

Microorganisms for Sustainability 2

Series Editor: Naveen Kumar Arora

Naheed Mojgani

Maryam Dadar *Editors*

Probiotic Bacteria and Postbiotic Metabolites: Role in Animal and Human Health



Springer

Microorganisms for Sustainability

Volume 2

Series Editor

Naveen Kumar Arora, Environmental Microbiology, School for Environmental Science, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, India

Microorganisms perform diverse roles on our planet most of which are important to make earth a habitable and sustainable ecosystem. Many properties of microorganisms are being utilized as low input biotechnology to solve various problems related to the environment, food security, nutrition, biodegradation, bioremediation, sustainable agriculture, bioenergy and biofuel, bio-based industries including microbial enzymes/ extremozymes, probiotics etc. The book series covers all the wider aspects and unravels the role of microbes towards achieving a sustainable world. It focuses on various microbial technologies related to sustenance of ecosystems and achieving targets of Sustainable Development Goals. Series brings together content on microbe based technologies for replacing harmful chemicals in agriculture, green alternatives to fossil fuels, use of microorganisms for reclamation of wastelands/ stress affected regions, bioremediation of contaminated habitats, biodegradation purposes. Volumes in the series also focus on the use of microbes for various industrial purposes including enzymes, extremophilic microbes and enzymes, effluent treatment, food products.

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Editors

Probiotic Bacteria and Postbiotic Metabolites: Role in Animal and Human Health

 Springer

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*To all those who have love for science and
realize the importance of microbes in healthy
environment and healthy life*

Preface

Since centuries, our ancestors employed microbes for preparing several traditional fermented products that at the time were considered health promoting. Although at that time the presence or importance of these microbes was not much realized, but with the passage of time the vital role played by these microorganisms in the evolution of life on earth and in maintenance of environmental health and our lives was highly acknowledged.

With the knowledge of integrative medicine, we have understood the direct relationship existing between health and diet. Hence, the significance of probiotic microbes, which exist mainly in our gut, has become the spotlight and forefront of vast research, gasping the attention of academics, students, industrialists, and most importantly consumers.

In this book, we have focused on the health aspects of probiotic microbes and their postbiotic metabolites, either added as an adjunct to food (dairy or nondairy foods) or in animal feed or as a supplement for human use with some health claims. Several metabolites produced by lactic acid bacteria have been known to improve the flavor, texture, and sensory characteristics of fermented foods with positive health impacts on the host when consumed in adequate amounts. The book also reviews the use of these microbes having metabolic functions, for the development of novel functional foods and functional pharmaceuticals. This book covers different aspects of probiotic bacteria and their metabolites in terms of their therapeutic and technological applications and benefits. We had put our maximum efforts to provide current knowledge and a holistic review of the related topics considering their wide use in plants, animals, and man, and it is our hope that the provided information compiled by the expert authors who contributed in this book would prove a significant contribution to the expanding knowledge of probiotics and postbiotics.

In the end, I highly acknowledge and appreciate the contributing authors not only for sharing their knowledge and expertise but also for their high sense of co-operations, patience. I express my sincere gratitude to all those who dedicated their time and energy in preparing these chapters.

Karaj, Iran
Karaj, Iran

Naheed Mojtani
Maryam Dadar

Contents

1	<i>Bacillus</i> spp. in Aquaculture - Mechanisms and Applications: An Update View	1
	Hien Van Doan	
2	Immunity and Gut Microbiome: Role of Probiotics and Prebiotics	61
	T. R. Keerthi, Rakhie Narayanan, K. Sreelekshmi, and C. Honey Chandran	
3	Preventive Effects of Probiotics and Prebiotics in Food Allergy: Potentials and Promise	85
	Youcef Shahali and Maryam Dadar	
4	An Overview of Dairy Microflora	101
	Deeba Noreen Baig and Samina Mehnaz	
5	Remarkable Metabolic Versatility of the Commensal Bacteria <i>Eubacterium hallii</i> and <i>Intestinimonas butyriciproducens</i>: Potential Next-Generation Therapeutic Microbes	139
	Jos F. M. L. Seegers, Thi Phuong Nam Bui, and Willem M. de Vos	
6	Anticarcinogenic Potential of Probiotic, Postbiotic Metabolites and Paraprobiotics on Human Cancer Cells	153
	Elham Noroozi, Majid Tebianian, Morteza Taghizadeh, Maryam Dadar, and Naheed Mojtani	
7	Postbiotic Metabolites of Probiotics in Animal Feeding	179
	Teck Chwen Loh, Hooi Ling Foo, and Hui Mei Chang	
8	Probiotics Application: Implications for Sustainable Aquaculture	191
	Milad Adel and Mahmoud A. O. Dawood	
9	Honeybee Gut: Reservoir of Probiotic Bacteria	221
	Samira Tootiaie, Mojtani Moharrami, and Naheed Mojtani	

10	Role of Probiotic Bacteria on Bioavailability of Functional Ingredients Under Fermentation Process	237
	Zeinab E. Mousavi and Seyed Mohammad Ali Mousavi	
11	Quality and Health Aspects of Dairy Foods as Affected by Probiotic Bacteria and Their Metabolites	257
	Mahdieh Iranmanesh	
12	Encountering the Antibiotic Resistance by Bioactive Components and Therapies: Probiotics, Phytochemicals and Phages	283
	Sheikh Ajaz Rasool, Muhammad Salman Rasool, and Munazza Ajaz	
13	Probiotic Bacteria as a Functional Delivery Vehicle for the Development of Live Oral Vaccines	319
	Maryam Dadar, Youcef Shahali, and Naheed Mojgani	
14	Promising Prospects of Probiotics and Postbiotics Derived from Lactic Acid Bacteria as Pharma Foods	337
	Hooi Ling Foo, Laiella Shaahierra Jann Hishamuddin, and Teck Chwen Loh	
15	Nondairy Foods as Potential Carriers of Probiotic Bacteria and Postbiotics	351
	Fereshteh Ansari and Hadi Pourjafar	

About the Series Editor

Naveen Kumar Arora, Ph.D. in microbiology, associate professor in the Department of Environmental Microbiology, Babasaheb Bhimrao Ambedkar University (a central university), Lucknow, Uttar Pradesh, India, is a renowned researcher in the field of environmental microbiology and biotechnology. His specific area of research is rhizosphere biology and PGPRs. He has more than 50 research papers published in premium international journals and several articles published in magazines and dailies. He is editor of three books, published by Springer. He is member of several national and international societies and reviewer of several international journals. He has delivered lectures in conferences and seminars around the globe. He has a long-standing interest in teaching at the PG level and is involved in taking courses in bacteriology, microbial physiology, environmental microbiology, agriculture microbiology, and industrial microbiology. He has been advisor to 57 postgraduate and 8 doctoral students. Recently, he was awarded for excellence in research by the honorable governor of Uttar Pradesh. Although an academician and researcher by profession, he has a huge obsession for the wildlife and its conservation and has authored a book, *Splendid Wilds*. He has a dedicated website www.naveenarora.co.in for the cause of wildlife and environment conservation.

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Naheed Mojgani, Ph.D., professor of microbiology at Razi Vaccine and Serum Research Institute, Iran, is renowned for her research work in the field of bacterial infectious diseases, probiotics, paraprobiotics, and postbiotics, conjugate and recombinant vaccines, etc. She has formulated and commercialized several probiotic supplements for man and animals. Her continuous efforts, dedication, and hard work in the field of probiotic have led her to be recognized in the country as an eminent specialist in the field. Recently, she has been awarded by the Ministry of Education and Ministry of Agriculture for her novel approach providing efficient therapy for diarrheal diseases. Additionally, she is committee member at Iranian National Standard Organization and National Veterinary Organization for writing and setting standards for probiotic products.

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Bacillus spp. in Aquaculture - Mechanisms and Applications: An Update View

1

Hien Van Doan

Abstract

Probiotics have been widely applied in aquaculture industry as sustainable and environmentally friendly tools to sustain host's health and the well-being. Among probiotics, *Bacillus* species have great potential applications in aquaculture because they can form the spores that makes them able to survive in the harsh environmental conditions. Moreover, they are nonpathogenic and nontoxic to aquacultural environments and animals. In addition, *Bacillus* species are able to produce antimicrobial substances making them more suitable candidates compared to other probiotics. In this chapter, we discussed the role of *Bacillus* in sustainable aquaculture as alternative strategies to enhance growth performance, disease resistance, and immune response of different aquaculture farmed animals.

Keywords

Bacillus · Aquaculture · Probiotics · Disease resistance

1.1 Introduction

Aquaculture is one of the world's fastest growing food sectors (Willer and Aldridge 2019). It is necessary to meet the global seafood demand, which is being accountable for 50% of the world's seafood consumption (Gómez et al. 2019). However, sustainable development of aquaculture industry is constantly defeated by the outbreak of diseases, which is considered as main obstacles to the economical

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1

profitability of the industry (FAO 2020). The outbreak of diseases is also linked to application of antibiotics, posing a significant danger to the public health (World Health Organization 2014). Thus, new and natural alternatives that prohibit the incidence of diseases and improve human and animal health are urgently needed. The use of probiotics, “live organisms that can give a health benefit to the host when administered in the appropriate amounts,” is a potential alternative to boost the global health (FAO/WHO 2001). The scientific community has been searching for the environmentally friendly solutions to prevent aquacultural disease, where probiotics emerged as crucial alternative to antibiotics due to advert effects of antibiotics, such as the modulation of microbiota in the aquaculture systems and the development of resistance bacteria (Kuebutornye et al. 2019; Resende et al. 2012; Ringø 2020; Wang et al. 2019a). Consequently, wide range of probiotics, such as *Bacillus*, *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Micrococcus*, *Pediococcus*, *Enterobacter*, *Vibrio*, *Pseudomonas*, *Rhodopseudomonas*, *Roseobacter*, and *Shewanella*, have been found and applied to improve growth performance, immune response, and disease resistance of farmed fish and shellfish (Abd El-Rhman et al. 2009; Adel et al. 2017; Feng et al. 2019; Kuebutornye et al. 2019; Li et al. 2006; Li et al. 2020; Ringø 2020; Yang et al. 2019). In aquaculture, probiotics have been applied as functional feed additives to boost host’s health and well-being via increasing growth, supplying nutrient, modulation gut microbiota, enhancing immunity, improving feed efficiency, increasing digestive enzyme activities and digestibility, and controlling diseases (Kuebutornye et al. 2019; Ringø 2020; Selim and Reda 2015).

Bacillus species are one of the most commonly used probiotics in the aquaculture industry because of their ability to form endospores, which is a benefit for industrial applications without losing their characteristics (Hong et al. 2005; Kuebutornye et al. 2019; Cutting 2011; Hai 2015). In addition, *Bacillus* is known to generate natural antimicrobial compounds, which are able to prohibit the proliferation of harmful bacteria in the aquaculture systems and host’s intestines (Abriouel et al. 2011; Caulier et al. 2019; Sumi et al. 2015). Similarly, *Bacillus* species are known to stimulate the digestive enzymes, antioxidant enzymes, relative immune gene expression, and stress-related genes, which in turn improve disease resistance of the host against pathogenic bacteria (Elshaghabee et al. 2017; Nayak 2010; Soltani et al. 2019). *Bacillus* species also increase the use of feed in fish, contributing to better growth rates (Mukherjee et al. 2019; Nair et al. 2020; Xia et al. 2020). Therefore, these chapters gather recent data on the role of *Bacillus* species in promoting growth performance, disease resistance, and immune response in aquaculture.

1.2 Mode of Action of Probiotics in Aquaculture

Probiotics can affect the host’s immune responses, as well as the interrelationship between these responses and their gastrointestinal microflora (Hemarajata and Versalovic 2013; La Fata et al. 2018; Yan and Polk 2011). Over the past decades, extensive researches on probiotics have provided insight into the significance of

probiotics and their modes of action and numerous mechanisms have been suggested (Santacroce et al. 2019; Shi et al. 2016).

1. Probiotics improve feed efficiency and growth rate of farmed fish and shellfish (Ringø 2020; Romano 2021). They also enhance the host's appetite and feed digestion via decomposition of indigestible components, enhance vitamin productions, and detox diet's substances (Ashaolu 2020; Cencic and Chingwaru 2010; Hoseinifar et al. 2018).
2. Probiotics could compete the exclusion of gastrointestinal harmful bacteria via the secretion of peroxide, bacteriocin, siderophore, and lysozyme enzymes (Vieco-Saiz et al. 2019; Yang et al. 2014). The physiological and immunological effects are considered as one of the most essential modes of action of probiotics (Klaenhammer et al. 2012; Plaza-Diaz et al. 2019; Vieco-Saiz et al. 2019).
3. Probiotics could enhance aquaculture animal's disease resistance to stress caused by various environmental threats during aquaculture activities (Hlordzi et al. 2020; Mohapatra et al. 2013; Reverter et al. 2020).

These mechanisms display the favorable impacts of probiotics in farmed fish and shellfish. Future studies, however, on the relationship between probiotics and hosts, including metagenomics and proteomic studies, is important to clarify mode of action of probiotics.

1.3 *Bacillus* Applications in Aquaculture

1.3.1 Improve Growth Performance

The utmost target of aquaculture practice is to acquire the rapidest growth and lowest production cost. To achieve this goal, several means have been established to boost growth rate and feed consumption by adding functional feed additives and growth natural growth promoters (Hernández et al. 2016; Katya et al. 2014). Probiotics are potential tools to maintain the normal growth, health, and well-being of farmed fish and shellfish because they serve as nutrients source, vitamins, and digestive enzymes. These substances for their part will contribute significantly on feed consumption, nutrients uptake, and host's growth rate (Lauriano et al. 2016; Nath et al. 2019). Probiotics consumption have been speculated to improve the host's appetite or boost organisms' digestibility (Irianto and Austin 2002). Probiotics can improve feed efficiency of fish and shellfish by stimulating the excretion of digestive enzymes and maintaining the balance of intestinal microbes, which lead to the improvement of nutrients absorption and utilization, as well as the survival and growth of the host (Ibrahim 2015; Irianto and Austin 2002). Studies on diets containing probiotics revealed the possible involvement of these probiotics on the improvement of intestinal microflora balance and the production of extracellular enzymes to elevate the feed efficiency and growth of cultured species as growth

promoters (Giri et al. 2013; Ringø et al. 2018). Most of the studies using *Bacillus* in aquaculture focus on growth performance and survival rate (Table 1.1).

1.3.1.1 Tilapias

During past decades, *Bacillus* spp. have been intensively applied in Nile tilapia aquaculture. Han et al. (2015) indicated that 10 weeks feeding trial with *B. licheniformis* significantly enhanced growth performance. However, there were no significant discrepancies in survival rate and feed conversion ratio (FCR) and in villi length and muscular layer thickness of anterior intestine among the treatments. In contrast, Iwashita et al. (2015) reveal that administration of the probiotic had no significant effect on the growth rates of Nile tilapias, although the fish fed probiotics had better feed conversion. Likewise, no significant difference in growth performance and FCR was observed in Nile tilapia fed *Bacillus amyloliquefaciens* (Silva et al. 2015). This can be explained due to the low temperatures during experimental period. Marcusso et al. (2015) reported that the homeostasis of Nile tilapia rearing at temperatures below 24 °C could be affected, enhancing the susceptibility to bacterial infections and impairing the growth performance. No effects were observed on the growth performance of Nile tilapia fed *Bacillus subtilis* (Aqua NZ and AP193) and *Bacillus subtilis* strains (Addo et al. 2017a, 2017b). These results are not unexpected given the short duration of this trial. This statement agrees with Apún-Molina et al. (2009) who observed a tendency toward improved growth in Nile tilapia fry (0.14 g) only after 75 d of feeding with diets composed of *Bacillus* or *Lactobacillus* probiotics. On the contrary, dietary inclusion of *Bacillus subtilis* significantly improved body weight, percent weight gain, specific growth rate, and feed conversion ratio (Liu et al. 2017). It is well documented that *Bacillus* exoenzymes are very efficient at metabolizing a large variety of carbohydrate, lipids, and proteins (Liu et al. 2009). The exoenzymatic activity of *Bacillus* spp. is one of the main reasons for its ability to improve digestive enzyme activities (Han et al. 2015). Higher enzyme activities in the digestive tract enhance digestive capability and growth performance of the host. It is widely accepted that the level of digestive enzyme activity is a useful comparative indicator of food utilization rate, digestive capacity, and growth performance of the host (Suzer et al. 2008; Ueberschär 1995). Liu et al. (2017) also reported that 4-week *B. subtilis* HAINUP40 diet supplementation significantly increased protease and amylase activities of tilapia. This is because *B. subtilis* HAINUP40 could secrete exoenzymes; the improvement of indigestive tract enzyme activities may be partially due to enzymes synthesized by the bacteria. However, the proportion of enzymes contributed by bacteria cannot be assessed since the probiotic may also stimulate the production of endogenous enzymes in the fish (Dawood et al. 2016; Suzer et al. 2008; Wu et al. 2012; Ziaei-Nejad et al. 2006). In the same trend, supplementation of *B. subtilis* and *B. licheniformis* or *B. subtilis* and *Bacillus licheniformis* (BS) combined with traditional Chinese medicine (TCM) significantly enhanced weight gain and specific growth rate of Nile tilapia and Mozambique tilapia (Abarike et al. 2018b; Abarike et al. 2018a; Gobi et al. 2018). It is known that an increase in the body weight gain in fish fed with probiotic supplemented diets, could contribute to the increase in digestive enzyme activity, increase in

Table 1.1 Weight gain (WG), specific growth rate (SGR), food conversion efficiency (FCE), food conversion ratio (FCR), protein efficiency ratio (PER), survival rate (SR), digestive enzyme, and disease resistance of fish and shellfish fed *Bacillus* probiotics. → no change, ↑ increase, ↓ decrease

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus licheniformis</i>	Commercial probiotic	0%, 0.02%, 0.04%, 0.06%, 0.08% and 0.1% containing live germ 2×10^{10} CFU/g) 10 weeks	Juvenile Nile tilapia (<i>O. niloticus</i>) 3.83 ± 0.03 g	WG, FBW, SGR, and SR ↑ FCR → Villi length → Muscular layer thickness of anterior intestinal → Resistance against to <i>S. initae</i> ↑	Han et al. (2015)
<i>Bacillus subtilis</i> (combined with <i>S. cerevisiae</i> and <i>A. oryzae</i>)	Commercial probiotic	0; 5 kg ⁻¹ probiotic mixture (<i>B. subtilis</i> 1.5×10^9 , <i>S. cerevisiae</i> 10^9 and <i>A. oryzae</i> 2×10^9); and 10 g kg ⁻¹ probiotic mixture (<i>B. subtilis</i> 3.0×10^9 , <i>S. cerevisiae</i> 2.0×10^9 and <i>A. oryzae</i> 4.0×10^9) (CFU g ⁻¹) 6 weeks	Juvenile Nile tilapia (<i>O. niloticus</i>) 25 ± 0.05 g	Growth rates → Resistance against to <i>A. hydrophila</i> and <i>S. initae</i> ↑	Iwashita et al. (2015)
<i>Bacillus amyloliquefaciens</i>	Commercial probiotic	0; 1×10^6 , 5×10^6 and 1×10^7 CFU g ⁻¹ 90 days	Nile tilapia (<i>O. niloticus</i>) 35 ± 5 g	Growth performance → Proximal composition → Blood glucose and hemoglobin ↓ Villi height and number of goblet cells ↑	Silva et al. (2015)

(continued)

Table 1.1 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus</i> NP5	Commercial probiotic	10^{10} CFU g^{-1} in feed with dose of 0.5, 1 and 2% 28 days	Nile tilapia (<i>O. niloticus</i>) 6.38 ± 0.05 g	Growth performance ↑	Utami and Suprayudi (2015)
<i>Bacillus subtilis</i> (Aqua NZ and AP193)	Commercial probiotic	4.2×10^7 CFU g^{-1} of feed 8 weeks	Nile tilapia (<i>O. niloticus</i>) 7.47 ± 0.11 g	WG and FCR → Thermal growth coefficient → Resistance against <i>A. hydrophila</i> ↑	Addo et al. (2017a)
<i>Bacillus subtilis</i> strains SB3086, SB3295, SB3615, and AP193	Commercial probiotic	4×10^7 CFU/g of feed in 21 days	Nile tilapia (<i>O. niloticus</i>) 16.5 ± 0.2 g	Growth performance → Resistance against <i>Streptococcus agalactiae</i> ↑	Addo et al. (2017b)
<i>Bacillus subtilis</i> HAINUP40	Isolated from the aquatic environment	10^8 CFU/g 8 weeks	Nile tilapia (<i>O. niloticus</i>) 95 ± 8 g	FW, WG, and SGR ↑ FCR ↓ Protease and amylase activity ↑ Total antioxidant capacity (T-AOC) ↑ Serum superoxide dismutase (SOD) ↑ Resistance against <i>S. agalactiae</i> ↑	Liu et al. (2017)
<i>B. subtilis</i> and <i>B. licheniformis</i>	Commercial probiotic	0, 3, 5, 7 and 10 $g\ kg^{-1}$ 4 weeks	Nile tilapia (<i>O. niloticus</i>) 53.01 ± 1.0 g	WG and SGR ↑ FCR ↓ Resistance against <i>S. agalactiae</i> ↑	Abarike et al. (2018a)

<i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i> (BS) combined with traditional Chinese medicine (TCM)	Commercial probiotic	0; TCM at 3 and BS at 7 (g/kg); TCM at 5 and BS at 5 (g/kg); TCM at 7 and BS at 3 (g/kg). 4 weeks	Nile tilapia (<i>O. niloticus</i>) 57 ± 2 g	WG and SGR ↑ FCR ↓ Resistance against <i>S. agalactiae</i> ↑	Abarike et al. (2018a)
<i>Bacillus licheniformis</i> Dahb1	Commercial probiotic	0, 10 ⁵ and 10 ⁷ CFU/g 4 weeks	Mozambique tilapia (<i>Oreochromis mossambicus</i>)	FW and SGR ↑ FCR ↓ Resistance against <i>A. hydrophila</i> ↑	Gobi et al. (2018)
<i>Bacillus licheniformis</i> and <i>B. subtilis</i>	Commercial probiotic	1 × 10 ⁶ CFU mL ⁻¹ was feed for <i>Artemia urmiana</i> nauplii and <i>Brachionus plicatilis</i> 8 h	Pacific white shrimp larvae (<i>Litopenaeus vannamei</i>)	Growth performance ↑ Survival rate ↑	Jamali et al. (2015)
<i>Bacillus licheniformis</i> and <i>Lactobacillus rhamnosus</i>	Commercial probiotic	<i>B. licheniformis</i> 10 ⁹ CFU/kg, <i>L. rhamnosus</i> 8 × 10 ⁸ CFU/kg 120 days	Pacific white shrimp (<i>L. vannamei</i>) PL14	WG, SGR, and WG ↑	Swapna et al. (2015)
<i>Bacillus</i> spp.	Isolated from pustulose ark	1 × 10 ⁶ , 2 × 10 ⁶ , 4 × 10 ⁶ , and 6 × 10 ⁶ CFU g feed ⁻¹ 32 days	Pacific white shrimp (<i>L. vannamei</i>) 1 ± 0.1 g	Growth performance ↑	Sánchez-Ortiz et al. (2016)
<i>Bacillus coagulans</i> ATCC 7050	Commercial probiotic	0 (BO), 1 × 10 ⁶ (BC1), 1 × 10 ⁷ (BC2), and 1 × 10 ⁸ (BC3) CFU g ⁻¹ feed) 56 days	Pacific white shrimp larvae (<i>L. vannamei</i>) 0.57 ± 0.001	FW, WG, and SGR ↑ FCR ↓ Condition factor ↑ Lipase, amylase, and trypsin ↑ Villus height ↑ Villus width ↑ Muscle thickness ↑	Amoah et al. (2019)

(continued)

Table 1.1 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i>	Commercial probiotic	1×10^4 and 1×10^8 CFU/g 60 days	Pacific white shrimp (<i>Litopenaeus vannamei</i>)	WG, total length, SGR, and SR ↑ Dry matter and crude protein ↑	Sadat Hoseini Madani et al. (2018)
<i>Bacillus</i> spp.	Isolate from shrimp gut	Added to water: 1×10^2 , 1×10^3 , 1×10^4 and 1×10^5 CFU/mL			Kewcharoen and Srisapoomte (2019)
<i>B. licheniformis</i>	Commercial probiotic	Control diet (CON), 0.2% MOS (MOS), 0.1% <i>B. licheniformis</i> (BL), 0.2% MOS plus 0.1% BL (SYN) 8 weeks	Pacific white shrimp (<i>Litopenaeus vannamei</i>)	WG, SGR, PER ↑ Villus number (VN) ↑ Villus height (VH) ↑ Thicker submucosa ↑ Propionic acid content ↑ Resistance against ammonia ↑	Chen et al. (2020a)
<i>B. licheniformis</i>		Basal diet (Control); 0.5% hydrolyzed yeast (HY); 0.1% <i>B. licheniformis</i> (BL) and 0.5% hydrolyzed yeast +0.1% <i>B. licheniformis</i> (SYN) 8 weeks	Pacific white shrimp (<i>Litopenaeus vannamei</i>)	Growth and body composition → PER ↑ Intestinal villus height ↑ Villus number (VN) ↑ Villus height (VH) ↑	Chen et al. (2020b)
<i>Bacillus cereus</i> and <i>Pediococcus acidilactici</i>	Commercial probiotic	<i>P. acidilactici</i> (106 CFU/mL) and <i>B. cereus</i> (106 CFU/mL) to the water pond 110 days	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 0.002 ± 0.001	WG and SR ↑	Khadenzade et al. (2020)

<i>Bacillus subtilis</i> WB60, <i>Pedococcus pentosaceus</i> , and <i>Lactococcus lactis</i>	Commercial probiotic	<i>B. subtilis</i> at 10^7 CFU/g diet, <i>B. subtilis</i> , <i>P. pentosaceus</i> , and <i>L. lactis</i> at 10^8 CFU/g diet, and oxytetracycline at 4 g/kg 8 weeks	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 1.41 ± 0.05	Growth performance ↑ Resistance against <i>Vibrio parahaemolyticus</i> ↑	Won et al. (2020a, 2020b)
<i>Bacillus subtilis</i> WB60 and <i>Lactobacillus plantarum</i> KCTC3928	Commercial probiotic	0; <i>B. subtilis</i> at 10^6 , 10^7 , 10^8 and <i>L. plantarum</i> at 10^6 , 10^7 , 10^8 CFU/g diet	Japanese eel (<i>Anguilla japonica</i>) 8.29 ± 0.06 g	WG, FE, and PER ↑ Resistance against <i>V. anguillarum</i> ↑	Lee et al. (2017)
<i>Bacillus subtilis</i> WB60 and mannanoligosaccharide (MOS)	Commercial probiotic	BS: 0.0, 0.5, and 1.0×10^7 CFU/g diet and MOS: 0 and 5 g/kg diet 8 weeks	Japanese eel (<i>Anguilla japonica</i>) 9.00 ± 0.11 g	WG, FW, SGR and PER ↑ Resistance against <i>Vibrio anguillarum</i> ↑	Lee et al. (2018)
<i>Bacillus subtilis</i> or <i>licheniformis</i>) and (mannan or fructo oligosaccharide)		0, Probiotics (1.0×10^8 CFU/g diet) and prebiotics (5 g/kg diet) 12 weeks	Japanese eel (<i>Anguilla japonica</i>) 12.8 ± 0.47	WG and SGR ↑ Intestinal villi length ↑ Resistance against <i>A. hydrophila</i> ↑	Park et al. (2020)
<i>B. megaterium</i> PTB 1.4	Commercial probiotic	0 and 1% 30 days	Catfish (<i>Clarias</i> sp.) 11.41 ± 0.23 g	Growth performance ↑ Protease and amylase enzymes ↑ Total amount of probiotic bacteria ↑	Afrilasari and Meryandini (2016)
<i>B. subtilis</i> , <i>B. amyloliquefaciens</i> , <i>B. cereus</i> and a commercial <i>B. amyloliquefaciens</i>	Isolated from the intestine of African catfish	10^{10} CFU/ml 60 days	African catfish (<i>Clarias gariepinus</i>) 75.23 ± 1.6	BW, WG, and SGR ↑ FCR ↓ Hemogram blood parameters ↑ Serum antioxidant and digestive enzymes ↑ Resistance against <i>Aeromonas sobria</i> ↑	Reda et al. (2018)

(continued)

Table 1.1 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus cereus</i> EN25	Isolated from mud of sea cucumber culturing water bodies.	0, 10 ⁵ , 10 ⁷ and 10 ⁹ CFU/g 30 days	Juvenile sea cucumber (<i>Apostichopus japonicus</i>) 0.375 ± 0.024 g	Growth performance → Resistance against <i>V. splendidus</i> ↑	Zhao et al. (2016)
<i>Bacillus baekryungensis</i> MS1	Isolated from a sea cucumber pond in winter	0 and 10 ⁷ CFU/ml 60 days	Sea cucumber (<i>Apostichopus japonicus</i>) 4.17 g ± 0.22 g	Growth performance ↑ Resistance to <i>Vibrio splendidus</i> ↑	Liu et al. (2020)
<i>Bacillus subtilis</i> and <i>Saccharomyces cerevisiae</i>	Commercial probiotic	<i>Bacillus subtilis</i> 10 ⁹ UFC/g and <i>Saccharomyces cerevisiae</i> 10 ⁹ UFC/g 90 days	Tambaqui (<i>Colossoma macropomum</i>) 2.13 ± 0.75 g	Growth performance → Body composition → Hematological parameters ↑ Resistance against <i>S. agalactiae</i> ↑	da Paixão et al. (2017)
<i>Bacillus cereus</i>	Commercial probiotic	0, 4.2 × 10 ⁴ , 3.9 × 10 ⁶ and 3.3 × 10 ⁸ CFU/g 120 days	Tambaqui (<i>Colossoma macropomum</i>) 0.94 ± 0.02 g	Weight and length gains ↑ Neutrophils and thrombocyte count ↑ Resistance against <i>Aeromonas hydrophila</i> ↑	Dias et al. (2018)
<i>B. licheniformis</i> and <i>B. subtilis</i>	Commercial probiotic	1.6 × 10 ⁹ CFU/g dry pellet in 60 days	Kutum (<i>Rutilus frisii</i>) 0.4 ± 0.1 g	FW, WG, and SGR ↑ Red blood cells ↑ White blood cells ↑ Neutrophils ↑ Lymphocytes ↑ Mean cell volume ↑ Mean cell hemoglobin ↑ Mean cell hemoglobin concentration ↑	Azarin et al. (2015)

<i>Bacillus</i> sp. PP9	Isolated from mirgial gut	2×10^4 , 2×10^5 and 2×10^6 CFU 60 days	Mirgal (<i>Cirrhinus mrigala</i>) 2.5 ± 0.20	Growth performance ↑ Maximum RNA DNA ratio ↑ FCR ↓ Intestinal protease and α-amylase activity ↑ Hepatic glutamic oxaloacetic transaminase ↑ Glutamate pyruvate transaminase levels ↑	Bandyopadhyay et al. (2015)
<i>B. subtilis</i> and <i>B. circulans</i>	Commercial probiotic	1×10^4 , 2×10^4 , 3×10^4 , and 4×10^4 CFU/g 30 days	Three spot gourami (<i>Trichopodus trichopterus</i>)	Larval growth → Larval resistance against the challenge ↑	Jafariyan et al. (2015)
<i>Bacillus coagulans</i>	Commercial probiotic	0 , 10^5 , 10^7 and 10^9 cfu g ⁻¹ 60 days	Freshwater prawn (<i>Macrobrachium rosenbergii</i>) 2.4 ± 0.35 g	Growth performance ↑ Feed utilization ↑ Protease, amylase, and lipase digestive enzymes ↑	Gupta et al. (2016)
<i>Virgibacillus proomii</i> and <i>Bacillus mojavensis</i>		5.8×10^4 , 9.6×10^4 , and 9.8×10^4 CFU/ml 60 days	Sea bass (<i>Dicentrarchus labrax</i>) larvae	Length, weight, and the survival rate ↑ FCR ↓ Phosphatase alkaline and amylase activities ↑	Hamza et al. (2016)
<i>Bacillus</i> spp.	Commercial probiotic	The live rotifers were enriched with: Algamac 3050; Algamac 3050 and a commercial mix of <i>Bacillus</i> spp. 0.5 g L ⁻¹ ; additional probiotics in water (5 g m ⁻³)	Florida pompano (<i>Trachinotus carolinus</i>) Larvae	Growth performance ↑ Survival rate → Trypsin-specific activity ↑ Alkaline phosphatase activity ↑	Hauville et al. (2016)

(continued)

Table 1.1 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus pumilus</i> SE5		0 and 1.0×10^8 CFU g ⁻¹ 60 days	Groupers (<i>Epinephelus coioides</i>) 14.6 ± 0.2 g	FW, WG, and SGR ↑ FCR ↓	Yan et al. (2016)
<i>Bacillus mycoides</i> (BS) and organic selenium (OS)		BS 10^8 CFU g ⁻¹ , OS 0.2 g kg ⁻¹ and combination BS, OS	Marron (<i>Cherax cainii</i>) 10.83 ± 0.28 g	Growth performance ↑ The glutathione peroxidase ↑ Total hemocyte counts ↑ Intestinal bacterial population ↑	Ambas et al. (2017)
<i>Bacillus amyloliquefaciens</i> -JFP2		0 and 1.4×10^6 (CFU/g) of feed 90 days	Rock Bream (<i>Oplegnathus fasciatus</i>) 25.4 ± 0.13 g	BW, WG, and SGR ↑ FCR ↓ Serum protein and glucose level ↑ Resistance against <i>Streptococcus iniae</i> ↑	Kim et al. (2017)
<i>B. siamensis</i> B44v	Isolated from Thai pickled vegetables (Phak-dong)	10^7 CFU/g feed	Hybrid catfish (<i>C. macrocephalus</i> × <i>C. gariepinus</i>)	Protease and cellulase enzymes ↑ Gastrointestinal conditions ↑ Improve growth ↑ Resistance against to <i>A. hydrophila</i> and <i>S. iniae</i> ↑	Meidong et al. (2017)
<i>Bacillus aerophilus</i> KADR3	Commercial probiotic	0, 10^7 , 10^8 and 10^9 CFU g ⁻¹ 6 weeks	Robita labeo (<i>Labeo rohita</i>) 35–40 g	Serum lysozyme activity ↑ Phagocytic activity ↑ Serum total protein, Respiratory burst activity ↑	Ramesh et al. (2015)

					Serum IgM levels ↑ Superoxide dismutase activity ↑ Alternative complement pathway activity ↑ Resistance against <i>A. hydrophila</i> ↑	Ramos et al. (2017)
<i>Bacillus subtilis</i> and <i>Bacillus cereus toyoi</i>	Commercial probiotic	0, 6 × 10 ³ and 1.5 × 10 ⁶ CFU g ⁻¹ of diet. 9 and 20 weeks	Rainbow trout (<i>Oncorhynchus mykiss</i>) and brown trout (<i>Salmo trutta</i>) 15.6 g		Growth performance → Body composition → Intestinal <i>lamina propria</i> ↑ Submucosa ↑	
<i>B. amyloliquefaciens</i> 54A and <i>B. pumilus</i> 47B	Isolated from gut of striped catfish	1 × 10 ⁸ , 3 × 10 ⁸ , and 5 × 10 ⁸ CFU g ⁻¹ feed 90 days	Striped catfish (<i>Pangasianodon hypophthalmus</i>)		WG ↑ SGR and FCR → Resistance against to <i>E. ictaluri</i> ↑	Truong Thy et al. (2017)
<i>Bacillus</i> sp. DDKRC1	Isolated from the gut of Asian seabass (<i>Lates calcarifer</i>)	0, 2.94 × 10 ⁷ CFU/100 g feed and diet fermented with <i>Bacillus</i> sp. DDKRC1 42 days	Tiger shrimp (<i>Penaeus monodon</i>) 2.73 ± 0.01		PER ↑ FCR ↓ Dry matter and cellulose digestibility ↑ Hemicellulose and lipid digestibility ↑ Cellulase, amylase, and protease activities ↑	De et al. (2018)
<i>Bacillus amyloliquefaciens</i> (GB) and <i>Yarrowia lipolytica</i> lipase 2 (YLL2)	Commercial probiotic	0, 5.0 g/kg GB-9, 4.0 g/kg YLL2, and 5.0 g/kg GB-9 + 4.0 g/kg YLL2 12 weeks	Hybrid sturgeon (<i>Acipenser schrenckii</i> ♂ and <i>Acipenser baerii</i> ♀) 5.0 g		Final weight ↑ Docosahexaenoic acid (DHA) ↑ Eicosapentaenoic acid (EPA) concentration ↑	Fei et al. (2018)

(continued)

Table 1.1 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus licheniformis</i>	Commercial probiotic	10^3 , 10^5 , and 10^7 CFU/mL 8 weeks	Abalone (<i>Haliotis discus hannai</i> Ino.) 4.17 ± 0.32 g	SGR and FI ↑ FCR ↓ Resistance to <i>V. parahaemolyticus</i> ↑	Gao et al. (2018)
<i>B. subtilis</i> E20	Commercial probiotic	0, 10^8 , 10^9 , and 10^{10} CFU kg ⁻¹ 56 days	Parrotfish (<i>Oplegnathus fasciatus</i>)	Growth performance ↑ Resistance against <i>V. alginolyticus</i> ↑	Liu et al. (2018)
<i>Bacillus aerius</i> B81e	Isolated from healthy hybrid catfish	0 and 10^7 CFU g ⁻¹ feed 60 days	Basa fish (<i>Pangasius bocourti</i>) 69 g	WG and SGR ↑ FCR ↓ Resistance against <i>A. hydrophila</i> ↑	Meidong et al. (2018)
<i>Bacillus subtilis</i>	Commercial probiotic	0, 1×10^4 , 1×10^6 , 1×10^8 , and 1×10^{10} CFU kg ⁻¹ diet 60 days	Red sea bream (<i>Pagrus major</i>) 3.99 ± 0.01	FW, WG, and SGR ↑ Feed utilization (FI, FCE, PER and PG) ↑ Amylase, protease, and lipase enzymes ↑	Zaineldin et al. (2018)
BetaPlus® (<i>B. subtilis</i> DSM 5750) <i>B. licheniformis</i> (DSM 5749)) and Isomaltooligosaccharides	Commercial probiotic	0 and 2 g kg ⁻¹ IMOS + 1 g kg ⁻¹ BetaPlus® in 7 weeks	Caspian Brown Trout (<i>Salmo trutta caspius</i>) 9 g	SR, BW, FW, and SGR ↑ FCR ↓ White blood cells ↑ Monocytes, neutrophils, and hematocrit ↑ Mean corpuscular volume and lymphocytes ↑ Serum triglycerides ↑ Cholesterol, total protein, and albumin ↓ Albumin/globulin ratio ↑	Aftabgard et al. (2019)

<i>Bacillus subtilis</i> and β -glucan	Commercial probiotic	1 g kg ⁻¹ β -glucan and 1×10^9 CFU kg ⁻¹ <i>B. subtilis</i> 70 days	Pengze crucian carp (<i>Carassius auratus</i> var. Pengze) 12.89 \pm 0.04 g	Growth performance \rightarrow Textures of muscle \uparrow Cholesterol activity \uparrow High-density lipoprotein \uparrow Low-density lipoprotein \downarrow Acid phosphatase activity \uparrow Alkaline phosphatase activity \uparrow Catalase activity \uparrow Fold height and microvillus height \uparrow Amylase, lipase, and trypsinase activities \uparrow	Cao et al. (2019)
<i>B. licheniformis</i> and <i>B. amyloliquefaciens</i>	Commercial probiotic	(1) probiotics supplemented to the water and live feed, (2) probiotics supplemented to the water only, and (3) no probiotic controls with 1×10^{10} CFU g ⁻¹ in 2×10^2 , 4×10^4 , 6×10^6 , 8×10^8 and 10×10^{10} CFU/100 g of feed 40 days	Larval common snook (<i>Centropomus undecimalis</i>)	Growth performance \uparrow Innate enzyme activities \uparrow Inhibition of opportunistic bacteria \uparrow Water quality parameters \uparrow	Tamecki et al. (2019)
<i>Bacillus subtilis</i>	Isolated from the shrimp gut		Indian prawn (<i>Penaeus indicus</i>) 16.8 \pm 0.11 g	Bacterial growth \uparrow Bacteriocin production \uparrow	Ook Kim et al. (2020)

(continued)

Table 1.1 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus licheniformis</i>	Isolated from grass carp	1×10^5 cfu/g and 1×10^6 cfu/g 56 day	Grass carp (<i>Ctenopharyngodon idella</i>) 16.5 g	WG and SGR ↑ Resistance against <i>A. hydrophila</i> ↑	Qin et al. (2020)

appetite, increase in the production of vitamin, breakdown of indigestible components, as well as possible improvement of intestine morphology (Irianto and Austin 2002). In addition, *Bacillus* spp. could secrete several digestive enzymes like protease, amylase, and lipase (Cai et al. 2019; Caulier et al. 2019).

1.3.1.2 Shrimps

Shrimp is a commercially important aquatic species with high economic value and good flavor, which has been widely farmed in the world, particularly in some Asia countries (Chen et al. 2020a). However, the shrimp industry has suffered severe economic losses because of the frequent outbreaks of diseases such as early mortality syndrome (EMS) and white spot syndrome virus (WSSV) (Alavandi et al. 2019; Castex et al. 2009; Chang et al. 2012). Chemotherapeutant and antibiotics are usually applied to settle this problem. Unfortunately, prolonged use of chemotherapeutant and antibiotics could lead to severe outcomes such as resistant bacteria, drug residues, and toxins, which pose a substantial threat to human beings and environment (Dash et al. 2015). Therefore, to seek an alternative way to solve this threat has caused increasing concern (Huynh et al. 2018). Probiotics have been widely applied in shrimp aquaculture. Jamali et al. (2015) revealed that dietary enrichment with *B. licheniformis* and *B. subtilis* significantly enhanced growth performance and survival rate of Pacific white shrimp, *Litopenaeus vannamei*. Elevation of growth performance has been demonstrated as the *Bacillus* could colonize shrimp digestive tract. In *P. monodon*, *Bacillus*, when used as a probiotic, was able to colonize both the culture water and the shrimp digestive tract; the *Bacillus* also was able to replace *Vibrio* spp. in the gut of the shrimp, thereby increasing shrimp survival (Rengpipat et al. 1998), via out-competing other bacteria for nutrients and space by producing antibiotics (Moriarty 1998; Verschuere et al. 2000). Similarly, significant improvement in growth performance of *L. vannamei* supplemented with *Bacillus* spp. has been reported in previous studies (Sadat Hoseini Madani et al. 2018; Sánchez-Ortiz et al. 2016; Swapna et al. 2015). Also, Amoah et al. (2019) indicated that dietary inclusion of *B. coagulans* significantly improved growth performance and feed utilization of Pacific white shrimp. The nutritive values as reported by Vijayavel and Balasubramanian (2006) is highly dependent on their biochemical constituents such as crude protein, crude lipid, ash content, and moisture, which also is noted to be an indication of improved meat quality. In addition, higher inclusion levels of probiotic BC at 1×10^8 CFU g⁻¹ feed in diets could modulate gut microflora of *L. vannamei* (Amoah et al. 2019), which play an ardent role in the digestive enzyme activities and the intestinal health. It has been well documented that digestive enzymes are known to break down food and absorb nutrients (Gobi et al. 2018). The digestive enzymes including amylase, lipase, and trypsin (Rawlings and Barrett 1994; Svendsen 2000) in this study significantly increased in the treated group compared to the untreated. Similar results of improved digestive enzyme activities in *Litopenaeus vannamei* (Zokaeifar et al. 2012) and *Fenneropenaeus indicus* (Ziaei-Nejad et al. 2006) have been established. Verschuere et al. (2000) in their work also noted that, *Bacillus* genus secretes a wide range of exoenzymes which aid in the nutritional enhancement of the host. More

recently, significant increase in growth performance, villus number, villus height, thicker submucosa, and propionic acid content has been reported in *L. vannamei* fed different *Bacillus* species (*B. licheniformis*, *B. cereus*, and *B. subtilis*) singularly or combined with other probiotics (*Pediococcus acidilactici*, *P. pentosaceus*, and *Lactococcus lactis*) (Chen et al. 2020a; Chen et al. 2020b; Khademzade et al. 2020; Won et al. 2020a).

Dietary supplementation of *Bacillus coagulans* on growth and feed utilization of freshwater prawn *Macrobrachium rosenbergii* showed that growth performance and feed utilization were found to be significantly higher ($P < 0.05$) in prawn fed 109 cfu g^{-1} diet. In addition, the specific activities of protease, amylase, and lipase digestive enzymes were significantly higher ($P < 0.05$) for 109 cfu g^{-1} diet (Gupta et al. 2016).

In Marron (*Cherax cainii*), Ambas et al. (2017) found that synbiotic use of *B. mycoides* and organic selenium (OS) significantly improved some immune parameters of marron, particularly the glutathione peroxidase, and to some extent total hemocyte counts. However, the synbiotic feed did not synergistically improve marron growth; in fact, the use of *B. mycoides*-supplemented diet alone demonstrated significantly higher growth in marron compared with the growth of marron fed on other test diets. A study conducted by Ock Kim et al. (2020), it was indicated that strain *Bacillus subtilis* isolated from the gut of *Penaeus indicus* and added at $2 \times 10^2 \text{ CFU } 100 \text{ g}^{-1}$ as probiotics in feed, resulted in weight gain of the juvenile shrimp ($16.8 \pm 0.11 \text{ g}$) after 40 days. The weight gain was $16.8 \pm 0.11 \text{ CFU } 100 \text{ g}^{-1}$ at $10 \times 10^2 \text{ CFU } 100 \text{ g}^{-1}$ probiotic concentration.

1.3.1.3 Catfish

To the best of our knowledge, there were few studies regarding the use of *Bacillus* spp. on this fish. Afrilasari and Meryandini (2016) reported that *Bacillus megaterium* PTB 1.4 increased the activity of digestive enzymes and the growth of catfish. It is known that isolate PTB 1.4 is *B. megaterium*, where *Bacillus* spp. group is known to have ability to produce extracellular enzymes (Moriarty 1998). Probiotic bacteria are capable of producing digestive enzymes that help fish use feed nutrients and digest (Bairagi et al. 2002). Generally, endogenous enzyme can be produced by fish, but the presence of probiotics can improve digestive enzyme. Probiotics improve digestive enzyme activity by stimulating the synthesis of endogenous enzyme in the digestive tract (Mohapatra et al. 2012). Similarly, combination of *B. subtilis*, *B. amyloliquefaciens*, *B. cereus*, and a commercial *B. amyloliquefaciens* significantly improved growth performance of *C. gariepinus* (Reda et al. 2018). This improvement could be attributed to the production of amylase and protease by the same strain (Selim et al. 2019). In addition, *Bacillus* sp. are capable to detoxify the harmful substance in feed, produce essential vitamins such as vitamin B12 and biotin, and increase the intestinal villus heights (Ramirez and Dixon 2003; Reda and Selim 2015; Sugita et al. 1992).

In hybrid catfish (*C. macrocephalus* \times *C. gariepinus*), Meidong et al. (2017) indicated that *Bacillus siamensis* strain B44v, selectively isolated from Thai pickled vegetables (Phak-dong), displayed a high potential as a probiotic in catfish culture.

Fish fed diet containing strain B44v (10^7 CFU g^{-1} feed) displayed not only no mortality but also growth improvement. The potential probiotic *B. siamensis* strain B44v could produce cellulase and protease, whereas the *Bacillus* sp. strain B51f produced protease and amylase enzymes. Ability to produce some hydrolytic enzymes is beneficial to the host. Enzymes increase the digestion of macromolecules in animal feed and improve feed intake by reducing digesta viscosity and increasing nutrient absorption in host animals (Ray et al. 2012).

For striped catfish, *Pangasianodon hypophthalmus*, the mixture of probiotics (*B. amyloliquefaciens* 54A and *B. pumilus* 47B) isolated from striped catfish at concentrations of 1×10^8 , 3×10^8 , and 5×10^8 CFU g^{-1} was added to the fish feed and conducted for 90 days. Truong Thy et al. (2017) reported that AWG (476.6 ± 7.81 g fish $^{-1}$) of fish fed probiotics at 5×10^8 CFU g^{-1} was significantly higher than the control (390 ± 25.7 g fish $^{-1}$) after 90 days of feeding, but there was no significant ($P > 0.05$) effect of probiotics on FCR and SGR. However, in basa fish, *Pangasius bocourti* (Meidong et al. 2018) reported that the administration of strain B81e isolated from the fish's gut (1×10^7 CFU g^{-1}) for 60 days had significant effects ($p < 0.05$) on weight gain, specific growth rate, and feed utilization efficiency of *P. bocourti*. This growth improvement might be related to the capability of the putative probiotics in producing extracellular protease and lipase within fish gut and thus exert beneficial effects to the digestive processes of the host fish as bacterial enzymes can help degrade the proteinaceous and lipid substrates (Ramesh et al. 2015; Ray et al. 2012). The significant reduction in FCR indicated that the fish utilized dietary nutrients more efficiently when feed was supplemented with strain B81e.

1.3.1.4 Japanese eel (*Anguilla japonica*)

Bacillus spp. supplementations have been recently applied in Japanese eel. Lee et al. (2017) indicated that dietary supplementation of *Bacillus subtilis* WB60 at 10^8 CFU g^{-1} in diet of Japanese eel (*Anguilla japonica*) resulted in better weight gain, feed efficiency, and protein efficiency ratio compared to the control and *Lactobacillus plantarum* diets. Similar results were observed in Japanese eel fed *Bacillus subtilis* WB60 and mannanoligosaccharide (MOS), as well as (*Bacillus subtilis* or licheniformis) and (mannan or fructooligosaccharide) (Lee et al. 2018; Park et al. 2020). There is growing evidence that gastrointestinal bacteria facilitate the decomposition of nutrients in the host organism and provide physiologically active materials, such as enzymes, amino acids, and vitamins (Cencic and Chingwaru 2010; Morowitz et al. 2011; Wang et al. 2020a). These materials can positively influence the digestive tract and improve feed digestion and utilization (Bairagi et al. 2004; Dawood et al. 2019; Ramirez and Dixon 2003; Wang et al. 2020b).

1.3.1.5 Sea Cucumber (*Apostichopus japonicus*)

Supplementation of *Bacillus cereus* EN25 at 0 (control), 10^5 , 10^7 , and 10^9 CFU g^{-1} for 30 days showed no significant effects on growth of sea cucumbers *A. japonicus* (Zhao et al. 2016). Growth performance of sea cucumbers was one of the important

indices to evaluate the effects of potential *Bacillus* spp. on culturing of sea cucumbers. Previous studies had proved that dietary *Bacillus* spp., such as indigenous *B. subtilis* T13 (Zhao et al. 2012), indigenous *B. cereus* (Yang et al. 2015), and commercial *B. subtilis* (Zhang et al. 2010), could improve the growth performance of sea cucumbers at suitable doses. This difference could be attributed to the differences in *Bacillus* strains, sizes of sea cucumbers, sources of sea cucumbers, experimental period, and experimental conditions. The present study was conducted with the same source of sea cucumbers at the same experimental period and conditions with Zhao et al. (2012), except *Bacillus* strain and initial sizes of sea cucumbers. Recently, Liu et al. (2020) indicated that dietary supplementation of *B. baekryungensis* MS1 at 10^7 cfu g^{-1} for a total of 60 days significantly improved the growth performance of the sea cucumber cultured under low temperature. This is related to the mode of action of probiotics, including the production of digestive enzymes, the production of antibacterial substances, immune stimulation, and interference of quorum sensing, all of which depend on the long-term growth and reproduction of probiotics. Studies have also shown that probiotics work by managing community assembly of the water and gut microbiota (Selim and Reda 2015; Wang et al. 2017a).

1.3.1.6 Tambaqui (*Colossoma macropomum*)

Dietary inclusion of *Bacillus subtilis* (10^9 UFC g^{-1}) and *Saccharomyces cerevisiae* (10^9 UFC g^{-1}) showed that no differences were found for the growth parameters between the treatments with probiotics (da Paixão et al. 2017). Although probiotics are supposed to be beneficial, the literature mentions possible synergistic effects. The total replacement of indigenous populations with probiotics may not be desirable to improve growth performance (Merrifield et al. 2010). The control of the endogenous balance between pathogenic and beneficial bacteria is still the target of many studies. According to Merrifield et al. (2010), the lack of improvements regarding growth and feed use may be explained by the level of gastrointestinal colonization that could be too high and any possible synergistic effect with the normal gut microbiota was negated. Thus, it is expected that the beneficial effects of probiotics for tambaquis are not on its performance but on its health and welfare. However, in another study with tambaqui, Dias et al. (2018) indicated that the use of the autochthonous bacteria *B. cereus* improves the growth performance, productivity, hematological profile, and survival of tambaqui juveniles. This enhanced growth performance of fish supplemented with probiotics is probably due to an improvement in digestion as well as an increase in the synthesis and absorption of nutrients (Hoseinifar et al. 2017). Similar results were obtained by El-Haroun et al. (2006) reporting increased growth performance and feed efficiency in tilapia fed the probiotics *Bacillus licheniformis* and *Bacillus subtilis*. According to these authors, the added probiotics improved digestibility, dietary protein, and energy utilization. These positive effects can be attributed to the capacity of the probiotics to promote an increase in the gut absorbent surface area, and stimulate and/or produce several enzymes on the intestinal tract, which improve digestibility and nutrient retention, leading to higher growth rates (El-Haroun et al. 2006; Ibrahem 2015).

1.3.1.7 Carp Species

Dietary administration of BioPlus 2B, a probiotic containing *Bacillus licheniformis* and *B. subtilis*, and Ferroin solution indicate that the combination of probiotic and Ferroin solution represents an effective dietary supplement for improving carcass quality, growth performance, and hematological parameters in kutum fry (Azarin et al. 2015). In mrigal fingerlings, *Cirrhinus mrigala* (avg.wt. 2.5 ± 0.20 g) were fed with three different doses (2×10^4 , 2×10^5 , and 2×10^6 CFU) of *Bacillus* sp. PP9 admixed with 100 g feed for a period of 60 days. It was found that the feed with *Bacillus* concentration of 2×10^4 CFU exhibited significantly higher growth and lower food conversion ratio compared to the control and other supplemented diets (Bandyopadhyay et al. 2015). More recently, Qin et al. (2020) found that dietary inclusion of *B. licheniformis* at the low-dose 1×10^5 cfu g^{-1} and the high-dose (HD) group with 1×10^6 cfu g^{-1} led to significantly ($p < 0.05$) improved percent weight gain (PWG) and specific growth rate (SGR) parameters. The improvement of growth performance parameters such as PWG and SGR with increasing concentrations of supplemented *B. licheniformis* FA6 observed in this study is in agreement with Han et al. (2015) observed a significant increase in the growth performance of tilapia fed with *B. licheniformis*. The increase in the growth performance of grass carp may due to the secretion of digestive enzymes by *B. licheniformis*, which improves feed digestibility (Kuebutornye et al. 2019).

In Pengze crucian carp, *Carassius auratus*, dietary supplementation with prebiotics β -glucan (BG group) and probiotics *Bacillus subtilis* (BS group) resulted in better growth performance than other groups whereas feed efficiency was unaffected by dietary treatments. The textures of muscle in terms of hardness, springiness, cohesiveness, gumminess, chewiness, and resilience were higher in BG and BS groups than the control group. Supplementation of β -glucan and *B. subtilis* acted as a hypolipidemic in terms of decreasing the total cholesterol, high-density lipoprotein, and low-density lipoprotein, whereas increased the immune responses in serum measured by acid phosphatase, alkaline phosphatase, and catalase activities. Dietary supplementation of β -glucan and *B. subtilis* significantly improved the fold height and microvillus height in contrast to basal diet. Moreover, β -glucan could significantly increase digestive capacity observed in terms of an increase in amylase and trypsin activities, and *B. subtilis* significantly increased amylase and lipase activities in intestine (Cao et al. 2019).

1.3.1.8 Trout

A commercial probiotic (4.2×10^9 CFU g^{-1} of additive) was supplemented to the experimental diets at 0% (control), 0.03% (P₁; 6×10^3 CFU g^{-1} of diet), or 0.06% (P₂; 1.5×10^6 CFU g^{-1} of diet) and fed to brown trout (*Salmo trutta*) and rainbow trout (*Oncorhynchus mykiss*) for 9 and 20 weeks, respectively. Rainbow trout showed significantly better growth performance than brown trout, regardless of the dietary treatment. No effect of dietary probiotic supplementation was detected on growth performance and body composition (Ramos et al. 2017). However, in Caspian Brown Trout (*Salmo trutta caspius*) Aftabgard et al. (2019) found that the combined effects of IMOS, a prebiotic, and BetaPlus[®], a probiotic containing

B. subtilis and *B. licheniformis*, demonstrated a better performance of select growth indices, including BWI and FCR, than fish that were fed the control diet; these results were probably due to improved nutrition and digestive processes (Cerezuela et al. 2011).

1.3.1.9 Other Aquacultured Species

Two probiotics (*Virgibacillus proomii* and *Bacillus mojavensis*) were used to study their effects on the digestive enzyme activity, survival, and growth of sea bass, *Dicentrarchus labrax* at various ontogenetic stages in three separate experiments (Hamza et al. 2016). The results indicated that the two probiotics *V. proomii* and *B. mojavensis* were adequate for improved growth performance and survival and for healthy gut microenvironment of the host (Hamza et al. 2016).

In the study of Hauville et al. (2016) Florida pompano (*Trachinotus carolinus*) larvae were fed either live feed enriched with Algamac 3050 (Control), Algamac 3050, and probiotics (PB), or the previous diet combined with a daily addition of probiotics to the tank water (PB+). The results indicated that a mix of *Bacillus* sp. can promote growth through an early maturation of the digestive system during the early larval stages of pompano and snook.

In grouper *Epinephelus coioides* (Yan et al. 2016, juveniles (14.6 ± 0.2 g) were fed either a basal control diet (without probiotic) or the basal diet supplemented with 1.0×10^8 CFU g^{-1} live (T1) and heat-inactivated *B. pumilus* SE5 (T2). The results indicated that the heat-inactivated probiotic significantly improved the final weight, weight gain (WG), and specific growth rate (SGR) at day 60 and significantly decreased the feed conversion ratio (FCR) at day 30 and 60, while the viable probiotic significantly decreased the FCR at day 60 ($P < 0.05$). This suggested that live and heat-inactivated *B. pumilus* could promote the efficient utilization of dietary nutrients. Interestingly, significant increased growth was only observed in fish fed the heat-inactivated *B. pumilus* containing diet for 60 days, but not in fish fed the live *B. pumilus* containing diet. Likewise, Hoseinifar et al. (2011) observed that dietary supplementation of 20 g kg^{-1} inactive brewer's yeast *Saccharomyces cerevisiae* var. *ellipsoideus* significantly improved the growth performance in juvenile beluga sturgeon (*Huso huso*). In rock bream, *Oplegnathus fasciatus*, Kim et al. (2017), revealed that supplementation of *B. amyloliquefaciens* spores at a concentration of 1.4×10^6 colony-forming units per gram (CFU g^{-1}) of feed for 90 days resulted in significant improvements in body weight (BW), weight gain (WG), specific growth rate (SGR), and food conversion ratio (FCR) when compared with control group fish.

In hybrid sturgeon, *Acipenser schrenckii* ♂ and *Acipenser baerii* ♀, fish were fed with *Bacillus amyloliquefaciens* (GB-9) and *Yarrowia lipolytica* lipase2 (YLL2): Diet 1 (0-control), Diet 2 (5.0 g kg^{-1} GB-9), Diet 3 (4.0 g kg^{-1} YLL2), and Diet 4 (5.0 g kg^{-1} GB-9 + 4.0 g kg^{-1} YLL2), respectively (Fei et al. 2018). The results indicated that supplementations of GB-9 + YLL2 resulted in a significant increase in final weight, Docosahexaenoic acid (DHA) and Eicosapentaenoic acid (EPA) concentration, compared with that of control ($p < 0.05$). This might be because the DHA and EPA hydrolyzed by YLL2 improved the poor establishment of the GB-9

in the gastrointestinal tract of hybrid sturgeon and might have promoted the growth of GB-9 (Menni et al. 2017). Similarly, combination of *B. licheniformis* and *B. amyloliquefaciens* indicated up to 2.5 times higher survival with probiotic addition, as well as 20% higher survival 7 days following a transport event. These benefits could not be explained by faster larval growth. In fact, CONT larvae were significantly longer than probiotic-treated larvae, likely due to decreased competition for food in CONT tanks which exhibited significantly lower survival. The other differing morphometric in this study was oil globule volume which was lowest in CONT larvae, suggesting that CONT larvae were consuming their endogenous reserves more quickly than probiotic-treated larvae. Retention of oil globules allows for a longer transition time to exogenous feeding, and studies indicate larvae that retain their endogenous reserves longer demonstrate increased survival (Avila and Juario 1987; Berkeley et al. 2004). The probiotic may alter development of the digestive tract and thus the start of exogenous feeding, as has been demonstrated in previous studies involving *Bacillus* probiotics and common snook (Hauville et al. 2016).

Dietary supplementation of *B. subtilis* has been reported to improve the growth performance, feed utilization, amylase, protease, and lipase enzymes of parrotfish (*Oplegnathus fasciatus*) and red sea bream (*Pagrus major*) (Liu et al. 2018; Zaineldin et al. 2018). The observed improvement in growth performance might be ascribed to the enhanced intestinal digestive enzyme activity and beneficial intestinal microbiota (Dawood et al. 2014; Liu et al. 2009; Sun et al. 2010). *Bacillus* sp. can produce certain essential micronutrients to promote better growth and feed utilization of hosts (Sanders et al. 2003). Further, *Bacillus* species may participate in digestion processes to break down nutrients such as carbohydrates, proteins, and lipids by producing extracellular enzymes (Liu et al. 2009; Sun et al. 2010). In abalone, *Haliotis discus hannai*, Gao et al. (2018) indicated that the food containing 10^5 cfu mL⁻¹ *Bacillus licheniformis* promoted food intake and growth of abalones. *Bacillus licheniformis* is an aerobic nonpathogenic bacterium that inhabits the intestinal microbial community in the form of spores, which can reduce intestinal pH, reduce ammonia concentration, and promote decomposition of starch and cellulose. Thus, it is generally considered to be a relatively stable probiotic (Hong et al. 2005; Vine et al. 2006).

1.3.2 Increase Disease Resistance

Probiotics have been proven as an effective tool for disease prevention in aquaculture (Hoseinifar et al. 2018). Probiotics can interact with or antagonize other enteric bacteria by resisting colonization or by directly inhibiting and reducing the incidence of opportunistic pathogens (Chiu et al. 2017). They can also improve host's health and well-being via physiological or immune modulation (Butt and Volkoff 2019). Probiotics can produce effective molecules that have bactericidal activity on intestinal pathogenic bacteria of the host, providing a barrier against the proliferation of opportunistic pathogens (Martínez Cruz et al. 2012; Seghouani et al. 2017). The

functional molecules produced during the bactericidal activity are antibiotics, bacteriocins, siderophores, enzymes and/or hydrogen peroxide as well as the alteration of the intestinal pH due to the generation of organic acids (Verschuere et al. 2000). The inhibition of intestinal related diseases has been reported in several cultured species by probiotic incorporation in aquafeeds (Ringø et al. 2018; Serra et al. 2019; Wanka et al. 2018). Thus, it can be confirmed that the ability of aquatic animals to avoid the infectious diseases mainly depends on the immunomodulatory effect that happened due to the administration of beneficial bacterial cells.

1.3.2.1 Tilapias

Dietary inclusion of *B. licheniformis* at 0%, 0.02%, 0.04%, 0.06%, 0.08%, and 0.1% containing live germ 2×10^{10} CFU/g for 10 weeks significantly increased disease resistance of Nile tilapia, *Oreochromis niloticus* against *Streptococcus iniae* (Han et al. 2015). *Bacillus* strains supplementation in diet could increase disease resistance in fish through the stimulation of both the cellular and humoral immune function, such as phagocytic activity, lysozyme activity, and complement activity (Arena et al. 2006; Queiroz and Boyd 1998; Sookchaiyaporn et al. 2020; Zhou et al. 2010). It was reported that *Bacillus* bacteria are able to outcompete other bacteria for nutrients and space and can exclude other bacteria through the production of antibiotics, and as usually lead to the enhanced immunity of fish (Cha et al. 2013). Similarly, dietary inclusion of *B. licheniformis* Dahb1 at 10^7 cfu g^{-1} could improve disease resistance of Mozambique tilapia (*Oreochromis mossambicus*) against *A. hydrophila* (Gobi et al. 2018). In terms of *Bacillus subtilis* HAINUP40, H. Liu et al. (2017) reported that dietary supplement of *B. subtilis* HAINUP40 at 10^8 cfu g^{-1} can effectively enhance disease resistance of Nile tilapia against *Streptococcus agalactiae*. In addition, combination of *B. subtilis* with *S. cerevisiae* and *A. oryzae*; *Bacillus subtilis* with Aqua NZ and AP193; *Bacillus subtilis* strains SB3086, SB3295, SB3615 with AP193; *B. subtilis* and *B. licheniformis*, and *Bacillus subtilis* and *Bacillus licheniformis* (BS) combined with traditional Chinese medicine (TCM) *A. hydrophila* and *S. iniae*. Higher intestinal *Bacillus* spp. counts can regulate the gut microbiota of fish, selectively stimulate other beneficial probiotic bacteria, and depress some potential harmful bacteria (Yang et al. 2012).

1.3.2.2 Shrimps

The efficiency of these isolates in controlling pathogens, which is a key factor in selecting appropriate bacteria as probiotics, was evaluated (Kesarcodei-Watson et al. 2008). Based on in vitro laboratory results, B4, B6, and B12 inhibited *V. parahaemolyticus*; however, only *B. subtilis* AQHPS001 (B12) showed the highest antagonistic property against VP_{AHPND} strains. However, among the VP_{AHPND} strains, there were different sizes of the inhibitory clear zone, and VP_{AHPNDAQH3.2} was the only strain that resisted B12. This suggests that there are varieties of VP_{AHPND} and that each strain may employ different mechanisms in response to the target B12 (Kewcharoen and Srisapoom 2019). Previous reports found that *Bacillus* spp. could produce many kinds of bacteriocins, such as subtilin, subtilosin, coagulins, megacins, bacillins, bacillomycins, mycosubtilins, toximycins, and

xanthobacidin, which could reduce pathogen colonization by directly inhibiting pathogens while having no resulting effects on the virulence resistance genes of pathogenic bacteria (Desriac et al. 2010; Hammami et al. 2012; Joseph et al. 2013). Zhao et al. (2015) also reported that *Bacillus* spp. could secrete quorum-quenching enzymes, which are expected to be quorum-sensing blockers to reduce disease infection. These results suggest that *B. subtilis* AQAHBS001 possesses more effective characteristics that are important for controlling the various harmful VP_{AHPND} strains than other candidates. For these reasons, it was further chosen to study its application on a laboratory scale. Similarly, dietary inclusion of *Bacillus subtilis* WB60, *Pediococcus pentosaceus*, and *Lactococcus lactis* at 10^8 CFU g⁻¹ could improve disease resistance of whiteleg shrimp *Litopenaeus vannamei* against *Vibrio parahaemolyticus* (Won et al. 2020b). Generally, administration of probiotics in the shrimp diet was shown to decrease mortality rates compared to the CON diet (Balcázar et al. 2007; Sapcharoen and Rengpipat 2013; Zhang et al. 2009). Previous studies demonstrated that probiotic supplementation can be used for modulating fish health and disease resistance (Wang et al. 2018; Zuo et al. 2019). Indeed, probiotics can beneficially influence the disease resistance of fish to pathogen bacteria by producing antimicrobial substances and competing with pathogens for physical occupation of space (Lim et al. 2020). As a result, the enhanced survival and cumulative survival rates could be due to probiotic supplementation. Chen et al. (2020a) recently indicated that dietary MOS and/or *B. licheniformis* supplementation could positively increase ammonia resistance of *Litopenaeus vannamei*. According to Chen et al. (2012), immune parameters decrease after ammonia stress, yet these parameters recover faster when they were initially stimulated by a probiotic. Faster recovery of immune parameters might have contributed to the increased survival after ammonia stress for the *Rps. palustris* fed shrimp.

1.3.2.3 Catfish

Meidong et al. (2017) revealed that *Bacillus siamensis* strain B44v and *Bacillus* sp. strain B51f, derived from indigenous fermented foods, displayed strongly antagonistic activity against the bacterial fish pathogens, *A. hydrophila* and *S. agalactiae*. Both strains effectively inhibited Gram-positive and Gram-negative bacteria, indicating their broad spectrum as a useful antagonistic property as the two most striking bacterial fish pathogens in aquaculture in Thailand belong to the genera the *Aeromonas* and *Streptococcus* (Maisak et al. 2013). Besides fish pathogens, the bacteriocin-like substance from *B. siamensis* strain B44v inhibited several foodborne pathogens suggesting potential applications in human foods (Sivamaruthi et al. 2018). Likewise, Reda et al. (2018) showed that supplementation of three autochthonous *Bacillus* strains (*B. subtilis*, *B. amyloliquefaciens*, and *B. cereus*) and a commercial *B. amyloliquefaciens* at a dose of 1×10^{10} CFU kg⁻¹ significantly increased disease resistance of African catfish against *Aeromonas sobria*. This may be returned to the ability of *Bacillus* spore to resist gastrointestinal conditions, survive and transit cross gastrointestinal tract, germinate and vegetate with heterologous antigen expression before being excreted (Duc et al. 2003). In striped catfish, Truong Thy et al. (2017) indicated that the mixed probiotics of *Bacillus*

amyloliquefaciens 54A and *B. pumilus* 47B isolated from striped catfish (*Pangasianodon hypophthalmus*) intestine significantly enhanced disease resistance of the fish against *Edwardsiella ictaluri* and ammonia tolerance. Antimicrobial activity of probiotics has been demonstrated on many in vitro and in vivo studies in animals. The study of Corr et al. (2007) reported trial mice received protection from *Lactobacillus salivarius* against *Listeria monocytogenes* involved bacteriocin produced by *L. salivarius*UCC118. Additionally, antimicrobial activities of probiotics against pathogens include secretion of hydrogen peroxide (Pridmore et al. 2008), lactic acid (Fayol-Messaoudi et al. 2005), competitive exclusion (Lee et al. 2003), and stimulation of immune system (Ryan et al. 2009). The positive effect on barrier function of probiotics is to protect the host intestine by prevention of pathogen attachment to epithelial cells on gut surface (Mennigen et al. 2009). In basa fish, *Pangasius bocourti*, Meidong et al. (2018) found that *B. aerius* B81e has beneficial effects on growth performance, innate immunity, and disease resistance of *P. bocourti* against *Aeromonas hydrophila* and *Streptococcus agalactiae*. Bacterial co-aggregation has considerable significance in the host gut as co-aggregation ability of bacterial probiotics might interfere with the ability of pathogenic bacteria to infect the host and can prevent colonization of the pathogens (Spencer and Chesson 1994). In addition, *B. aerius* B81e has an absence of hemolysin and is susceptible to most of the common antibiotics tested which demonstrated that it is likely a nonpathogen and has an inability to transfer antibiotic-resistant genes to recipient bacteria in the host gut, thus preventing the development of antibiotic-resistant pathogens (Meidong et al. 2018).

1.3.2.4 Japanese eel (*Anguilla japonica*)

The combination of *Bacillus subtilis* WB60 and *Lactobacillus plantarum* KCTC3928 or *Bacillus subtilis* WB60 and mannanoligosaccharide (MOS) significantly improved disease resistance of Japanese eel against *V. anguillarum* (Lee et al. 2017, 2018). Similarly, Park et al. (2020) reported that dietary inclusion of *B. subtilis* with FOS (BSF) and *B. licheniformis* significantly increased disease resistance against *Aeromonas hydrophila*. Significant increase in disease resistance in these works may be attributable to the stimulation of cellular and humoral immune function.

1.3.3 Sea Cucumber (*Apostichopus japonicus*)

Zhao et al. (2016) indicated that the cumulative mortality after *V. splendidus* challenge decreased significantly in sea cucumbers fed with EN25 at 10^7 CFU g⁻¹ ($P < 0.05$). The present study confirmed dietary *B. cereus* EN25 at 10^7 CFU g⁻¹ could significantly improve disease resistance in juvenile *A. japonicus*. Recently, Liu et al. (2020) showed that *B. baekryungensis* MS1 significantly reduced the mortality of sea cucumbers infected with *Vibrio splendidus*. By regulating the expression of immune-related genes and signaling pathways, *B. baekryungensis* MS1 improved

the immunity of sea cucumber in winter and effectively controlled the infection of pathogenic bacteria such as *V. splendidus*.

1.3.4 Tambaqui (*Collossoma macropomum*)

da Paixão et al. (2017) indicated that supplementation of two probiotics *Bacillus subtilis* and *Saccharomyces cerevisiae* at 10^9 UFC g^{-1} significantly increased disease resistance of tambaqui, *Collossoma macropomum*, against *Streptococcus agalactiae*. Similarly, Dias et al. (2018) reported that *B. cereus* (4.2×10^4 , 3.9×10^6 and 3.3×10^8 CFU g^{-1}) supplemented as probiotics to *C. macropomum* for 120 days significantly increased disease resistance against *Aeromonas hydrophila*. The probiotic promoted a nonspecific response against bacterial infection, increasing fish survival after challenge with *A. hydrophila*.

1.3.5 Other Species

In rock bream, *Oplegnathus fasciatus*, Kim et al. (2017) demonstrated the benefit of incorporation of *B. amyloliquefaciens* as a feed supplement to improve the health status of *Oplegnathus fasciatus* challenged with *Streptococcus iniae*. The enhancement of the innate immune response with a *B. amyloliquefaciens* enriched probiotic diet and decreased mortality rate, thereby protecting the fish against *S. iniae*. Similarly, dietary inclusion of *B. subtilis* at 10^8 CFU kg^{-1} significantly increased disease resistance of parrotfish, *Oplegnathus fasciatus*, against *Vibrio alginolyticus* (Liu et al. 2018). The growth performance and health status improvement of aquatic animal might be involved with the gut microbiota change after probiotic administration. The previous study has also demonstrated the positive effects of *B. subtilis* E20 in terms of intestinal presence and subsequent health benefits for *L. vannamei* (Liu et al. 2009; Tseng et al. 2009) and *E. coioides* (Liu et al. 2010). In the same trend, dietary inclusion of *Bacillus licheniformis* significantly improved disease resistance of abalone, *Haliotis discus hannai* Ino., against *V. parahaemolyticus* and grass carp, *Ctenopharyngodon idella*, against *A. hydrophila* (Gao et al. 2018; Qin et al. 2020).

1.4 Immune Effects of *Bacillus*

Enhancement of host immunity is one important benefit of probiotic diet supplementation (Kuebutornye et al. 2019). As stated by Verschuere et al. (2000), probiotics can modulate innate immunity through the modulation of humoral immune responses and expression of immune-related genes. Effects of *Bacillus* on immune response of different fish and shellfish are displayed in Table 1.2.

Table 1.2 Immune responses of fish and shellfish fed different *Bacillus* probiotics. → no change, ↑ increase, ↓ decrease

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>B. amyloliquefaciens</i>	Commercial probiotic	0; 1×10^4 and 1×10^6 CFU/g 30 days	Nile tilapia (<i>O. niloticus</i>) 27.7 ± 0.22 g	Serum killing percentages ↑ Phagocytic activities ↑ Lysozyme activities ↑ Nitric oxide assay ↑ The percentage of serum killing ↑ Serum nitric oxide activity ↑ Serum lysozyme activity ↑	(Selim & Reda 2015)
<i>Bacillus subtilis</i> (combined with <i>S. cerevisiae</i> and <i>A. oryzae</i>)	Commercial probiotic	0; 5 g kg ⁻¹ probiotic mixture (<i>B. subtilis</i> 1.5×10^9 , <i>S. cerevisiae</i> 10^9 and <i>A. oryzae</i> 2×10^9); and 10 g kg ⁻¹ probiotic mixture (<i>B. subtilis</i> 3.0×10^9 , <i>S. cerevisiae</i> 2.0×10^9 and <i>A. oryzae</i> 4.0×10^9) (CFU g ⁻¹) 6 weeks	Juvenile Nile tilapia (<i>O. niloticus</i>) 25 ± 0.05 g	Respiratory burst activity ↑ Erythrocyte fragility ↑ Levels of white blood cells ↑	(Iwashita et al. 2015)
<i>Bacillus licheniformis</i>	Commercial probiotic	0%, 0.02%, 0.04%, 0.06%, 0.08% and 0.1% containing live germ 2×10^{10} (CFU/g) 10 weeks	Juvenile Nile tilapia (<i>O. niloticus</i>) 3.83 ± 0.03 g	Lysozyme activity ↑ Content of complement C3 ↑	(Han et al. 2015)
<i>B. subtilis</i> and <i>B. licheniformis</i>	Commercial probiotic	0, 3, 5, 7 and 10 g kg ⁻¹ 4 weeks	Nile tilapia (<i>O. niloticus</i>) 53.01 ± 1.0 g	Lysozyme and protease activity ↑ Anti-protease activity ↑ Superoxide dismutase activity ↑	(Abarike et al. 2018a)

<p><i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i> (BS) combined with traditional Chinese medicine (TCM)</p>	<p>Commercial probiotic</p>	<p>0; TCM at 3 and BS at 7 (g/kg); TCM at 5 and BS at 5 (g/kg); TCM at 7 and BS at 3 (g/kg) 4 weeks</p>	<p>Nile tilapia (<i>O. niloticus</i>) 57 ± 2 g</p>	<p>Immunoglobulin M level ↑ Myeloperoxidase activity ↑ Expression of C-lysozyme ↑ Heat shock protein 70 ↑ β-defensin ↑ Transforming growth factor beta ↑ Small body size decapentaplegic homolog 3 ↑ Lysozyme activity ↑ Superoxide dismutase activity ↑ Catalase, protease, and antiprotease ↑ Expression of C-lysozyme ↑ Heat shock protein 70 ↑ β-defensin ↑ Transforming growth factor beta ↑ Alkaline phosphatase ↑ Myeloperoxidase ↑ Lysozyme ↑ Reactive oxygen species ↑ Reactive nitrogen species ↑ Superoxide dismutase ↑ Glutathione peroxidase ↑ Respiratory burst activity ↑ Serum lysozyme activity ↑</p> <p>(Abarike et al. 2018b)</p>
<p><i>Bacillus licheniformis</i> Dahb1</p>	<p>Commercial probiotic</p>	<p>0, 10⁵ and 10⁷ CFU/g 4 weeks</p>	<p>Mozambique tilapia (<i>Oreochromis mossambicus</i>)</p>	<p>(Gobi et al. 2018)</p>
<p><i>Bacillus subtilis</i> HAINUP40</p>	<p>Isolated from the aquatic environment</p>	<p>10⁸ CFU/g 8 weeks</p>	<p>Nile tilapia (<i>Oreochromis niloticus</i>) 95 ± 8 g</p>	<p>(Liu et al. 2017)</p>

(continued)

Table 1.2 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus cereus</i> AQAHBS01	Commercial probiotic	Exp 1: $0, 1.0 \times 10^4$ and 1.0×10^5 CFU mL ⁻¹ in 42 days on tanks Exp 2: $0, 1.0 \times 10^7$ and 1.0×10^8 CFU g ⁻¹ 42 days on cages	Nile tilapia (<i>Oreochromis niloticus</i>) 20.20 ± 0.17 g	Serum lysozyme ↑ Peroxidase activity ↑ Alkaline phosphatase activity ↑ Total superoxide dismutase activity ↑ Autochthonous gut bacteria community ↑ Potentially beneficial bacteria ↑	(Wang et al. 2017b)
<i>Bacillus pumilus</i> AQAHBS01	Isolated from farmed fish	$10^6, 10^7, 10^8$ and 10^9 CFU/g 30 days	Nile tilapia (<i>Oreochromis niloticus</i>) 50 g	Phagocytic activity ↑ Superoxide anion levels ↑	(Srisapoom & Areechon 2017)
<i>Bacillus subtilis</i> strains SB3086, SB3295, SB3615, and AP193	Commercial probiotic	4×10^7 CFU/g of feed in 21 days	Nile tilapia (<i>Oreochromis niloticus</i>) 16.5 ± 0.2 g	Serum bactericidal activity ↑ Lysozyme activity ↑	(Addo et al. 2017b)
<i>Bacillus subtilis</i> (Aqua NZ and AP193)	Commercial probiotic	4.2×10^7 CFU g ⁻¹ of feed 8 weeks	Nile tilapia (<i>Oreochromis niloticus</i>) 59.5 ± 0.99 g	Lysozyme activity → Respiratory burst activity →	(Addo et al. 2017a)
<i>Bacillus cereus</i> NY5 and <i>Alcaligenes faecalis</i> Y311	Nile tilapia intestine	1.0×10^4 CFU mL ⁻¹ 3 months	Nile tilapia (<i>Oreochromis niloticus</i>) 5.20 ± 0.17 g	The total superoxide dismutase activities ↑ Alkaline phosphatase activities ↑	(Wang et al. 2020a, 2020b)

<i>Bacillus licheniformis</i> HG48B		1×10^6 and 1×10^8 CFU g ⁻¹ 60 days	Pacific white shrimp (<i>Litopenaeus</i> <i>vannamei</i>) 0.57 ± 0.001 g	Lysozyme activity ↑ Phosphatase activity ↑ Superoxide dismutase (SOD) ↓ Total protein (TP) ↑ Albumin (ALB) in serum ↑ Glutathione peroxidase (GSH-Px) ↑	(Amoah et al. 2019)
<i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i>	Commercial probiotic	1×10^4 and 1×10^8 CFU/ g 60 days	Pacific white shrimp (<i>Litopenaeus</i> <i>vannamei</i>)	Lysozyme and hemocyte cell count ↑	(Sadat Hoseini Madani et al. 2018)
<i>B. licheniformis</i>	Commercial probiotic	Control diet (CON), 0.2% MOS (MOS), 0.1% <i>B.</i> <i>licheniformis</i> (BL), 0.2% MOS plus 0.1% BL (SYN) 8 weeks	Pacific white shrimp (<i>Litopenaeus</i> <i>vannamei</i>)	Expression levels of catalase ↑ Expression levels of glutathion peroxidase ↑ Expression of superoxide dismutase (SOD) ↑ Expression of penaeidin -3a (Pen-3a) ↑ Expression of heat shock protein (Hsp-70) ↑	(Chen et al. 2020a)
<i>B. licheniformis</i>		Basal diet (Control); 0.5% hydrolyzed yeast (HY); 0.1% <i>B.</i> <i>licheniformis</i> (BL) and 0.5% hydrolyzed yeast + 0.1% <i>B.</i> <i>licheniformis</i> (SYN) 8 weeks	Pacific white shrimp (<i>Litopenaeus</i> <i>vannamei</i>) 2.0 ± 0.01 g	MDA ↓ Expression of CAT, GPX, and SOD ↑ Expression of Pen-3a and PPO ↑ Pen-3a and SOD ↓	(Chen et al. 2020b)

(continued)

Table 1.2 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus licheniformis</i> MA132, <i>B. subtilis</i> MA143 and <i>B. subtilis</i> subsp. <i>subtilis</i> GA1B1	Isolated from pustulose ark <i>Anadara tuberculosa</i>	$0, 1 \times 10^6$, 2×10^6 , 4×10^6 , and 6×10^6 CFU g ⁻¹ of feed. 32 days	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 1 ± 0.1 g	Expression of proPO gene ↑ Expression of LvToll1 and SOD genes ↑ expression of the Hsp70 gene ↓ Expression of TGase gene →	(Sánchez-Ortiz et al. 2016)
<i>Bacillus</i> spp	Isolated from pustulose ark	1×10^6 , 2×10^6 , 4×10^6 , and 6×10^6 CFU g feed ⁻¹ 32 days	Pacific white shrimp (<i>L. vannamei</i>) 1 ± 0.1 g	proPO gene ↑ LvToll1 gene ↑ SOD gene ↑ TGase gene →	(Sánchez-Ortiz et al. 2016)
<i>Bacillus subtilis</i> WB60, <i>Pedotococcus pentosaceus</i> , and <i>Lactococcus lactis</i>	Commercial probiotic	<i>B. subtilis</i> at 10^7 CFU/g diet, <i>B. subtilis</i> , <i>P. pentosaceus</i> , and <i>L. lactis</i> at 10^8 CFU/g diet, and oxytetracycline at 4 g/kg 8 weeks	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 1.41 ± 0.05 g	Superoxide dismutase activity ↑ Lysozyme activity ↑ Immune-related gene expression ↑	(Won et al. 2020)
<i>Bacillus cereus</i> and <i>Pedotococcus acidilactici</i>	Commercial probiotic	<i>P. acidilactici</i> (10^6 CFU/mL) and <i>B. cereus</i> (10^6 CFU/mL) to the water pond 110 days	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 0.002 ± 0.001 g	Total hemocyte count ↑ Total protein ↑ Lysozyme activity ↑	(Khademzade et al. 2020)
<i>Bacillus aryabhatai</i> TBRC8450	Commercial probiotic	1×10^8 CFU/g diet 6 weeks	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 0.9 ± 0.1 g	C-type lectin ↑ Penaeidin-3 ↑ Heat shock protein 60 ↑ Thioredoxin, and ferritin ↑ phenoloxidase activity ↑ Total antioxidant activity ↑ Total hemocyte count → Superoxide dismutase →	(Tepaamorndech et al. 2019)

<i>Bacillus subtilis</i> E20		10^9 cfu (kg diet) ⁻¹ 8 weeks	Pacific white shrimp (<i>Litopenaeus vannamei</i>) 3.78 ± 0.21 g	Antioxidant enzymes gene ↑ Pattern recognition protein genes ↑ Antimicrobial molecule ↑ Hexosamine biosynthesis pathway ↑ UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase ↑	(Chien et al. 2020)
<i>Bacillus</i> sp. DDKRC1	Isolated from the gut of Asian seabass (<i>Lates calcarifer</i>)	0, 2.94 × 10 ⁷ CFU/100 g feed and diet fermented with <i>Bacillus</i> sp. DDKRC1 42 days	Tiger shrimp (<i>Penaeus monodon</i>) 2.73 ± 0.01 g	Total heterotrophic count ↑ Amylolytic ↑ Cellulolytic and proteolytic bacterial counts ↑ Phagocytic activity ↑	(De et al. 2018)
<i>Bacillus coagulans</i>	Commercial probiotic	0, 10 ⁵ , 10 ⁷ and 10 ⁹ cfu g ⁻¹ 60 days	Freshwater prawn (<i>Macrobrachium rosenbergii</i>) 2.4 ± 0.35 g	Lysozyme activity ↑ Respiratory burst activity ↑	(Gupta et al. 2016)
<i>Bacillus</i> sp. PP9	Isolated from mrigal gut	2 × 10 ⁴ , 2 × 10 ⁵ and 2 × 10 ⁶ CFU 60 days	Mrigal (<i>Cirrhinus mrigala</i>) 2.5 ± 0.20 g	Hemoglobin percentage ↑ Total erythrocyte count ↑ Total leukocyte count ↑ Corpuscular hemoglobin ↑ Total serum protein ↑ Albumin globulin ratio ↑ Serum bactericidal activity ↑	(Bandyopadhyay et al. 2015)

(continued)

Table 1.2 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus subtilis</i> KADR1	Commercial probiotic	10^6 ; 10^8 and 10^{10} CFU/g 4 weeks	<i>Labeo rohita</i>	Serum lysozyme ↑ Phagocytosis ↑ Serum total protein ↑ Respiratory burst ↑ Serum IgM levels ↑ Superoxide dismutase ↑ Alternative complement pathway ↑	(Ramesh & Souissi 2018)
<i>Bacillus subtilis</i> FPTB13 and chitin	Isolated from an indigenous fermented fish product "Shidal"	<i>B. subtilis</i> 10^9 cells g^{-1} , chitin 2% and the combination 2 weeks	Labeo catla (<i>Catla catla</i>) 40.0 ± 1.9 g	Oxygen radical production ↑ Myeloperoxidase content ↑ Lysozyme activity ↑ Total protein content and alkaline ↑ Phosphatase activity ↑	(Sangma & Kamilya 2015)
<i>B. subtilis</i> , <i>B. licheniformis</i> , and <i>B. cereus</i>		0; 1×10^5 cfu/g of <i>B. subtilis</i> ; 1×10^5 cfu/g of <i>B. subtilis</i> and <i>B. licheniformis</i> and 1×10^5 cfu/g of <i>B. subtilis</i> , <i>B. licheniformis</i> , and <i>B. cereus</i> 45 days	Common carp (<i>Cyprinus carpio</i>) 57.40 ± 0.43 g	Phagocytic percentage ↑ Phagocytic index ↑ Serum immunoglobulin M ↑ Serum lysozyme activity ↑ Intestinal mucosal secretory immunoglobulin A ↑ Peripheral blood lymphocyte proliferation ratio ↑ Superoxide dismutase activity ↑ Glutathione peroxidase activity ↑ Catalase activity ↑ Total antioxidant maleic dialdehyde activity ↑ Glutathione activity ↑	(Wang et al. 2017a)

<i>Bacillus subtilis</i>		10 ⁹ CFU/g 60 days	Gibel carp (<i>Carassius auratus gibelio</i>) 60.51 ± 0.51 g	Protective effects against lead toxicity ↑ Superoxide dismutase ↑ Catalase and glutathione ↑ Lysozyme and IgM levels ↑ immune-related genes ↑	(Yin et al. 2018)
<i>Bacillus amyloliquefaciens</i>		0, 10 ⁵ , 10 ⁷ and 10 ⁹ CFU/g 70 days	Roho labeo (<i>Labeo rohita</i>) 20.23 g	Serum protein and globulin ↑ Albumin, lysozyme, and IgM ↑ Malondialdehyde ↑ Catalase, and superoxide dismutase ↑ Serum aspartate transaminase ↑ Serum alanine transaminase activity ↑ Liver malondialdehyde level ↑	(Nandi et al. 2018)
<i>Bacillus subtilis</i> and β-glucan	Commercial probiotic	1 g kg ⁻¹ β-glucan and 1 × 10 ⁹ CFU kg ⁻¹ <i>B. subtilis</i> 70 days	Penge crucian carp (<i>Carassius auratus</i> var. Pengeze) 12.89 ± 0.04 g	Acid phosphatase activity ↑ Alkaline phosphatase activity ↑ Glutathione peroxidase activity ↑ Glutathione activity ↓ Catalase activity ↓ Total superoxide dismutase activity ↓	(Cao et al. 2019)

(continued)

Table 1.2 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus amyloliquefaciens</i> FPTB16		10^7 , 10^8 and 10^9 cells g^{-1} diet 4 weeks	Indian major carp (<i>Catla catla</i>) 25.98 ± 2.57 g	Oxygen radical production \uparrow Serum lysozyme activity \uparrow Total serum protein content \uparrow Myeloperoxidase activity \uparrow Alkaline phosphatase activity \uparrow Expression of IL-1 β , TNF- α , C3 and iNOS \uparrow IFN- γ expression \downarrow	(Singh et al. 2017)
<i>Bacillus subtilis</i>	Isolated from the gut of grass carp	0, high-fat diet, and high-fat diet + <i>B. subtilis</i> (1×10^7 CFU g^{-1}) for 8 weeks	Grass carp (<i>Ctenopharyngodon idellus</i>) 50.24 ± 1.38 g	Serum low-density lipoprotein cholesterol \uparrow Aspartate aminotransferase \uparrow Hepatic mRNA expression of fatty acid synthase \downarrow Carnitine palmitoyl transferases \uparrow Glutathione \uparrow Hydrogen peroxide (H_2O_2) \downarrow Malondialdehyde (MDA) contents \downarrow	(Zhao et al. 2020)
<i>Bacillus licheniformis</i>	Isolated from grass carp	1×10^5 cfu/g and 1×10^6 cfu/g 56 days	Grass carp (<i>Ctenopharyngodon idella</i>) 16.5 g	Superoxide dismutase (SOD) activity \uparrow Malondialdehyde (MDA) levels \downarrow Antioxidant enzymes <i>MnSOD</i> \uparrow Catalase (CAT) in the intestine \uparrow Proinflammatory cytokines \downarrow Anti-inflammatory cytokine \uparrow <i>ZO-1</i> , <i>occludin</i> , and <i>claudin-c</i> \uparrow	(Qin et al. 2020)

<i>B. subtilis</i> YB-1 and <i>B. cereus</i> YB-2	Commercial probiotic	0, 10 ⁷ and 10 ¹⁰ cfu/g diet 32 days	Sea cucumber (<i>Apostichopus japonicus</i>) 50 ± 0.5 g	Phagocytic activity ↑ Superoxide anion production ↑ Lysozyme activity ↑ Catalase activity ↑ Phenoloxidase activity ↑	(Li et al. 2015)
<i>Bacillus baekryungensis</i> MS1	Isolated from a sea cucumber pond in winter	0 and 10 ⁷ CFU/ml 60 days	Sea cucumber (<i>Apostichopus japonicus</i>) 4.17 g ± 0.22 g	↑ Superoxide dismutase activity Catalase activity ↑ Alkaline phosphatase activity ↑ Acid phosphatase activity ↓ Nitric oxide synthetase activity ↑ Phagocytosis and respiratory burst ↑ Ubiquitin-mediated proteolysis pathway ↑	(Liu et al. 2020)
<i>Bacillus cereus</i> EN25	Isolated from mud of sea cucumber culturing water bodies	0, 10 ⁵ , 10 ⁷ and 10 ⁹ CFU/g for 30 days	Juvenile sea cucumber (<i>Apostichopus japonicus</i>) 0.375 ± 0.024 g	Total coelomocytes count → Acid phosphatase activity → Phagocytosis activity ↑ Respiratory burst activity ↑ Total nitric oxide synthase activity ↑ Superoxide dismutase activity ↑	(Zhao et al. 2016)
<i>B. amyloliquefaciens</i> 54A and <i>B. pumilus</i> 47B	Isolated from gut of striped catfish	1 × 10 ⁸ , 3 × 10 ⁸ , and 5 × 10 ⁸ CFU g ⁻¹ feed 90 days	Striped catfish (<i>Pangasianodon hypophthalmus</i>)	Phagocytic activity ↑ Respiratory bursts ↑ Lysozyme activity ↑	(Truong Thy et al. 2017)

(continued)

Table 1.2 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus aerius</i> B81e	Isolated from healthy hybrid catfish	0 and 10^7 CFU g^{-1} feed 60 days	Basa fish (<i>Pangasius bocourti</i>) 69 g	Serum lysozyme activity ↑ Bactericidal activity ↑ Alternative complement activity ↑ Phagocytic activity ↑ Respiratory burst activity ↑	(Meidong et al. 2018)
<i>B. subtilis</i> , <i>B. amyloliquefaciens</i> , <i>B. cereus</i> and a commercial <i>B. amyloliquefaciens</i>	Isolated from the intestine of African catfish	10^{10} CFU/ml 60 days	African catfish (<i>Clarias gariepinus</i>) 75.23 ± 1.6 g	Lysozyme activity ↑ Nitric oxide and IgM ↑ Myostatin cDNA levels ↑ PACAP expression ↑	(Reda et al. 2018)
<i>Bacillus subtilis</i> WB60 and <i>Lactobacillus plantarum</i> KCTC3928	Commercial probiotic	0; <i>B. subtilis</i> at 10^6 , 10^7 , 10^8 and <i>L. plantarum</i> at 10^6 , 10^7 , 10^8 CFU/g diet	Japanese eel (<i>Anguilla japonica</i>) 8.29 ± 0.06 g	Lysozyme activity ↑ Superoxide dismutase (SOD) ↑ Myeloperoxidase (MPO) ↑ Level of intestine glyceraldehyde-3-phosphate dehydrogenase (GAPDH) ↑ Heat shock protein 70, 90 ↑ Immunoglobulin (IgM) ↑	(Lee et al. 2017)
<i>Bacillus subtilis</i> WB60 and mannanoligosaccharide (MOS)	Commercial probiotic	BS: 0.0, 0.5, and 1.0×10^7 CFU/g diet and MOS: 0 and 5 g/kg diet. 8 weeks	Japanese eel (<i>Anguilla japonica</i>) 9.00 ± 0.11 g	Nonspecific enzymatic activities ↑ Heat shock protein 70 mRNA levels ↑ Immunoglobulin M expressions ↑	(Lee et al. 2018)
<i>Bacillus subtilis</i> or <i>licheniformis</i> and (mannan or fructo oligosaccharide)		0, Probiotics (1.0×10^8 CFU/g diet) and prebiotics (5 g/kg diet) 12 weeks	Japanese eel (<i>Anguilla japonica</i>) 12.8 ± 0.47 g	Expression of heat shock protein 70 ↑ Expression of immunoglobulin M ↑	(Park et al. 2020)

<i>B. subtilis</i> E20	Commercial probiotic	0, 10 ⁸ , 10 ⁹ , and 10 ¹⁰ CFU kg ⁻¹ 56 days	Parrotfish (<i>Oplegnathus fasciatus</i>)	Lyszyme activity ↑ Respiratory burst ↑ Phagocytic activity ↑	(Liu et al. 2018)
<i>B. velezensis</i> V4 and <i>Rhodotorula mucilaginosa</i> compound	Isolated from the water of RAS rearing salmonid	0; <i>B. velezensis</i> V4 5 × 10 ⁶ , <i>R. mucilaginosa</i> 5 × 10 ⁷ (CFU g ⁻¹), (<i>B. velezensis</i> V4 1.5 × 10 ⁷ , <i>R. mucilaginosa</i> 1.5 × 10 ⁸ (CFU g ⁻¹), and <i>B. velezensis</i> V4 2.5 × 10 ⁷ , <i>R. mucilaginosa</i> 2.5 × 10 ⁸ (CFU g ⁻¹) 62 days	Juvenile Atlantic salmon (<i>Salmo salar</i> L.) 180.18 ± 3.64 g	Acid phosphatase ↑ IgM ↑ Nitric oxide ↑ Glutamic pyruvic transaminase ↓ Glutamic oxalacetic transaminase ↑ Lysozyme ↑ Total superoxide dismutase malondialdehyde ↑ Glutathione ↑ Glutathione peroxidase ↑ Total antioxidant capacity ↑ Malondialdehyde ↑	(Wang et al. 2019a, 2019b)
<i>Bacillus subtilis</i>	Commercial probiotic	0, 1 × 10 ⁴ , 1 × 10 ⁶ , 1 × 10 ⁸ , and 1 × 10 ¹⁰ CFU kg ⁻¹ diet 60 days	Red sea bream (<i>Pagrus major</i>) 3.99 ± 0.01 g	Hematocrit and hemoglobin values ↑ Nitro blue tetrazolium value ↑ Serum bactericidal activity ↑ Serum lysozyme activity ↑ Serum peroxidase activity ↑ Catalase activity ↑	(Zaineldin et al. 2018)
<i>B. subtilis</i> and <i>B. licheniformis</i>	Commercial probiotic	0.6 g/kg 84 days	Turbots (<i>Scophthalmus maximus</i>) 95.8 ± 17.7 g	Plasma lysozyme activity → Neutrophil reactive oxygen species (ROS) → Production, and total plasma protein levels → Plasma glucose and triglyceride ↑ Glucose levels ↑ Cortisol levels ↓	(Fuchs et al. 2017)

(continued)

Table 1.2 (continued)

Species	Source	Doses and duration	Fish species	Parameters investigated	References
<i>Bacillus</i> sp. SJ-10 plus β -glucooligosaccharides	Identified from traditional Korean fermented fish	0; 1×10^8 CFU g ⁻¹ BSJ-10; 0.1% BGO, and 1×10^8 CFU g ⁻¹ BSJ-10 + 0.1% BGO. 8 weeks	Olive flounder (<i>Paralichthys olivaceus</i>) 10 \pm 0.25 g	Respiratory burst activity \uparrow Superoxide dismutase \uparrow Lysozyme activity \uparrow Expression of interleukin (IL)-1 β \uparrow Tumor necrosis factor (TNF)- α \uparrow	(Hasan et al. 2018)
<i>Bacillus amyloliquefaciens</i> R8		0 and 92×10^6 CFU g ⁻¹ 30 days	Zebrafish (<i>Danio rerio</i>) 0.48 g	Xylanase activity \uparrow mRNA expressions of glycolysis-related genes \uparrow Enzyme activities \uparrow Expression of innate immune-related genes \uparrow Expressions of oxidative stress-related genes \uparrow	(Lin et al. 2019)
<i>Bacillus pumilus</i> SE5		0 and 1.0×10^8 CFU g ⁻¹ 60 days	Groupers (<i>Epinephelus coioides</i>) 14.6 \pm 0.2 g	Phagocytic activity \uparrow Serum complement C3 and IgM levels \uparrow SOD activity \uparrow Expression of TLR2 and pro-inflammatory cytokines \uparrow	(Yan et al. 2016)
<i>Bacillus amyloliquefaciens</i> (GB) and Yarrowia lipolytica lipase 2 (YLL2)	Commercial probiotic	0, 5.0 g/kg GB-9, 4.0 g/kg YLL2, and 5.0 g/kg GB-9 + 4.0 g/kg YLL2 12 weeks	Hybrid sturgeon (<i>Acipenser schrenkii</i> σ and <i>Acipenser baeri</i> ♀) 5.0 g	Skin mucus lysozyme activity \uparrow Leukocytes phagocytosis activity \uparrow Reactive oxygen species level \uparrow Alternative complement pathway activity \uparrow Peroxidase and lysozyme activity \uparrow	(Fei et al. 2018)

<i>Bacillus subtilis</i> and <i>Bacillus cereus toyoi</i>	Commercial probiotic	0, 6×10^3 and 1.5×10^6 CFU g ⁻¹ of diet. 9 and 20 weeks	Rainbow trout (<i>Oncorhynchus mykiss</i>) and brown trout (<i>Salmo trutta</i>) 15.6 g	Plasma lysozyme activity ↑ Alternative complement activity ↑ Peroxidase activity ↑	(Ramos et al. 2017)
<i>Bacillus amyloliquefaciens</i> -JFP2		0 and 1.4×10^6 (CFU/g) of feed 90 days	Rock Bream (<i>Oplegnathus fasciatus</i>) 25.4 ± 0.13 g	Serum antioxidant and lysozyme activity ↑ Triglyceride and total cholesterol ↓ Alanine aminotransferase ↑ Aspartate aminotransferase ↑	(Kim et al. 2017)
BetaPlus® (<i>B. subtilis</i> , <i>B. licheniformis</i> and Isomaltooligosaccharides)	Commercial probiotic	0 and 2 g kg ⁻¹ IMOS + 1 g kg ⁻¹ BetaPlus® in 7 weeks	Caspian Brown Trout (<i>Salmo trutta caspius</i>) 9 g	Immunoglobulin M levels ↑ Alanine aminotransferase activity ↑ Lactate dehydrogenase activity ↑	(Aftabgard et al. 2019)
<i>Bacillus licheniformis</i>	Commercial probiotic	10^3 , 10^5 , and 10^7 CFU/mL 8 weeks	Abalone (<i>Haliotis discus hannai</i> Ino.) 4.17 ± 0.32 g	Blood lymphocytes ↑ Activity of acid phosphatase ↑ Expression level of heat shock protein 70 ↑ Phagocytic activity ↑ Myeloperoxidase and catalase ↑ Expression levels of CAT ↑ Expression of thioredoxin ↑ Superoxide dismutase (SOD) ↑ Respiratory burst of blood lymphocytes ↑ Expression levels of Mn-SOD ↑	(Gao et al. 2018)

1.4.1 Tilapias

Selim and Reda (2015) found that *Bacillus amyloliquefaciens* spores supplementation at concentrations of 1×10^6 (G3) and 1×10^4 (G2) colony-forming units per gram (CFU g^{-1}) of feed significantly enhanced serum killing, serum nitric oxide, serum lysozyme activities, as well as IL-1 and TNF α mRNA levels in the kidneys of Nile tilapia, *O. niloticus*. The cell wall components of both Gram-positive and Gram-negative bacteria are able to stimulate cytokine production (Henderson et al. 1999). Probiotic bacteria colonize in the gut and are involved with the gut-associated lymphoid tissue to stimulate systemic signals that end with cytokine production (Kesarcodi-Watson et al. 2008; Rangavajhyala et al. 1997; Rescigno et al. 2001; Ringø 2011). Similarly, dietary inclusion of *B. subtilis* singularly or *B. subtilis* combined with *S. cerevisiae* and *A. oryzae*; *B. subtilis* with *B. licheniformis*; *B. subtilis* and *Bacillus licheniformis* (BS) combined with traditional Chinese medicine (TCM), and *B. subtilis* with Aqua NZ and AP193 significantly enhanced innate immune response, growth, relative immune, and antioxidant gene expressions of Nile tilapia (Abarike et al. 2018a; Abarike et al. 2018b; Addo et al. 2017a, 2017b; Iwashita et al. 2015; Liu et al. 2017; Wang et al. 2020a). Dietary inclusion of *B. licheniformis* has been found to increase alkaline phosphatase, myeloperoxidase, lysozyme, reactive oxygen species, reactive nitrogen species, superoxide dismutase, and glutathione peroxidase of Mozambique tilapia (*Oreochromis mossambicus*) (Gobi et al. 2018). Also, supplementation of *Bacillus licheniformis* HGA8B significantly improved lysozyme activity and content of complement C3 (Han et al. 2015). It is well documented that, the immune system can be nonspecifically modulated by probiotics (Hoseinifar et al. 2015; Lazado and Caipang 2014; Nayak 2010). Moreover, colony formation and adhesion of probiotics in the intestine of fish are necessary to enhance the immune responses (Ausubel 2005). Interaction between probiotic cells and immune system are through microbe associated molecular patterns (MAMPs) consisting of specific cell wall polysaccharides, peptidoglycan, lipoprotein anchors, and lipoteichoic acids (Hosoi et al. 2003). Cells or components of immune system can interact with MAMPs by pattern recognition receptor such as toll-like receptors, C-type receptor, and nucleotide oligomerization domain-like receptors (Bron et al. 2012; Kleerebezem et al. 2010). This fact may indicate that, addition of fresh culture of *B. licheniformis* to the diet maintains a high level of probiotics in the diet and improve the immune responses in fish. Similar results have been reported in Nile tilapia fed *B. cereus* and *B. pumilus* (Srisapoomee and Areechon 2017; Wang et al. 2017b).

1.4.2 Shrimps

In shrimp, *B. licheniformis* has been intensively applied in Pacific white shrimp (*Litopenaeus vannamei*). Amoah et al. (2019) indicated that dietary inclusion of 1×10^8 CFU g^{-1} feed significantly enhanced activity of lysozyme (LYZ), acid phosphatase (ACP), superoxide dismutase (SOD), total protein (TP), albumin (ALB)

in serum, glutathione peroxidase (GSH-Px) in serum and liver of Nile tilapia. Similarly, dietary administration of *B. licheniformis* significantly upregulated the expression of catalase, glutathione peroxidase, superoxide dismutase (SOD), penaeidin-3a (Pen-3a), and heat shock protein (Hsp-70) genes of Pacific white shrimp, *Litopenaeus vannamei* (Chen et al. 2020a, 2020b). In addition, the combination of *B. licheniformis* with *B. subtilis* significantly enhanced lysozyme and hemocyte cell count and upregulated the expression of proPO, LvToll1 and SOD, Hsp70, and TGase genes (Sadat Hoseini Madani et al. 2018; Sánchez-Ortiz et al. 2016). Likewise, dietary inclusion of *B. subtilis* E20 singularly or combined with other probiotics significantly innate immune response and related immune gene expression of Pacific white shrimp, *Litopenaeus vannamei* (Chien et al. 2020; Won et al. 2020a). Also, Khademzade et al. (2020) reported that dietary inclusion of *Bacillus cereus* and *Pediococcus acidilactici* significantly enhanced total hemocyte count, total protein, and lysozyme activities of *L. vannamei*. Similar results were found in tiger shrimp and freshwater pawn fed *Bacillus* sp. and *Bacillus coagulans* where significant increase in total heterotrophic count, amylolytic, cellulolytic, and proteolytic bacterial counts, phagocytic, lysozyme, and respiratory burst activities was recorded (De et al. 2018; Gupta et al. 2016). At molecular levels, Sánchez-Ortiz et al. (2016) indicated that dietary supplementation of *Bacillus* spp. resulted in upregulation of proPO, LvToll1, SOD genes, except the TGase gene expression. Similarly, Tepasamorndech et al. (2019) revealed that dietary inclusion of *Bacillus aryabhattai* TBRC8450 significantly upregulated C-type lectin, penaeidin-3, and heat shock protein 60 genes, as well as enhanced thioredoxin, ferritin, phenoloxidase, and total antioxidant activities of Pacific white shrimp, *Litopenaeus vannamei*. However, no significant increase in total hemocyte count, and superoxide dismutase were observed (Tepasamorndech et al. 2019).

1.4.3 Carps

In mrigal, *Cirrhinus mrigala*, Bandyopadhyay et al. (2015) indicated that dietary inclusion of *Bacillus* sp. PP9 significantly improved hemoglobin percentage, total erythrocyte count, total leukocyte count, corpuscular hemoglobin, total serum protein, albumin globulin ratio, and serum bactericidal activity. Similarly, dietary supplementation of *B. subtilis* singularly or combined with other *Bacillus* sp. and prebiotics significantly stimulated hematological, antioxidant, and immunological parameters of *Labeo rohita* (Ramesh and Souissi 2018); *Labeo catla*, *Catla catla* (Sangma and Kamilya 2015); common carp, *Cyprinus carpio* (Wang et al. 2017a); grass carp, *Ctenopharyngodon idellus* (Zhao et al. 2020), and Pengze crucian carp, *Carassius auratus* var. Pengze (Cao et al. 2019). At gene level, Yin et al. (2018) found that supplementation of *B. subtilis* resulted in higher protective effects against lead toxicity, superoxide dismutase, catalase and glutathione, lysozyme and IgM levels, as well as immune-related genes of gibel carp, *Carassius auratus gibelio*. Likewise, dietary inclusion of *B. amyloliquefaciens* significantly stimulated innate immune response, antioxidant, and relative immune gene expressions of roho laqueo,

Labeo rohita (Nandi et al. 2018); Indian major carp, *Catla catla* Singh et al. (2017), and grass carp, *Ctenopharyngodon idella* (Qin et al. 2020).

1.4.4 Sea Cucumber (*Apostichopus japonicus*)

Supplementation of *B. cereus* singularly or combined with *B. subtilis* significantly enhanced total coelomocytes count, acid phosphatase, phagocytosis, respiratory burst, total nitric oxide synthase, catalase, phenoloxidase, and superoxide dismutase activities (Li et al. 2015). Recently, Liu et al. (2020) indicated that dietary administration of *B. baekryungensis* significantly enhanced superoxide dismutase, catalase, alkaline phosphatase, acid phosphatase, nitric oxide synthetase, phagocytosis, respiratory burst activities, and ubiquitin-mediated proteolysis pathway. Ubiquitin-mediated proteolysis plays an important role in the dynamic regulation of host defense against pathogen infection. It has been reported that a number of key joint molecules in the natural immune and antiviral signaling pathways can be modified by ubiquitination to regulate the antiviral immune response of the body (Chuang and Ulevitch 2004; Liu and Chen 2011). Ubiquitination plays an important role in the Toll-like receptor (TLR) signaling pathway. The activation of this pathway leads to the upregulated expression of Toll-like receptors and enhances nonspecific immunity (Bhoj and Chen 2009). The upregulation of *TLR* in this study is consistent with the above theory. In the immune system, mTOR signaling plays an important role in maintaining immune homeostasis, for example, the survival and migration of natural immune cells and the secretion of inflammatory factors (Katholnig et al. 2013; Weichhart et al. 2008). Studies have found that the mTOR signaling pathway negatively regulates nonspecific immune responses (Weichhart et al. 2008). Therefore, the downregulation of the mTOR pathway in sea cucumber is beneficial to improve sea cucumber immunity.

1.4.5 Catfish

In striped catfish, *Pangasianodon hypophthalmus*, Truong Thy et al. (2017) reported that dietary inclusion of *B. amyloliquefaciens* and *B. pumilus* significantly enhanced phagocytic, respiratory bursts, and lysozyme activities. Similar results were observed in basa fish, *Pangasius bocourti* fed *B. aeriis* (Meidong et al. 2018). Likewise, combination of *B. subtilis*, *B. amyloliquefaciens*, *B. cereus*, and *B. amyloliquefaciens* (Reda et al. 2018).

1.4.6 Japanese eel

Dietary inclusion of *B. subtilis* and *Lactobacillus plantarum* significantly enhanced lysozyme, superoxide dismutase (SOD), myeloperoxidase (MPO), level of intestine glyceraldehyde-3-phosphate dehydrogenase (GAPDH), heat shock protein 70, 90,

and immunoglobulin (IgM). Similarly, dietary inclusion of *B. subtilis* and mannanoligosaccharide (MOS) significantly improved nonspecific enzymatic activities, heat shock protein 70 mRNA levels, and immunoglobulin M expressions (Lee et al. 2018). More recently, Park et al. (2020) indicated that dietary inclusion of *B. subtilis* or *B. licheniformis* and mannan or fructo oligosaccharide upregulated heat shock protein 70 and immunoglobulin M genes.

1.4.7 Other Species

Dietary inclusion of *B. subtilis* singularly or combined with *B. licheniformis*, *Bacillus cereus toyoi*, and isomaltooligosaccharides significantly stimulated hematological, innate immune response, antioxidant, and gene expression of parrotfish, *Oplegnathus fasciatus* (Liu et al. 2018); red sea bream, *Pagrus major* (Zaineldin et al. 2018); turbot, *Scophthalmus maximus* (Fuchs et al. 2017); rainbow trout, *Oncorhynchus mykiss* and brown trout, *Salmo trutta* (Ramos et al. 2017), and Caspian brown trout, *Salmo trutta caspicus* (Aftabgard et al. 2019). Regarding *B. amyloliquefaciens*, dietary inclusion of *B. amyloliquefaciens* singularly or combined with *Yarrowia lipolytica* lipase 2 (YLL2), *B. licheniformis* significantly enhanced innate immune response, antioxidant, and gene expression of rock bream, *Oplegnathus fasciatus* (Kim et al. 2017); hybrid sturgeon, *Acipenser schrenckii* ♂ and *Acipenser baerii* ♀ (Fei et al. 2018), and zebrafish, *Danio rerio* (Lin et al. 2019).

In juvenile Atlantic salmon (*Salmo salar* L.), Wang et al. (2019a) reported that *B. velezensis* V4 and *Rhodotorula mucilaginosa* compound led to an increase in acid phosphatase, IgM, nitric oxide, glutamic pyruvic transaminase, glutamic oxalacetic transaminase, lysozyme, total superoxide dismutase malondialdehyde, glutathione, glutathione peroxide, total antioxidant capacity, and malondialdehyde. Similarly, dietary inclusion of *Bacillus licheniformis* significantly enhanced hematological, innate immune response, and Mn-SOD gene expression (Gao et al. 2018). Also, significant increase in innate immune response and relative immune gene expressions were observed in grouper, *Epinephelus coioides*, fed *Bacillus pumilus* (Yan et al. 2016) and in olive flounder, *Paralichthys olivaceus*, fed *Bacillus* sp. SJ-10 plus β -glucooligosaccharides (Hasan et al. 2018).

1.5 Conclusion

This chapter addressed the role of *Bacillus* probiotics in sustainable aquaculture. Although a wide range of researches have indicated beneficial effects of *Bacillus* species on grow rate, immunity, and disease resistance of farmed fish and shellfish, the investigated effects were species specific. In order to evaluate in vivo adherence and colonization of *Bacillus* bacteria within the complex microbial ecosystem of the intestine, detection of green fluorescence protein (GFP) tagged strains or fluorescence in situ hybridization (FISH) targeting 16S rRNA to identify the probiotics on

the mucus surface must be carried out. Furthermore, mucus-associated (autochthonous) microbiome must be investigated by next-generation sequencing (NGS), transcriptomic, metagenomics or proteomic profiling, and not the allochthonous microbiome; mostly investigated *per se*. In addition, we recommend that gnotobiotic approaches are used in future studies, as the gnotobiotic approaches have been reported to have important roles to understand the function of gut microbiota on numerous biological processes of the host. Moreover, data is needed to understand the mechanisms by which the immune system of the intestinal mucosa discriminates between pathogenic, probiotics, and commensal microorganisms.

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Immunity and Gut Microbiome: Role of Probiotics and Prebiotics

2

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Abstract

The chapter comprises the role of gut microbiome and beneficial bacteria (probiotic) to boost the overall health. The GI tract is described as the body's largest immune organ. The intestinal microbiota has a vital role in the body's defence system. The most important factor that determines gut health is the microflora or gut flora. Our gut comprises diverse and hundreds of trillion bacteria and it comes in both good, i.e. beneficial bacteria, and bad, i.e. harmful bacteria. So it is mandatory to keep the beneficial bacteria for a better health. Microbes considered to be beneficial usually ferment carbohydrates, do not produce toxins and may have a range of potential benefits for the host. Such microbes include *Bifidobacterium*, *Eubacterium* and *Lactobacillus*. These beneficial bacteria are called probiotic. To get flourish good bacteria in the gut we need to feed it with a proper nutrient called prebiotic. A prebiotic is a special type of soluble non-digestible plant fibres that nourish the beneficial good bacteria in the gut. The synergy of the probiotic and prebiotic components in the gut provides a stable and relatively uniform gut microbiome and thereby boost the gut health and immune system.

Supplementations of prebiotics improve the establishment of microbial community which benefits the overall health. By metabolizing these fibres gastrointestinal tract community produces short-chain fatty acids which elicit many immune pathways and recruit immune cells to the gut. The pattern recognition receptors of immune cells recognize the pathogen-associated molecular pattern and initiate a cascade of immune pathways that ends in production of cytokines or helps in recruiting more immune cells. However, the specialized macrophages

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and neutrophils of gut regulate the overexpression of inflammatory cytokines and help to protect the gut lumen from inflammation.

Keywords

Gut microbiota · Immunomodulation · Probiotics · Prebiotics · Synbiotics · Postbiotics

2.1 Introduction

In human body, the gastrointestinal (GI) tract represents the largest contact area between the body and the external environment. GI tract is the natural habitat of trillions of microflora collectively known as gut microbiota or microflora. Microflora coevolved in a symbiotic relationship with the human intestinal mucosa in such a way that the indigenous microbiota is essential for gut homeostasis. So, the microbiota is considered as ‘Super organisms’ and is an integral part of the GI tract.

The GI tract harbours millions of bacteria which continuously stimulate the immune system both by its own structural component and by the metabolic products. The gut flora elicits not only a local immune response but also systemic response, thereby affecting whole body. Use of microorganisms that can contribute to a healthy gut, the probiotics, is common nowadays. The micro organisms inhabiting the gut environment act as immune eliciting agents and also their metabolites. Both cell-mediated and humoral immune systems get upregulated. But the gut immune system has a capacity to regulate the immune response to commensal bacteria.

Nutrients also affect gut immunity, and strategies that restore a healthy gut microbial community by affecting the microbial composition are being developed as new therapeutic approaches to treat several inflammatory diseases. The use of probiotics and prebiotics is a promising strategy for the reduction and prevention of GI infections. One of the main differences between probiotics and prebiotics is that probiotics are viable food supplements whereas prebiotics are nonviable food component. Prebiotics are non-digestible oligosaccharides, remain intact through the digestive system, and act as nutrients for already established microflora. These are oligosaccharide that overcomes several limitations of introducing probiotic bacteria into the GI tract. Therefore, using prebiotics is possibly a more practical and efficient way to manipulate the gut microflora. Prebiotics are defined as functional components of food which are metabolized by particular commensal bacteria in the gut conferring various health benefits to the host. Prebiotics reach the large intestine without changing their chemical and structural properties. Prebiotics are capable to escape the digestive processes in the upper part of the gut due to their molecular and structural composition, which makes them essentially resistant to our digestive enzymes.

Most of the studies about prebiotics have been focused on fructans, such as inulin, fructo- oligosaccharides (FOS) and galacto-oligosaccharides (GOS). They are also valuable functional ingredients for the food industry with the potential to improve

the sensory properties of food. Other important prebiotics include lactulose, Xylooligosaccharides (XOS) and Mannan-oligosaccharides (MOS). These prebiotics stimulate the growth of bacteria in the colon, where lactobacilli and bifidobacteria are respectively preferred. As a product of the beneficial fermentation, short-chain fatty acid (SCFA) are produced, mainly the butyrate. The most studied SCFA is butyrate. Butyrate is the major energy source of colonic epithelial cells that affect the proliferation and barrier function of the colonic epithelium and reduce DNA damage. Other roles of prebiotics include reducing the level of cholesterol, reducing constipation, stimulating immune system, reduction of antibiotic-associated diarrhoea, reduction in inflammation and symptoms associated with inflammatory bowel disease, protective effects for prevention of colon cancer, and increasing the uptake of minerals, including calcium, magnesium iron, etc.

Numerous studies prove that a number of mechanisms mediating the health benefits of beneficial bacterial cells require viability. However, recent evidence suggests that bacterial viability is not necessary to attain the health-promoting activity. The newest member of biotic family (including probiotic, prebiotic, synbiotic, postbiotic,), the postbiotics also known as metabiotics, or simply metabolites, can confer health promotion in the host. The cell-free supernatants (CFS) refer to soluble factors (products or metabolic by products) secreted by live bacteria or released after bacterial lysis. These by-products offer physiological benefits to the host by providing additional bioactivity. Such soluble factors have been collected from different bacterial strains; examples include SCFAs, enzymes, peptides, teichoic acids, peptidoglycan-derived muropeptides, endo and exopolysaccharides, cell surface proteins, vitamins, plasmalogens, and organic acids.

Synbiotics refer to nutritional supplements combining probiotics and prebiotic food ingredients and in a form of synergism that improves the survival and implantation of live microbial dietary supplements in the GI tract, either by stimulating growth or by metabolically activating the health-promoting bacteria. Synbiotics products offer the potential to develop prebiotics targeted at specific probiotic strains to optimize health benefits.

This chapter mainly focused on the effects of dietary components, commensal bacteria and their metabolites in host immune system.

2.2 An Introduction to Gut Microbiome

The human GI tract harbours very complex population of microorganisms collectively called the gut microbiome that influences the host metabolism, homeostasis and pathogenesis. The gut microbiota has evolved with host and forms a mutually beneficial relationship and their number has been estimated to exceed 10^{14} (Cani et al. 2008). The colonization of gut is generally believed to begin from birth onwards and the members colonized immediately depend on the mode of delivery. Vaginally delivered infants harbour abundant Lactobacilli and Bifidobacteria during the first few days which is an indication of its abundance in vagina (Aagaard et al.

2012; Dominguez-Bello et al. 2010) while infants of caesarean session harbour *Clostridium* sp. The gut of a healthy adult is predominantly constituted by phylum Firmicutes and Bacteroidetes followed by Actinobacteria and Verrucomicrobia. Gut microbiota exhibits great variation in their distribution throughout the GI tract (Ramakrishna 2007). Streptococcus is the dominant genus in the oesophagus, duodenum and jejunum. In addition to Streptococcus, Prevotella, Veillonella and Rothia inhabit the stomach. A few number of *Helicobacter pylori* is also seen as a commensal in stomach. Besides Firmicutes and Bacteroidetes, human colon also inhabits pathogens like Salmonella, Vibrio, *E. coli* and camphylobacter but constitutes less than 0.1% of the entire gut microbiome. The intestinal microbiota exhibits an axial difference from intestinal lumen to mucosal surface. Bifidobacterium, Enterobacteriaceae, Enterococcus, Clostridium, Lactobacillus, Ruminococcus, Streptococcus and Bacteroides predominate in the lumen while Lactobacillus, Enterococcus, Clostridium and Akkermansia predominate in mucosal layer (Jandhyala et al. 2015). Age, diet, antibiotic consumption, host genetics, and life events are some of the factors which alter the normal gut microbiota.

2.3 Gut Immune System

Gut is the primary interface between the environment and immune system. It is important that the gut immune system must eliminate invading pathogens and simultaneously maintain self-tolerance to avoid autoimmunity. The homeostasis between the two is essential to maintain host health (Chassaing et al. 2014).

2.3.1 Immune Barriers in the Gut

Gut interacts with all other organs and it is the connection link between external environment and internal organs. Many microorganisms including pathogens and food antigens are ingested along with food. It is the gut which determines what needed and what not. The gut plays a major role in preventing the pathogens. At the same time the immune systems get boosted. The lining of the gut, mucus itself is a barrier and it is the first line of defence against pathogens and antigens throughout the gut. But in *Helicobacter pylori* infection, gastric neoplasia, colorectal polyps and cancer, the composition of mucin has altered (Jass and Walsh 2001). The next line of physical barrier is the gastrointestinal epithelium. It is primarily composed of enterocytes which selectively transport nutrients, electrolytes and water to underlying cells by various pumps and thereby eliminating the antigens entering into immune system (Chassaing et al. 2014). Beyond a physical barrier, intestinal epithelial cells (IEC) secrete cytokines and chemokines which regulate chemotaxis of both innate and adaptive immune cells. Neutrophils are recruited to the gut by epithelia derived chemokine IL-8 and epithelial neutrophil attractant 78. The monocyte chemotactic protein (MCP 1), RANTES/CC L5 and macrophage inflammatory protein (MIP1 α) regulate the chemotaxis of monocytes. T cells are recruited by

interferon inducible protein (IP-10) and interferon γ . IEC also secretes proinflammatory cytokines TNF- α and IL-6, nitric oxide synthase, cyclooxygenase and reactive oxygen species (ROS). Another structural component is Paneth cells which contain defensin-rich granules (defensin 5 and 6) and can regulate composition and number of microbes. They also secrete antibacterial peptides like lysozyme and secretory phospholipase A2. The microfold cells or M cells in the epithelium are the main site of invasion of pathogens and normal microbiota. The main function of M cells is antigen sampling that is the uptake of antigen and microorganisms and presentation to lymphoid follicle. Hence they are also the site of immunological functions. Intestinal macrophages play an important role in gut immune homeostasis. They do not respond to TLR ligand and secrete proinflammatory cytokines or generate ROS or nitric oxide. But they express high levels of CD 36 which facilitates phagocytosis and apoptosis. Intestinal macrophages differ from other tissue macrophages in its property of “inflammation anergy” in which macrophage maintains the overexpression of proinflammatory cytokines to normal flora (Smythies et al. 2005). Intestinal dendritic cells are also distinguishable from other tissues. They also maintain a tolerogenic immune response by decreased expression of pattern recognition receptors, increased levels of anti-inflammatory cytokine IL-10, low level of antigen presentation by reducing co-stimulatory molecules, and favouring differentiation of Treg and IgA secreting B cells (Coombes and Powrie 2009). Secretory IgA gives protection against *Vibrio cholera*, Salmonella, rotavirus, and *Escherichia coli*. Another obstacle to activation of gut immune system is the controlled activation of pattern recognition receptors (PRR). TLR-2 (Toll like receptor 2) and TLR-4, specific for bacterial peptidoglycan and lipopolysaccharide (LPS), respectively, are abundant in IEC when they are migrating to the surface epithelium but are barely expressed once they reach the surface. Moreover, the cofactors for TLR 4 activation, LPS binding protein, CD 14, and myeloid differentiating factor are also limited in the intestine. Likewise, TLR 5, specific for flagellin is expressed only on the basolateral side to respond only if invaded by flagellated microorganisms (Vamadevan et al. 2010; Carvalho et al. 2012). In addition to all the microbial metabolites especially short-chain fatty acids produced by gut microbes play a vital role in intestinal immunity by regulating Treg cells (Smith et al. 2013).

2.4 Gut Microbiota and Immunity

The gut microbial community can regulate local as well as systemic immune responses. As the gut contains commensal and beneficial bacteria as well as opportunistic pathogens, the immune system always maintains a balance that will not disturb the beneficial bacteria, but when there is any increase in pathogens or antigens it will act immediately to eliminate the effect. The normal flora of the gut has a profound role in shaping the immune system. Its effect not only confines to gut but also to other organs.

2.4.1 Gut-Associated Lymphoid Tissue (GALT) Development

The role of microbiota in GALT development was evident from studies in germ-free (GF) mice. GALT includes Peyer's patches, crypt patches and isolated lymphoid follicle (ILF). Microbial stimulation is required for the development of these tissues. It was observed that the maturation of ILF was incomplete in mice deficient of PRRs like TLR2, TLR3, NOD2 (nucleotide binding oligomerization domain 2) and MyD88 (myeloid differentiation primary response protein 88) suggesting the role of microbial stimulation for proper development of an immune system (Hendricks et al. 2014).

2.4.2 Modulation of Innate Immune Cells

As mentioned earlier, antigen-presenting cells (APCs) of gut have co-evolved with gut microbiota and develop the ability to protect from invading pathogens but maintaining tolerance to normal flora. The dendritic cells (DCs) of Peyer's patches produce high levels of anti-inflammatory cytokine IL-10 when compared to splenic dendritic cells (Iwasaki and Kelsall 1999). Likewise, the intestinal macrophages developed the inflammation synergy, the non-inflammatory profile. However, experiments in GF animal showed a reduction in the number of intestinal dendritic cells but colonization with *E. coli* was sufficient for recruiting DCs to intestine. Similarly, macrophage activity was reduced in GF mice and major histocompatibility complex class II was also absent (Mikkelsen et al. 2004). The gut flora influences the neutrophil activity also. The peripheral blood neutrophils of GF rats exhibited decreased phagocytic activity and impaired generation of free radicals (Ohkubo et al. 1999). The role of gut microbes in systemic immune system is evident from the enhanced activity of bone marrow neutrophils when cytosolic receptor–nucleotide oligomerization domain 1 (NOD 1) gets activated by peptidoglycans of gut microbiota (Clarke et al. 2010). Overall for the complete maturation and activation of phagocytic cells microbial stimulation is required either the whole organism or the structural components (antigens). Natural killer (NK) cells produce IFN γ and perforins to eliminate damaged and infected cells. But the specialized NK cells, NKp46⁺ of intestine is limited in its production; instead they express IL-22 and the nuclear hormone receptor retinoic acid receptor-related orphan receptor gamma t (ROR γ t). The absence of this NKp46⁺ in GF mice explains the role of microbes in gut for its development (Yan and Polk 2002). Mice lacking IL-22 producing NKp46⁺ cells were susceptible to pathogenic infection. An important immune barrier in gut is IECs. They produce various antimicrobials among which defensins and cathelicidins are important. There are two types of defensins, alpha and beta. Human β -defensin 1, 2, and 3 and mice β -defensin 2/3 can regulate the chemotaxis of immature DCs and memory T cells. Human β -defensin 3 enhances the expression of co-stimulatory factors CD 40, CD 80 and CD 86 on monocyte and myeloid DCs. The major function of cathelicidins is antibacterial activity. It shows broad activity towards gram positive and gram negative bacteria. Other antimicrobials secreted by

IECs include antimicrobial C-type lectins, angiogenin 4, phospholipase A2 type IIA and lysozyme C (Muniz et al. 2012). But in GF mice a lower cell proliferation and expression of genes for these antimicrobial was observed (Reikvam et al. 2011).

2.4.3 Modulation of Adaptive Immune System

CD4⁺ cells are the most important component of adaptive immune system. Upon stimulation by microbiota CD4⁺ cells in Lamina propria (LP) differentiates into its subtype Th1, Th2, Th17 and Treg cells. In GF mice there is a decrease in CD4⁺ cells of LP and defects in spleen and mesenteric lymph nodes were observed. The polysaccharide A of *Bacteroides fragilis* induces a Th1 systemic response and also suppresses Th17 response by signalling through TLR 2 on Treg cells. Conversely, segmented filamentous bacteria induce LP Th17 cell response (Macpherson et al. 2002). Similarly, CD8⁺ cells, commonly seen in intraepithelial compartment of gut, are also minimal in GF mice indicating the critical role of microbial stimulation for maintaining CD8⁺ population. Gut microbiota also stimulates the cytolytic activity of $\gamma\delta$ T cells, the connecting link between innate and adaptive immunity and their number is very high in intestine compared to lymph node and spleen. Peyer's patches are rich in IgA secreting plasma cells but are considerably low in GF mice. To induce IgA production in GF mice a large dose of bacteria approximately 10⁹ CFU/ml was required (Hapfelmeier et al. 2010).

2.5 Communication of Gut Microbiota to Other Organs

Gut microbiota communicates to other organs mainly through metabolic, endocrine, autonomous nervous system and immune pathways. Bacterial fermentation in intestine produces many metabolites. Fermentation of dietary fibres produces many SCFA like acetate, propionate, butyrate, etc. SCFAs have profound role in many signalling pathways. The GALT comprises 70% of the body's immune system and can be considered as the largest immune organ of the body. Enterohormones, metabolites, immune cells and cytokines derived from this complex mucosal and submucosal network have systemic impacts on other organs such as the kidney, cardiovascular system, bone marrow and brain via the circulation (Yang et al. 2018). Here we mainly discuss on the immune axis between gut microbiota and other organs (Fig. 2.1).

The gut lung axis is bidirectional. The metabolites produced by gut microbes enter the blood stream and reach the lungs, and the immune factors from lungs also elicit an immune response in gut. The immune cells induced by antigens move through the lymphatic system between gut and lungs and thereby elicit immune response in both organs. Kalliomäki et al. (2001) showed that reduction in *Bifidobacteria* and increase in *Clostridia* in gut are associated with asthma. Respiratory tract infection by influenza virus reduces *Lactobacilli* and *Lactococci* and increases *Enterobacteriaceae*. A study in Canadian children whom at the risk of

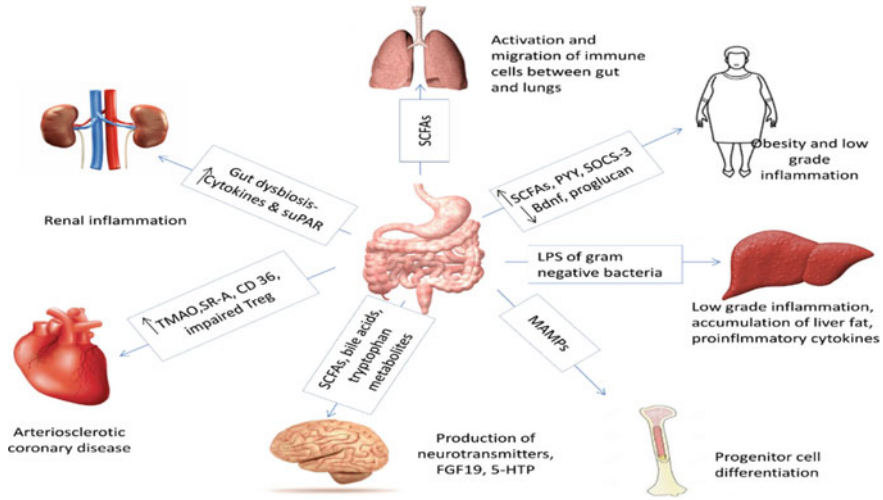


Fig. 2.1 Communication of gut to other systems. Microbial products or microbially derived host metabolites exerts effect on different organs in different ways

asthma showed decreased number of *Veillonella*, *Rothia*, *Lachnospira* and *Faecalibacteria* (Arrieta et al. 2015). The gut microbiota not only modulates gut immune system but also immune progenitor cells in bone marrow. Renal dysfunctions have been seen in patients receiving bone marrow transplants which indicate the role of bone marrow in kidney inflammation. In the immune pathway, immune cells originating from the bone marrow encounter dysbiotic microbiota and become overactivated within the intestine. Inflammatory cells, cytokines and soluble urokinase plasminogen activator surface receptor (suPAR) generated in the gut contribute to renal inflammation via the circulation (Hingorani et al. 2007; Hahm et al. 2017).

Nutrients and bacterial components reach liver by portal circulation. LPS of gram negative bacteria circulating through blood triggers low-grade inflammation by TLR signalling. Besides, they also enhance accumulation of liver fat but this is not evident in mice lacking LPS receptor CD14/TLR4 (Cani et al. 2008). Duparc et al. (2017) demonstrated that a deletion of Myd88 in hepatic cells affects gut microbiota. Administration of *Bifidobacterium longum* plus inulin type fructans significantly reduces inflammatory markers (TNF- α and C-reactive proteins), Steatosis and non-alcoholic steatohepatitis index (Malaguamnera et al. 2012). In alcoholic liver disease, gut permeability increased due to disruption of tight junction by alcohol and aldehyde causes the entry of LPS, endotoxin and bacterial DNA into circulation and thereby enters liver. As a result, the Kupffer cells in liver produces proinflammatory cytokines through TLR4 or TLR9 (Yoon-Seok and Ekihiro 2013).

Gut microbiome also improves cardiovascular diseases. The accumulation of foam cells in subendothelium constitutes the first step in arteriosclerosis. The gut microbiome derived trimethylamine N-oxide (TMAO) increases the expression of

the receptor SR-A and CD 36 which can ultimately lead to the formation of foam cells. TMAO can also activate NLRP3 inflammasome (Wright et al. 2000; Duewell et al. 2012). Also impaired Treg cell increases the incidence of arteriosclerosis (Duewell et al. 2012). The gut invasion by probiotic can prevent arteriosclerotic coronary diseases.

A comparative study in GF and conventionally raised mice showed that conventionally raised mice with gut colonization were prone to become obese than GF mice when consumed with high carbohydrate high fat diet. The proposed mechanism is that the SCFAs produced by gut bacteria binds with GPR41 (G-protein coupled receptor) and GPR43 (FFAR3 and FFAR2) and promotes nutrient uptake and adipose tissue development. GPR41 also induces the secretion of pancreatic peptide YY (PYY) which increases the transit time. As the transit time increases, more nutrients will be absorbed, mainly glucose, which also contributes to obesity (Samuel et al. 2008). A similar study by Schéle et al. (2013) also showed weight gain in conventionally raised mice. They showed a reduced expression of two genes for antiobesity peptide, brain derived neurotrophic factor (Bdnf) and proglucagon (precursor of glucagon like peptide 1, GLP-1). In the presence of gut microbiota, leptin signalling inhibitor SOCS-3 was upregulated, thereby reducing the sensitivity to leptin. Since the leptin signal was not received by hypothalamus, mice became obese. Leptin is a neurohormone which is secreted by adipocytes. Its level is proportional to fat mass. As the size of adipocytes increases, more leptin is secreted. Leptin has proinflammatory properties and upregulates TNF- α , IL-16 and IL-12. This might be a reason of low-grade inflammation in obese persons. Leptin is also involved in innate and adaptive immunity. It significantly increases CD4⁺ and CD8⁺ cells and is also involved in DC maturation, proliferation of monocytes, neutrophil chemotaxis, reactive oxygen species generation, NK cell proliferation and activation of various pathways (IRS-1, PI3k/Akt, NF-kB and STAT-3) for production of interleukins (Naylor and Petri Jr 2016).

Gut microbiota communicates to the brain directly or indirectly through microbe-derived products. The gut brain axis involves neural, immune and endocrine pathways. The metabolic products of gut bacteria interact with ganglionated plexus of enteric nervous system and aids in peristalsis. Inflammation of GI tract increases anxiety like response and anorexia. It is clear that dysbiosis of the gut causes such behavioural changes. The gut microbe modulates CNS by neuroimmune and neuroendocrine pathways through metabolites like SCFA, bile acids and tryptophan metabolites. In addition, the microbiota produce or can stimulate the production of γ -aminobutyric acid, norepinephrine, dopamine and serotonin. The bile acids induce the production of fibroblast growth factor (FGF19), enter the circulation and cross blood brain barrier, and activate arcuate nucleus of hypothalamus which regulates glucose and energy metabolism (Tomlinson et al. 2002). Gut microbes contribute to the development and function of microglial cells in CNS. Defective and compromised glial cells found in GF mice can be normalized by SCFA supplementation or colonization with microbes (Erny et al. 2015). SCFAs also aid in the release of norepinephrine by activation of GPR 41 (Kimura et al. 2011). Serotonin (5-hydroxytryptamine, 5-HTP) is an important neurotransmitter which has immune

functions also. Above 90% of body's 5-HTP is present in enterochromaffin cells of intestine. The indigenous spore-forming bacteria of gut, *Clostridium* sp. promotes the biosynthesis. The SCFA produced by fermentation induces TPH1 gene expression and leads to the utilization of tryptophan for 5-HTP. It regulates cytokine secretion in macrophages and monocytes and reduces the level of TNF- α , IL-1 β and also neutrophil recruitment to the inflammation site and T cell activation (Yano et al. 2015).

2.6 Probiotics in Immunomodulation

The composition of gut microbiota may vary with age, clinical status, diet, mental stress, antibiotic consumption, etc. Thus, a dysbiosis of gut leads to impaired immune system which ultimately leads to inflammatory bowel disease (IBD) and polyps in gut. The scope of probiotics lies here. Probiotics are live microorganisms which when administered in adequate amounts confer a health benefit to the host (FAO/WHO 2001). The use of microorganisms for improving health was first appeared in the book of Ilya Ilyich Metchnikof in early twentieth century. Now probiotics are available in many fermented dairy and non-dairy products as well as capsules and probiotic drinks. Health benefits of probiotics are numerous. It can be exploited for all gut-related problems as evident from recent studies. Antipathogenicity, immunomodulation and anticancer effects of probiotics are the major research areas. Probiotics exert their beneficial effects through their metabolites, competitive exclusion of pathogens and by boosting innate and adaptive immunity of the host.

Most extensively studied organisms in immunomodulation are *Lactobacillus* and *Bifidobacteria*, the classic probiotics. The commercial strain *Lactobacillus rhamnosus* GG can be used to treat inflammatory bowel disease (IBD) since it showed equal effect as that of mesalazine, the drug for IBD (Zocco et al. 2006), and also exhibits anti-apoptotic property by activating Akt/protein kinase B. *Lactobacillus casei* can induce IL-12 production by TLR-2, TLR-4 or TLR-9 deficient macrophage but not by MyD88 deficient macrophage (Ichikawa et al. 2007). Another Strain, *L. casei* DN114001, downregulates TNF- α production by inflamed mucosa in Crohn's disease (CD) patients (Borrueal et al. 2001). Dietary supplementation of *L. rhamnosus* HN001 and *L. casei* Shirota enhances the number and cytolytic activity of NK cells in the peripheral blood in adults (Dong et al. 2010; Gill et al. 2001). The mutant strain of *L. acidophilus* NCK2025 lacking normal lipoteichoic acid lowers the level of IL-12 and TNF α but enhanced IL-10 in DCs than its wild type (Gill et al. 2001). Administration of *B. lactis*, *L. rhamnosus* and *B. breve* can upregulate Treg cells, thereby reducing allergic response (Sagar et al. 2014).

An improvement in lung cancer was observed when *Enterococcus hirae* and *Barnesiella intestinihominis* were given along with chemotherapeutics (Daillère et al. 2016). The colon cancer cell lines CaCO-2 and HT-29 secrete IL-8 when stimulated by TNF- α . But pretreatment of CaCO-2 by *L. rhamnosus* GG reduces the

level of IL-8 and inhibited the secretion of IL-8 in HT-29 when treated with *Bifidobacterium* genomic DNA. Clinical trials in humans proved the efficiency of various probiotics in IBD treatment. Administration of probiotic tablet VSL#3 (consisting of *L. plantarum*, *L. delbrueckii* subsp. *bulgaricus*, *L. casei*, *L. acidophilus*, *Bifidobacterium breve*, *B. longum*, *B. infantis*, and *Streptococcus salivarius* subsp. *thermophilus*) for 9 months reduced the relapse rate of pouchitis. Similarly, fermented milk containing *Bifidobacterium* improves ulcerative colitis (Gionchetti et al. 2000). Oral administration of a combination of *Lactobacillus helveticus* R0052 and *Bifidobacterium longum* R0175 for a period of one month has been reported to improve depression, anxiety, and lower the level of the stress hormone cortisol in humans (Messaoudi et al. 2011). A three-week consumption of a probiotic-containing milk drink that contained *Lactobacillus casei* Shirota showed improved mood in healthy volunteers (Benton et al. 2007).

The commensals as well as probiotics have profound effect on the overall homeostasis of the body. The survivability of these beneficial organisms in gut can be increased by administration of additional substances called prebiotics.

2.7 Prebiotics

The human gastrointestinal microbiota is one of the most densely populated microbial communities that provide metabolic, immunological and protective functions that play an important role in human health (Jumpertz et al. 2011; Goldsmith and Sartor 2014; Wang et al. 2011). Genetics, host physiology (Age of host, diseases, stress, etc.), and environmental factors including living conditions and use of medications are the number of factors influenced by the gastrointestinal microbiota (Wang et al. 2011; Greenblum et al. 2012; Wang et al. 2012a; Goodrich et al. 2014). However, the key environmental factor is a diet that mediates the composition and metabolic function of the gastrointestinal microbiota. Actually, the consumption of specific dietary ingredients, fibre and prebiotics is an important strategy that stimulates the functions of gut microbiota. Some dietary fibres can also be classified as prebiotics. Prebiotics are widely defined as a food ingredient that is composed of oligosaccharides, that are non-digestible by the host and has a beneficial effect on host health through selective stimulation of the growth and activity of specific members of the gut microbiota (Vieira et al. 2013). These types of food supplements have innumerable and composite effects on the intestinal microbiota and gut immune system. The US recommended daily fibre intake is 25–38 g but only an average of 15 g is consumed (American Dietetic Association), recommending dietary prebiotics could positively influence total fibre intake.

The major source of prebiotics is dietary fibre. They occur naturally in fruits and vegetables including chicory root, Jerusalem Artichokes, Raw dandelion Greens, Garlic, Leeks, Onion, Asparagus, Wheat Bran, Banana, Barley, Oats, Apple, Konjac root, Cocoa, Burdock root, Flaxseeds, Yacon root, Jicama root, sea weeds, etc. But they are present in the form of nutritional supplements for maximum health benefits. Prebiotics are also found in human milk, cow's milk, and yoghurt in the form of

galactooligosaccharides. The most important prebiotic, inulin, is generally found in plants, bacteria and some fungi. It is known in more than 36,000 fruits and vegetables (Chicory, Banana, Onion, etc.). Soybean oligosaccharides (SOS) are another type of naturally occurring oligosaccharides present in soybean, which consist of raffinose and stachyose.

Another major naturally occurring prebiotics is acacia gum. More than 20 studies have been performed since the late 1970s to understand the relationships between acacia gum and the colonic microflora. It is a soluble dietary fibre obtained from the stems and branches of *Acacia Senegal* and *Acacia seyal*. It is composed mainly of complex polysaccharides (95%) that consist of highly branched galactan polymers, with galactose and/or arabinose side chains, possibly terminated by rhamnose or glucuronic acid residues (Cherbut et al. 2003b). It is present in different names including gum Arabic, Gum Hashab, Kordofanian gum and Acacia gum. 80% above production is used by the food industry for various applications such as food additives, emulsification, encapsulation, coating, gum candies, thickener, demulcent, suspension agent, and foam stabilizer in cosmetics, bath and body products, and other skincare applications, etc. Gum is traditionally consumed by African and Indian population to improve digestive comfort and intestinal transit. Acacia gum induces bifidogenic effect, specific stimulation of SCFAs production and high gut tolerance. Guar gum, in its intact state, is a gel-forming galactomannan made from the endosperm of the plant *Cyamopsis tetragonolobus*, and is composed primarily of high molecular weight polysaccharides ([1,4]-linked β -D-mannopyranosyl units with [1,6]-linked α -D-galactopyranosyl side-chain residues (Kolida et al. 2000). Guar is commonly used in dairy, bakery, cereal and meat products.

Besides a range of naturally occurring prebiotics, there are synthetic prebiotics including Lactosucrose (LS) produced by combining lactose and sucrose using β -fructofuranosidase, Lactulose produced from lactose (it is not hydrolysed and absorbed in the small intestine), and Isomaltooligosaccharide (IMO) produced from starch (it can be digested in the small intestine) (Mudgil et al. 2014). Glucooligosaccharides are synthesized with glucosyl transferase, which is produced by *Leuconostoc mesenteroides* or may be extracted from β -glucan of oak tree. XOS can be hydrolysed by Bifidobacteria and Lactobacilli are found to be more effective than FOS in increasing the population of the probiotics and in decreasing the number in harmful bacteria.

Prebiotics provide nutrition to the host, inhibit the growth of potential pathogens and promote beneficial microbiota. The latter causes fermentation of non-digestible fibres, saves energy, synthesizes vitamin B and K, produces SCFA and polyamines, leads to improvement in gastrointestinal motility and function, reduces the level of cholesterol and stimulates the immune system. Other benefits of prebiotic consumption include reduction in the prevalence and duration of infectious and antibiotic-associated diarrhoea, reduction in inflammation and symptoms associated with inflammatory bowel disease, protective effects for prevention of colon cancer, enhancement of the bioavailability and uptake of minerals, including calcium, magnesium and possibly iron, lowering some risk factors for cardiovascular

diseases, promotion of satiety and weight loss and prevention of obesity, reduced constipation and gas formation, etc. (Tomar et al. 2015).

2.7.1 Role of Prebiotics in Gut Immunity

Non-digestible carbohydrates of plant origin are the main substrates of gut microflora and include resistant starch as well as non-starch polysaccharides such as cellulose, hemicellulose, pectin and inulin which are referred to as dietary fibre. But breakdown of dietary fibres is different, based on the matrix and the type of polysaccharides present. Mucus, slough epithelial cells, lysed bacteria, etc. are the other principal substrates of the gut microflora. These substrates provide carbon and energy for growth of the gut microorganisms.

The bacterial metabolism in the human colon is primarily anaerobic, because more than 99% of the bacteria encountered in an adult's faecal flora are strict anaerobes (Moore and Holdeman 1974). The available substrates are broken down to the SCFAs acetate, propionate, butyrate and the gases hydrogen (H₂) and carbon dioxide (CO₂). Formate, Valerate and Caproate are formed in small amounts only. Lactate, ethanol and succinate are intermediate which are also converted to SCFAs. The most studied SCFAs is butyrate. The major energy source of colonic epithelial cells is butyrate that affects the proliferation and barrier function of the colonic epithelium and reduces oxidative DNA damage (Gibson et al. 1999; Wang et al. 2012b). This energy source is transported into cells via monocarboxylated transporters, such as MCT-1107 (Ritzhaupt et al. 1998). Butyrates modulate the immune system in different ways. Initial studies using primary human leukocytes found that butyrate inhibits IL-12 production by *S. aureus* stimulated human monocytes (Säemann et al. 2000). The same study also found that in anti-CD3 stimulated monocytes, butyrate enhanced IL-10 and IL-4 secretion, but inhibited IL-2 and IFN- γ release, presenting an anti-inflammatory profile for butyrate. Other in vitro studies have found that butyrate inhibits vascular cell adhesion molecule (VCAM-1)-mediated leukocyte adhesion to endothelial cells (Menzel et al. 2004). Ex vivo studies in mice found that butyrate suppresses colonic immune activation through Fas-mediated apoptosis of T cells through histone deacetylase (HDAC) 1-dependent Fas upregulation. This work also provided evidence that butyrate inhibits IFN- γ -mediated inflammatory signalling, particularly through STAT1 and iNOS, and that loss of butyrate signalling induces increased expression of inflammatory genes in mice (Zimmerman et al. 2012). Other in vitro findings demonstrate that butyrate inhibits the IFN- α /STAT1 axis (Klampfer et al. 2003), which is important because enhanced activation of STAT1 occurs in CD patients (Schreiber et al. 2002). Human ex vivo studies found that butyrate was able to decrease pro-inflammatory cytokine (TNF- β , IL-1b, IL-6) mRNA expression as well as TNF secretion in intestinal biopsies and peripheral blood mononuclear cells of CD patients, through inhibition of NF κ B (Segain et al. 2000).

Acetate is the second most abundant short-chain fatty acids in the colon. Many researchers reported the anti-inflammatory effects of acetate on the inflammatory

response (Maslowski et al. 2009; Kim et al. 2013; Smith et al. 2013), but most studies mainly focused on butyrate. The receptors GPR41 (Ffar1), GPR109A and GPR43 (Ffar2) were identified as receptors of butyrate, propionate and acetate, respectively (Brown et al. 2003). GPR41 is primarily expressed by adipose tissue and is also present at very low levels in peripheral blood mononuclear cells (PBMCs). GPR43 expression is entirely related to the immune system and is particularly high on polymorph nuclear cells (eosinophils and neutrophils). Maslowski et al. (2009) showed that mice that lack the Gpr43 gene have increased inflammation and a poor ability to resolve inflammation because their immune cells cannot bind to SCFAs. Hence they were more susceptible to IBD. However, the effect of activation of acetate/Gpr43 helps to increase the clinical and inflammatory response in experimental mice. Intestinal bacteria are useful in the elevation of human health, but certain components of microflora in genetically susceptible individuals contribute to various pathological disorders, including inflammatory bowel disease (IBD). A change in gut microbiota composition is considered as one of many factors involved in the pathogenesis of either inflammatory bowel disease or irritable bowel syndrome. For these reasons, the use of prebiotics in IBD such as Crohn's disease, ulcerative colitis and pouchitis is very important because they restore the balance of GI microflora, reducing and preventing intestinal inflammation (Cherbut et al. 2003a; Schultz et al. 2004; Furrle et al. 2005; Kelly et al. 2005). These diseases are characterized by persistent mucosal inflammation at different levels of the GIT (Guarner 2007). In the GIT, the inflammatory capacity of commensal bacteria varies because some bacteria are pro-inflammatory, whereas others attenuate inflammatory responses.

Prebiotics fermentation in large intestine also produces propionate that shows anti-inflammatory effects with respect to colon cancer (Makivuokko et al. 2009). Acetate is largely produced in the colon but reaches a high concentration in the blood, so we could observe systemic anti-inflammatory effects of this SCFA in other diseases, such as asthma and arthritis and also decrease in the luminal pH. A low pH can stimulate the growth of Lactobacilli and Bifidobacteria which are adapted to low pH. While a low pH suppresses growth of harmful bacteria. SCFAs may play an important role for the optimal functioning of the colonic epithelium and the absorption of various cations including Ca^{2+} , Mg^{2+} and Fe^{2+} .

Recent study investigated the effects of prebiotic oligosaccharide on microbiota composition and immune function (NK cells, phagocytosis and cytokines) in healthy elderly volunteers. The study also found significant positive effect on immune response, evidenced by an improvement in NK cell activity and phagocytosis, increased secretion of the anti-inflammatory cytokines, IL-10, and decreased secretion of proinflammatory cytokines (IL-6, IL-1 β and TNF- α) (Vulevic et al. 2008). Oral lactulose increases stool water content (Hebden et al. 1999) and increases stool frequency in constipation (Bass and Dennis 1981; Freedman et al. 1997). This beneficial effect arises out of a combination of increased bacterial mass, increased stool water as well as increased colonic tone resulting in accelerated transit (Jouet et al. 2006). Numerous other poorly absorbed storage carbohydrates are used for

their laxative effect with important effects on gut microbiota although their specific mechanism of action is less well worked out than for lactulose.

Prebiotics can administer along with live bacteria (probiotics) that are most able to utilize that energy source to improve the health benefits to the host. The synergistic combinations of probiotics and prebiotics are called synbiotics. Probiotics, prebiotics and synbiotics can influence the intestinal microbiota and modulate the immune response. In the study on the effect of the synbiotic product containing a blend of probiotics (*Lactobacillus casei*, *Lactobacillus rhamnosus*, *Streptococcus thermophilus*, *Bifidobacterium breve*, *Lactobacillus acidophilus*, *Bifidobacterium longum*, *Lactobacillus bulgaricus*) and fructooligosaccharides, 52 adults participated for 28 weeks. It was found that supplementation with the synbiotic resulted in the inhibition of NF κ B and reduced production of TNF- α (Eslamparast et al. 2014). The use of a synbiotic containing five probiotics (*Lactobacillus plantarum*, *Lactobacillus delbrueckii* spp. *bulgaricus*, *Lactobacillus acidophilus*, *Lactobacillus rhamnosus*, *Bifidobacterium bifidum*) and inulin as a prebiotic in adult subjects with NASH (non-alcoholic steatohepatitis) confirmed a significant reduction of IHTG (intrahepatic triacylglycerol) within six months (Wong et al. 2013). It is also known that lipopolysaccharides (LPSs) induce proinflammatory cytokines, such as the tumour necrosis factor alpha (TNF- α), playing a crucial role in insulin resistance and inflammatory cell uptake in NAFLD (non-alcoholic fatty liver disease). Other beneficial effects of synbiotics include improved hepatic function in patients suffering from cirrhosis, prevention of bacterial translocation and reduced incidence of nosocomial infections in patient post-surgical procedures and similar intervention.

2.8 Postbiotic Modulation of Immune System

2.8.1 Postbiotics and Host Microbiota

Mechanism of actions of postbiotics is not fully elucidated. One of the possible immunomodulatory effects by postbiotics in humans could be derived from an in vitro experiment showing the innate response of macrophages to non-viable *Lactobacillus casei* cells. Heat killed bacterial cell suspension increases in expression of proinflammatory cytokines and increases the transcription of Toll-like receptors (TLR-2, TLR-3, TLR-4 and TLR-9) (Wang et al. 2013). But the heat treated *Bifidobacterium* cells induce cellular immune and anti-inflammatory responses by inhibiting IL-8 secretion in intestinal epithelial cells obtained from patients with ulcerative colitis (Imaoka et al. 2008).

The postbiotic compounds from *Lactobacilli* spp. can exert immunomodulation activity by increasing levels of Th1-associated cytokines and reducing Th2-associated cytokines (Ou et al. 2011). Likewise, retinoic acid produced by *L. reuteri* 17,938 influences the phenotype and function of mucosal like dendritic cells and also increases the level of IL-10, CD103 and CD1d and downregulates inflammation-associated genes like NF κ B and TNF (Haileselassie et al. 2016).

Similar findings were reported in another research conducted by Sokol et al. (2008), who reported that increased IL-8 levels in Caco-2 cells when exposed to intracellular extracts and the supernatant fraction of *Faecalibacterium prausnitzii*. Cultural supernatants of *Lactobacillus rhamnosus* GG collected at different stages of growth (middle and late exponential, stationary, and overnight) were able to protect human colonic smooth muscle cells (HSMCs) against lipopolysaccharide (LPS)-induced myogenic damage. Increased level of protective effect was observed with supernatants of the late stationary phase, which reverted 84.1% of LPS-induced cell shortening, and inhibited 85.5% of acetylcholine-induced contraction and 92.7% LPS-induced IL-6 secretion (Cicenia et al. 2016).

Exopolysaccharides and extracellular vesicles (EV) are two important fermentation products that are associated with health benefits. Exopolysaccharide from *Lactobacillus plantarum* 70,810 was found to function as antitumor agents in vitro by inhibiting the proliferation of HepG-2, BGC-823 and HT-29 tumour cells (Wang et al. 2014). Extracellular vesicles are spherical lipid bilayer structures that can be secreted by both gram negative and gram positive bacteria. Extracellular vesicles have ability to carry a different type of compounds such as nucleic acids, proteins, phospholipids, polysaccharides and glycolipids. EVs can be differentiated into two; they are outer membrane vesicles (OMVs) for gram negative bacteria and membrane vesicles (MVs) for gram positive bacteria. EVs derived from *Akkermansia muciniphila* and commensal *Escherichia coli* have shown respectively to decrease gut permeability and activate signalling through the intestinal epithelial barrier in vitro (Chelakkot et al. 2018; Fábrega et al. 2016). However, human clinical trials are needed to establish safety and potential for the use of EVs as therapeutic agents in humans.

The potential of innate and adaptive immunity to trigger inflammation in response to abundant microbial compounds including lipoteichoic acids and S-layer proteins was elucidated by Konstantinov et al. (2013). The major metabolite of gut bacteria, the SCFA, has numerous health-promoting activities such as butyrate enhances the intestinal barrier function and mucosal immunity and butyrate and small amount of propionate act as histone deacetylase (HDAC) inhibitors, etc. As a result, they promote anti-inflammatory and immune effects through suppression of lamina propria macrophages and cause differentiation of dendritic cells from bone marrow stem cells (Koh et al. 2016; Johnstone 2002; Singh et al. 2010; Lukovac et al. 2014). SCFAs can also activate some SCFAs specific G-protein-coupled receptors (GPRs) present on gut epithelial cells and others. It helps to modulate cellular activity (Gill et al. 2018). SCFAs have antitumor effects, anti-inflammatory effects on the colonic epithelium, protection from development of immune disorders and control of obesity. Table 2.1 illustrates the important gut bacterial products/metabolites which elicit an immunomodulatory effect. All these studies suggest that postbiotics have ability to increase health by providing better and specific physiological effects, although the exact mechanisms remain to be elucidated.

Table 2.1 Gut microbial metabolites or postbiotics and their role in immunity

Postbiotic metabolites/ compounds	Immunomodulatory functions	Reference
Butyrate	Boost extra thymic Treg cell generation in mice	Arpaia et al. (2013)
	Differentiation of colonic Treg cells	Furusawa et al. (2013)
	Downregulation of LPS induced proinflammatory mediators like NO, IL-6 and IL-12 in macrophages in vitro	Chang et al. (2014)
Butyrate and propionate	Downregulation of proinflammatory cytokines IL-6, IL-12p40, CCL3, CCL4, CCL5, CCL-9, CCL10, CCL11 in human monocyte derived DC	Nastasi et al. (2015)
Butyrate and acetate	Increased GPR43 expression and decreased proinflammatory monocyte chemoattractant protein MCP-1, IL- β and inhibit oxidative stress in high glucose treated glomerular mesangial cells	Huang et al. (2017)
Aryl hydrocarbon receptor ligand	Necessary for the postnatal expansion of ROR γ t	Kiss et al. (2011)
Polyamines	Increased production of sIgA in rats	Buts et al. (1993)
	Enhances the integrity of IECs	Chen et al. (2007)
	Modulates adaptive immunity by accelerating the maturation of CD4 ⁺ and CD8 ⁺ T cells	Pérez-Cano et al. (2010)
Polysaccharide A	Anti-inflammatory effect by increasing the levels of IL-10	Round et al. (2011)
	Maintains balance between T _H 1 and T _H 2 cells in GF mice	Mazmanian et al. (2005)
Formyl peptides	Helps in recruiting leukocytes and production of proinflammatory cytokines	Liu et al. (2014)
D-glycero β -D-Manno-heptose-1,7-bisphosphate	Stimulates innate immune response by activating NF κ B pathway	Gaudet et al. (2015)

LPS lipopolysaccharide, *NO* nitric oxide, *IL* interleukin, *CCL* chemokines, *DC* dendritic cells, *ROR γ t* retinoic acid receptor related orphan nuclear receptor gamma, *sIgA* secretory immunoglobulin A, *IEC* intestinal epithelial cells

2.9 Conclusion

Gut is the largest immune organ of the body and it is considered as the second brain due to the complex enteric, endocrine, neuron and immune networks. The food and microbiota in the gut influences all organs through these networks. If the microorganisms inhabiting the gut are beneficial, body homeostasis will be maintained; otherwise it gets disrupted. Administration of probiotic is an alternative to a dysbiotic gut. Prebiotics are given along with probiotics for their establishment and survival. The synergistic effects of both improve gut health. Fermentation of

prebiotics in gut produces metabolites which circulates through the body and activates different systems. Usage of synbiotics is an approach to prevent aberrations in the gut. The latest trend in the biological modulation of immunity is the administration of microbial by-products, metabolites or inactivated cells itself. Upon further studies and clinical trials, the postbiotics can be used as non-specific immune boosting vaccines which can activate the low-immune children as well as adult.

It is important to maintain proper health and immunity through natural means, since we are facing new challenges day by day. In current pandemic COVID 19, several positive cases were asymptomatic or they may be immune. Boosting immunity through functional food helps in preventing infection and staying healthy. As this chapter indicates, consuming healthy food always improves the health through the nutrients and metabolites that are present in it or by the by-products of gut microflora. Age and health status of an individual are always a critical factor that increases the severity of infection, but a proper diet and hygiene does help improving the condition.

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Preventive Effects of Probiotics and Prebiotics in Food Allergy: Potentials and Promise

3

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Abstract

The significant increase in food allergy severity and prevalence stresses the need for efficient preventive strategies to reduce life-threatening allergic reactions, particularly among children. At present, there is no cure for food allergy and the eviction of triggers remains the main preventive strategy. The gut microbiome was found to play a key role in the development and pathogenesis of food allergy, opening new therapeutic possibilities. Differences in gut microbiomes were reported between allergic and healthy individuals, suggesting that imbalances in the gut microbial environment likely precede the development of food allergy. The administration of probiotics and prebiotics has been proposed as a safe non-allergen specific therapy with promising outcomes for food allergy treatment. Although numerous studies support the effective role of the probiotics and prebiotics against different allergy conditions, these beneficial impacts appeared to be highly strain specific and particularly observed in pediatric studies. This chapter tries to address the potentials of prebiotics and probiotics in the prevention or treatment of food allergy in the light of preclinical and clinical investigations.

Keywords

Probiotics · Prebiotics · Gut microbiota · Food Allergy

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85

3.1 Introduction

According to the National Institute of Allergy and Infectious Diseases and Guidelines for the Diagnosis and Management of Food Allergy promoted by the National Institutes of Health (NIAID/NIH) in the United States, food allergy is described as an unfavorable immune response to food properties that affects approximately 5% of adults and 8% of children (Sicherer and Sampson 2006; Boyce et al. 2011). It impacts negatively the life quality of millions of people worldwide, significantly contributes to morbidity, and is related to important medical costs (Rona et al. 2007; Boyce et al. 2011). The significant increase in food allergy severity and prevalence stresses the need for efficient preventive strategies to reduce life-threatening allergic reaction, chiefly among children with 0–14 years old (Sicherer and Sampson 2014). The immediate symptoms affecting the respiratory, skin, cardiovascular, or gastrointestinal systems are mainly the result of immunoglobulin (Ig) E-mediated food allergic reactions (Boyce et al. 2011; Sicherer and Sampson 2014). Numerous epidemiological investigations reported an important increment in hospital admissions for severe food-allergic reactions in children in the USA, the UK, Australia, Iran, and Italy over the last 10 years (Ahanchian et al. 2016; Canani et al. 2013; Mullins et al. 2015; Nocerino et al. 2015; Paparo et al. 2019; Turner et al. 2015). Although more than 170 food allergens have already been described, the most common and serious allergic reactions are caused by a restricted list of food including egg, tree nuts, peanuts, milk, shellfish, fish, soy, wheat, and seeds, with national and geographical variations (Boyce et al. 2011; Sicherer and Sampson 2014; Chafen et al. 2010). At present, there is no specific cure for food allergy and the diagnosis of the offending allergen (s) allowing the eviction of triggers remains the main preventive strategy. However, the accidental consumption of food allergens is not uncommon and the treatment of symptoms with glucocorticoids, antihistamines, or epinephrine in case of systemic reactions is often recommended (Burks et al. 2018; Oyoshi et al. 2014; Sicherer and Sampson 2014). On the other hand, in the past decade, potential therapeutic alternatives for food allergy have been advocated. These emerging therapies are concentrated on suppressing Th2 effector cells, increasing levels of allergen-specific IgA or IgG, decreasing levels of allergen-specific IgE, or increasing regulatory T cells by different allergen nonspecific and allergen-specific approaches (Berin 2014; Paparo et al. 2019). Considering the variable efficacy and safety of allergen-specific therapies (subcutaneous, epicutaneous, sublingual, oral immunotherapy and heat treatment of food), strict risk evaluation and mitigation strategies are required when using these methods. Among numerous uncertainties reported for these approaches, we can mention the observation of adverse events, the onset of eosinophilic esophagitis, desensitization without proper immunological tolerance, the lack of long-term efficacy and difficulties to determine optimal dose and duration (Rachid and Keet 2018).

Besides, the gut microbiome was found to play a key role in the development and pathogenesis of food allergy, opening new therapeutic possibilities. Differences in gut microbiomes were reported between allergic and healthy individuals, suggesting

that imbalances in the gut microbial environment likely precede the development of food allergy (Bunyavanich 2019). In this respect, pioneer studies revealed that the commensal gut microbiota function and composition significantly affect the immune tolerance mechanisms following antigen exposure and its dysregulation may lead to the development of food allergy (Paparo et al. 2019). Recently, the administration of probiotics and prebiotics has been proposed as a novel non-allergen specific therapy with promising outcomes for food allergy treatment. Probiotics are described as live microorganisms that when consumed in adequate amounts as oral supplements or as a food component induce a health benefit on the host by regulating its microbiota (Hill et al. 2014). The functions of probiotics are commonly regulated through the toll-like receptors or TLRs (innate immune system), inducing the production of regulatory cytokines (TGF-beta and IL-10), improvement of T helper1 differentiation, increased intestinal release of IgA (Rautava et al. 2012), although these impacts could be different according to the food matrix, probiotic strain, timing, and dose (Heine 2018). This chapter tries to highlight the potentials of prebiotics and probiotics in the prevention or treatment of food allergy in the light of preclinical and clinical investigations.

3.2 Safety of Probiotics and Prebiotics

The safety of probiotics is an important asset leading to its widespread consumption in various forms (Castellazzi et al. 2013). A wide range of people around the world ingest probiotics daily because of their purported health benefits and the global market of probiotic products is steadily expanding (Novik and Savich 2020). *Lactobacilli*, *lactococci*, and *bifidobacteria* have been recognized as safe (GRAS) by the United States Food and Drug Administration (FDA). This designation indicates that these bacteria are considered safe to be added to food, thereby exempting them from usual tolerance requirements for food additives. Several safety properties have been taken into account such as the absence of associated disease, including endocarditis or bacteremia, the absence of antibiotic resistance gene transformation in the gastrointestinal flora, as well as the absence of metabolic or toxic impacts on the gastrointestinal system (Aureli et al. 2011). Principally, the safe properties of a probiotic strain are associated with the absence of virulence factors and the absence of clinical or veterinary resistance to antibiotics (Daliri et al. 2019). Besides, the Italian Ministry of Health along with the Scientific Committee on Animal Nutrition of the EU (SCAN) and the EFSA panel on additives, products and substances used in animal feed (FEEDAP) proposed to add “the absence of evidence regarding the possible transfer of genes related to antibiotic resistant” as an essential parameter for microorganism safety confirmation (Ahanchian et al. 2016; Snyderman 2008). Furthermore, the confirmation of safety and efficacy of probiotic strains is important for different bacterial strains of the same species which may reveal variable effects on the host immune system (Aureli et al. 2011). In recent years, the administration of probiotic products has increased in different medical conditions, because of their efficacy and safety in clinical practice. However,

although limited, there are also some risks related to the consumption of probiotics such as an inappropriate immune response in vulnerable populations, the capability of some strains to transfer antibiotic resistance genes to pathogens and deleterious metabolic activities and/or production of host-deleterious metabolites (Daliri et al. 2019). These risks are considerably reduced by the use of prebiotics which represent the substrate that is selectively utilized by beneficial host microorganisms (Gibson et al. 2017). Thus, prebiotics are used as nutrients for favorable microorganisms found in the host such as resident microorganisms and specific probiotics (Monteagudo-Mera et al. 2019). It is supposed that prebiotics could stimulate modifications in the gut environment toward a different host microbial ecosystem through their selective employment by host microorganisms. The effects of prebiotics on various functional pathways including immunomodulatory effects, inhibition of pathogenic bacteria, induction of metabolic function and barrier function have been repeatedly emphasized (Quigley 2019). The fructo-oligosaccharides, galactooligosaccharides and inulin are considered as safe prebiotics because of their long history of safe use in many countries (Cremon et al. 2018; Quigley 2019). However, new prebiotic and probiotic components with different effective impacts on the host immune system have emerged. Some of these components have been designated as ‘novel foods’ in the EU. These novel foods are evaluated on a case-to-case basis and different production methods or sources might be reported as novel (Kumar et al. 2015).

3.3 Probiotics/Prebiotics and Immunity

The terms probiotics and prebiotics are comprehensive, and various genera, species, and strains show differential effects on the immune system (Bron et al. 2012). Several important cofounding factors such as commensal bacteria and diet could influence the gut immune system. Although specific metabolites/food components (prebiotics) and live microorganisms (probiotics) may regulate and restore the gut microbial composition, an accurate knowledge of the associated molecular pathways behind their impacts on the immune system may provide insights into therapeutic potential for many diseases, such as allergy (Vieira et al. 2013). Several investigations showed that TLRs, Nod-like receptors (NLRs), and pattern recognition receptors (PRRs) play a key role in the development of immune tolerance mediated by probiotics (Abreu 2010; Kamada et al. 2013). The outcomes of TLRs stimulation result into the overexpression of pro-inflammatory regulators that facilitate the responses of host’s immune systems. Furthermore, some cytoplasmic proteins, NLRs, could modulate the activation of PRRs and inflammatory responses through the commensal microbiota that is directly involved in the gut homeostasis (Yeretssian 2012). However, disorders in the interactions of PRR-microbiota, in gut mucosal compartment and various cell types, often lead to the development of diseases and intensified inflammation (Lavelle et al. 2010; Maynard et al. 2012). The beneficial effects of probiotics in the host have been supported by a plethora of *in vivo* studies based on clinical experiments or animal models, suggesting their

effectiveness in the necrotizing enterocolitis; post-antibiotic-related diarrhea; certain pediatric allergic disorders; prevention or treatment of acute viral gastroenteritis; and inflammatory bowel disease (IBD) (Cruchet et al. 2015). The efficient role of probiotics in the alleviation of numerous dysfunctions of the gastrointestinal system has also been reported (Vieira et al. 2013). One of the major mechanisms by which probiotics may decrease gut disorder symptoms is through the elevation of short-chain fatty acids (SCFAs) production in the colon that decrease the intestinal permeability and the invasion of pathogenic microorganisms (Morais and Jacob 2006; Szajewska and Kołodziej 2015). Several probiotic effector molecules such as the cell wall components of bacteria including lipoteichoic acid and peptidoglycan along with specific proteins effectively contribute to the immune response (Klaenhammer et al. 2012). Moreover, the regulation of several receptor-mediated signaling cascades playing a key role in the modulation of the human immune system is considered as one of the most important functions of these probiotic effector molecules (Bron et al. 2012). Probiotics also regulate the function of epithelial cells, natural killers and dendritic cells (Yahfoufi et al. 2018). These beneficial bacteria could stimulate the Treg cells and polarize the immune pathways toward Th1.

Prebiotics as not digestible food ingredients are composed of oligosaccharides that show several profitable impacts on host health by selective induction of the growth and/or function of particular microbes present in the gut microbiota (Gibson 1998). Fiber carbohydrates such as gums, pectin, cellulose, lignin, and beta-glucan are not digested in the upper gastrointestinal tract. However, residential gut bacteria selectively ferment these components into SCFAs, especially propionate, acetate, lactate, and butyrate which are fermented when reaching the colon (Horrocks and De Dombal 1978). The majority of the bacteria in the colon are severe anaerobes getting energy from fermentation. The other profitable role of prebiotics is the stimulation of the immune system through the regulation of beneficial microbes' population in the gut, particularly bifidobacteria and lactic acid bacteria. Also the expression of cytokines is another important pathway influenced by the consumption of specific probiotics and prebiotics (Shokryazdan et al. 2017). The mechanism for the beneficial impact of prebiotics on immune system is still largely unknown. Interestingly, the prebiotic metabolites are involved in the modulation of Treg cells, cytokines, and chemokines (Yahfoufi et al. 2018), while prebiotic fibers, by promoting short-chain fatty acids (SCFA) like propionate, lead to the regulation of hepatic lipogenic enzymes. In addition, it was found that inulin supplementation led to increased SCFA levels in the caecum of treated animals (Vieira et al. 2013; Artiss et al. 2006). Other possible effects of prebiotics are the modulation of mucin production, an increase in the number of lymphocyte and/or leucocyte in gut-associated lymphoid tissues (GALT) and peripheral blood, as well as elevated IgA secretion by the GALT.

3.4 Food Allergy and Microbiota

Numerous microorganisms localized in the gastrointestinal tract influence the function and shaping of host adaptive and innate immune responses. Several studies based on both clinical and animal experimentation showed that abnormalities in the microbiota composition (dysbiosis) can lead to allergic disorders through their effects on immune system. Food allergies are reported frequently in preschool children of developing and developed countries with a prevalence reaching 7% and 10%, respectively (Prescott et al. 2013). However, the etiology of food allergy is complex. The environmental/developmental/genetic combined effects involved in the food allergy may explain the global rising trends in recent decades. The key role of microbiome in the development of food allergy is now well documented (Bunyavanich 2019). A changed susceptibility to allergic disorders could thus be linked to the microbial exposure in early childhood (Cahenzli et al. 2013). Furthermore, the comparison of genetically similar populations in Finland and Russia provided more insights into the close interactions between the host microbiome, food allergy, and environment (Haahtela et al. 2015). Experiments on animals revealed that mice with food allergy have a particular gut microbiota signature that could be responsible for increased allergic susceptibility (Rivas et al. 2013). It has thus been suggested that a particular microbiota composition related to food allergy could lead to allergic sensitization and life-threatening anaphylaxis reaction. Several investigation data proposed that dysregulations in the composition of intestinal microbiota in infants are involved in the food allergy pathogenesis, although the precise composition and structure of the intestinal microbiota in human with food allergy still need to be clarified (Matsui et al. 2019). A study using high-throughput 454 sequencing to target hypervariable V1-V3 regions of the 16S rRNA gene in the feces investigated the microbial composition and diversity of 34 infants with food allergy. The results of this study confirmed remarkable modifications in the fecal microbiota of infants suffering from food allergy, showing a significant association with the development of food allergy (Ling et al. 2014). In the food allergy population, the abundance of *Firmicutes* phylum dramatically increased, while the concentration of *Proteobacteria*, *Actinobacteria*, and *Bacteroidetes* phyla significantly decreased. Furthermore, the phyla of *Clostridiaceae* organisms were commonly found in infants suffering from food allergy. Detailed analysis of microbiota community suggested that the dysbiosis of fecal microbiota is associated with several food allergy-related key phylotypes and may play an effective role in the development of food allergy. Another study also revealed that mice and infants with food allergy had increased IgE and decreased IgA binding to fecal bacteria (Abdel-Gadir et al. 2019). Interestingly, bacteriotherapy stimulated the expression of the transcription factor ROR- γ t by Treg cells in a MyD88-dependent manner. These results were of importance as the transcription factor ROR- γ t was found to be deficient and ineffectively produced by the microbiota of infants and mice affected by food allergy. Protection by bacteriotherapy is, however, abrogated following the deletion of Myd88 or Rorc in Treg cells. Thus, by activating a MyD88/ROR- γ t pathway in nascent Treg cells, commensal microbiota is able to protect against food allergy,

while, inversely, microbial imbalance and dysbiosis may promote disease (Abdel-Gadir et al. 2019; Aitoro et al. 2017). Comparison of fecal microbiota in a mouse model of food allergy showed that the development of the disease could be related to a specific microbiota composition (Diesner et al. 2016; Hussain et al. 2019). Different animal studies investigated the possible association of food allergy with intestinal microbiota. For example, a study reported that Germ-free (GF) mice are more likely susceptible to oral sensitization with cow's milk protein and ovalbumin compared to wild-type control mice (Cahenzli et al. 2013). Moreover, mice with antibiotic-related modifications in their microbiota were more severely affected by food allergy when compared to untreated mice (Bashir et al. 2004). Interestingly, the regulation of the microbiota of GF mice with commensals such as *Bacteroides fragilis* and *Clostridia* or short-chain fatty acids and prebiotics promoted the induction of Treg cells and reduced allergic sensitization (Geuking et al. 2011; Smith et al. 2013; Lathrop et al. 2011). Surprisingly, significant reduction in allergic diarrhea and increased levels of Treg cells were also reported among mice exposed to the human microbiota, thereby suggesting that protection or susceptibility to food allergy could be transmitted (Atarashi et al. 2013). In human, the pathogenesis of food allergy, atopic dermatitis, and asthma has been associated with altered microbiota composition (Marrs et al. 2013). However, further investigations are needed to determine implicated microbial species and their influence on the development of allergies. Preclinical and clinical studies on the efficacy of different probiotics and prebiotics on food allergy are addressed in the rest of the chapter.

3.5 Preclinical Studies on the Efficacy of Probiotics and Prebiotics in Food Allergy

As discussed above, gut microbiota and its metabolites such as short-chain fatty acids play a key role in immune tolerance (Paparo et al. 2019). In vivo benefits of probiotics are difficult to assess through in vitro studies as the extrapolation of the results is not possible (Berni Canani et al. 2012). The first in vivo studies on the effect of probiotics on food allergy were performed in Finland and revealed that hydrolysis of caseins with *L. casei* GG-derived enzymes resulted in molecules with suppressive effects on lymphocyte proliferation. These preliminary results suggested that intestinal bacteria can promote the downregulation of hypersensitivity reactions to ingested proteins in patients with food allergy (Sütas et al. 1996). It was found that the probiotic effects on immune tolerance to food allergens could be due to the regulation of gut microbiota function and composition through the elevation of butyrate production (Canani et al. 2016) and immune tolerogenic pathways through the induction of beta-defensins, sIgA production (Hardy et al. 2013), cytokines regulation and through improving the mucus thickness and gut permeability (Kim et al. 2008; Niers et al. 2005; Turner et al. 2015). Furthermore, the evaluation of probiotic and prebiotic impacts on immune cell responses has been performed by in vitro induction of mononuclear cells in human peripheral blood under selected strains of probiotics and prebiotics. The treatment of mononuclear cells of human

peripheral blood with lactic acid bacteria (LAB) strains such as *Bifidobacterium adolescentis* and *Lactobacillus plantarum* induced the production of IFN- γ by T cells and the regulatory cytokine IL-10 by dendritic cells and monocytes (Cross and Gill 2001; Karlsson et al. 2004; Mohamadzadeh et al. 2005). The incubation of mononuclear cells of human peripheral blood with a mixture of probiotics including *L. acidophilus* W55, *B. infantis* W52, *L. casei* W56, *L. salivarius* W57, *L. lactis* W58, *B. lactis* W18, and *B. longum* W51 in children with food allergy induces the production of Th1 and regulatory cytokines and proliferation of T cell (Flinterman et al. 2007). Furthermore, after 3 months of incubation with these mixture, the increase in B and T cell proliferation and a decrease in production of IgE were also reported in children with food allergy (Flinterman et al. 2007). In addition, a mixture of probiotics *L. rhamnosus* GG and *B. breve* regulated the function of IL-23 and IL-17 inflammatory cytokines, resulting in a decrease in histone acetylation and an increase in DNA methylation in a 3D coculture model of mononuclear cells from human peripheral blood and intestinal epithelial cells used as an in vitro model of the intestinal mucosal immune system (Ghadimi et al. 2008). Animal models for food allergy were also regularly applied as experimental approaches to assess probiotics and prebiotics effects. Differential effects of oral ingestion of three LAB strains including *B. infantis* 11.322, *L. plantarum* 08.923 (Lp), and *B. coagulans* 09.712 (Bc) in a murine model induced by shrimp allergen were reported on the reduction of Th2-driven intestinal inflammation and other symptoms related to food-induced anaphylaxis (Fu et al. 2017). Oral supplementation of these probiotics remarkably increased the population of CD4+ FoxP3+ T cells and alleviated anaphylaxis symptoms in sensitized mice by FoxP3 upregulation, GATA-3 downregulation, and mTORC inhibition (Fu et al. 2017). The therapeutic and preventive effects of oral *Clostridium butyricum* CGMCC0313-1 on anaphylactic symptoms in sensitized mice by a β -lactoglobulin (BLG) showed that this bacteria could increase CD4+ CD25+FoxP3Treg cell and sIgA and alleviate anaphylaxis symptoms in the spleen of sensitized mice (Zhang et al. 2017). Another study showed that casein immunogenicity after oral sensitization to cow's milk could be induced in neonatal monocolonization of germ-free mice by *L. casei* BL23 (Maiga et al. 2017). It was also revealed that oral ingestion of *B. infantis* improved the allergic conditions through the reduction of the Th2 cytokines release in the spleen and ovalbumin-specific IgG1 and IgE contents in the sera of ovalbumin-sensitized mice. Furthermore, the analysis of gut microbiota showed that the probiotics-regulated protection was induced by overexpression of Rikenella and Coprococcus at genus level (Yang et al. 2017). A decrease in IgE, IL-4, and IL-13 levels was reported following the administration of *B. infantis* CGMCC313-2 in BLG-sensitized mice (Liu et al. 2017). Another study reported that oral ingestion of VSL#3 probiotic-mixture remarkably ameliorate the anaphylactic reactions through the decrease of the Th2 immune responses in sensitized mice (Sicherer and Sampson 2018). Also, the treatment of probiotic mixture with mouse spleen cells in sensitized mice increased the production of IL-10 and IFN- γ , while decreasing the allergen-induced IL-5 and IL-13 production (Schiavi et al. 2011). An oral supplementation of *Lactobacillus rhamnosus* GG with cholera toxin B-subunit as adjuvant decreased the

cow's milk allergy in the sensitized Balb/C mice through the regulation of immune responses by shifting Th2-dominated trends toward Th1-dominated responses (Thang et al. 2011). Similar studies have been showed that the oral administration of *Lactobacillus rhamnosus* GG induced a remarkable decrease of allergic reaction and of specific production of IgE and IL-4, IL-5, IL-13, in a BLG-sensitized mouse model (Aitoro et al. 2017). Probiotics also ferment prebiotics or fiber-rich diets to SCFAs, including acetate, propionate, and butyrate. Evidence data proposed that SCFAs, especially butyrate, are involved in the homeostasis of mucosal system by the modulation of epithelial barrier integrity and stimulation of Tregs (Canani et al. 2015). The deficiency of butyrate has been reported in patients with food allergy symptom (Canani et al. 2016). Therefore, it is possible that various kinds of dysbiosis led to similar impacts in SCFAs or other production of microbiota-derived metabolites resulting in allergy occurrence. Clostridia species are known as the main source of SCFAs in the colon that has been involved in the modulation of proportions and activation of Tregs functions in the colon (Arpaia et al. 2013; Smith et al. 2013). SCFAs also stimulate G-protein-coupled receptors involved in the induction of colonic macrophages and dendritic cells, the secretion of IL-10 and increase Tregs in the mesenteric lymph nodes. Tregs are a prominent source of tolerogenic cytokines, like TGF- β and IL-10 that control inflammatory and allergic responses (Paparo et al. 2019). Another study also reported that dietary vitamin A together with fiber/SCFAs in a healthy gut microbiota could protect the food allergy development through the conservation of a tolerogenic mucosal environment and increase function of tolerogenic CD103+ dendritic cells, resulting to heighten differentiation of Tregs. In addition, mice lacking GPR109A or GPR43 receptors for SCFAs showed fewer CD103 + dendritic cells and increased food allergy symptom (Tan et al. 2016). These researches suggest that the effective role of different prebiotics on food allergy could be related to their direct effects on the gut microbiota.

3.6 Clinical Data on the Probiotics Efficacy in Food Allergy

The pioneer studies suggesting the potential of probiotic bacteria to prevent allergic diseases and regulate the immune response originate from Finland (Majamaa and Isolauri 1997). There are several investigations on the importance of the gut microbiota composition in the food allergy pathogenesis that have been supported by clinical research on the effective role of the probiotics against allergy conditions. These protective impacts appeared to be strain specific and particularly reported in the pediatric age (Paparo et al. 2019). On the other hand, tolerance and safety of prebiotic-containing starter infant formula supplemented with *Lactobacillus paracasei* and *Bifidobacterium animalis* have been reported to be an effective approach to improve the beneficial bacteria in the intestine to develop a gut flora (Vieira et al. 2013). However, in a randomized double-blind placebo-controlled trial, it has been reported that 12 months administration of hydrolyzed formula of *B. lactis* BB12 and *L. casei* CRL431 could not affect the immune tolerance responses to

cow's milk proteins in infants with cow's milk allergy (Hol et al. 2008). Conversely another study showed that the supplementation of hydrolyzed casein formula (EHCF) with the *L. rhamnosus* strain GG is capable to increase the immune tolerance acquisition in infants with cow's milk allergy (Berni Canani et al. 2012). After 12-month treatment period, the group receiving EHCF+ *L. rhamnosus* strain GG (78.9%) showed higher proportion of children acquiring tolerance to cow's milk proteins when compared to other groups (Canani et al. 2013). More confirmation of a lower incidence of other atopic manifestations as well as a better resolution of IgE-regulated cow's milk allergy also was reported after treatment with EHCF+ *L. rhamnosus* strain GG after 3-year follow-up in pediatric cohort study (Canani et al. 2017). These beneficial effects could be because of regulation of *L. rhamnosus* strain GG-related immune functions by different pathways such as mast cells, enterocytes, monocytes, Tregs cell, and DCs (Canani et al. 2013; Ghadimi et al. 2008; Mileti et al. 2009) and by an expansion of butyrate-producing gut microbiota (Canani et al. 2016). Accordingly, supplementation of EHCF with *L. rhamnosus* strain GG in infants with eczema and/or CMA resulted in beneficial effects on the reducing of inflammation and gastrointestinal symptoms (Isolauri et al. 2000; Kalliomäki et al. 2010). Furthermore, it has been showed that the administration of *L. rhamnosus* strain GG for 4–12 weeks could significantly reduce in atopic dermatitis score in children aged 4–48 months. These children expressed less Scoring of Atopic Dermatitis (SCORAD) in the three components, including area of affected skin, intensity of atopic dermatitis, and patient symptoms, with a significant decrease in the mean change of intensity from baseline compared with placebo (Wu et al. 2017). Moreover, the combination of a prebiotic (galactooligosaccharides) with four probiotics (*L. rhamnosus* strain GG, *L. rhamnosus* LC705, *B. breve* Bb99, and *Propionibacterium freudenreichii* ssp. shermanii) decreased the incidence of atopic eczema and eczema and tended to decrease IgE-related diseases by modulating the infant's gut microbiota (Kukkonen et al. 2007). The same combination of probiotics without prebiotic did not show any significant impacts (Viljanen et al. 2005). The addition of prebiotic may have been the critical difference, although clear evidence of its bifidogenic effect is still lacking. Probiotics have been also proposed to reinforce the effectiveness of immunotherapy (Rachid and Keet 2018). Another randomized double-blind placebo-controlled trial study in 62 children (1–10 years) with peanut allergy showed that the probiotic *L. rhamnosus* CGMCC 1.3724 and peanut oral immunotherapy (PPOIT) could show effective impacts on the regulation of the peanut-specific immune response (Tang et al. 2015). For a total of 18 months, children received a fixed dose of probiotic (or placebo) along with peanut oral immunotherapy (or placebo) once daily. PPOIT induced high rates of desensitization (90%) and was related to decreased peanut-specific IgE levels and peanut skin prick test responses and increased levels of peanut-specific IgG4. Further investigations comparing food allergy with probiotic and prebiotics in different situation will be hotly demanded to evaluate associated mechanisms and relative contributions of probiotics versus prebiotics.

3.7 Conclusion

The key role of microbiome in the development of food allergy is now well documented and numerous investigations highlighted the importance of the gut microbiota composition in the food allergy pathogenesis. Microbial exposure was found to influence the development of oral tolerance, particularly in childhood. Dysbiosis and low diversity of gut microbiota have been linked to the pathogenesis of food allergy. The therapeutic strategy of the prebiotics and probiotics administration is to restore the gut microbiota in order to improve the microbiome immune support leading to a better tolerance to allergens. Numerous studies assessed allergy-preventive capacity of probiotics and prebiotics in food allergy and some very promising results were obtained following the administration of specific probiotic strains. Prebiotics also represent an interesting and safe alternative to some probiotics in allergy prevention, but more studies on various types and combinations of prebiotics are needed in the context of rigorous clinical investigations. Although, the use of probiotics in the prevention of food allergy and eczema among children led to new therapeutic perspectives, many variables such as the duration and mode of delivery, feeding type, optimal dose and strain combination merit to be addressed in future studies to confirm their effectiveness in the primary prevention of allergic disease.

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An Overview of Dairy Microflora

4

Deeba Noreen Baig and Samina Mehnaz

Abstract

An assembly of bacterial and fungal communities in the milk and dairy products presents a complete picture of dairy born microflora. Fermentation and pasteurization processes are crucial for the maintenance of microflora. Chemical composition and initial colonization of bacteria and fungi define the mutualistic pattern of microbial communities. The abundance and variety of microbial communities in milk are highly variable and depend upon many factors ranging from the health of milking animals to the milking practices, storage, and transportation methods. Probiotics are beneficial microbes, specifically lactic acid bacteria such as *Lactobacilli* and *Bifidobacteria* are generally regarded as safe (GRAS) microorganisms that benefit the host physiology upon ingestion. Lactic acid bacteria are the predominant group in all dairy microbiota that display a diverse range of strains associated with the milk from different animals. Few dairy microbes behave as pathogens as well as the cause of food spoilage. Human diseases from milk-borne pathogens are usually due to raw milk or products made from raw milk. However, the enormous medicinal and health-promoting impact of microbes and their additives overcome the limited effects of few harmful bacteria in the dairy environment. In addition to the known advantages of dairy bacteria, the phenomenon of psychobiotics is introducing a new therapeutic channel for the treatment of many psychological disorders.

Keywords

Dairy microflora · Probiotics · Lactic acid bacteria · Nutraceutical · Psychobiotics

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101

4.1 Introduction

Dairy microflora refers to the assemblage of microorganisms present in milk and its associated products. Milk is an important food for human consumption and was considered as a drink of ancient times that aided in the survival of generations. For centuries it has served as a cure for a variety of diseases and as an instant source of energy (Shori 2012). Today, it is considered to host a complex microbial community with great diversity. The microbial quality of milk products is highly dependent on their initial microflora colonization. Each kind of milk and dairy products develops a specific microflora composition. The most common dairy associated microflora includes *Lactobacillus*, *Bifidobacterium*, *Enterococcus*, *Streptococcus*, *Pediococcus*, *Propionibacterium*, and *Leuconostoc* bacterial genera, and *Saccharomyces* and *Aspergillus* yeast genera (Abushelaibi et al. 2017; Amara and Shibl 2015; Ogier and Serror 2008).

Fermentation is one of the common and primitive methods for processing and preservation of the microbial community that has been used worldwide. This method conserves the food and makes sure that the food is safe for human consumption by boosting their desired microbial composition. As a source of probiotics, raw and fermented forms of milk are well known around the world. A combination of fresh and lyophilized, one or more pure microorganisms (starter cultures) are routinely used for the fermentation of dairy products (Ahmed and Kanwal 2004; Lourens-Hattingh and Viljoen 2001; Vinderola et al. 2000). Sugars are metabolized into lactic acid, which enables food preservation by providing an acidic environment that is hostile for spoilage microorganisms (Hati et al. 2013). The diversity of microorganisms is highly varied in raw and fermented milk, as well as in dairy products like yogurt, cheese, kefir, and dahi. The quality of dairy products entirely depends on the viable count of microbiota in fresh milk, breeding area, nutritive condition, breed type, age of the animal, stage of lactation, and milking practices (Khaskheli et al. 2005). Milk microbiota exploration relies on both culture-dependent and molecular culture-independent approaches, including sequencing of 16S rRNA clone libraries and metabolomics, based on 16S rRNA gene amplicon sequencing (Gill et al. 2006; Verdier-Metz et al. 2012).

4.2 Different Sources of Milk Microbes

Various bovine and non-bovine milk sources have been reported in the account of diverse microflora. Generally, all types of milk carry a variety of bacterial and fungal strains in its raw and fermented forms. However, complete specie level identification and accurate count of viable and non-viable microorganisms in pasteurized and fermented forms are not known yet. Modern high-throughput sequencing technologies (including second- and third-generation sequencing and combinations thereof) enabled the detection and inventory of animal-specific complex microbial communities. Milk microbiota is well documented in various hosts like cows (Addis et al. 2016; Falentin et al. 2016; Oikonomou et al. 2014), goats, sheep, camel,

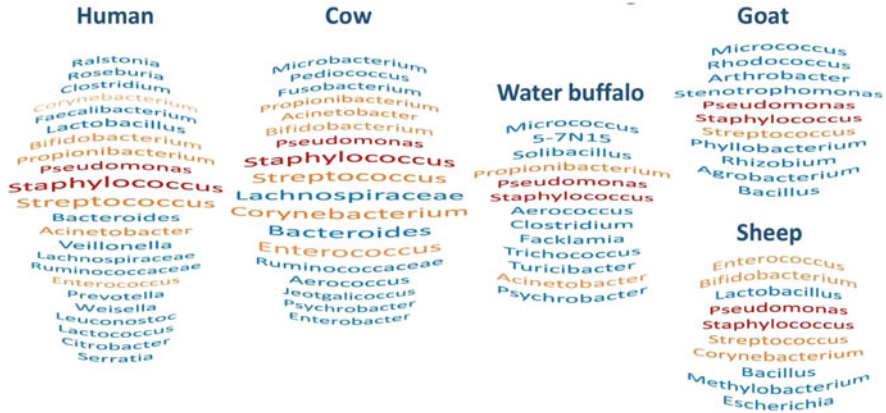


Fig. 4.1 Milk-associated microbiota in humans, cow, water buffalo, sheep, and goat. Major taxa. Red and orange taxa are shared between all human and animal species or present in three species out of five, respectively. For humans and bovines, taxa size reveals citation frequency

donkeys, buffalo, deer, reindeer, mice (Catozzi et al. 2017; De Los DoloresSoto et al. 2017; McInnis et al. 2015; Quigley et al. 2013; Treven et al. 2015), and human (Hunt et al. 2011; Jost and Lacroix 2013; Fitzstevens et al. 2017). Nevertheless, significant differences have been reported in the milk bacterial communities of different ruminants, such as water deer, reindeer, and goat, suggesting host-microbial adaptation, although the influence of environment and herd management should not be excluded. Recently, a comparison of bovine and human milk microbiota exhibited the clear metataxonomic picture and revealed the presence of common genera including *Bifidobacterium*, *Staphylococcus*, *Pseudomonas*, *Streptococcus*, *Propionibacterium*, *Corynebacterium*, *Bacteroides*, and *Enterococcus* which are among the most reported taxa in scientific reports related to bovine and human microbiota (Fig. 4.1) (Oikonomou et al. 2014).

4.2.1 Cow Milk

Culture-independent approaches described cow milk microbiota as one of the complex and diverse community comprised of 146 bacterial strains, with *Bacteroides*, *Bifidobacterium*, *Corynebacterium*, *Enterococcus*, *Propionibacterium*, *Pseudomonas*, *Staphylococcus*, and *Streptococcus* being the predominant taxa (Addis et al. 2016; Boix-Amorós et al. 2016; Cabrera-Rubio et al. 2012; Derakhshani and Naghizadeh 2018; Hoque et al. 2019; Jiménez et al. 2015; Murphy et al. 2017; Oikonomou et al. 2014; Urbaniak et al. 2016). Similar milk bacterial profiles were noticed through the shotgun metagenomic approach (Jiménez et al. 2015; Pärnänen et al. 2018) and described the presence of fungal, protozoal, and viral DNA. Colostrum microbiome depends on the lactation number and major

taxonomic profile; and diversity of primiparous colostrum microbiome includes the presence of *Staphylococcus*, *Prevotella*, *Ruminococcaceae*, *Bacteroidales*, *Clostridiales*, and *Pseudomonas* (Lima et al. 2018).

4.2.2 Buffalo Milk

Differential microbial communities and diversity in buffalo milk include major taxa of *Micrococcus*, *Propionibacterium*, *Solibacillus*, *Staphylococcus*, *Aerococcus*, *Facklamia*, *Trichococcus*, *Turicibacter*, *Clostridium*, *Acinetobacter*, *Psychrobacter*, and *Pseudomonas* through Ion Torrent 16S rRNA gene sequencing (Catozzi et al. 2017).

4.2.3 Sheep Milk

Sheep milk is reported to have various genera of lactic acid bacteria. These genera are identified as *Bacillus*, *Enterococcus*, *Lactobacillus*, *Lactococcus*, and *Leuconostoc*. The species identified for these genera are *Bacillus shackletonii*, *E. casseliflavus*, *E. durans*, *E. faecium*, *Lactobacillus rhamnosus*, *Lactobacillus acidophilus*, *Lactobacillus plantarum*, *Lactobacillus casei*, *Lactobacillus delbrueckii*, *Lactococcus lactis* ssp. *cremoris*, *Lactococcus lactis* ssp. *lactis*, *Lactococcus lactis* subsp. *biovar diacetylactis*, and *Leuconostoc* spp. (Acurcio et al. 2014; Aziz et al. 2009; Medina et al. 2011; Patil et al. 2019).

4.2.4 Goat Milk

Lactic acid bacteria isolated from the goat milk belonged to the genera *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, and *Streptococcus*. Isolated species are identified as *Enterococcus faecium*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus hirae*, *Enterococcus avium*, *Lactobacillus acidophilus*, *Lactobacillus delbrueckii* subsp. *bulgaricus*, *Lactobacillus fermentum*, *Lactobacillus lactis* subsp. *lactis*, *Lactobacillus paracasei*, *Lactobacillus plantarum*, *Lactobacillus rhamnosus*, *Lactobacillus reutei*, *Lactobacillus casei*, *Lactobacillus bulgaricus*, *Lactobacillus brevis*, *Lactobacillus curvatus*, *Leuconostoc mesenteroides* subsp. *mesenteroides*, *Leuconostoc mesenteroides* subsp. *dextranicum*, *Lactococcus plantarum*, *Lactococcus lactis* subsp. *lactis*, *Lactococcus raffinolactis*, *Pediococcus pentosaceus*, *Streptococcus thermophiles*, *Streptococcus salivarius* subsp. *thermophilus* (Medina et al. 2011; Mittu and Girdhar 2015; Perin and Nero 2014; Pisano et al. 2019).

4.2.5 Camel Milk

Nowadays an increasing attention is being focused towards consumption of camel milk. Its composition is closer to human milk than cow's milk; therefore it is better for humans especially for infants and children. Camel milk is an enriched source of *Lactococcus*, *Lactobacillus*, *Enterococcus*, *Streptococcus*, *Weissella*, and *Pediococcus*. Isolated strains belonged to *Enterococcus durans*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Lactobacillus brevis*, *Lactobacillus salivarius*, *Lactobacillus reuteri*, *Lactobacillus fermentum*, *Lactobacillus plantarum*, *Lactobacillus pentosus*, *Lactobacillus helveticus*, *Lactococcus garvieae*, *Lactococcus lactis*, *Leuconostoc pseudomesenteroides*, *Leuconostoc mesenteroides*, *Pediococcus pentosaceus*, *Pediococcus acidilactici*, *Weissella sp. t4r2c13*, *Weissella paramesenteroides*, *Weissella confusa*, *Streptococcus infantarius subsp. infantarius*, *Streptococcus equinus*, and *Str. thermophilus* (Abushelaibi et al. 2017; Amara and Shibl 2015; Bin Masalam et al. 2018; Edalati et al. 2019; Fguiri et al. 2015; Ogier and Serror 2008; Rahmeh et al. 2019).

4.3 Sources of Contaminant Microbes in Milk

The microbiological quality of dairy products reflects good hygienic practices during the milking process; raw milk contamination may occur in diseased or infected animals with environmental bacteria (Kongo et al. 2008). The detection of mesophilic aerobes and total coliforms is a clear indication of *E. coli* contamination; in addition to this the presence of *L. monocytogenes* and *Salmonella spp.* revealed poor microbiological quality of dairy products and cause interference with the native microbiota of milk. The predominant bacterial species isolated at the dairy farm comes from the water, feedstuffs, and milking equipment. In this context, *Bacillus licheniformis* and *Bacillus pallidus* act as entry points being in the form of highly heat-resistant spores in raw milk. The contamination risk of such aerobic spore-forming bacteria could lead to spoilage of milk and dairy products. The fecal material attached to the udder skin of milking animals is another source of contamination. Many species of *Lactobacillus* and *Enterococcus* are major fecal genera in the milk from rural and farm animals.

4.4 Indigenous Bacterial Community Composition

4.4.1 Raw Milk

The abundance and variety of microbial communities in raw milk varies and depends upon many factors ranging from the health of milking animal, to the milking practices, storage, and transportation methods (Kable et al. 2019; Skeie et al. 2019). The immediate cold storage of fresh milk reduces the bacterial growth and keeps milk in its native load of microflora (Li et al. 2018). The breeding practices,

lactation period, and availability of feeding plants in specific geographic location of herd are important factors for the change of microbial community patterns in the milk (Kable et al. 2019; Li et al. 2018; Parente et al. 2020; Skeie et al. 2019).

Modern high-throughput metagenomic sequencing of milk is a robust tool for the identification and estimation of indigenous microbiota of milk (Ercolini 2013; Zhang et al. 2019). Recently, Li et al. (2016) reported *Proteobacteria* as predominant group in fresh buffalo milk; however the population of abundance of *Firmicutes* increased and *Proteobacteria* and *Bacteroidetes* decreased significantly during the 24 h of cold storage. Looking at the genera-level microbial population pattern, *Streptococcus*, *Lactococcus*, and *Pseudomonas* were found in the fresh milk, and after 24 h of refrigeration the abundance of *Lactococcus* and *Streptococcus* populations increased significantly ($P < 0.05$), with the *Lactococcus* population contributing up to 38.6% of the total microflora (Li et al. 2016). One of the noticeable aspects was the robust growth of *Pseudomonas* and *Acinetobacter* genera (62%) in 72 h of cold storage (Fig. 4.2; Li et al. 2016).

4.4.2 Pasteurized Milk

Due to risk of pathogen contamination in milk produced from healthy animals under sanitary milk conditions, pasteurization of milk prior to consumption destroys pathogens, and provides hygienic milk (Fusco et al. 2020; Melini et al. 2017). Occasionally, human illness has been linked to pasteurized milk products but these cases usually have been a result of contamination of the product after pasteurization or due to improper pasteurization.

Despite the pasteurization process, a diverse bacterial population is a key characteristic feature of milk. According to Li et al. (2016), *Paenibacillus* is a dominated taxon at genus level in the microbial population. Other predominant bacterial populations appeared after prolonged storage, were psychotropic in nature, and were mostly associated with the spoilage of dairy products (Li et al. 2016). However, pasteurization appeared sufficient for eliminating contaminants from the *Pseudomonas* and *Acinetobacter* genera. However, there is a crucial need for developing novel technologies for controlling the proliferation of *Paenibacillus* to extend the shelf life of pasteurized milk products (Doll et al. 2017; Li et al. 2016).

Pasteurized milk bacterial composition did not significantly change during a storage period of 7 days; however the population of *Lactococcus* increased, while *Streptococcus* reportedly decreased (Li et al. 2016). At phylum level, *Firmicutes* and *Proteobacteria* contributed to more than 90% of the microbial composition after 7 days of storage. However, after 14 days of storage period, there was a significant increase in the population of *Firmicutes*, with a decrease in the population of *Proteobacteria* (Li et al. 2016). The analysis of the pasteurized milk after 21 days of storage showed that the *Firmicutes* increased and contributed to 90% of the total composition, along with *Paenibacillus* which increased to 80% in the bacterial population (Fig. 4.3; Li et al. 2016).

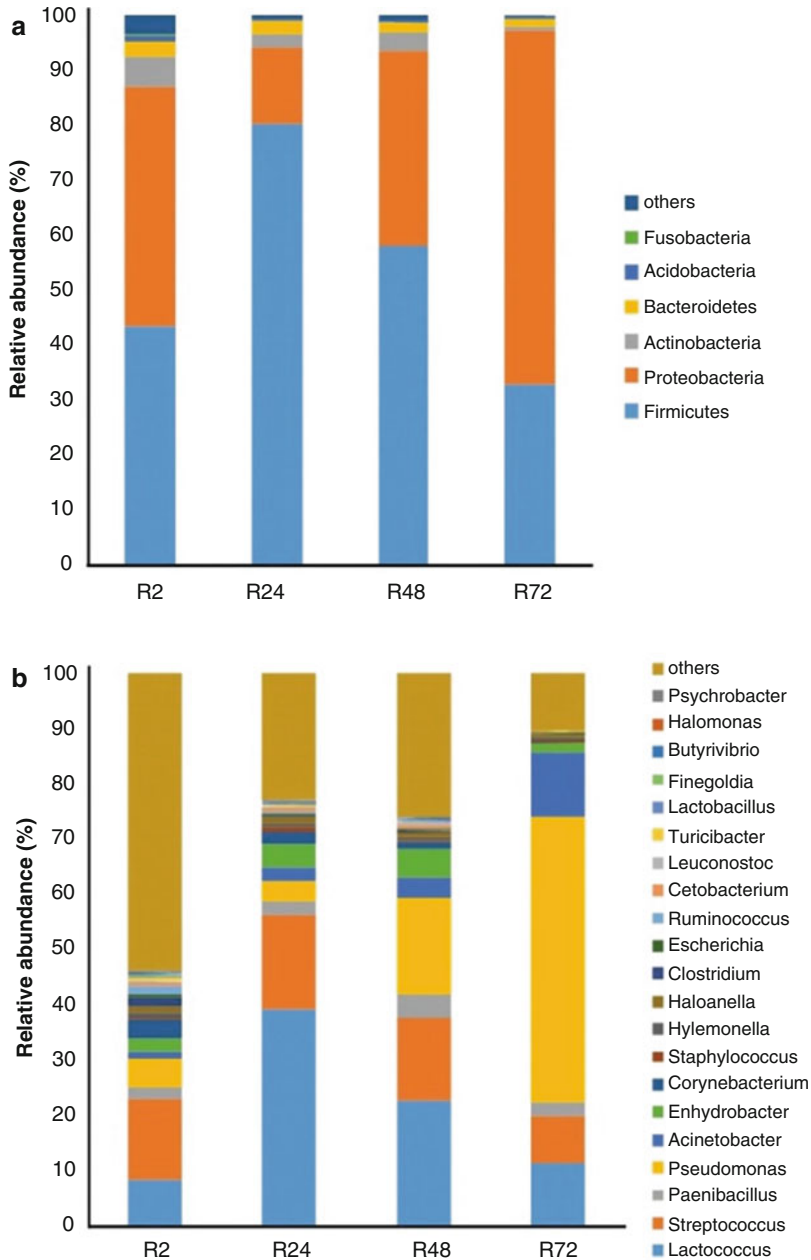


Fig. 4.2 Composition of the indigenous microflora, at the phyla (a) and genus (b) levels, in raw milk samples stored under refrigerated temperatures. Data represent the mean percentage from the metagenomics analysis of three separate raw milk samples. R₂ = raw milk samples stored for 2 h, R₂₄ = raw milk samples stored for 24 h, R₄₈ = raw milk samples stored for 48 h, R₇₂ = raw milk samples stored for 72 h (Li et al. 2016)

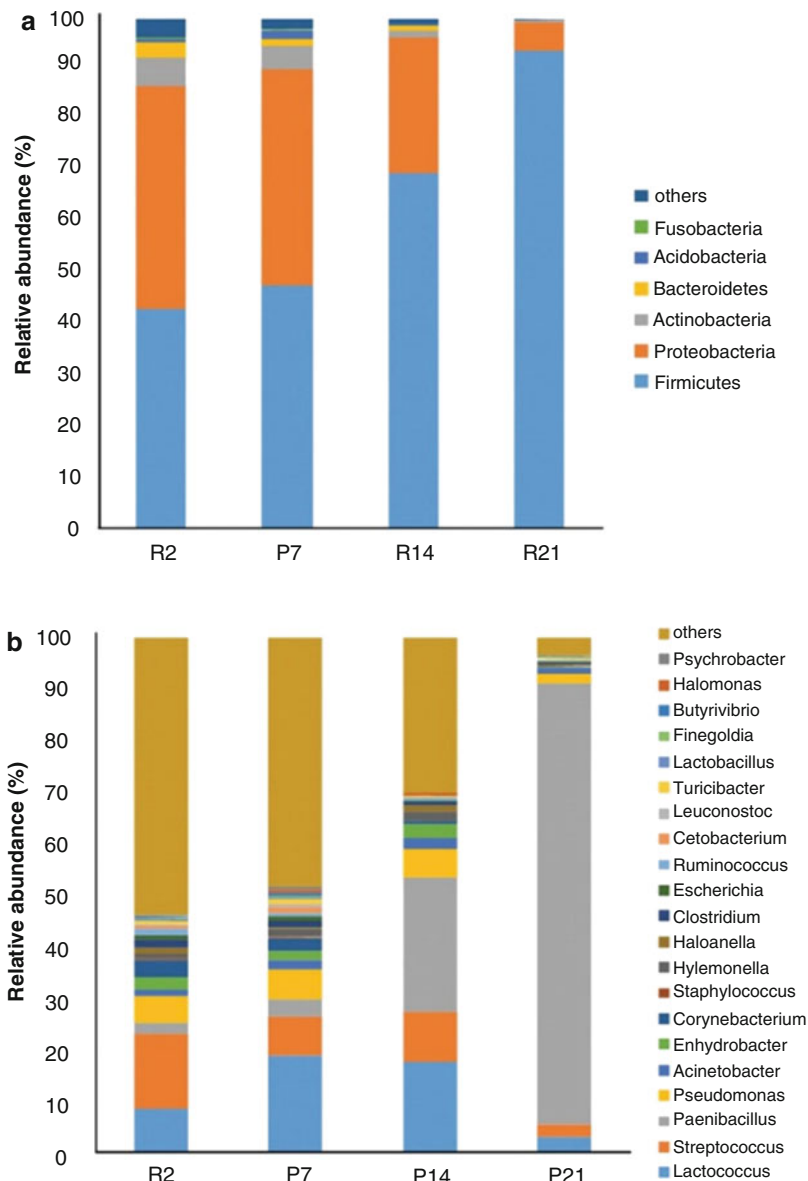


Fig. 4.3 Composition of the indigenous **microflora**, at both the phyla (**a**) and genus (**b**) levels, in **pasteurized milk** stored at refrigerated temperature. Data represent the mean percentages from the **metagenomic** analysis of 3 separate raw milk samples. R₂ = raw milk samples stored for 2 h, P₇ = pasteurized milk samples stored for 7 days, P₁₄ = pasteurized milk samples stored for 14 days, P₂₁ = pasteurized milk samples stored for 21 days (Li et al. 2016)

4.4.3 Fermented Milk

Fermented milk and its associated products are the richest and traditional source of probiotic microorganisms (Bernardeau et al. 2006). Naturally fermented milk has a variable microbial diversity in each of the resultant products, which contributes to their taste and texture (Zhong et al. 2016). Fermentation results in the functionally active microbial population to increase the bioavailability of nutrients for the consumers, while degrading toxic components to enhance the safety and bio-preservation of the final product (Tamang et al. 2016a). Low pH, fermented environment is an ideal medium to flourish beneficial microbial population (Savadogo et al. 2006; Sun et al. 2020). Fermented milk associated lactic acid bacteria (LAB) include *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, *Weissella*, *Bifidobacterium*, etc. these species of these genera are widely present in all types of milk (Axelsson et al. 2012; Tamang et al. 2016b).

Gao et al. (2017) reported *Lactococcus* as most predominant and *Lactobacillus* as subdominant genera in the milk samples collected in different times of year. Other genera found are *Leuconostoc*, *Streptococcus*, *Enterococcus*, *Chryseobacterium*, *Acetobacter*, *Weissella*, *Dysgonomonas*, *Macroccoccus*, *Xenophilus*, *Pseudoclavibacter*, and *Corynebacterium* in variable proportions. Among fungal genera, *Pichia*, *Kluyveromyces*, and *Geotrichum* are found predominantly in the milk through the year. However, *Naumovozyma* and *Hanseniastora* are subdominant genera (Fig. 4.4; Gao et al. 2017).

4.5 Types of Microbes

4.5.1 Beneficial Microbes

Beneficial bacteria are well known as “Probiotics” (usually lactic acid bacteria such as *Lactobacilli* and *Bifidobacteria*) that benefit the host physiology upon ingestion. Food and Agriculture Organization (FAO) and World Health Organization (WHO) defined probiotics as “Live microorganisms which when administered in adequate amount confers a health benefit on the host”. They have become very popular over the past two decades due to their countless benefits to human health and for this reason they have been incorporated in many food-related products, mainly fermented products. Probiotic strains are marketed in the form of capsules, powder, or fermented products. The global market of probiotics is rapidly increasing annually due to consumers’ interest in optimizing their health with functional foods (Di Cerbo and Palmieri 2015).

Lactic acid bacteria are generally regarded as safe (GRAS) microorganisms and are gram positive, facultative aerobes or anaerobes with bacilli, coccobacilli, or cocci morphology. These are non-respiratory, catalase-negative, acid-tolerant, and non-spore-forming bacteria, grouped on the basis of physiological, morphological, and metabolic constellation. These bacteria are normally associated with human and animal healthy mucosal surfaces and are a part of various animal and plant niches.

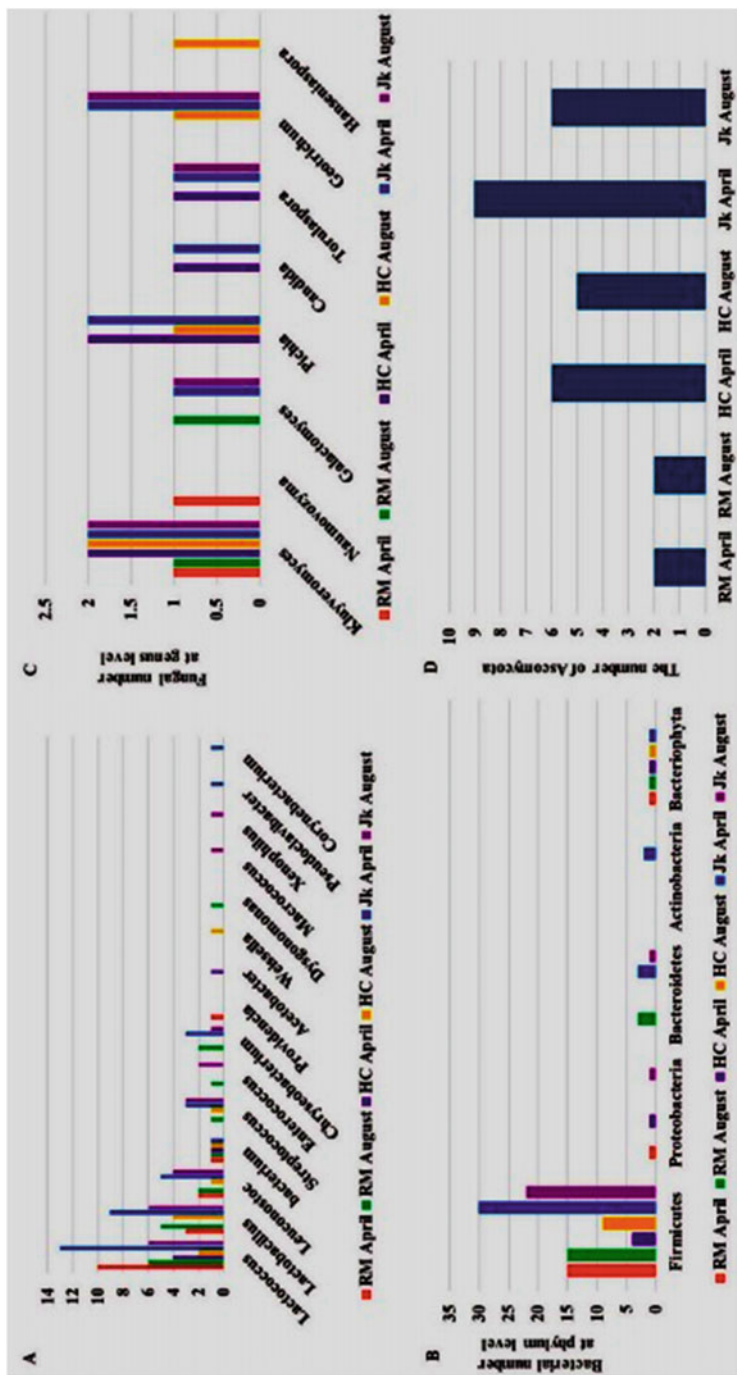


Fig. 4.4 Composition of the indigenous microflora, at the bacterial genus (a) and phyla (b) levels, and fungal genus (c) and Ascomycota (d) levels in raw and fermented milk samples. Data represents the number from the metagenomics analysis of two raw milk samples, and four fermented milk samples. RM April = raw milk samples collected in April, RM August = raw milk samples collected in August, HC April = Hurood Cheese samples collected in April, HC August = Hurood Cheese samples collected in August, Jk April = Jeuke samples collected in April, and Jk August = Jeuke samples collected in August (Gao et al. 2017)

Historically, the core genera of lactic acid bacteria include *Pediococcus*, *Lactobacillus*, *Streptococcus*, and *Leuconostoc*; however, nowadays there are 20 taxonomic revised genera. The significant LAB genera from food technology point of view are *Lactococcus*, *Leuconostoc*, *Lactobacillus*, *Enterococcus*, *Pediococcus*, *Aerococcus*, *Carnobacterium*, *Tetragenococcus*, *Vagococcus*, *Oenococcus*, and *Weissella* (Makarova et al. 2006).

Fermented milk associated LAB play a crucial role in the production of fermented beverages and other dairy products. They are strictly fermentative and produce lactic acid as a major product during the course of sugar fermentation. They are classified into two major groups based upon their fermentation potential, e.g., homofermentative or heterofermentative. Homofermentative LAB produces twice the energy from glucose fermentation as compared to heterofermentative. Homofermentation occurs through Embden Meyerhof Parna's pathway, whereas heterofermentation occurs either through hexose monophosphate or pentose phosphate pathway. The end product in the former case is mainly lactic acid, while in the latter ethanol/acetic acid and CO₂ are also significantly produced (Bassyouni et al. 2012; Çetin 2011; Rattanachaiakunsoon and Phumkachorn 2010).

A higher intake of fermented dairy products would reduce the risk of immune and metabolic disorders that will reduce the risk of obesity. Metabolizable nutrients and beneficial microorganism are incorporated due to the intestinal microbiota flourishing with the consumption of fermented dairy products. Yogurt is one of the dairy products that is well known for its numerous health benefits due to the probiotics. The intestinal health is maintained with the restoration of healthy balance between the good and bad bacteria from the probiotic intake. Moreover, it enhances the humoral and cellular immunity (Borchers et al. 2009). Despite general gut microenvironment, every individual's gut has a unique pattern of microbial community, and thus the response towards the use of probiotics is different.

Flu-like symptoms and upper respiratory infections are decreased with consumption of probiotics, as there is an immunity boost with the production of IgA antibodies, T lymphocytes, and natural killer cells. Crohn's disease, colorectal cancer, celiac disease, ulcerative colitis, and irritable bowel are some of the diseases that are improved with the use of yogurt. The severity of diarrhea is reduced with the use of probiotics, as it is among the side effects of consuming antibiotics. Therefore, doctors have suggested the use of yogurt for patients taking an antibiotic course to prevent the risk of antibiotic associated diarrhea. A study showed how certain strains of good bacteria present in the probiotics will help reduce the time of infectious diarrhea (Kechagia et al. 2013).

Another interesting research shows how the probiotics impact the mental health, as there is link between the brain and gut called the gut-brain axis (Mayer et al. 2014). Yogurt has proven to help reduce anxiety and stress which further improves the mental health of the individual. The *Bifidobacterium* and *Lactobacillus* strains for 1–2 months have been proven to positively affect the memory, obsessive compulsive disorder, autism, depression, and much more. Probiotic supplements introduced in the diet for 8 weeks decreased 40 patient's depression levels along with C-reactive protein that causes inflammation.

Probiotics have been declared to be healthy for all those suffering from chronic heart illnesses, such as angina, cardiovascular disease (CVD), heart attack, etc. due to their potential to reduce pressure and cholesterol by lowering the low-density lipoproteins (LDL). Moreover, probiotic microbes help with digestion, as the cholesterol is broken down into bile, which adds digestion. The benefit of having probiotics is the prevention of the reabsorption of the broken-down cholesterol in the blood. Studies suggest the reduction of allergies and eczema in children and infants with the consumption of probiotics in the form of milk or yogurt.

The health-promoting properties of conjugated linoleic acid (CLA) include anticarcinogenic, antiatherogenic, anti-inflammatory, and antidiabetic activity, as well as the ability to reduce body fat (Sosa-Castañeda et al. 2015). Although it is a native component of milk, the amount consumed in foods is far from that required in order to obtain desired beneficial effects. Thus, increasing the CLA content in dairy foods through milk fermentation with specific LAB offers a promising alternative. An effective way to increase CLA uptake in humans is to increase its level in dairy products by using strains with high production potential.

4.5.2 Pathogenic Microbes

Mammary glands of milking animal are natural reservoirs of microbes. Many of these bacteria are not harmful to humans, but some may be harmful to humans even though the animals are not affected and appear healthy. As listed in Table 4.1, the bacteria present in dairy products may cause disease or spoilage. Human diseases from milk-borne pathogens are usually due to the consumption of raw milk or products made from raw milk such as fresh cheeses. Till now, major dairy microorganisms are predominately associated with *Brucella* spp., *Campylobacter jejuni*, *Coxiella burnetii*, *Salmonella enterica*, *Listeria monocytogenes*, *Mycobacterium bovis*, *Mycobacterium paratuberculosis*, *Yersinia enterocolitica*, and *Escherichia coli* O157:H7 (Table 4.1).

4.5.2.1 *Brucella* spp.

Brucella species (spp.) are found in many animal species including cattle, sheep, and goats. *Brucella* spp. are destroyed by pasteurization. *Brucella* spp. cause illness with symptoms that are flu-like and include fever, sweats, headaches, back pain, and physical weakness. In some cases, long-lasting symptoms of fever, joint pain, and fatigue may occur.

4.5.2.2 *Campylobacter jejuni*

Campylobacter jejuni is found in the intestinal tract, udder, and feces of cattle, in poultry and wild birds, and in contaminated water sources. *C. jejuni* is destroyed by pasteurization. *C. jejuni* is one of the most common bacterial causes of diarrheal illness. *C. jejuni* generally causes illness 2–5 days after exposure, and illness typically lasts 5–10 days. Symptoms of campylobacteriosis include diarrhea, bloody diarrhea, abdominal pain, cramping, nausea, vomiting, and fever. Patients with

Table 4.1 Dairy pathogenic bacteria and associated diseases

Organism	Source of microorganism	Disease condition	Reference
<i>Campylobacter jejuni</i>	Intestinal tract and feces	Gastroenteritis	Facciola et al. (2017)
<i>Coxiella burnetii</i>	Infected cattle, sheep, and goats	Q fever	
<i>Escherichia coli</i> O157:H7	Intestinal tract, and feces	Gastroenteritis, Hemolytic uremic syndrome (HUS)	
<i>Listeria monocytogenes</i>	Water, soil, and environment	Listeriosis	Radoshevich and Cossart (2018)
<i>Mycobacterium bovis</i> or <i>tuberculosis</i>	Infected animals	Tuberculosis	Lan et al. (2016)
<i>Mycobacterium paratuberculosis</i>	Infected animals	Johne's (ruminants)	Whittington et al. (2019)
<i>Salmonella</i> spp.	Feces, and environment	Gastroenteritis, Typhoid fever	
<i>Yersinia enterocolitica</i>	Environment, water, and infected animals	Gastroenteritis	Sabina et al. (2011)

Campylobacteriosis usually recover without specific treatment other than fluid and electrolyte replacement. In some persons with a compromised immune system, *C. jejuni* infection can lead to the more serious diseases like Guillan-Barré syndrome and Reiter syndrome. Guillan-Barré syndrome is a disorder that results in temporary neuromuscular paralysis, although 20% of those infected may have long-term disability and it may cause death. Reiter syndrome is a reactive arthritis that may affect multiple joints, particularly the knee joint. The prevalence of *C. jejuni* is very widespread. It has been reported in bulk tank raw milk samples in Illinois, Michigan, Minnesota, Ohio, Pennsylvania, South Dakota, Tennessee, Virginia, and Wisconsin, suggesting that the organism is ubiquitous. In these studies, *C. jejuni* was found in 0.4–12.3% of the bulk tank milk samples (Facciola et al. 2017; Jayarao et al. 2006).

4.5.2.3 *Coxiella burnetii*

Coxiella burnetii is a pathogen shed in the milk, urine, and feces of cattle, goats, and sheep. *C. burnetii* is considered to be the most heat-resistant, non-spore-forming pathogen commonly found in milk, and the established conditions for milk pasteurization are specifically designed to destroy this organism. *C. burnetii* causes Q fever, an illness characterized by a sudden onset of high fever, severe headache, nausea, vomiting, diarrhea, abdominal pain, chest pain, chills, sweats, sore throat, non-productive cough, and general malaise. Fever can last for 1–2 weeks. Most patients recover without any treatment, although *C. burnetii* may result in death. The prevalence of *Coxiella burnetii* was >94% in raw milk samples from the North-eastern, Midwestern, and Western regions of the USA tested between 2001 and 2003 (Kim et al. 2005).

4.5.2.4 *Escherichia coli* O157:H7

Escherichia coli O157:H7 is one strain in a large family of bacteria. Strains of *E. coli* are considered fecal coliforms. Most strains of *E. coli* do not cause illness and live in the intestinal tracts of healthy humans and animals. *E. coli* O157:H7 is found in the intestinal tract and feces of cattle and destroyed by pasteurization. *E. coli* O157:H7 produces toxins that cause illness in humans. Symptoms of illness include bloody diarrhea and abdominal cramps. In some cases, particularly in young children, *E. coli* O157:H7 infection causes hemolytic uremic syndrome, which destroys red blood cells and causes kidney damage or failure, and in some cases death. The prevalence of *E. coli* O157:H7 and Shiga-toxin producing *E. coli* have been reported for bulk tank raw milk samples in Minnesota, Pennsylvania, South Dakota, Wisconsin, and Ontario. *E. coli* O157:H7 was found in 0.87–10% of the bulk tank milk samples tested (Jayarao et al. 2001, 2006).

4.5.2.5 *Listeria monocytogenes*

Listeria monocytogenes is found in soil and water and has been isolated from a large number of environmental sources. It is destroyed by pasteurization, but if food products are contaminated after pasteurization, it can grow at refrigerator temperatures. Illness can occur as sporadic events or larger outbreaks. *L. monocytogenes* typically causes illness in pregnant adults, newborns, the elderly, and patients with compromised immune systems, but healthy adults and children may also become infected. Symptoms of Listeriosis include flu-like symptoms, fever, muscle aches, stiff neck, headache, septicemia, meningitis, miscarriage, still-birth, premature delivery, abortion, or death. The prevalence of *L. monocytogenes* has been reported for bulk tank raw milk samples in individual states (or grouped by region) for California, Colorado, Florida, Idaho, Illinois, Indiana, Iowa, Kentucky, Massachusetts, Michigan, Minnesota, Missouri, Nebraska, New Mexico, New York, Ohio, Pennsylvania, South Dakota, Tennessee, Texas, Washington, Wisconsin, Vermont, Virginia, and in Alberta and Ontario, Canada. *Listeria monocytogenes* was found in up to 12% of the bulk tank milk samples tested (Jayarao et al. 2001, 2006; Van Kessel et al. 2004) illustrating the widespread presence of *L. monocytogenes* in unpasteurized milk.

4.5.2.6 *Mycobacterium bovis* and *Mycobacterium tuberculosis*

Mycobacterium bovis and *Mycobacterium tuberculosis* are found in infected cattle worldwide. Both of these organisms are destroyed by pasteurization. *Mycobacterium bovis* and *Mycobacterium tuberculosis* cause tuberculosis, a lung disease. Tuberculosis in the USA is not very common today, although historically milk was a common source of tuberculosis. Tuberculosis is a concern in many parts of the world. *Mycobacterium paratuberculosis* causes Johne's disease in cattle. It has been suggested that *M. paratuberculosis* may be associated with Crohn's disease, an intestinal disorder, in humans, but this has not been confirmed (Peden 2000; Whittington et al. 2019).

4.5.2.7 *Salmonella* spp.

Salmonella species (spp.) contain several strains that cause illness in humans; the most common are the serotypes Enteritidis and Typhimurium. *Salmonella* has been found in the intestinal tracts of all warm-blooded animals including humans. *Salmonella* is destroyed by pasteurization. *Salmonella* spp. causes illness that can develop 12–72 h after exposure, and can last 4–7 days. Symptoms of Salmonellosis include diarrhea, abdominal cramps, and fever. Most people recover without treatment other than fluid and electrolyte replacement. Some cases may be severe and require hospitalization. A small number of people may develop Reiter syndrome, which is a reactive arthritis that may affect multiple joints, particularly the knee joint. The prevalence of *Salmonella* spp. has been reported for bulk tank milk samples in individual states (or grouped by region) for California, Colorado, Florida, Idaho, Illinois, Indiana, Iowa, Kentucky, Michigan, Minnesota, Missouri, New Mexico, New York, Ohio, Pennsylvania, South Dakota, Tennessee, Texas, Washington, Wisconsin, Vermont, Virginia, and Ontario, Canada. *Salmonella* spp. were found in 0.17–8.9% of the bulk tank milk samples tested (Jayarao et al. 2001, 2006; Van Kessel et al. 2004), indicating the widespread presence of *Salmonella* in unpasteurized milk.

4.5.2.8 *Yersinia enterocolitica*

Yersinia enterocolitica is found in the intestinal tract of farm animals, especially pigs, and in the environment. *Y. enterocolitica* is destroyed by pasteurization, but if food products are contaminated after pasteurization, *Y. enterocolitica* can grow at refrigerator temperature. *Yersinia enterocolitica* causes illness with symptoms of fever, abdominal pain, and diarrhea. The prevalence of *Yersinia enterocolitica* has been reported for bulk tank milk samples in Michigan, Minnesota, Pennsylvania, South Dakota, Tennessee, Wisconsin, Virginia, and Ontario, Canada. *Yersinia enterocolitica* was found in 1.2–18% of the bulk tank milk samples tested (Jayarao et al. 2001, 2006; Sabina et al. 2011).

4.5.2.9 Other Pathogens

Coliforms are a large group of bacteria that are found in the intestines of warm-blooded animals. Most coliforms are not pathogenic, but their presence indicates contamination, usually from fecal sources. Coliforms are destroyed by pasteurization. The prevalence of coliforms was detected in 62–95% of the raw bulk tank milk tested in regions that included California, Colorado, Florida, Idaho, Illinois, Indiana, Iowa, Kentucky, Michigan, Minnesota, Missouri, New Mexico, New York, Ohio, Pennsylvania, South Dakota, Tennessee, Texas, Washington, Wisconsin, Vermont, and Virginia (Jayarao et al. 2001, 2006; Van Kessel et al. 2004).

Psychotropic bacteria are capable of growing at 44.6 °F (7 °C) or less. This group of microbes is a concern in dairy products because they grow at refrigerator temperature and cause spoilage, often resulting in off-flavors. The most common psychrotrophs are in the genus *Pseudomonas*. These organisms are killed by pasteurization, but may occur in milk from contamination after pasteurization. Some bacterial pathogens are psychrotrophic, including *Listeria monocytogenes*, *Yersinia*

enterocolitica, some *E. coli* strains, and some *Bacillus* strains (Radoshevich and Cossart 2018; Sabina et al. 2011).

4.6 Microbial Additives

Milk itself is a natural source for a variety of bacteria; the group of lactic acid bacteria is one of the prime sources of microbial additives. Many health-promoting effects are achieved from bioactive molecules produced by dairy fermented products. In contrast to the conventional concept of probiotic (ingestion of alive bacteria for the production of metabolites within human gut), a biologically functional food concept is based on the endogenous production of healthy metabolites in the fermented products, as a result of the metabolic response of bacterial machinery. The main biologically active molecules produced by LAB during dairy fermentation are vitamins, gamma-aminobutyric acid, bioactive peptides, bacteriocins, enzymes, conjugated linoleic acid, and exopolysaccharides.

4.6.1 Bioactive peptides

In the process of milk fermentation, lactic acid bacteria digest many proteins into short peptides through proteolytic activity. These peptides are biologically functional and exhibit antioxidative, antimicrobial, antihypertensive, immunomodulatory, and antithrombotic properties (Nongonierma and FitzGerald 2015). One of the most important bioactive peptides is Angiotensin-I-converting enzyme (ACE) inhibitory peptides. ACE inhibitory peptides display strong antihypertensive features and have been reported from a number of dairies (Fitzgerald and Murray 2006; Pritchard et al. 2010). Initially, ACE-inhibitory peptides, Ile-Pro-Pro (IPP), and Val-Pro-Pro (VPP) were extracted from milk fermented by *L. helveticus* (Slattery et al. 2010). Later on, other lactic acid bacteria including *L. rhamnosus*, *L. plantarum*, *L. delbrueckii*, *L. acidophilus*, *Lactococcus lactis*, and *S. thermophilus* were reported as dairy starter cultures in the industry as a source of inhibitory peptides of ACE (Hafeez et al. 2014). β -casein (SLVYPFPGPI) is another bioactive peptide produced by *L. delbrueckii* in fermented milk (Qian et al. 2011). Similarly, two short peptides are produced by the hydrolysis of α -S2 casein during the process of fermentation; both peptides are antimicrobial and display protective function against many human pathogens including *Saccharomyces thermophilus*, *E. coli*, *Helicobacter pylori*, *Staphylococcus aureus*, *Streptococcus pyogenes*, and *Listeria monocytogenes* (Nagpal et al. 2011). Lactoferrin is another source of antimicrobial peptides (Zivkovic et al. 2013). Peptic digestion of lactoferrin produces short peptides that displayed antimicrobial activity against a broad range of bacteria including *E. coli*, *Listeria*, *Salmonella*, *Campylobacter*, and many fungal strains, however, non-toxic to *Bifidobacterium* (Quintieri et al. 2013; Shah 2007).

4.6.2 Bacteriocins

Bacteriocins are major ribosomal antimicrobial peptides known to inhibit adhesion and invasions of pathogens through direct microbial interaction or by altering the exterior environment leading to slow to no growth of microbes (Hernández-Ledesma et al. 2014). Different types of ribosomal short peptides and their respective immunity proteins are produced by many lactic acid bacteria, which provide a broad range of antimicrobial activity against major human pathogens. Thus, bacteriocin producers are a potential alternative to pharmaceutically synthesized antibiotics and offer a means of controlling pathogen-induced inflammation (Cotter et al. 2013). Many lactic acid bacteria are generally regarded as safe (GRAS) for human consumption. These are the ideal source of bacteriocin production on a commercial scale (Nes et al. 2007). Because of the strong antimicrobial characteristics of bacteriocin, the producing strains also use as natural food-preservatives.

Nisin is the most used for food preservation due to its antimicrobial effect against spoilage and disease-associated bacteria like *Listeria* and clostridia spores. Plantaricin C is another broad-spectrum peptide produced by *L. plantarum* and documented as an immunomodulator for dendritic cells (Meijerink et al. 2010). Briefly, the use of bacteriocins directly or bacteriocin-producing bacteria as a starter culture for the generation of bacteriocins through fermentation became an efficient health-promoting strategy. Similarly, the use of lacticin-producing strain of *Lactococcus lactis* greatly inhibits the growth of *Listeria monocytogenes* in Cheddar cheese (Chen and Hoover 2003). Many other lactic acid bacteria like *L. acidophilus*, *Pediococcus acidilactici*, and *Leuconostoc mesenteroides* known for their specific bacteriocins can be added as an adjunct in many food fermentations processes as food preservatives (Anjum et al. 2014). Besides the production of antimicrobial peptides, these bacteria pose many other advantages to enhance flavor, texture, and nutritional value of the product (Gaggia et al. 2011; Jiang et al. 2012; Grosu-Tudor et al. 2013; Mitra et al. 2010; Khan et al. 2010; Tamang et al. 2009).

4.6.3 Enzymes

Many *Lactobacillus*, *Lactococcus*, and *Streptococci* species can ferment milk by producing hydrolytic enzymes. The proteolytic machinery of lactic acid bacteria (LAB) comprises membrane-bound aminopeptidases, endopeptidases, and proteinases for the production of hydrolysates. Fermentation-associated microbes depend on the degradation of milk proteins to get free amino acid residues and short peptides required for their growth. Yogurt and other conventional fermented dairy products associated with bacteria reduce lactose intolerance and improve lactose digestion by degrading lactose through the activity of microbial β -galactosidase (De Vrese et al. 2001; Patel et al. 2013).

4.6.4 Vitamins

Although milk contains many vitamins, however, in the fermented milk the vitamin producer lactic acid bacteria enhance the nutritional value of the product. Many species of *Lactobacillus* and *Bifidobacterium* genera secrete vitamin B complex (B1, B2, B7, B9, B12) during the fermentation process. Dietary depletion of vitamin B1 (thiamine) and vitamin B2 (riboflavin) can dysregulate glucose metabolism in the brain and lead to both skin and liver diseases, respectively (Russo et al. 2014). Some *Propionibacteria* and lactic acid bacteria can produce cobalamin, folic acid, and biotin, such as *L. casei* richly produce thiamine and riboflavin in fermented milk (Hugenholtz et al. 2002; Drywień et al. 2015).

Vitamin B7 (Biotin) deficiency can be genetic or dietary that affects the skin and hair health. Starter culture of lactic acid bacteria, e.g., *L. helveticus* and *Propionibacteria*, ferment and produce biotin-enriched milk products (Patel et al. 2013). The deficiency of vitamin B9 (Folate) is linked to neural tube impairment and cardiac issues. Limited strains of lactic acid bacteria including *Streptococcus thermophilus* CRL803/CRL415, *L. amylovorus*, and *L. bulgaricus* are designated as vital for dairy folate enrichment (Laiño et al. 2014). Among *Bifidobacteria*, *B. catenulatum* is known as rich folate producer.

Plants, animals, and fungi are unable to produce, thus bacteria are the exclusive source of vitamin B12 (cobalamin) (LeBlanc et al. 2011). It has been demonstrated that vitamin B12 cobalamin can be synthesized by some bacteria such as *L. reuteri*, *Propionibacterium freudenreichii*, and *B. animalis* (Gu et al. 2015; Moslemi et al. 2016; Patel et al. 2013; Van Wyk et al. 2011). *Propionibacterium freudenreichii* is able to secrete vitamin B12 and the pseudovitamin B12 isoforms during the milk fermentation process. Pseudovitamin B12 converts into vitamin B12 to enhance the bioavailability of cobalamin (Deptula et al. 2017).

Vitamin K is essential for arterial de-calcification to reduce the risk of cardiovascular disorders. Its deficiency can cause medical ailments such as osteoporosis and hemorrhage (LeBlanc et al. 2011). Vitamin K in nature exists in the forms of phyloquinone (vitamin K1) and menaquinone (vitamin K2). Menaquinone is microbial vitamin synthesized by *Lactococcus lactis*, a common starter culture for the industrial production of sour cream, cheese, kefir, and buttermilk (Walther et al. 2013).

4.6.5 Gamma-Aminobutyric Acid

Gamma-aminobutyric acid (GABA) is one of the exclusive inhibitory neurotransmitters (INT) of the central nervous system (CNS). Glutamate decarboxylase (GAD) catalyzes glutamate in the process of α -decarboxylation and synthesizes GABA (Tajabadi et al. 2015). Interestingly, *Bacteroides* genus is the largest GABA producer group; for example, *Bacteroides fragilis* produces GABA, polysaccharide A, and sphingolipids; the latter two are evident for the health of immune and gut systems (Tan et al. 2019; Troy and Kasper 2010). In addition to

Bacteroides, several lactic acid bacteria have been reported as the source of GABA producers including *Lactococcus lactis*, *Lactobacilli* (*L. paracasei*, *L. brevis*, *L. delbrueckii*, *L. plantarum*, *L. helveticus*, *L. buchneri*), *Streptococcus thermophilus*, and *Bifidobacterium* spp. (Barrett et al. 2012; Li and Cao 2010) which are most promising candidates.

Few strains, *S. salivarius* fmb5, *L. casei* Shirota, and *L. plantarum* NDC75017, were selected for commercial production of GABA-enriched fermented milk drink (Chen et al. 2016; Inoue et al. 2003; Shan et al. 2015). Similarly, yogurt and cheese enriched with GABA were produced by using the strain *S. thermophiles* APC151, *L. brevis* OPY-1, and *Lactococcus lactis* (Linares et al. 2016; Park and Oh 2007; Pouliot-Mathieu et al. 2013).

4.6.6 Conjugated Linoleic Acid

Polyunsaturated fatty acids (PUFA) are important metabolites of lactic acid and bifidobacteria bacteria such as conjugated linoleic acid (CLA) produced by conversion of linoleic acid. Many LAB and bifidobacterial strains like *L. casei*, *L. plantarum*, *Lactococcus lactis*, *L. rhamnosus*, *L. acidophilus*, *B. bifidum*, and *B. animalis* were reported to produce CLA in dairy products (Florence et al. 2009; Sosa-Castañeda et al. 2015; Van Nieuwenhove et al. 2007; Yang et al. 2015). These strains also used to add extra CLA contents in cheese and yogurt as adjunct cultures (Van Nieuwenhove et al. 2007).

4.6.7 Exopolysaccharides

Exopolysaccharides (EPS) are complex carbohydrates produced by a group of lactic acid bacteria, Propionibacteria, and bifidobacteria in the form of secretions during the fermentation process of dairy products and support the immune system by promoting host beneficial microflora (Salazar et al. 2016). Lactic acid bacteria including *L. delbrueckii*, *L. mucosae*, *Lactobacillus kefiranofaciens*, *Lactococcus lactis*, and *S. thermophilus* are predominant EPS-producing species in the yogurt and cheese and boost immune-stimulatory effects and reduce cholesterol levels (Darilmaz and Gumustekin 2012; Makino et al. 2016; Ryan et al. 2015). Specifically, *Lactobacillus kefiranofaciens* produce EPS metabolites, which dramatically inhibit the invasion of pathogens like *Listeria monocytogenes* and *Salmonella enteritidis* in the enterocytes (Jeong et al. 2017; Medrano et al. 2008). Antimicrobial effects of these metabolites may extend to other microbial species in the gut microflora.

In addition to health-promoting effects, EPS greatly enhance the quality, sensory and rheological features of dairy products. For example, *Bifidobacterium longum* and *S. thermophiles* are well known for immune-modulatory effects and high EPS production that directly reduces syneresis and improves the texture and viscosity of

fermented ice-cream and yogurt (Dertli et al. 2016; Han et al. 2017; Hidalgo-Cantabrana et al. 2012; Prasanna et al. 2013).

4.6.8 Other Bio-Functional Molecules

Carbohydrate-fermenting microbes also secrete many neuroactive molecules including Clostridia metabolites, short-chain fatty acids, histamine, and diacylglycerol kinase (Karl et al. 2018; Shaw 2017). Mycelial fungi *Aspergillus*, *Actinomucor*, *Monascus*, *Amylomyces*, *Mucor*, *Rhizopus*, and *Neurospora* also produce various carbohydrate enzymes including β -galactosidase, α -amylase, pectinase, maltase, cellulase, amyloglucosidase, hemi-cellulase as well as lipase and proteases.

4.7 Industrial Importance of Dairy Microbes

The dairy starter culture is used on a large scale in the food industries for the manufacturing of butter, cheese, yogurt, kefir, sour cream, and other fermented milk products. The principle purpose of the starter culture is to convert lactose and other sugars present in milk to lactic acid. The industrially important lactic acid bacteria are used as a starter culture for the preparation of many important food products and they impart various sensory characteristics to them, i.e., aroma, texture, viscosity, and flavor; henceforth, an increase in the use of LAB probiotics has been observed in the recent years. Dairy industry has become an integral part of food industries worldwide. Henceforth, the demand for starter culture is growing by leaps and bounds over the past few years. Lactic acid bacteria have also been reported to play a crucial role in the cheese ripening and giving it perfect consistency, flavor, and aroma (Hannon et al. 2003). Apart from this, many antimicrobial short peptides, exopolysaccharides, and enzymes are associated with dairy microbes to enhance nutritional value and shelf life of product.

The growth of the dairy starter culture market is driven by the growth of dairy industry. The overall increase in the production of dairy products and growing demand for dairy-based products is expected to boost the demand for the dairy starter culture globally.

4.8 Nutraceutical Properties of Milk Microbiota

Milk proteins exhibit a wide range of nutraceuticals and biological properties. Most of the dairy proteins are specific in biological functions and display many health-promoting effects. These short peptides are inactive within the endogenously secreting proteins and can be cleaved by proteolytic activity of gastrointestinal enzymes upon ingestion of milk or fermentation process. Proteins are the essential components of dairy products that have a variety of applications in several food industries.

4.8.1 Antihypertensive

Although many fermented food products exhibit medicinal characteristics, however, fermented dairy products are exceptional in the nutraceutical contents. Regular consumption of fermented dairy products displayed anticholesterol and antihypertensive properties, thus reducing the risk of cardiovascular diseases. In addition to milk proteins, fermented milk-associated probiotic bacteria secrete some proteins and metabolites and exert an overall positive impact on the health of the consumer. Kefir and Calpis contain many short peptides that are responsible for hypotensive effects. Some lactic acid bacteria functionally antihypertensive such as *L. rhamnosus*, *L. plantarum*, *L. delbrueckii* ssp. *bulgaricus*, *Lactococcus Lactis*, *L. acidophilus*, and *S. thermophilus* in fermented milk are the commercial source of ACE inhibitory peptides (Hafeez et al. 2014), and thus greatly reduces elevated blood pressure (Shah 2015).

4.8.2 Anticarcinogenic

Many dairy raw and fermentation-associated bacteria like *L. acidophilus* inhibit the conversion of paracarcinogenic molecules into carcinogenic forms by reducing specific enzymes including azoreductase β -glucuronidase, and nitroreductase in human, hence, trigger and boost body immunity. In this context, South Asian fermented milk product *dahi* (yogurt) is the most known anticarcinogenic dairy product. Daily use of yogurt can reduce the risk of cervical, bladder, and colon cancer (Mohania et al. 2014).

4.8.3 Gastrointestinal Support

Many fermented dairy lactic acid bacteria significantly reduce a load of gastrointestinal diseases (Verna and Lucak 2010). Intake of *Lactobacillus* species in the food improves the symptoms of ulcerative colitis, paucities, and inflammatory bowel disease (Orel and Trop 2014). Similarly, *L. rhamnosus* specifically treat severe diarrheal issue (Szajewska et al. 2007). Moreover, probiotics in fermented dairy products manifest immunomodulatory effects and thus inhibit the growth of pathogens in the gastrointestinal tract (Balamurugan et al. 2003).

4.8.4 Anti-allergic Effects

Lactobacillus kefiranofaciens has an anti-allergic effect. In the process of fermentation, cleavage, and degradation of casein proteins of allergenic reactivity thus increases tolerance (Alessandri et al. 2012). Several species of *Lactobacillus* captured attention because of their ability to produce interleukins and interferons, and thus significantly reduce allergic reactions due to food or dermatitis. Yogurt is a rich

probiotic supplement that increases glucose tolerance and reduces oxidative stress, hyperglycemia, dyslipidemia, hyperinsulinemia, indicating a lower risk of diabetes (Yadav et al. 2007).

4.8.5 Alleviation of Lactose Intolerance

Lactose intolerance both in children and in adults arises because of the unavailability of β -D-galactosidase (Shah 2015). Lactic acid bacteria including *L. delbrueckii* and *S. thermophilus* strains are capable to secrete high contents of β -D-galactosidase which improve the symptoms of lactose malabsorption in lactose intolerant people. Consumption of fresh yogurt (with live yogurt cultures) has demonstrated better lactose digestion and absorption than with the consumption of a pasteurized product. *Kefir* can minimize the symptoms of lactose intolerance by providing an extra source of β -galactosidase (Hertzler and Clancy 2003).

4.8.6 Brain Gut Axis Aid

Many mental conditions including psychiatric, neurodevelopmental and neurodegenerative disorders can be potentially treated with the psychobiotic microbes. These bacteria include many species of *Lactobacillus*, *Lactococcus*, *Bifidobacterium*, *Streptococcus* and few species of *Bacillus* and *Clostridium* genera. Appropriate dose management of these microbes display psychotropic potential by the production of neuroactive molecules, such as neurotransmitters (GABA, serotonin, norepinephrine, acetylcholine, glutamate), neuropeptides (neuropeptide Y, glucagon-like peptide-1 and 2, Tyr-Tyr peptide), and other molecules like cholecystokinin and substance P for the regulation of brain-associated protein like brain-derived neurotrophic factor (BDNF). The regulation of neuronal proteins is important to modulate specific behavior types. Psychobiotics employ antidepressant, anti-anxiety, and antidepressant properties, and improve sleep quality and energy metabolism of brain through enteric neural network, systemic, humoral, and metabolic mechanisms in the body and establish a brain gut axis. The bacteria-brain communication is important in the modulation of behaviors related to the central nervous system (Hao et al. 2019).

4.9 Dairy Psychobiotics

Lactobacillus and *Bifidobacterium* have reportedly shown potential psychobiotic activity when present in higher numbers in the human gut microbiome. Dairy products which undergo fermentation have proven to be a chief reliable source of *Lactobacillus* species. Species of *Lactobacillus* are reported to produce a variety of neurotransmitters, and their precursors *in vitro*. The gut microflora plays an important role in the regulation of bioavailability of the precursor molecules for

neurotransmitters. In the brain, dopamine is converted to norepinephrine through an enzyme known as dopamine- β -hydroxylase. The inhibitors of this enzyme 4-hydroxyphenylacetate, and 4-cresol, are metabolites produced by *Clostridia*, a class of *Firmicutes*. Similarly, the microbes that ferment carbohydrates produce a short-chain fatty acid, known as butyrate that has been reported to impact the intestinal entero-chromaffin cells by stimulating them to synthesize serotonin (5-HT). As shown in Table 4.2, these precursor molecules for neurotransmitters and other metabolites produced by the probiotic microbes are neuroactive molecules, and have an influence on the modulation of enteric nervous system signaling, which in turn impacts the gut-brain axis (Yong et al. 2020).

4.9.1 *Lactobacillus rhamnosus*

Lactobacillus rhamnosus has been a commercially available probiotic for quite some time. It has been reported that *L. rhamnosus* is able to metabolize glutamate and gamma amino-butyric acid (GABA), which are the excitatory and inhibitory neurotransmitters, respectively. *L. rhamnosus* *in vitro* has reportedly utilized microbial enzymes glutamate decarboxylase to produce GABA and glutaminase to produce glutamate. Studies on mice models have shown that an intervention of *L. rhamnosus* in the diet resulted in alleviation of anxious and depressive behaviors. The alteration was brought about in the expression of mRNA of the receptors of GABA. However, the reduced anxious and depressive behavior of the mice was also dependent on the neural signaling from the intact vagus nerve. GABA produced by the gut microbiota is reported to utilize the H⁺/GABA symporter to cross the intestinal barrier *in vitro*. The enteric neurons and the vagus afferents have a large number of GABA receptors and transporters, since it is a chief inhibitory neurotransmitter. These GABA receptors and transporters are possibly utilized by GABA molecules which are produced by microbes, such as *L. rhamnosus* (Bravo et al. 2011; Nielsen et al. 2012; Lin 2013; Yong et al. 2020).

4.9.2 *Lactobacillus casei*

Lactobacillus casei has a potential for maintaining gut health, and is known for its industrial value as a starter culture for fermentation. A dietary intervention of milk containing *L. casei* resulted in a reportedly uplifted mood in individuals. In the analysis of saliva collected from individuals who reported to be stressed, it was found that cortisol levels were high. Consequently, the high cortisol levels resulted in abdominal disturbances and flu symptoms. However, in the clinical trials, an intervention with *L. casei* reportedly alleviated the abdominal and flu symptoms, and reduced the stress frequency by lowering the cortisol levels. Similar to *L. rhamnosus*, *L. casei* was also able to produce GABA, which is involved in inhibition mechanisms. The presence of *L. casei* in a probiotic comprising a mixture of similar species resulted in a reduction in the depression levels of individuals diagnosed with

Table 4.2 The neurotransmitters produced by probiotics and their regulatory functions

Neurotransmitter	Regulatory functions	Probiotics	References
Gamma-aminobutyric acid (GABA)	<ul style="list-style-type: none"> • Hippocampal neurogenesis • HPA axis regulation • Mood 	<i>L. brevis</i> <i>L. rhamnosus</i> <i>L. reuteri</i> <i>L. paracasei</i> <i>L. plantarum</i> <i>L. bulgaricus</i> <i>L. helveticus</i> <i>L. casei</i>	Barrett et al. (2012), Oleskin et al. (2014)
Serotonin (5-HT)	<ul style="list-style-type: none"> • Impulsivity • Aggression • Appetite • Circadian rhythm • Learning • HPA axis regulation • Mood 	<i>L. plantarum</i> <i>L. helveticus</i>	Oleskin et al. (2014)
Dopamine (DA)	<ul style="list-style-type: none"> • Motivation • Concentration • Psychomotor speed • Ability to experience pleasure • Mood 	<i>L. plantarum</i> <i>L. helveticus</i> <i>L. casei</i> <i>L. bulgaricus</i>	Oleskin et al. (2014)
Norepinephrine (NE)	<ul style="list-style-type: none"> • Aggression • Cognitive function • Sleep • Sympathetic activity • HPA axis regulation • Mood 	<i>L. helveticus</i> <i>L. casei</i> <i>L. bulgaricus</i>	Oleskin et al. (2014)
Glutamate (Glu)	<ul style="list-style-type: none"> • Gastrointestinal reflexes • Intestinal motility • HPA axis regulation • Mood 	<i>L. rhamnosus</i> <i>L. reuteri</i> <i>L. plantarum</i> <i>L. paracasei</i> <i>L. helveticus</i> <i>L. casei</i> <i>L. bulgaricus</i>	Oleskin et al. (2014)
Histamine	<ul style="list-style-type: none"> • Motivation • Learning • Memory • Appetite • Sleep • Sympathetic activity • Mood 	<i>L. plantarum</i> <i>L. reuteri</i>	
Acetylcholine (ACh)	<ul style="list-style-type: none"> • Cognition • Synaptic plasticity • Analgesia • Sleep • HPA axis regulation • Mood 	<i>L. plantarum</i>	

clinical depression, and those exhibiting depressive symptoms. The production of microbial GABA by *L. casei* shows that there is a possibility to have similar mechanisms, and the resultant antidepressant effect like *L. rhamnosus* (Kato-Kataoka et al. 2016; Oleskin et al. 2014; Takada et al. 2016; Yong et al. 2020).

4.9.3 *Lactobacillus brevis*

Lactobacillus brevis has a possible overlap in the underlying mechanisms for GABA production, with *L. rhamnosus* and *L. casei*, though reportedly the central GABAergic system remains uninfluenced by its presence. *L. brevis* utilizes the microbial glutamate decarboxylase to produce GABA. An increase in the total GABA content was observed in a quantitative analysis of milk fermented with a starter culture of *L. brevis*. A study on rat models for depression found that *L. brevis* exhibited antidepressive potential, much like fluoxetine, after a dietary intervention of milk fermented with *L. brevis*. Since GABA is the primary inhibitory neurotransmitter, it plays an important role in sleep quality and REM cycle, and hence its imbalance may result in sleep disorders. Sleep disorders such as insomnia are mostly treated by an increased dosage of GABA through diet, or by treatment with pharmacological benzodiazepine which targets GABA receptors. In mice models, the presence of *L. brevis* in the diet has reportedly improved the quality of sleep; therefore it shows great potential to be a therapeutic intervention for treatment of insomnia in people suffering from major depressive disorder (Ko et al. 2013; Miyazaki et al. 2014; Yamatsu et al. 2015; Yong et al. 2020).

4.9.4 *Lactobacillus reuteri*

Lactobacillus reuteri is a probiotic that enhances the immune system. *L. reuteri* is reported to have anti-inflammatory effects on the human body. Hydrogen peroxide is a chief metabolite produced by *L. reuteri*, that inhibits the activity of indoleamine 2,3 dioxygenase through peroxidase-mediated catalyzed reactions. Indoleamine 2,3 dioxygenase is reported to impact levels of kynurenine, and the microbial hydrogen peroxide can possibly cross the intestinal epithelial lining, and reduce the activity of indoleamine 2,3 dioxygenase. Hence, the suppressed activity of this key enzyme lowers the kynurenine levels. *L. reuteri* utilizes microbial histidine decarboxylase to produce histamine from the metabolism of dietary L-histidine. Diacylglycerol kinase is also a microbial enzyme produced by *L. reuteri*, which metabolizes diacylglycerol to phosphatidic acid which plays a role in the microbial histamine anti-inflammatory activity. Both the microbial histamine and the enzyme diacylglycerol kinase produced by *L. reuteri* have been reported to interact with the histamine receptors and enhance the immune response by reducing the inflammatory cytokines in the gastrointestinal tract (Jang et al. 2019; Réus et al. 2015; Yong et al. 2020).

4.9.5 *Lactobacillus plantarum*

Lactobacillus plantarum has been reported to utilize fatty acid synthase II-thioesterase to synthesize butyrate following a butyrogenic pathway mediated by glutamine. Studies on mammals have reported that a dietary intervention of *L. plantarum* has antidepressive effects. It has also been reported that there was an overall increase in levels of butyrate, as *L. plantarum* not only produces butyrate as a metabolite, it also favors the colonization of *Bacteroidetes*, *Lactobacillus*, and *Roseburia* which are also butyrate-producing bacteria. Supplements containing *L. plantarum* have exhibited the enhancement of hippocampal brain-derived neurotrophic factor. Similarly, analysis of butyrate levels from the cecum showed an elevation after the administration of *L. plantarum* (Botta et al. 2017; Dhaliwal et al. 2018; Yong et al. 2020).

4.9.6 *Lactobacillus gasseri*

Lactobacillus gasseri is known for its anti-inflammatory effect on the immune system. Heat-killed or live form of *L. gasseri*, both have the ability to alter the levels of gut microbiome by favoring the colonization of few microbes over others in the gastrointestinal tract. A study reported that consumption of milk containing probiotics including *L. gasseri* showed an altered gut microflora composition in stressed individuals. *L. gasseri* is reported to produce gasserins which have antibacterial properties against possible pathogens present in the gastrointestinal tract. An introduction of live *L. gasseri* resulted in reduced growth of inflammatory bacterial populations such as *Enterobacteriaceae*, *Clostridium cluster IV group*, and *Veillonella*, along with altered levels of short-chain fatty acids. The heat-killed form of *L. gasseri* reportedly increased the population of *Dorea longicatena*, while decreasing *Bacteroides vulgatus*. *L. gasseri* when administered in heat-killed form across multiple studies showed that it does not have a unique microbial target, but alters the gut microflora composition towards a favorable anti-inflammatory environment (Nishida et al. 2017; Sawada et al. 2017; Yong et al. 2020).

4.9.7 *Lactobacillus helveticus*

Lactobacillus helveticus is a probiotic that imparts multiple health benefits to the human body. *L. helveticus* has been reported to increase immunity by protection against pathogenic bacterial colonization, along with prevention of diseases of the gastrointestinal tract. In patients diagnosed with clinical depression and symptoms related to depression, a probiotic intervention was introduced which included *L. helveticus* and *Bifidobacterium longum*, and a positive result was observed as depressive symptoms were reduced. In a study involving cognitively impaired rodent models, it was reported that an intervention of *L. helveticus* enhanced cognitive performance and memory. Similarly, *L. helveticus* introduced as a dietary

intervention improved cognition abilities such as attention, memory, and learning as reported by studies on animal models and human participants (Liang et al. 2015; Oleskin et al. 2014; Yong et al. 2020).

4.9.8 *Lactobacillus paracasei*

Lactobacillus paracasei belongs to the *Lactobacillus casei* group which also includes *L. rhamnosus* and *L. casei*. The *Lactobacillus casei* group is the most used *Lactobacillus* species, and is used as a potential therapeutic agent for health, along with being of industrial and commercial use. Lactocepain is a protein that is produced by *L. paracasei*, it is a serine protease, and hence is sensitive to high temperatures. However, studies have demonstrated that whether alive or heat-killed, *L. paracasei* exhibits antidepressive and mood uplifting mechanisms. Reportedly while an intervention of heat-killed *L. paracasei* resulted in elevated levels of dopamine in the brain, introduction of live *L. paracasei* increased the levels of serotonin. In a study on mice models, where depression was induced by corticosterone, oral administration of both forms of *L. paracasei* demonstrated potential for antidepressive agents in par with fluoxetine. Similarly, in a study done on healthy individuals in stressful times, a dietary intervention of *L. paracasei* in its heat-killed form kept the mood stable and prevented it from deteriorating (Chunchai et al. 2018; Réus et al. 2015; Wei et al. 2019; Yong et al. 2020).

4.9.9 *Lactobacillus kefiranofaciens*

Lactobacillus kefiranofaciens is reported to have a variety of physiological alterations as a result of its administration. In a study on chronically stressed depressive mice models, the oral administration of *L. kefiranofaciens* showed a marked improvement in their behavior: alleviated depressive and stress-related mood. *L. kefiranofaciens* is reported to affect the Tryptophan/Kynurenine metabolic pathway by increasing the levels of tryptophan in circulation in the body, and hence reducing the Kynurenine/Tryptophan ratio. The presence of *L. kefiranofaciens* also favors the abundance of beneficial gut microbiome such as *Akkermansia*, *Bifidobacteriaceae*, and *Lachnospiraceae*, while reducing the abundance of *Proteobacteria* in the gastrointestinal tract. *L. kefiranofaciens* impacts the immune system by increasing the level of splenic IL-10, and decreasing the levels of splenic IL-6 and IFN- γ levels. The exopolysaccharide is being considered the potential focal point for future researches, as it seems to play a role in the *L. kefirifaciens*' ability to mediate the hypothalamus-pituitary-axis, the immune system, the tryptophan/kynurenine metabolic pathway, and the colonization of gut microbiome (Jeong et al. 2017; Sun et al. 2020; Yong et al. 2020).

4.9.10 *Bifidobacterium breve*

Bifidobacterium breve is a probiotic widely known for its antidepressant potential. There has been no widely reported success in understanding and clarifying the exact mechanism of action of *B. breve*. However, a metabolite produced by *B. breve*, benzoic acid, was reported in a study to play a role in the antidepressive mechanism. *B. breve* introduced to schizophrenic patients showed reduced depressive symptoms, and hence is prescribed as an antidepressive agent. It was also reported that *B. breve* uplifted mood, and enhanced cognition in cognitively impaired elderly individuals (Okubo et al. 2019; Yong et al. 2020).

4.9.11 *Clostridium butyricum*

Clostridium butyricum belongs to *Clostridia* which are a class of bacteria responsible for fermenting free sugars and carbohydrates. *C. butyricum*, as the name suggests, produces a metabolite known as butyrate as a result of carbohydrate fermentation. Similar to *L. paracasei* and *B. infantis*, *C. butyricum* has a potential to upregulate the central BDNF-5HT system through a mechanism involving its metabolite, butyrate. This microbial butyrate-mediated upregulation results in reduced depressive symptoms. Despite being a potential antidepressant agent, not all strains of *C. butyricum* are safe for consumption, as few are reportedly pathogenic and can cause gastrointestinal complications (Anderberg et al. 2016; Cassir et al. 2016; Yong et al. 2020).

4.10 Conclusions

Conclusively, total dairy microflora presents a complete profile of differential bacterial and fungal communities that predominately depends on the chemical composition of milk. Lactic acid bacteria are the most versatile group in all dairy microbiota that display a variety of strains associated with the milk of different animals. The health-promoting advantages of microbes and their additives are overwhelming the few effects of few harmful bacteria in the dairy environment. Despite many benefits of dairy associated bacteria, the emergence of psychobiotics is directing a new avenue towards personalized treatment of many psychological disorders and enhancing the need to explore new microbes with therapeutic potential (Table 4.2).

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Remarkable Metabolic Versatility of the Commensal Bacteria *Eubacterium hallii* and *Intestinimonas butyriciproducens*: Potential Next-Generation Therapeutic Microbes

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Abstract

Our gastrointestinal tract is host to a wide variety of bacteria, together referred to as the microbiota. These bacteria influence our health and well-being through many different mechanisms. Most of these effects are the result of metabolites that are being produced by these bacteria or through triggering the expression of metabolites by the host. In this chapter we will highlight two bacterial species that have remarkable metabolic features that make them prime candidates for the development as next-generation probiotics. The first is *Eubacterium hallii*, a bacterium that is capable of producing two important short-chain fatty acids (SCFAs), propionate and butyrate. The other bacterium is *Intestinimonas butyriciproducens*, a bacterium that is capable of producing butyrate from not only sugars but also lysine and even glycated lysine. Both species also can produce pseudovitamin B12. We will discuss conditions that can result in the production of specific metabolites and the implications this can have on human health.

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5.1 Introduction

The human body is host to trillions of microorganisms, mostly bacteria. These microorganisms can be found on every surface that is in contact with the outer world such as our skin, our digestive tract, the lungs, and even the eye (Willcox 2013). By far the largest bacterial community is found in our gut. The importance of these bacteria in relation to our health has long been overlooked, but even Hippocrates, who by many is seen as the founding father of modern medicine, apparently already claimed “all disease begins in the gut.”

The first person in more recent times who recognized that bacteria might play an important role in health was the Russian biologist Elie Metchnikoff. While his theory on how to improve health by manipulating the intestinal microbiota with host-friendly bacteria in yoghurt (probiotics) caught the attention for a while (Metchnikoff 1907), in the coming years it would drift out of attention, largely due also to the difficulty of growing gut bacteria in the lab.

Someone whose contribution should not go unmentioned is Carl Woese, an American microbiologist who, together with George Fox, defined the Archaea as a separate kingdom from bacteria, based on 16S ribosomal RNA sequence (Woese and Fox 1977). With the emergence of modern technologies such as polymerase chain reaction and next-generation DNA sequencing came the possibility to quickly distinguish different bacteria on the basis of 16S rRNA sequence and detect and identify bacteria that could not be detected before by classical growth experiments. Not only the identification of bacteria has made considerable progress, also cultivation conditions have evolved and as a result over 1000 different, mainly anaerobic species from our gut can now be cultivated *in vitro* (Rajilić-Stojanović and de Vos 2014).

In the wake of research that followed, it became increasingly clear that the bacterial populations that surround us produce many substances essential to our bodies and thus play a major role in health and disease. From that came the realization that there is an intricate relationship between the food that we eat, the microbes in our gut, the metabolites they produce, and how they affect our body (Fig. 5.1, Holmes et al. 2012; Patterson et al. 2014). The main metabolites produced by the bacteria in our gut are the short-chain fatty acids acetate, propionate, and butyrate (Den Besten et al. 2013). Acetate, the most abundant SCFA from our gut, is a primary carbon source for other gut bacteria, who convert this to either propionate or butyrate (Bui et al. 2014; Moens et al. 2017; Schwab et al. 2017). Of all SCFA acetate is the one that is systemically most available (Boets et al. 2017). Propionate plays an important role in glucose metabolism through the liver and is thought to lower lipogenesis and serum cholesterol levels, although most studies for this have been conducted in rodents and would need confirmation for humans (Lin et al. 1995). Butyrate is taken up directly by the colonocytes that line our gut for which it serves as a direct source of energy. As a result, butyrate directly contributes to a healthy gut. In addition, these SCFA have an important role as signaling molecules, thereby affecting many factors such as satiety, secretion of hormones, and glucose

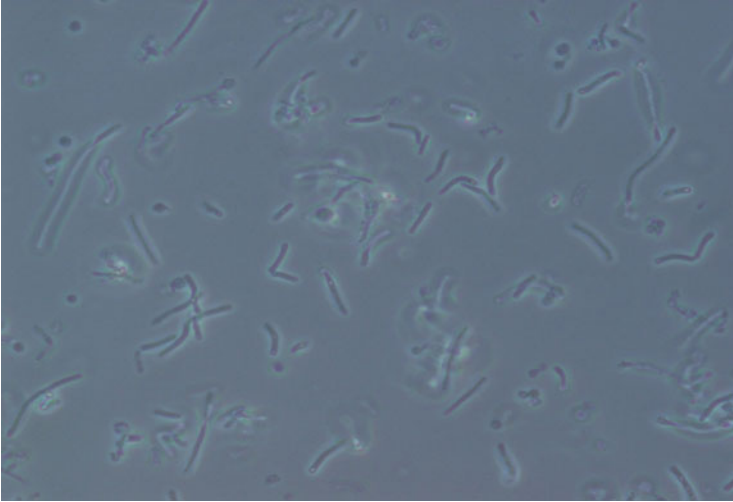


Fig. 5.1 Microscopic picture of *E. hallii*. Swellings, appearing in the form of vacuole-like structures under certain growth conditions, can clearly be observed

metabolism (Den Besten et al. 2013; Bolognini et al. 2016; Morrison and Preston 2016).

Other important metabolites that can be produced by gut bacteria are vitamins (notably K and B) and several neuroactive molecules that can either directly serve as or induce the expression of neurotransmitters and hormones (Oleskin and Shenderov 2019).

Following the elucidation of the human genome, analysis of the genetic composition of the microbiota, the microbiome, revealed its vast genetic potential. Whereas the human genome encodes approximately 23,000 genes, the gut microbiome encodes over ten million genes (Li et al. 2014). This not only reflects genetic power, but also a high level of flexibility. The ten million genes are divided in over 1000 different bacterial species, countless viruses and fungi and yeasts. Each individual will carry an estimate amount of 400 different bacteria and the composition of this is highly diverse between individuals (Qin et al. 2010). Remarkably, the genetic composition is less variable, allowing the microbiota to execute all of its functions, regardless of its species composition.

Within this high variety there are a number of key species that are shared by all individuals. These bacteria perform functions that serve our body, but also contribute to the stability of the highly complex ecosystem which they are part of. Here we describe one of those key species, *Eubacterium hallii* that has recently been renamed to *Anaerobutyricum* spp. but for simplicity we keep the original name. *E. hallii* has a remarkable metabolic versatility and produces metabolites that do not only serve its host but are also important for maintenance of a stable microbiota. We also include another species, *Intestinimonas butyriciproducens* that is highly specialized and adapted to the nutrients that are provided by its hosts.

5.2 *Eubacterium hallii*

5.2.1 General Description

Eubacterium hallii is a member of the *Lachnospiraceae* and based on 16S rRNA sequence analysis belongs to Clostridium cluster XIVa (Collins et al. 1994; Harmsen et al. 2002), a cluster that comprises many of the most prominent butyrate-producing bacteria in the gut. It has been detected as common commensal in human microbiota and recognized as a core species due to its frequent presence in all humans (Shetty et al. 2017). It is a common gut bacterium that can be detected in at least 63–81% of the population (Engels et al. 2016). With a diameter of 0.8–2.4 μm and 4.7 to more than 25 μm in length (De Vos et al. 2009) these bacteria are among the larger bacteria that can be found in our gut. Subterminal and terminal swellings can be observed, but cultures do not survive heating at 80 °C for 10 min (Fig. 5.1).

Because of its high metabolic flexibility *E. hallii* can easily adapt to the different conditions that are found in the gastrointestinal tract. As a result, this bacterium can be found in the small intestine as well as in the colon. Its metabolites can be used by other bacteria and as such *E. hallii* takes a central role in the microbiota, defining it as a key species. Also, it produces metabolites that are essential to human health. The role of butyrate and propionate in this respect are well documented. Moreover, *E. hallii* plays an important role in insulin resistance. In a double blinded study that was performed in The Netherlands, where volunteers that were diagnosed with metabolic syndrome received either fecal matter from lean donors or fecal matter of their own through a nasal duodenal tube, an improvement in peripheral insulin sensitivity could be observed in the former group. This improved insulin sensitivity was accompanied by an increase in the abundance of *E. hallii* that was observed in small intestinal biopsies (Vrieze et al. 2012). In subsequent animal trials, where mice were fed live *E. hallii*, a similar improvement of insulin sensitivity could be observed (Udayappan et al. 2016). Studies on the mode of action to explain this improvement are ongoing.

The omnipresence of this bacterium and its involvement with insulin resistance shows the importance of these bacteria. Through its metabolic diversity it is able to interact both with other members of the microbiota and its host. In the next section, the remarkable versatility of this bacterium is further explained.

5.3 Metabolic Diversity

E. hallii is a metabolically versatile species in the gastrointestinal tract. As *E. hallii* is not able to grow on complex polysaccharides this bacterium is mainly involved in secondary fermentation of simple compounds that arise as metabolites from other gut bacteria (Duncan et al. 2004; Schwab et al. 2017). *E. hallii* can grow very well in dietary-derived sugars such as glucose, fructose, galactose, sucrose, maltose, mannose, and sorbitol with butyrate as the major end metabolite of fermentation. In addition, *E. hallii* has been shown to metabolize the mucin-derived substrate

N-acetylglucosamine (Belzer et al. 2017), thus facilitating the interaction with mucin degrading bacteria. Compared to other butyrate-producing bacteria, *E. hallii* has a relatively broad spectrum of substrates for its growth which is one of several advantages for *E. hallii* to survive in the gut where competition is high, especially for simple substrates. In addition, *E. hallii* is able to efficiently convert both D- and L-lactate to butyrate in the presence of acetate (Duncan et al. 2004; Louis et al. 2010). This can be a of mechanism to prevent lactate accumulation in the gut (Shetty et al. 2018). Accumulation of lactate has been observed in patients with gastrointestinal conditions (Hove et al. 1994) and the capability of removing access of lactate by *E. hallii* can therefore be an important factor in maintaining intestinal health.

E. hallii has been proposed to contribute to propionate production in the gut via a conversion of 1,2-propanediol (Engels et al. 2016). *E. hallii* is capable of converting 1,2-propanediol to propionate using 1,2-propanediol metabolic pathway. Although this metabolic pathway has been detected in several other bacteria, including *Flavonifractor plautii*, *Intestinimonas butyriciproducens*, and *Veillonella* spp. (Engels et al. 2016). The conversion of 1,2-propanediol to propionate has been demonstrated experimentally only for *E. hallii* and *Lactobacillus reuteri* (Gänzle 2015; Engels et al. 2016).

5.3.1 Butyrate Pathway

Genomic analysis of *E. hallii* revealed the presence of a glycolytic pathway for conversion of sugars to pyruvate while employing butyryl-CoA transferase pathway for butyrate production (Fig. 5.2a). This pathway differentiates from the other butyrogenic pathways at the terminal step which involves butyryl-CoA:acetate CoA transferase for butyrate production. This CoA transferase transfers CoA group from butyryl-CoA to acetate to form butyrate and acetyl-CoA as end products. Either CO₂/H₂ or formate is also produced along this pathway which might confer an opportunity for cross-feed with hydrogenotrophic microbes. In addition, in order to use lactate *E. hallii* first converts it to pyruvate and follow all other steps in butyryl-CoA:acetate CoA transferase to make butyrate. The energy is mainly conserved via the conversion from crotonyl-CoA to butyryl-CoA which involves butyryl-CoA dehydrogenase electron-transferring flavoprotein complex that generates a proton gradient via a membrane-associated NADH-ferredoxin oxidoreductase (Li et al. 2008).

5.3.2 Propionate Pathway

E. hallii is known to not only produce butyrate but also propionate. An entire adenosylcobalamin-dependent dehydratase PduCDE operon was found in the genome which confers the ability to convert 1,2-propanediol to propionate (Fig. 5.2b). This conversion is relatively fast and obtains only a small amount of energy via a last step from propionyl-phosphate to propionate. Remarkably, the

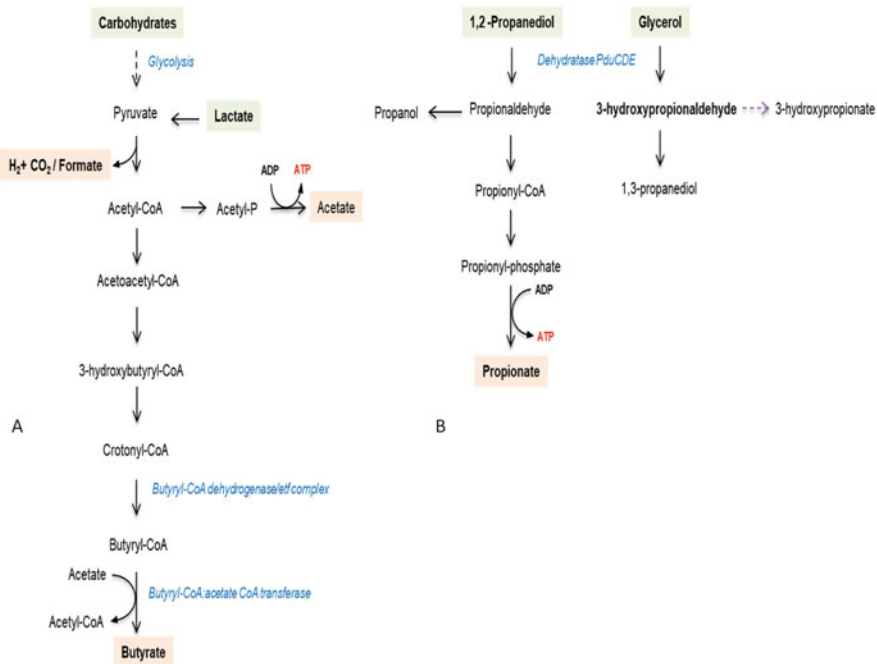


Fig. 5.2 Metabolic pathways of *E. hallii* for butyrate (a) and propionate (b) production

propanediol pathway was found to be widely spread in several intestinal taxa and contribute to approximately 31% of propionate turnover in the gut (Engels et al. 2016). This is indicative of the notable role of *E. hallii* on formation of propionate in the gut.

5.3.3 Additional Metabolites

Next to the generation of two significant short-chain fatty acids, *E. hallii* is capable of producing several other interesting metabolites. Strikingly, it was found that *E. hallii* was able to convert glycerol to 3-hydroxypropionaldehyde (reuterin) via the same dehydratase PduCDE as is used for the conversion of 1,2-propanediol to propionate (Fig. 5.3b). Reuterin is known as antimicrobial compound and toxic to bacteria. In spite of that, *E. hallii* was able to metabolize a small amount of produced reuterin relatively fast (Engels et al. 2016), which might be important to eliminate the toxicity of this compound at small quantities in the gut.

In addition, it was found that *E. hallii* was capable of producing pseudovitamin B12 (Belzer et al. 2017). Vitamin B12 is known as a modulator in shaping the structure and function of human gut microbial community (Degnan et al. 2014). It is believed that pseudovitamin B12 cannot be used efficiently by humans and other animals. Moreover, the receptors necessary for vitamin B12 absorption are only

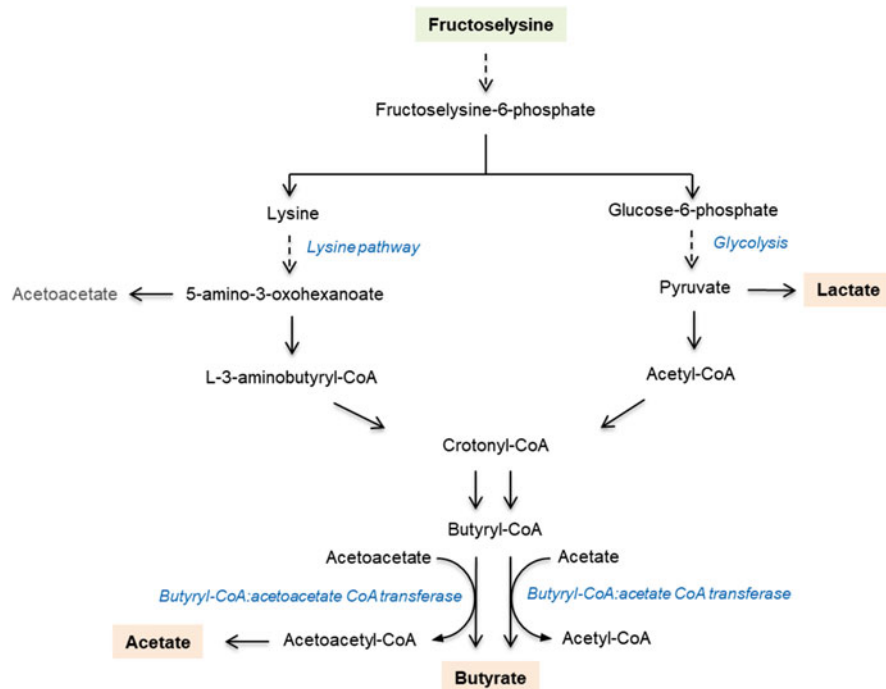


Fig. 5.3 Metabolic pathway of *Intestinimonas butyriciproducens* for butyrate production

found in the small intestine (Seetharam and Alpers 1982). However, animal experiments suggest that pseudovitamin B12 delivered orally may be bioavailable.

Finally, *E. hallii* was found to be able to transform the carcinogenic heterocyclic amine 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine (PhIP) to noncarcinogenic PhIP-M1 (Fekry et al. 2016). PhIP is a component that is found in well-cooked meats and is believed to contribute to the carcinogenicity of processed meats.

5.3.4 Interaction with Other Commensals

E. hallii has been reported to interact with many different commensal bacteria. This includes the production of butyrate by *E. hallii* from the metabolites resulting from starch/fructose-oligosaccharides degradation by *Bifidobacterium adolescentis* (Duncan et al. 2004; Belenguer et al. 2006). Another example is the utilization by *E. hallii* of sugars, released from mucin degradation by *Akkermansia muciniphila* to produce butyrate (Belzer et al. 2017). Conversely, *E. hallii* is capable of producing pseudovitamin B12, which is used for metabolizing 1,2 propanediol to propionate but can also be used by *A. muciniphila* to activate the methylmalonyl-CoA pathway, converting succinate to propionate. It has been shown that *E. hallii* might compete with *Desulfovibrio* for lactate consumption in the gut (Marquet et al. 2009) as lactate

is mainly fermented to butyrate in the gut (Bourriaud et al. 2005). It was observed that *E. hallii* converted 1,2-propanediol produced by infant bifidobacteria from L-fucose and fucosyllactose to propionate (Schwab et al. 2017). In parallel, *E. hallii* also used intermediate lactate/acetate produced by bifidobacteria to produce butyrate.

5.4 *Intestinimonas butyriciproducens*

5.4.1 General Description

In a bid to identify commensals that are capable of utilizing noncarbohydrate sources for their carbon needs, mouse fecal samples were prepared and cultured on reduced agar medium, containing yeast extract, rumen fluid, and lactic acid as main energy and carbon sources. One specific strain was identified that was only distantly related to any at the time known recognized species. This species was close related to the butyrate-producing bacterium *Flavonifractor plautii* (>94.5% similarity for 16S rRNA sequence), but clustered as a separate genus and was designated *Intestinimonas butyriciproducens* (Kläring et al. 2013). It was the first species that was found to produce butyrate from lysine. Moreover, it was found that *I. butyriciproducens* was able to convert the Amadori product fructoselysine to butyrate. Amadori products such as fructose-lysine have become part of our food since we are able to cook our foods and are formed through heating of reducing sugars with amino acids in a nonenzymatic Maillard reaction. An interesting question that arises from this is if this bacterium has evolved as part of our microbiota since we started consuming cooked foods. Hence it would be of interest to see if other mammals (apart from human and laboratory mice), who do not normally consume cooked foods, would also harbor *I. butyriciproducens*. To date no examples are known.

5.4.2 Metabolic Diversity

I. butyriciproducens is not able to degrade polysaccharides or disaccharides. This species grew poorly in hexose sugars, but the growth was much enhanced in the presence of acetate. *I. butyriciproducens* was able to ferment glucose, galactose, and arabinose to mainly butyrate and minor amounts of ethanol and lactate while no growth was observed on mannitol, cellobiose, raffinose, xylose, D-mannose, sucrose, or sorbitol (Bui et al. 2016). Growth on lactate and acetate was also observed (unpublished data). No hydrogen was detected on any substrate. Genomic analysis showed the presence of a complete glycolysis and butyryl-CoA transferase pathway. In accordance to this, it was shown that associated proteins were overproduced when growing on glucose (Bui et al. 2015). Of this pathway, the conversion of crotonyl-CoA to butyryl-CoA involved a butyryl-CoA dehydrogenase

(Bcd) electron-transferring flavoprotein (Etf) complex that generates a proton motive force via a membrane-integrated Rnf complex (Li et al. 2008).

Remarkably, *I. butyriciproducens* grew much better on lysine as a primary carbon source, converting it to equimolar amounts of butyrate and acetate. The entire lysine pathway was detected in the genome. It has been reported that the lysine to butyrate pathway is the second abundant pathway for butyrate synthesis in the gastrointestinal tract (Vital et al. 2014), suggesting a key role of *Intestinimonas* in colonic butyrate turnover.

The lysine metabolic pathway consists of a sequence of reactions from lysine to L-3-aminobutyryl-CoA which are performed by proteins of which the coding genes are located in a single operon. The conversion from crotonyl-CoA to butyryl-CoA is a major step for generation of energy. Generally, for butyrate formation from butyryl-CoA the butyryl-CoA:acetate CoA transferase pathway is used. For the butyrate formation pathway from lysine, however, it was found that butyryl-CoA:acetoacetate CoA transferase is also used, which transfers CoA from butyryl-CoA to acetoacetate to form butyrate. When growing on fructoselysine, these two pathways are operating simultaneously (Bui et al. 2015). These pathways are depicted in Fig. 5.3. Fructoselysine is first converted to fructoselysine-6-phosphate and subsequently cleaved to lysine and glucose-6-phosphate. While glucose-6-phosphate is used via glycolysis and butyryl-CoA pathway, lysine is further metabolized via lysine pathway. Butyrate, acetate, and ammonium were all detected as major end products. Lactate was formed in small amounts. Several strains of *I. butyriciproducens* have been isolated from different hosts, all of which shared the same metabolic activities for lysine and fructoselysine.

Similar to *E. hallii*, *I. butyriciproducens* produces pseudovitamin B12, which is beneficial for intestinal microbes and, either directly or indirectly, for the host.

Interestingly, an entire dehydratase PduCDE operon was also found on the genome of *I. butyriciproducens*, indicating the potential capability of converting 1,2-propanediol to propionate (Engels et al. 2016). This still needs to be proven experimentally.

5.5 Probiotic Potential

Both *I. butyriciproducens* and *E. hallii* show features that are reminiscent of human lifestyle. As mentioned previously, the conversion of fructoselysine to butyrate could be an adaptation to the consumption of Amadori products, which are the result of thermo treatment of food products. Similarly, the capability of *E. hallii* to convert PhIP, a component that is derived from well-cooked meat, could well be an adaptation of our microbiota to food that is normally confined to humans. The Amadori products have been associated with the aging process and chronic diseases (Deppe et al. 2011). Fructoselysine is among the most common Amadori products and also a precursor of Advanced Glycation Endproducts (AGEs). AGEs are implicated in the development of cancer and diabetic complications (Brownlee 1994) and therefore the removal of (predecessors of) AGEs could be an important

step in reducing the risk of cancer and diabetics. Similarly, reducing levels of PhIP could have a reducing effect on the risk of cancer development (Fekry et al. 2016).

These anticarcinogenic properties are just two reasons why *E. hallii* and *I. butyriciproducens* are prime candidates for the development as potential therapeutic strains. Another reason is that both strains produce butyrate, a short-chain fatty acid that has also been associated with lowering the risk of (colonic) cancer and a number of other beneficial health traits, including maintenance of blood glucose levels (McNabney and Henagan 2017). Indeed, *E. hallii* has been identified as a bacterium that can have a positive influence on insulin resistance (Vrieze et al. 2012; Udayappan et al. 2016). Simultaneously propionate is also linked to glucose metabolism and insulin production (Chambers et al. 2015; Pingitore et al. 2017), suggesting that the effects on glucose metabolism observed with *E. hallii* could also result from its ability to produce propionate.

E. hallii is also a keystone species as it has vast interactions with other bacteria from the microbiota. On the one hand, it uses the metabolites acetate and lactate that are produced by other bacteria from the fermentation of complex carbohydrates; on the other hand, it produces certain metabolites that can have a profound influence on the stability of the microbial ecosystem. As mentioned previously, (pseudo) vitamin B12 is essential for metabolic processes of several other bacteria such as *Akkermansia muciniphila* (Belzer et al. 2017), while reuterin is a bacteriocin that affects the composition of its close surroundings by killing bacteria.

A complicating factor in developing human gut-derived bacteria as potential probiotics is the ubiquitous presence of specific antibiotic resistance genes. These have emerged in the bacterial population as a result of widespread use of antibiotics over the last decades and bear the inherent risk of being spread to invading pathogens, complicating the treatment of infections (Thiemann et al. 2016). Preselecting of strains that have a preferred antibiotic resistance profile can therefore be a tedious step and might not always be successful. Notably tetracycline resistance genes are omnipresent in the human microbiota of all geographic regions (Hu et al. 2013). Indeed, *E. hallii* L2-7 also carries an active TetO gene. To be able to use this strain for probiotic purposes we used a mutagenic approach for the selection of naturally occurring tetracycline-sensitive strains (unpublished results).

Concluding it can be stated that the high versatility of these strains makes them prime candidates to be developed as next-generation therapeutic strains. First and foremost, both bacteria produce butyrate which has proven health implications. In addition, *Intestinimonas* has a high potential because of its ability to reduce the burden of Amadori products that could potentially develop into carcinogenic AGEs and turn it into a beneficial compound (butyrate). *E. hallii* has an even wider scope of use as it can influence the health of the host through a direct interaction by producing butyrate and propionate as well as its ability to transform the carcinogenic dietary compound PhIP to PhIP-M1. Indirectly, it can influence the health of its host by influencing the health state of the microbiota through the production of pseudovitamin B12 and reuterin.

More recently another potential application became apparent where the presence of *E. hallii* was associated with protection against *Clostridioides difficile* infection (Crobach et al. 2020).

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Anticarcinogenic Potential of Probiotic, Postbiotic Metabolites and Paraprobiotics on Human Cancer Cells

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Abstract

The performance of probiotic bacteria and their metabolites in the control and treatment of various cancers has been shown by a number of clinical studies. Among probiotic bacteria, lactic acid bacteria are well known for their beneficial role in colonic health, where they also exert anticarcinogenic effects. These beneficial bacteria can inhibit the occurrence of cancer by (1) lowering PH, (2) reducing the level of pro-carcinogenic enzymes, (3) enhancing cell proliferation by inhibiting normal cell apoptosis and by promoting cell differentiation and cytoprotective activities, (4) suppressing inflammation-induced cell apoptosis, (5) enhancing innate immunity, (6) promoting various gut homeostasis, and (7) displaying antioxidant activity. Several research findings showed that probiotic metabolites (postbiotics) can regulate cell proliferation in colorectal cancer and might be considered a therapeutic alternative for treating chemoresistant colorectal cancer. These metabolites including short-chain fatty acids, exopolysaccharides, vitamins, bacteriocin, H_2O_2 , etc. are known to be involved in decreasing the viability of cancer cells and the induction of apoptosis by influencing different signaling pathway. Despite the general definition that probiotics are live microorganisms, a variety of biological responses have been reported from administering dead and frequently heat-killed (Paraprobiotic)

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probiotic bacterial cultures to various mammals. The preparations of dead cells have also been fractionated and various cellular components shown to produce a range of biological responses. Many of the biological responses found with the heat-killed probiotic bacterial cells are not antimicrobial effects but are, rather, immunomodulating effects. Owing to the fact that probiotics, paraprobiotics and metabiotics or postbiotics metabolites are the most widely studied biological therapeutic alternatives for the treatment of cancer; hence in this chapter their functions and mechanism of action would be elucidated.

Keywords

Probiotics · Paraprobiotics · Postbiotics · Metabiotic · Bacteriocin · Exopolysaccharide · Short-chain fatty acids · Biosurfactants · Cancer

6.1 Introduction

Despite the fact that cancer risk indisputably depends on genetic factors, and immunological conditions of the host, but most important of all the gut microbiome has known to play considerable role in cancer cases. According to reports, any imbalance in the gut microbiome compositions might result in disorders such as cancer, malignancy, inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), fatty liver diseases, obesity, type 2 diabetes mellitus, asthma, cardiovascular, psychiatric disorders, and immune-mediated diseases (Barteneva et al. 2017; Marques et al. 2017). Such modification of the gut microbiota is referred to as dysbiosis is of paramount importance as they play potential role in initiation and progression of several diseases in humans and animals (Azad et al. 2018). Vast population of these bacteria present in the digestive tract of the host could either prevent cancer cell growth or slow down the process.

Gut microbiota is occupied by members of bacteria belonging to the family Bacteroidetes and *Firmicutes*. Among these, lactic acid bacteria (LAB) are the most dominant flora residing in the gut of a healthy individual that are recognized as GRAS (generally recognized as safe). Majority of the LAB species are widely used as probiotics in a number of food products and supplements. The term probiotic refers to the live microorganisms that provide health benefits to the host when consumed in sufficient amounts (Liu et al. 2015; Lüke et al. 2016; Maghsood et al. 2018; Voigt et al. 2009). Some of the therapeutic effects of probiotic LAB are their antitumor activities that inhibit the carcinogens present in the gastrointestinal tract by stimulating the immune response. Owing to their immune modulating role, these bacteria are also known as “immunobiotics” (Bedada et al. 2020; Ghanavati et al. 2020; Kumar et al. 2012; Sharma and Shukla 2016). According to reports, the occurrence of cancer is usually prevented by these bacteria by (1) lowering pH, (2) reducing the level of pro-carcinogenic enzymes (Kahouli et al. 2013), (3) enhancing cell proliferation by inhibiting normal cell apoptosis and by promoting cell differentiation and cytoprotective activities (Sivamaruthi et al. 2020),

(4) suppressing inflammation-induced cell apoptosis (Kumar et al. 2010), (5) enhancing innate immunity, (6) promoting various gut homeostasis (dos Reis et al. 2017), and (7) displaying antioxidant activity (Kaur and Kaur 2015).

Apart from probiotic bacteria, the dead cells of these bacteria are shown to demonstrate variety of biological responses. These nonviable probiotic bacterial cells are regarded as “Paraprobiotics” or “Probiotic ghost cells” (Sharma and Singh Saharan 2014). Similar to live probiotic cells, the dead cells of probiotic bacteria are known to bring about a number of biological responses in the hosts. Although their exact mechanism of action is yet not fully explored, they are believed to provide health benefits by the ability of their cell wall and other cellular components to boost the immune system, and inhibit the pathogens by adherence to the intestinal walls, etc. (Fujiki et al. 2012). Furthermore, the responses exerted by these live and dead bacteria might also be due to the secretory metabolites released in the cell free supernatant fluids by either the live bacteria or released after the cell lysis, respectively (Aguilar-Toalá et al. 2018). These secretory metabolites released by the probiotic bacteria are often termed as “postbiotics” or “metabiotics” and are known to exert beneficial effects in the gastrointestinal tract of the host (Sharma and Shukla 2016). Organic acids, bacteriocin, and H_2O_2 are some of these metabolites from probiotic bacteria that have significant role in decreasing the viability of colorectal cancer cells and the induction of apoptosis by influencing different signaling pathway (Jacouton et al. 2017).

6.2 Cancers

Abnormal growth of cells that harms an organ of the body is defined as cancerous cells. Cancer usually arises from the transformation of normal cells into tumor cells in a multistage process that generally progresses from a pre-cancerous lesion to a malignant tumor. The most common types of cancers include the following:

- Lung (2.09 million cases)
- Breast (2.09 million cases)
- Colorectal (1.80 million cases)
- Prostate (1.28 million cases)
- Skin cancer (nonmelanoma) (1.04 million cases)
- Stomach (1.03 million cases)

While the most common causes of cancer death include cancers of:

- Lung (1.76 million deaths)
- Colorectal (862,000 deaths)
- Stomach (783,000 deaths)
- Liver (782,000 deaths)
- Breast (627,000 deaths)

These changes are the result of the interaction between a person's genetic factors and three categories of external agents, including:

- Physical carcinogens, such as ultraviolet and ionizing radiation
- Chemical carcinogens, such as asbestos, components of tobacco smoke, aflatoxin (a food contaminant), and arsenic (a drinking water contaminant)
- Biological carcinogens, such as infections from certain viruses, bacteria, or parasites.

Aging is another fundamental factor for the development of cancer. The incidence of cancer rises dramatically with age, most likely due to a build-up of risks for specific cancers that increase with age. The overall risk accumulation is combined with the tendency for cellular repair mechanisms to be less effective as a person grows older (WHO).

Use of tobacco and alcohol, unhealthy diet, and physical inactivity are major cancer risk factors worldwide and are also the four shared risk factors for other noncommunicable diseases. Some chronic infections are risk factors for cancer and have major relevance in low- and middle-income countries. Approximately 15% of cancers diagnosed in 2012 were attributed to carcinogenic infections, including *Helicobacter pylori*, Human papillomavirus (HPV), Hepatitis B virus, Hepatitis C virus, and Epstein-Barr virus.

According to WHO reports, Hepatitis B and C virus and some types of HPV increase the risk for liver and cervical cancer, respectively. Infection with HIV substantially increases the risk of cancers such as cervical cancer.

A correct cancer diagnosis is essential for adequate and effective treatment because every cancer type requires a specific treatment regimen that encompasses one or more modalities such as surgery, radiotherapy, and chemotherapy. The primary goal is generally to cure cancer or to considerably prolong life. Improving the patient's quality of life is also an important goal. This can be achieved by supportive or palliative care and psychosocial support and most important of all by healthy diet. In this context, probiotic food products are of high importance as the beneficial bacteria in these products can manipulate the microbiome of the gut in a manner leading to desired health outcomes. Hence, the use of these bacteria for the prevention and treatment of various types of cancers has been of key research interest (Dicks et al. 2018; Zhong et al. 2014).

6.3 Anticancer Effects of Probiotic Bacteria

Probiotics are nonpathogenic live microorganisms that provide health benefits when are consumed in sufficient amounts (Mehra et al. 2012). Probiotic bacteria and yeasts are known to colonize, multiply, and produce variety of bioactive substances that accounts for their beneficial effects in the gastrointestinal tract of the host (Forsyth et al. 2009). Probiotics may be highly beneficial to the host as it has been described that they can maintain epithelial integrity, compete for adhesion and nutrition with

pathogens, and stimulate cell-mediated immunity, IgA production, and gut associated lymphoid tissue (Goldin and Gorbach 1980).

These beneficial bacteria are vastly studied for their anti-inflammatory effects (Jacouton et al. 2017), playing significant role in the treatment of variety of cancer types (Fig. 6.1). The underlying mechanisms for the anticancer effects of probiotic bacteria are versatile including suppression of the growth of microbiota implicated in the production of mutagens and carcinogens, alteration in carcinogen metabolism, and protection of DNA from oxide damage as well as regulation of immune system (Jacouton et al. 2017). In addition, they have been shown to change expression of different genes participating in cell death and apoptosis, invasion and metastasis, cancer stem cell maintenance, as well as cell cycle control. Probiotic actions such as adhesion of lactic acid bacteria or their components to epithelial cells as well as release of soluble factors have been proposed to be important for the suppression of neoplastic cells (Oelschlaeger 2010).

Diet is known to play a major role in the pathogenesis of cancer especially colon cancer, among which red meat and animal fats are the main enemies. On the other hand, reports have indicated that fruits and vegetables might have preventive effects on such types of cancers. With the recognition of importance of diet in the control and prevention of a number of diseases, the demand for functional foods that are claimed to have health benefits are highly sought for.

Goldin and Gorbach (1980) were among the first to demonstrate the association between a diet enriched with *Lactobacillus* and a reduced incidence of colon cancer (40% vs. 77% in controls). In another study, a traditional fermented milk product was shown to inhibit *in vitro* proliferation of MCF-7 breast cancer cells, but not normal mammary epithelial cells.

Generally, the importance of probiotics has been shown in different *in vitro*, *in vivo* animals and clinical trials in humans (Tables 6.1 and 6.2). In a recent study we were able to demonstrate *in vitro* and *in vivo* anticancer effects of a live and heat-killed *L. casei* strain isolated from local dairy product (Noorozi et al. 2021). While, previously, Orlando et al., 2009 had reported antiproliferative effects of L.GG on gastric and colon cancer cells. They found that the highest concentrations of L.GG homogenate and cytoplasm extracts reduced the percentage of cell viability to nearly 55% and 65% in DLD-1(colon) and HGC-27 (gastric) cancer cell lines (Oelschlaeger 2010).

Special attention has been given to the effects of probiotics in reduction of invasion and metastasis in cancer cells. Invasion and metastasis have been regarded as important hallmarks of malignant cells which are endowed to them through diverse and complex genetic or epigenetic aberrations as well as extrinsic signals, such as those relayed from their microenvironment (Górska et al. 2019).

While, during *in vivo* studies conducted by Jacouton et al. it was shown that dairy strain of probiotic *L. casei* BL23 possessed potential anti-inflammatory and antitumor effects when administered orally to 6–8 weeks old female mice. The protective effect demonstrated by this probiotic strain was through reduction in cell proliferations and apoptosis induction. Apoptosis or programmed cell death is necessary in the treatment of cancer (Jacouton et al. 2017).

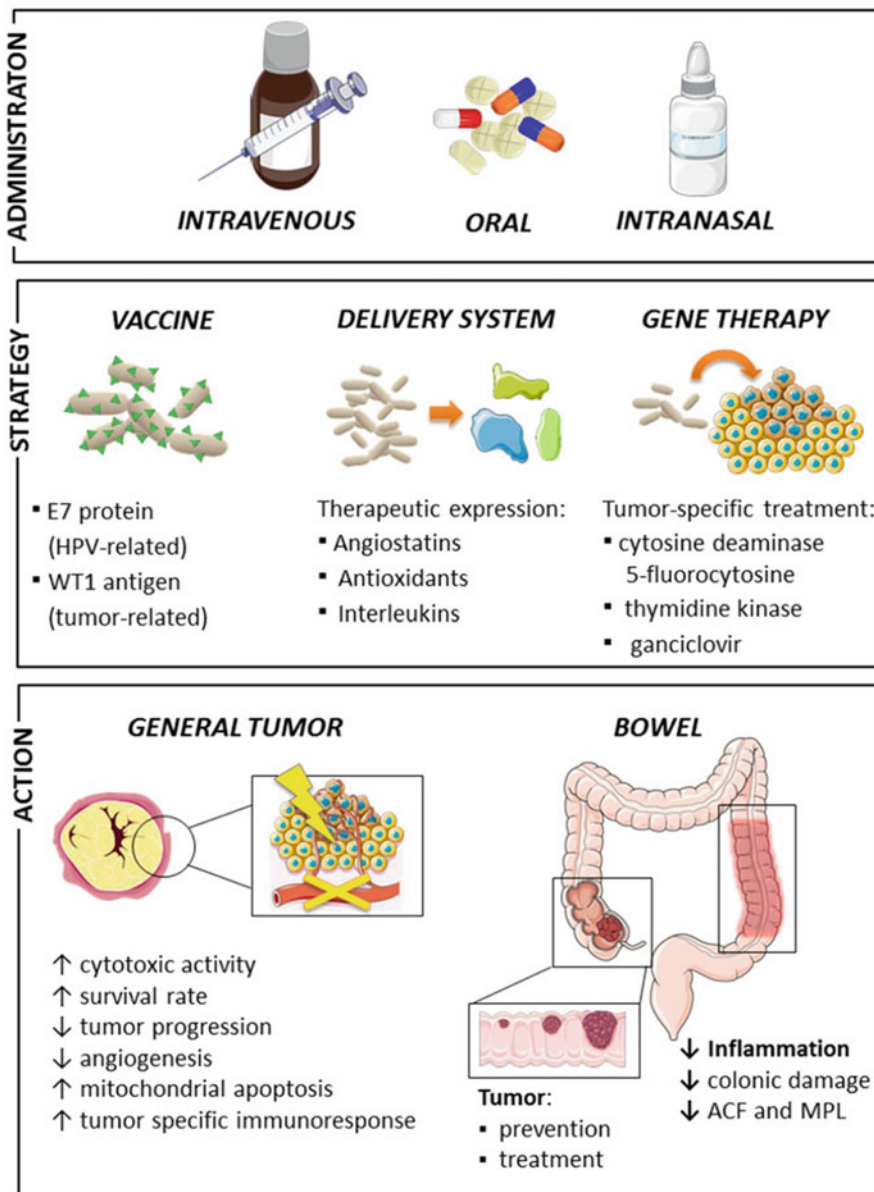


Fig. 6.1 Summary of the possible applications of probiotic bacteria in the treatment and prevention of cancer (Górska et al. 2019), downwards arrow depicts decrease, upwards arrow depicts an increase; ACF aberrant crypt foci; MPL multiple plaque lesions

Table 6.1 General effects of probiotics on cancer cells (in vitro studies)

Probiotic strain/details of experiment	Cell line	Effect	Reference
<i>Lactobacillus rhamnosus GG</i> , <i>Bifidobacterium lactis Bb12</i>	Caco-2	↑ Apoptosis	Altonsy et al. (2010)
<i>Lactobacillus casei ATCC 393</i>	HT29 and CT26	Induction of apoptosis	Tiptiri-Kourpeti et al. (2016)
<i>Lactococcus lactis NK34</i>	HT-29, LoVo, AGS	>80% ↓ Cell proliferation	
<i>Bifidobacterium infantis</i> , <i>Lactobacillus paracasei</i> , <i>Bifidobacterium bifidum</i>	MCF7	↓ Cell proliferation	Han et al. (2015)
<i>Lactobacillus paracasei IMPC2.1</i> , <i>Lactobacillus rhamnosus GG</i> /heat killed/	DLD-1	↓ Cell proliferation Induction of apoptosis	Orlando et al. (2012)
<i>Lactobacillus pentosus B281</i> , <i>Lactobacillus plantarum B282</i> /cell free supernatant used/	Caco-2 and HT-29	↓ Cell proliferation Cell cycle arrest (G1)	Oelschlaeger (2010)
<i>Lactobacillus casei CRL431</i>		↓ Cell proliferation	Saxami et al. (2016)
<i>Bacillus polyfermenticus</i> /AOM stimulation/	NMC460	↓ Cell colony formation in cancer cells(N/E on normal colonocytes)	Ma et al. (2010)
<i>Bacillus polyfermenticus KU3</i>	LoVo, HT-29, AGS	↓ Cell proliferation	Lee et al. (2015)
<i>Lactobacillus rhamnosus</i> , <i>Lactobacillus crispatus</i> /cell-free supernatant used/	HT-29	↑ Apoptosis	
<i>Lactobacillus gasseri</i> and <i>Lactobacillus crispatus</i> /cell-free supernatant used/	Hela, HNCf	↓ Cell proliferation	Motevaseli et al. (2013)
<i>Lactobacillus lactis IL-17A</i>	TH17	↑ Apoptosis	Jacouton et al. (2017)

↓ Decrease; ↑ increase; N/E no effect. Human colonic cancer cells: Caco-2, HT-29, SW1116, HCT116, SW480, DLD-1, LoVo, Human colonic epithelial cells: NMC460. Human gastric adenocarcinoma cells: AGS Mus musculus colon carcinoma cells: CT26. Cervical cancer: Hela. Head and neck cancer: HNCf. Lung cancer: TH17

The immunomodulatory potential of *L. casei* BL23 is mediated through IL-22 cytokine downregulation, and an antiproliferative property, mediated through Bik, caspase-7, and caspase-9 upregulation (Tiptiri-Kourpeti et al. 2016).

During an *in vitro* and *in vivo* study, it was shown that live *L. casei* ATCC393 and its components exert potent antiproliferative, growth inhibitory, and pro-apoptotic effects. These researchers reported that oral administration of live *L. casei* ATCC 393 and its components to the mice displayed antiproliferative effects, and suggested

Table 6.2 General effects of probiotics in tumor-induced animal models (in vivo studies)

Probiotic strain	Animal model	Induction	Treatment	Result	Reference
<i>Lactobacillus acidophilus</i> , <i>Lactobacillus casei</i>	Rat	DMH	40 weeks	↓ TI ↓ TV ↓ TM	Arvind and Sinha (2009)
<i>Bifidobacterium lactis</i> KCTC 5727	SPF C57BL rat		19 weeks	↓ TI ↓ TV	Kim et al. (2010)
<i>Bacillus polyfermenticus</i>	CD-1 mice	DLD-1 cells injection	20 weeks	↓ TI ↓ TV	Ma et al. (2010)
<i>Lactobacillus plantarum</i>	BALB/ c mice	CT26 cells injection	14 weeks	↓TV, Induction of necrosis	Hu et al. (2015), Walia et al. (2015)
<i>Lactobacillus plantarum</i> (AdF10), <i>Lactobacillus rhamnosus</i> GG	SD rats	DMH 4 weeks	12 weeks	↓ TI ↓ TV ↓ TM	
<i>Lactobacillus casei</i> BL23	C57BL/ 6 mice	DMH	10 weeks	↓ TI	Tiptiri-Kourpeti et al. (2016)

↓ Decrease, TI tumor incidence, TV tumor volume, TM tumor multiplicity, DMH 1,2 dimethylhydrazine dihydrochloride

that the mechanisms underlying this effect were tumor necrosis factor related apoptosis-inducing ligand TRAIL upregulation and surviving downregulation (Tiptiri-Kourpeti et al. 2016).

Lactobacilli can stimulate immune cells of the host including dendritic or natural killer (NK) cells or T helper type 1 (TH1) response, which participates in precancerous or anticancerous cell. Oral administration of probiotic *L. acidophilus* isolated from traditional homemade yogurt and neonatal stool reduces tumor growth by immune response modulation or changing the cytokine milieu reducing growth rate of tumor, increasing proliferation of lymphocyte, protecting TH cells, and activating antitumoral cell in in vivo breast cancer murine model, 8–10-week-old Balb/C female mice (Fujiki et al. 2012).

Notably, gut *L. acidophilus* activates NK cells, a major source of interferon (IFN)- γ and play vital role in antitumor immunity. Thus, the mechanism by which *L. acidophilus* prevents tumor growth is by innate anticancer cells activation. *L. acidophilus* produces IFN- γ from splenocyte to increase anticancer property, antiangiogenesis, and NK activity (Fujiki et al. 2012). Additionally, probiotic *Lactococcus lactis* (*L. lactis*) NK34 with a dose 10^6 CFU was shown to possess strong anticancer and anti-inflammatory effects by inhibiting the proliferation of cancer cells such as human lung carcinoma cell line (SK-MES-1), human colon adenocarcinoma cell line (DLD-1, HT-29), human colon adenocarcinoma cell line (LoVo), human stomach adenocarcinoma cell line (AGS), and human breast adenocarcinoma cell line (MCF-7 cells). *L. lactis* NK34 demonstrated anti-inflammatory property by inhibiting lipopolysaccharide-induced RAW 264.7 cells that produce

nitric oxide, and proinflammatory cytokines such as interleukin-18, tumor necrosis factor- α , and cyclooxygenase-2 were decreased (Tiptiri-Kourpeti et al. 2016). Probiotic *L. lactis* has been used as a fermentation starter in dairy or fermented foods and is considered as a safe microbe with GRAS (Generally recognized as safe) status.

Fast acidifying lactic acid bacteria, *Streptococcus thermophilus* (*S. thermophilus*) M17PTZA496 and *S. thermophilus* TH982 have been reported to possess probiotic properties, anticancer activity, and folate-producing ability *in vitro*. Of most commercially available strains of probiotics, thermophilic *S. thermophilus* is extensively used as starter culture for many dairy products next to *L. lactis* (Bedada et al. 2020). According to these studies, *S. thermophilus* MTH17CL396, TH982, and M17PTZA496 inhibited HT-29 cells significantly. The significant antiproliferative potential of these strains on HT-29 cancer cells was concluded to be the result of lactic acid produced by these bacteria. Various mechanisms are revealed as to how lactic acid bacteria prevent colon cancer, such as carcinogens binding and degrading, immune response increment, antimutagenic compounds production, and physico-chemical conditions change in the colon (Bedada et al. 2020; Sanders et al. 2018). Probiotics are used to fight against cancer by enhancing immune response or protecting against gastrointestinal infections. A pro-inflammatory cytokine, interleukin-17A is produced by TH17-cells and used in autoimmune disease and host defense. Recombinant *L. lactis* IL-17A produced and secreted cytokine, Interleukin-17A in murine fibroblasts 3 T3 L1 cells line and human papilloma virus induced cancer in mouse allograft model. This indicates the role of IL 17A in cancer (Kumar et al. 2010; Sanders et al. 2018). Figure 6.1 summarizes most significant findings from *in vitro* and *in vivo* studies regarding anticancer effects of probiotic bacteria and the therapeutic options (Górska et al. 2019).

6.4 Anticancer Effects of Postbiotic Metabolites Produced by Probiotic Bacteria

Probiotics colonize, multiply, and produce variety of bioactive substances termed “metabiotics,” accounting for their beneficial effects in gastrointestinal tract (GIT) diseases. These metabolites produced by probiotics help in maintaining homeostasis in the gut and enhance the growth of friendly bacteria that inhibit the conversion of procarcinogens into carcinogens by decreasing harmful enzyme levels such as nitroreductase, β -glucuronidase, and β -glucosidase enzymes (Sharma 2019). Postbiotics are defined as the soluble factors (products or metabolic byproducts), secreted by live bacteria during metabolism, like hydrogen peroxide, active ribosomal proteins like bacteriocins, exopolysaccharides, etc. or released after bacterial lysis, such as enzymes, peptides, teichoic acids, peptidoglycan-derived muropeptides, polysaccharides, cell surface proteins, and organic acids. A variety of these metabolites, such as plantaricin, exopolysaccharides (EPS), lactic acid, acetic acid, and γ -aminobutyric acid, have been shown to possess the ability to enhance body immunity, antitumor, and antiseptic activity (Dicks et al. 2018; Kaur and Kaur 2015; Sharma 2019). Apart from these, the short-chain fatty acids (SCF) in

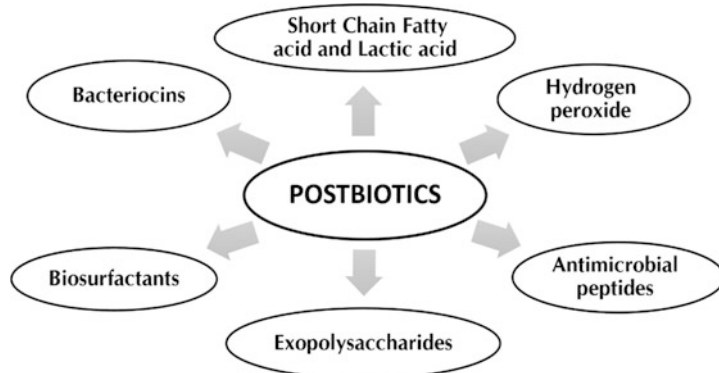


Fig. 6.2 Some biological functions of postbiotic metabolites produced by probiotic bacteria

the postbiotics are known to induce chemopreventive enzymes glutathione S transferase and glutathione transferase pi and impart genetic stability to colon cells. Some most important biological functions of postbiotic metabolites are shown in Fig. 6.2.

Molecules and metabolites derived from probiotic bacteria can prevent tumor development through modulation of immune systems of the host. For instance, bacterial lipopolysaccharide (LPS), a key component of gram-negative bacteria outer membrane, activates toll-like receptor 4, consequently activating immune T cell-mediated response against tumor cells (Sanders et al. 2018; Sharma 2019).

In the last decade, the postbiotic metabolites extracted from beneficial bacteria especially LAB have gained immense importance owing to their clear chemical structure, safety dose parameters, long shelf life, and the content of various signaling molecules that might have anti-inflammatory, immunomodulatory, anti-obesogenic, antihypertensive, hypocholesterolemic, antiproliferative, and antioxidant activities. As pointed out by Zhang et al., *L. acidophilus* and *L. casei* produce compounds that inhibit the growth of breast cancer cell line, MCF7. *L. acidophilus* 606 prevents the proliferation of human pancreatic tumor cell line by soluble polysaccharides production. These properties suggest that postbiotics may contribute to the improvement of host health by improving specific physiological functions, even though the exact mechanisms have not been entirely elucidated (Dicks et al. 2018; Kaur and Kaur 2015).

6.4.1 Short-Chain Fatty Acids (SCFAs)

The potential therapeutic role of probiotic bacteria in the gut is linked to their ability to produce a number of metabolites including short-chain fatty acids (SCFA) like lactic acid, acetic acid, butyric acid, propionic acids, etc. (Kahouli et al. 2013; Sharma and Shukla 2016).

SCFAs, conjugated linoleic acid and other anticarcinogenic products produced by Lactobacilli extracts induce apoptosis in cancer cells. In a report, the antiproliferative

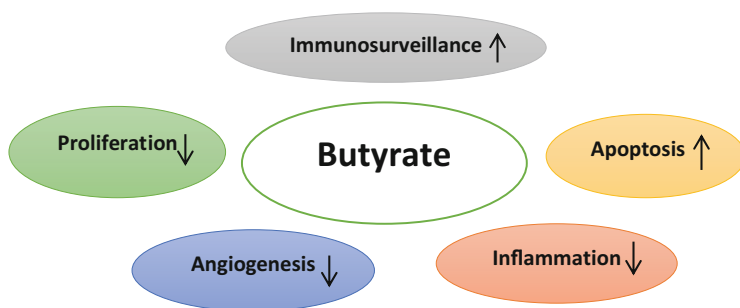


Fig. 6.3 Potential mechanisms by which the antineoplastic actions of butyrate may be mediated (Williams et al. 2003)

potential of probiotics *L. fermentum* NCIMB 5221, 2797, and 8829 was linked to their ability to produce SCFAs *in vitro* and their ability to persist in an intestinal fluid (Kahouli et al. 2013).

In another research report, SCFAs metabolites produced by probiotic *Propionibacterium freudenreichii* was shown to damage colorectal adenocarcinoma cells by producing apoptosis *in vitro*. Similarly, probiotics *Pediococcus pentosaceus* FP3, *Lactobacillus salivarius* FP35, *Lactobacillus salivarius* FP25, and *E. faecium* FP51 also inhibit proliferation of colon cancer cells by SCFAs bioproduction, mostly propionic and butyric acids. Similarly, conjugated linoleic acids produced by probiotic bacteria have the ability to form anticarcinogenic effects *in vitro* and *in vivo*. Another probiotic strain, *L. reuteri* NCIMB 701,359 has demonstrated anticarcinogenic effects owing to its ability to produce propionate (Kahouli et al. 2013; Sharma and Shukla 2016; Sivamaruthi et al. 2020).

Butyrate produced by fermentation of high amylose starch was reported to reduce the overall oxidative stress in gut and may also activate different procarcinogen metabolizing enzymes to aid in colon cancer prevention (Kahouli et al. 2013; Sharma and Shukla 2016; Sivamaruthi et al. 2020). Butyrate acts as the preferred source of energy for colonocytes and has anti-inflammatory and anticancerous properties (Fig. 6.3). Butyrate participates in the mobility of the colon, reduces inflammation, increases visceral irrigation, induces apoptosis, inhibits the progression of tumor cells, and contributes with the prevention of colorectal cancer (Williams et al. 2003). Unlike butyrate, acetate has been reported to be an instigator of cancers including liver, brain, prostate, and breast cancer. In cancer cells, acetate can serve as a source of nutrition required for lipid biosynthesis and can acetylate histones, leading to epigenetic modifications. It can also lead to the considerable posttranslational modification of proteins, altering their functions (Schug et al. 2016).

6.4.2 Bacteriocins

The potential use of bacteriocins in anticancer therapy is due to their inhibition of DNA and membrane protein synthesis, inducing apoptosis or cytotoxicity in tumor cells. Bacteriocins are ribosomally synthesized cationic peptides that are produced by almost all groups of bacteria. The first bacteriocin was discovered in the year 1925 by Gratia from *Escherichia coli* and later named as colicin. Since then, large number of bacteriocins have been identified from a diverse group of bacterial strains. Their physiological functions in bacteria seem to inhibit the growth of competing microorganisms in a particular biological niche by killing them. Microorganisms colonizing the gut may produce bacteriocins in an attempt to outcompete pathogens. Production of bacteriocins in a harsh and complex environment such as the gastrointestinal tract (GIT) may be below minimal inhibitory concentration (MIC) levels. At such low levels, the stability of bacteriocins may be compromised. Despite this, most bacteria in the gut have the ability to produce bacteriocins, distributed throughout the GIT. Most bacteriocins are extremely potent, exhibiting antimicrobial activity at nanomolar concentrations, as opposed to the peptide antimicrobials produced by eukaryotic cells, which normally have 10²–10³-fold lower activities. Interestingly, the producer cells are immune to their own bacteriocins. The classification of bacteriocins has been revised from time to time. The latest classification arranges bacteriocins into three major classes based on their structural and physicochemical properties (Aguilar-Toalá et al. 2018; Kaur and Kaur 2015).

Several studies have shown that some bacteriocins have anticancer properties and demonstrate selective action toward cancer cells. Although the exact mechanism of the cancer cell specificity has not been studied, the various factors that could account for the selective action of these bacteriocins could be explained based on the generalized cell surface variations of cancer cells from the normal cells. Bacteriocins have a higher affinity for cancer cells due to the general negative charge of cancer cells. This could be explained by the fact that, the bi-layered phospholipid membrane of normal mammalian cells is asymmetric with respect to the distribution of phospholipids on the inner and outer surface. However, in cancer cells there is loss in asymmetry with respect to phospholipid types. Cancer cell membrane is known to carry a predominantly negative charge due to high levels of the anionic phosphatidylserine, O-glycosylated mucins, sialylated gangliosides, and heparin sulfates. Bacteriocins are cationic peptides by nature and thus they preferentially bind to negatively charged cell membrane of cancer cells as compared to normal cell membranes which are neutral in charge. Secondly, the selective binding of bacteriocins to cancer cells can be explained due to differences in the membrane fluidity of cancer cells. Cancer cells have higher membrane fluidity as compared to normal cells and this facilitates easy membrane destabilization. Lastly, the membranes of cancer cells contain a significantly higher number of microvilli compared to normal cells that increases the surface area of cancer cells, which results in the binding of a greater number of antimicrobial peptides to the cancer cell membrane as compared to normal cells (Dicks et al. 2018; Kaur and Kaur 2015).

Table 6.3 Some well-known bacteriocins having anticancer activities against various cancer cell lines

Bacteriocin	Producer organism	Cancer cell lines	References
Colicin E3	<i>E. coli</i>	HeLa, HS913T	Fuska et al. (1979), Šmarda et al. (1978)
Colicin A	<i>E. coli</i>	HS913T, SKUT-1, BT474, ZR75, SKBR3, MRC5	Chumchalova and Šmarda (2003)
Colicin E1	<i>E. coli</i>	MCF7, HS913T	Chumchalova and Šmarda (2003)
MicrocinE492	<i>K. pneumonia</i>	Hela, Jurkat, RJ2.25	Hetz Flores et al. (2002)
Pediocin PA-1	<i>P. acidilactici</i> PAC1.0	A-549, DLD-1	Beaulieu et al. (2007)
Pediocin K2a2-3	<i>P. acidilactici</i> K2a2-3	HT2a, HeLa	Villarante et al. (2011)
Pediocin CP2	<i>P. acidilactici</i>	HeLa, MCF7, Sp2/0-Ag14, HepG2	Kumar et al. (2012)
Pyocin S2	<i>P. aeruginosa</i> 42A	HepG2, Im9HeLa, AS-II, mKS-ATU-7	Abdi-Ali et al. (2004), Watanabe and Saito (1980)
Nisin	<i>L. lactis</i>	MCF7, HepG2	Paiva et al. (2011)
Bovicin	<i>S. bovis</i>	HC5 MCF7, HepG2	Paiva et al. (2012)
Plantaricin A	<i>L. plantarum</i> C11	Jurkat, GH4, Reh, Jurkat, PC12, N2A, GH4	Sand et al. (2007, 2010, 2013), Zhao et al. (2006)

Nisin is a food grade bacteriocin that has been used as bio-preservative in dairy products. In a study, head and neck squamous cell carcinoma (HNSCC) cells treated with nisin showed that this agent induced DNA fragmentation and apoptosis on three different cancer cell lines. Apoptosis in HNSCC cells, caused by nisin, is associated with calcium influx and upregulation of CHAC1 (cation transport regulator and apoptosis mediator). In another study, the size of tumors in mice with oral cancer was reduced when treated with nisin. The authors concluded that the selective action of nisin was due to structural differences in the composition of the plasma membranes between HNSCC cells and primary keratinocytes (Dicks et al. 2018). Table 6.3 depicts anticancer effects of some bacteriocins produced by gram-negative and gram-positive bacteria.

The class IIc human defensins like bacteriocin, laterosporulin 10, displays cytotoxic effects against several cell lines and causes necrotic and apoptotic cell death at high and low concentrations, respectively. According to these studies, at high concentrations (10 mM), more than 95% of normal prostate epithelial cells remained viable, whereas 80% of cancer cells lost their viability. As with cytotoxicity against normal cells, the concentrations used to be effective against cancerous cells may be higher than the levels crossing the GBB (gut-blood barrier). However, the higher affinity for cancerous cells may result in bacteriocins targeting these cells. Immune priming by bacteriocins may also assist in the elimination of cancer cells. The possibility of bacteriocins crossing the GBB is intriguing, and from the literature, it is clear that they are capable of effecting the host if they do cross. However, if they

do cross and if they exert an effect requires further investigation (Dicks et al. 2018; Kaur and Kaur 2015).

6.4.3 Exopolysaccharides

Exopolysaccharides (EPS) are biological high-molecular long-chain extracellular polysaccharides surrounding the envelope of most bacteria. EPS are mainly involved in cell adhesion and protection, and often covalently bound to the cell surface in the form of capsules, or secreted into the extracellular environment in the form of slime (Sivakumar et al. 2012). EPS constitutes rhamnose, galactose, glucose, arabinose, and mannose. The diversity in the sugar composition, chain linkage, and molecular weight of EPS are known to be responsible for their antiproliferative activities (Ismail and Nampoothiri 2013; Wang et al. 2014a). Possible mechanism by which EPS exert their anticancer activity includes: (1) prevention of tumorigenesis, (2) induction of cancer cell apoptosis, and (3) immune modulation.

During last decade, several LAB have been investigated for their EPS-producing ability and their health benefits such as immunomodulatory, antitumor, antibiofilm, and antioxidant activity analyzed (Angelin and Kavitha 2020; Degeest et al. 2002). EPS extracted from probiotics plays a fundamental role in prevention and treatment of cancer. As Fig. 6.4 depicts, EPS of probiotic LAB have antimicrobial, immunomodulatory, anti-inflammatory, antioxidant, antitumor, antiviral, antidiabetic, anti-ulcer, and cholesterol lowering activities (Hussain et al. 2017; Patel et al. 2012; Angelin and Kavitha 2020)).

Several scientific data indicate that lactic acid bacteria found in the gut have a role in regression of cancer through their effect on immunomodulation. These bacteria

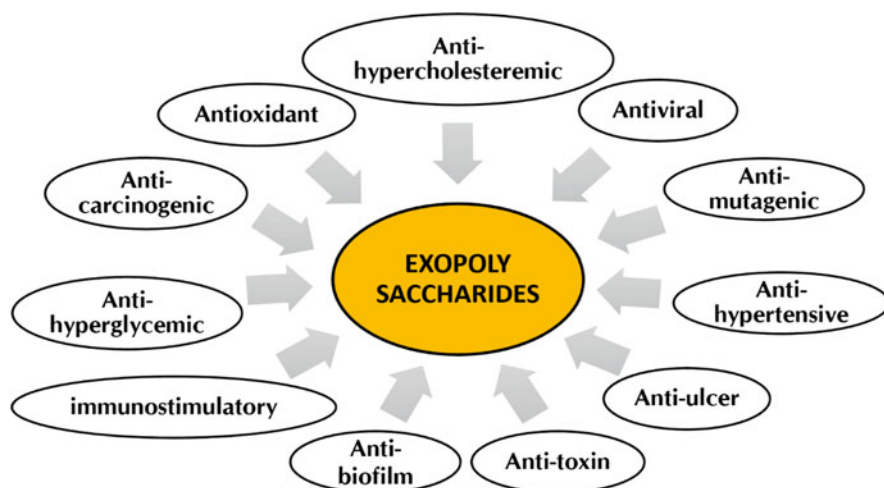


Fig. 6.4 Biological activities of exopolysaccharides produced by LAB

can activate phagocytes to remove early-stage tumor cells. In a recent report, Wu and his colleagues (2021) reported that EPS extracted from LAB are noncytotoxic to normal cells while promote tumor cell apoptosis and cell cycle arrest (Wu et al. 2020). The antitumor and antioxidant properties of EPS produced by *L. acidophilus*, *L. gasseri*, *L. plantarum*, and *L. rhamnosus* have been reported earlier (Adesulu-Dahunsi et al. 2018; Sungur et al. 2017).

In a study, the EPS of *L. fermentum* Lf2 given orally to BALB/c mice mixed with yoghurt samples was shown to increase SCFA concentrations such as acetate and butyrate. As mentioned in earlier section, these fatty acids are volatiles produced by gut microbiota and have intestinal anti-inflammatory properties (Ale et al. 2019).

Reports from Sungur and his colleagues (2017) showed that 400 µg/mL of EPS G10 extracted from *L. gasseri* could significantly inhibit HeLa cell line proliferations. According to these researchers, the enhanced antiproliferative activity observed was related to upregulation of BAX in HeLa cells and an increase in Caspase 3 protein expression that activates apoptosis (Sungur et al. 2017). Similar to these findings, EPS (MSR101) extracted from *L. kefir* showed apoptotic effect on HT-29 cancerous cells via upregulation of the expression of cytochrome-c, BAX, BAD, caspase-3, caspase-8, and caspase-9 (Rajoka et al. 2019). *L. acidophilus* 20,079 EPS has a direct cytotoxic effect on the tumor cells by mechanisms of apoptosis, immune response stimulation, and NF-κB inflammatory pathway inactivation. The effect of *L. acidophilus* 20,079 extracted EPS on colon is a promising therapeutic target for cancer. Cell wall components of *L. acidophilus* and *L. casei* act as anticancer substances. *L. plantarum* 70,810 extracted EPS prevents the proliferation of hepatocellular carcinoma cell line. Additionally, EPS produced by probiotic lactic acid bacteria such as *L. plantarum* GD2, *L. rhamnosus* E9, *L. brevis* LB63 isolated from healthy infant feces and *Lactobacillus delbrueckii sp. bulgaricus* B3 isolated from yogurt has shown anticancer effect on colon cancer cells (HT-29) (Sharma and Shukla 2016). Lactobacilli EPS induces apoptosis in CRC in vitro through Caspase 3 and 9 and BAX increased expression and decreased Bcl-2 and survivin. Vital molecular pathways target and different forms of cell death induction by components of probiotic yeasts are considered as potential therapeutic tools against CRC. EPSs produced by probiotic *Kluyveromyces marxianus* (*K. marxianus*) and *Pichia kudriavzevii* (*P. kudriavzevii*) inhibit various colon cancer cell lines (Dicks et al. 2018; Sharma and Shukla 2016).

Moreover, probiotic *Bifidobacterium breve* (*B. breve*) lw01 EPS improves immune development and possesses anticancer and anti-inflammation effects (Sharma and Shukla 2016). According to these researchers EPS shows anticancer property against head and neck squamous cell carcinoma cell line by controlling apoptosis and cell cycle arrest. The investigators suggested that *B. breve* lw01 EPS can be used to assist genetic and metabolic engineering and might play role in application of functional food or drug industries.

6.4.4 Biosurfactants

Several studies reported the prospective of LABS as biosurfactant producers and their potential role in biomedical and food research (Fariq and Saeed 2016; Fracchia et al. 2012; Thavasi et al. 2011). Biosurfactants (BS) are the diverse polymeric molecules synthesized during the late log or early stationary phase of the growth cycle of an organism, secreted extracellularly or cell wall-bound. These compounds are generally localized on the microbial surface and made of amphiphilic molecule, comprising both hydrophobic and hydrophilic moieties (Banat et al. 2010). As shown in Table 6.4, the major group of biosurfactants comprises phospholipids,

Table 6.4 Structural composition of biosurfactants derived from various LAB strains

No	Bacteria	Biosurfactant produced	References
1.	<i>L. acidophilus</i> RC14	Rich in protein, high amount of polysaccharides and Phosphate content	Velraeds et al. (1996)
2.	<i>S. thermophilus</i>	Glycolipid	Busscher and Van der Mei (1997)
3.	<i>L. acidophilus</i>	Surlactin	Velraeds et al. (1996)
4.	<i>S. mutans</i> NS	Rhamnolipid like	van Hoogmoed et al. (2004)
5.	<i>S. thermophiles</i> A	Glycolipid	Rodrigues et al. (2006)
6.	<i>L. casei</i>	Glycoprotein	Golek et al. (2009)
7.	<i>L. lactis</i>	Xylolipids	Saravanakumari and Mani (2010)
8.	<i>L. acidophilus</i>	Glycoprotein	Tahmourespour et al. (2011)
9.	<i>L. plantarum</i>	Glycolipids	Sauvageau et al. (2012)
10.	<i>L. plantarum</i>	Glycoprotein	Madhu and Prapulla (2014)
11.	<i>L. pentosus</i>	Glycolipids	Vecino et al. (2014)
12.	<i>L. casei</i> MRTL3	Glycolipids	Sharma et al. (2014)
13.	<i>E. faecium</i> MRTL9	Xylolipids	Sharma et al. (2015)
14.	<i>L. helveticus</i> MRTL91	Glycolipids (Xylolipids)	Sharma et al. (2015)
15.	<i>L. pentosus</i>	Glycolipopeptide	Vecino et al. (2015)
16.	<i>L. gasserii</i> P ₆₅ and <i>L. jensenii</i> P _{6A}	Glycolipoproteins	Morais et al. (2017)
17.	<i>L. lactis</i> 53	Glycoprotein	Rodrigues et al. (2006)
18.	<i>L. paracasei</i>	Glycoprotein	Gudina et al. (2010)
19.	<i>L. pentosus</i>	Glycoprotein	Moldes et al. (2013)
20.	<i>Bacillus subtilis</i> ATCC 6633	Lipopeptide	Dehghan-Noudeh et al. (2005)

fatty acids, glycolipids, lipopeptides, lipoproteins, polymeric surfactants, and particulate surfactants.

These bioactive compounds have recently emerged as promising molecules for their structural versatility, novelty, and diverse properties that are potentially useful for many therapeutic applications. One of the most important therapeutic effects of biosurfactants is their anticancer actions and their ability to regulate cancer progression processes (Gudiña et al. 2013).

The ability of these biomolecules to interact with cell membranes of several organisms and/or with the surrounding environments can be viewed as potential cancer therapeutics (Rodrigues 2011). The glycoproteins derived from *L. paracasei* were shown to have antitumor activity against breast cancer cell lines. According to the results of these researchers, the biocompound produced by the mentioned probiotic LAB was able to decrease cell viability after 48 h and reported cell cycle arrest in the tested cell lines. Lipopeptides have also been extensively studied for their potential antitumor activity. In another report, growth inhibition activity of mannosylerythritol lipids against human leukemia cells was stated (Isoda and Nakahara 1997).

Cao et al. (2010, 2011) demonstrated that surfactin induces apoptosis in human breast cancer MCF7 cells through a ROS/JNK-mediated mitochondrial/caspase pathway (Cao et al. 2010; Cao et al. 2011). While Kim et al. (2007) evaluated the effect of surfactin on the human colon carcinoma cell line LoVo and showed that the lipopeptide presents a strong growth inhibitory activity by inducing apoptosis and cell cycle arrest (Kim et al. 2010). Lee et al. (2012) demonstrated that surfactin inhibited the growth of MCF7 human breast cancer cells in a dose-dependent manner (Lee et al. 2012). In addition, several other lipopeptides (isoforms of surfactin and fengycin) were also found to have potent cytotoxic effects against the human colon cancer cell lines HCT15 and HT29 (Sivapathasekaran et al. 2010). While Durate and his colleagues were able to show the effect of biosurfactants on viability and proliferation of human breast cancer cells (Duarte et al. 2014).

However, an important drawback of using surfactin as a chemotherapeutic agent is its hemolytic activity (Dehghan-Noudeh et al. 2005) that has been reported for concentrations above 0.05 g/L. Since surfactin has never been tested in humans, to prevent future complications several strategies have been explored envisaging its use as a safe therapeutic agent. Symmank et al. (2002) reported several minor modifications of the surfactin molecule by altering surfactin synthetase. These modifications changed the molecule toxicity profile, resulting in a “new” lipopeptide with improved activity and not revealing any signs of toxicity or hemolytic activity. Another interesting approach consists in the incorporation of surfactin in nanoparticles in order to provide a directed as in order to provide a directed administration and in situ release of the cyclic peptide (Symmank et al. 2002).

Since there is an enormous diversity of microbial surfactants, the attention of the scientific community in the search for new molecules with interesting antitumor activities is continuously increasing, as well as in looking deeply into their mechanisms of action. Therefore, clinical applications of specifically probiotic biosurfactants yet need to be explored. In addition, further research is required to

unravel the mechanism of their action in human body which would assist in their target sited applications without interfering with other body microflora. Moreover, investigation on genetics of probiotic bacteria in regulation of biosurfactants is vital for their optimum production and potential applications in health sector.

6.5 Anticancer Effects of Paraprobiotics (Dead Probiotic Cells)

In contrast to probiotics, paraprobiotics are defined as dead or nonviable probiotic bacterial cells or cell components that confer health benefits when administered in adequate doses. They are also referred to as ghost or inactivated probiotics and mainly constitute ruptured cell components of probiotic cells such as teichoic acids, peptidoglycan-derived muropeptides, pili, fimbriae, flagella, polysaccharides, biosurfactants, etc. Some paraprobiotic products have been commercialized and present in the market with the trade name of Lactéol Fort® from PUMC Pharmaceutical Co., Ltd. and Fermenti Lattici Tindalizzati® from Frau, AF United Spa (Taverniti and Guglielmetti 2011).

The anticancerous activity of paraprobiotics has been reported by many; in fact, the suppressive potentials of dead probiotic have been shown to be superior to live probiotic. According to these statements, administration of high doses of dead probiotic reduced a number of tumors considerably compared with pure live probiotic. Dead probiotics showed fewer colonic tumors, longer colons, and less weight loss compared with pure live probiotic *L. plantarum* (Taverniti and Guglielmetti 2011; Wang et al. 2014b). This property was due to the effects of inflammation suppression, apoptosis, and enhanced IgA secretion. Figure 6.5 dictates some proposed mechanism of action of paraprobiotics (Fig. 6.5).

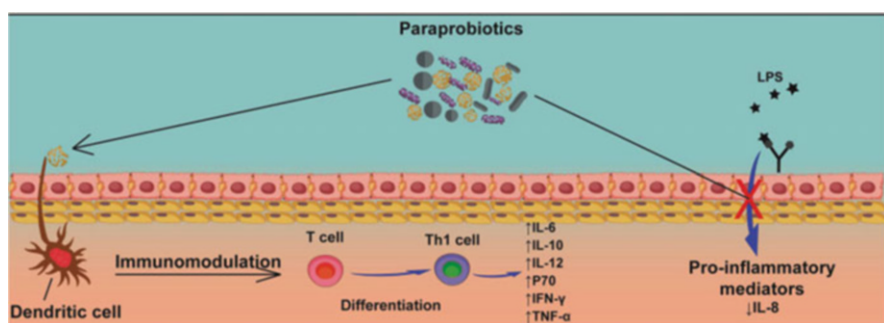


Fig. 6.5 Diagrammatic representation of mechanism of action of paraprobiotic; the inactivated or dead probiotic bacterial cells are known to exert their effects by immunomodulation of T cells by dendritic cells, stimulating their differentiation into Th1 cells, promoting the production of anti-inflammatory cytokines. Another proposed mechanism includes inhibition of signaling pathways related to LPS stimulation, resulting in a reduction of proinflammatory mediators, like IL-8 (Batista et al. 2020)

In a study, combined administration of live and dead probiotics was shown to significantly reduce proinflammatory cytokines and inflammatory genes overexpression, and suppressive potentials than separate administration of either groups. All the experimental AOM/DSS control animals group possessed colon tumors, but administration with dead *L. plantarum* suppressed the development of neoplasia significantly. The mechanism by which dead probiotic sustains the status of mucosal immune system is by increasing levels of secretory IgA. This indicates that the antitumor property of dead probiotic is related with the easier uptake of dead probiotic by more cells than pure live probiotic and the stronger secretory immune responses (Sharma and Shukla 2016).

Recent report indicated that, the application of heat-inactivated probiotic *Enterococcus faecalis* (*E. faecalis*) protects against dextran sodium sulfate-induced CRC and ameliorates intestinal inflammation severity in wild-type mice. *E. faecalis* paraprobiotic fractions provided protection to experimental animals against dextran sodium sulfate-induced colitis and CRC by reducing intestinal inflammation severity through phagocytosis attenuation. It was concluded that heat-killed probiotic *E. faecalis* is safe and useful for inflammation-associated colon carcinogenesis attenuation by inhibition of IL-1 β secretion induction in macrophages (Sharma and Shukla 2016).

6.6 Conclusions

Probiotics are known to exert various health benefits such as immunomodulation, inactivation of carcinogens, and maintenance of gut integrity, but the present review represents their role in cancer prevention and treatment. However, owing to their viable status these beneficial bacteria might impose some adverse effects in certain immunosuppressed individuals, which in turn might limit their use. Thus, attempts are being made to the dead counterpart (paraprobiotics) of these viable bacteria or their secretory substances (postbiotic metabolites/metabiotics) that might be safer alternative and effective bio-interventions. The significant role of these metabolites has been shown to possess remarkable antimutagenic, anti-inflammatory, antiproliferative potentials attributed to their epigenetic effects in one or the other way, and may target cancer at different stages. Hence, paraprobiotic and metabiotics independently or in conjunction with other approaches could be considered as a potent prophylactic/or therapeutic modulator for cancer or other diseases in the post-antibiotic era. However, there is a high need for human/clinical trials focusing on the validation of health claims of these bioactive molecules. The trials in immunocompromised subjects would be further augmentable to investigate the tolerance of immunocompromised subjects on these biomolecules. On the other hand, there is a lack of knowledge regarding the stability of paraprobiotics and postbiotics under *in vitro* and *in vivo* digestive conditions to comprehend specific mechanistic actions by interacting with the ligands. These biomolecules may eliminate the adverse effects and reduce the difficulties in the maintenance of viability of probiotics, but yet enough information regarding their human clinical trials is not available that

could elucidate their mechanism of action and propose their safe use in human especially for the treatment of variety of cancer.

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Postbiotic Metabolites of Probiotics in Animal Feeding

7

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Abstract

The gut is consistently exposed to broad harmful pathogens from the external environment. It also acts as a barrier against infections, involves in digestion, nutrient absorption, and immune response. Any disruption and dysfunction in the gut microenvironment can cause huge implications on the general well-being of the host. Hence, a good gut health, which is an integral component of the diet, gut microbiota, and intestinal mucus layer, is vital to maintain the normal function of physiological and metabolic activities in the body. In this chapter, we highlighted the positive effects of supplementation of dietary postbiotic on growth performance, gut microbiota, intestinal morphology, immune response, meat quality, and expression of genes related to the barrier function and immunity in livestock. The inclusion of antibiotic growth promoters to achieve good intestinal health and performance which led to the emergence of antibiotic resistance gene and

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179

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antibiotic residue level in the food product as well as beneficial compounds detected in the postbiotic are discussed in more detail.

Keywords

Probiotics · Postbiotics · Gut microbiota · Animal feeding

7.1 Introduction

The gut is a vital organ involved in nutrient digestion and absorption, metabolism, and immunity. It is highly exposed to the extrinsic pathogens (Yegani and Korver 2008). Failure or disruption on the digestion and nutrient absorption could affect the optimum performance and health of the birds. The intestinal mucosal is one of the critical determinants in the gut health and performance of the birds; it protects the internal environment against various harmful agents from the external environment, aids nutrient absorption, and acts as lubricant and site for microflora colonization (Rinttila and Apajalahti 2013).

The main factor that is responsible for the gut health and performance in a poultry flock is the gut microbiota. Even though it helps to shape the gut structure and morphology, which aid in the digestion and nutrient absorption, a good colonization of commensal microflora also protects against the pathogenic invasion and immune response (Sugiharto 2016). Also, a well-balanced intestinal mucosal barrier function is associated with the internal homeostasis between the mucus layer, epithelial cells, gut microflora, and immune cells (Schenk and Mueller 2008). The diet, nutrition, and infectious disease agents have been identified as the prominent factors that interrupt with the mucin dynamics in the gut. In turn, it will affect the well-being and performance of the birds (Yegani and Korver 2008).

Antibiotic growth promoter (AGP) has been included sub-therapeutically in the feed extensively to achieve optimum gut health. The extensive application of AGP in livestock nutrition may produce public health consequences as the resistance develops in many pathogenic bacterial species in exposed animals. It was reported that *E. coli* isolated from pigs' faeces were resistant to various commonly used antibiotics such as neomycin, oxytetracycline, nalidixic acid, and chloramphenicol (Loh et al. 2013). Similar findings were also reported in the Netherlands (Van de Bogaard et al. 2001). AGP has been widely used to maintain the equilibrium of the gut ecosystem as well as to improve the growth performance of birds (Huyghebaert et al. 2011).

Nonetheless, the usage of AGP for long periods has led to the emergence of antibiotic resistance gene (Shazali et al. 2014) and exceeded permitted residue levels in animal products (Van de Bogaard et al. 2001). Genes encoding for this resistance can also be transferred to other formerly susceptible bacteria, thereby posing a threat to both animal and human health (Montagne et al. 2003). Due to the rising concern of food safety and security from the public, the inclusion of AGP in animal feed is either restricted or outright banned in many countries (Ohimain and Ofongo 2012).

However, with the ban and restriction to the use of AGPs in poultry nutrition, other natural and safe alternatives are required to maintain the well dynamic gut microbiota in chickens (Sugiharto 2016).

Another natural alternative to replace AGP is the postbiotic. Unlike probiotic which deals with living cells, postbiotic is the secondary metabolic or the molecules secreted by the probiotic during the metabolic activity (Tsilingiri and Rescigno 2013). The postbiotic contains bacteriocin, enzymes, and other unelucidated protein compounds. It also contains organic acids such as lactic acid, acetic acid, and other short-chain fatty acids (Lee et al. 2019). It has been proven that postbiotics have antimicrobial and anti-inflammatory functions, prevent the proliferation of pathogens by lowering the pH in the gut environment (Kareem et al. 2014), stimulate cytotoxicity effect on cancer cells (Chuah et al. 2019) and act as an antioxidant agent (Humam et al. 2019; Izuddin et al. 2020). In the in vitro studies, the metabolites produced from *Lactiplantibacillus plantarum* (*L. plantarum*) were able to inhibit the growth of pathogenic bacteria such as *Listeria monocytogenes*, *Salmonella typhimurium*, *Escherichia coli*, and Vancomycin-Resistant *Enterococci* and *Paediococcus acidilactici* (Kareem et al. 2014; Loh et al. 2010). Furthermore, enhancement in the growth performance, faecal lactic acid bacteria, intestinal morphology and immune status were observed when metabolite combinations were added to the feed of broilers (Thanh et al. 2009), laying hens (Choe et al. 2012), pigs (Thu et al. 2011), and lambs (Izuddin et al. 2020).

7.2 Postbiotics

Postbiotics, the metabiotics or metabolites are the cell-free extracts or soluble factors (metabolic by-products) secreted by live bacteria or released after bacterial lysis (Aguilar-Toala et al. 2018). The hosts are benefitted physiologically by the capacity of the metabolites to induce additional bioactivity (Cicenia et al. 2014). Substances such as organic acids, bacteriocins, enzymes, cell surface proteins, peptides, polysaccharides (endo- and exo-), and plasmalogens are few examples of soluble factors that are commonly found in postbiotic metabolite (Lee et al. 2019; Thu et al. 2011; Aguilar-Toala et al. 2018; Lim et al. 2019; Malashree et al. 2019; Toe et al. 2019). Furthermore, their broad inhibitory activities against several pathogenic bacteria have been reported. For instance, reduced colonization of pathogenic bacteria such as *E. coli*, *Salmonella*, and *Enterobacteriaceae* in the gastrointestinal tract was reported in poultry following supplementation with various lactic acid bacteria (LAB) metabolites (Humam et al. 2019; Izuddin et al. 2020; Thanh et al. 2009; Choe et al. 2012; Loh et al. 2009; Kareem et al. 2016a).

Although the underlining mechanisms regarding the beneficial implications of postbiotics on livestock health are not well understood, there is scientific-based evidence to show that these metabolites possess various functional characteristics such as antimicrobial, immunomodulatory antioxidant, and other unconfirmed properties. Currently, these properties are known to influence gut microbiota and

metabolic pathways associated with physiological, immunological, and hormonal functions (Foo et al. 2019; Yang et al. 2019).

7.3 Implications of Postbiotic Supplementation on Growth Performance

The growth performance in poultry is measured using parameters such as total feed intake, feed conversion ratio (FCR), body weight gain (BWG), as well as factors relating to egg production and meat quality. Postbiotic efficacy is determined by various mechanisms involved in their ability to increase the beneficial bacteria population to protect mucosal surfaces from pathogens, which include direct competition between them for adhesion and the rate of regeneration (Aguilar-Toala et al. 2018). Also, postbiotics have both bactericidal and bacteriostatic properties, thus reducing the proliferation of pathogenic bacteria in the gastrointestinal tract (Loh et al. 2010; Rosyidah et al. 2011; Loh et al. 2014; Kareem et al. 2016b). The *L. plantarum* postbiotics have been documented to exert an antimicrobial effect on different pathogenic bacteria (Thanh et al. 2009). Thu et al. (2011) used the inhibitory activity test to assess such a relationship with the application of *P. acidilactici* as an indicator microbe. Their findings showed that postbiotic combinations (TL1, RG14, RG11, and RS5) have stronger inhibitory activity as compared with a single strain. Presence of a large amount of lactic acid and acetic acid, as well as bacteriocins inhibitory compound, is suggestive of contributing to such event. These mechanisms of actions enhance better growth performance in poultry.

Based on the inhibitory activities observed on the pathogens using postbiotics from *L. plantarum* (Thanh et al. 2010), an experiment was conducted to investigate the effect of a different combination of postbiotics on growth performance in broiler chickens (Thanh et al. 2009). Postbiotic treatment groups had greater BW, WG, ADG, and the best FCR compared to the negative control (fed basal diet only). Based on the improved growth performance found after postbiotic supplementation in piglets (Thu et al. 2011), the authors also evaluated if such beneficial effects could be replicated in laying hens (Loh et al. 2014). There was a significant reduction in faecal pH and specific pathogenic bacteria and improvement in faecal LAB following the addition of postbiotics, whereas there was no significant difference in overall feed intake, egg mass, and FCR among the treatment groups. The use of postbiotics combinations of *L. plantarum* strains in laying hens resulted in significantly higher laying performance and other parameters relating to gut microbiota and small intestine histomorphology (Choe et al. 2012). Thus, the latter study indicated the need for further evaluation on the potential benefits of various postbiotics combination on growth performance and immune response in poultry. Metabolite combinations and single strains of postbiotics could confer varying impact on the growth performance of broiler chickens. Kareem (2016) investigated the growth performance in broiler chickens after supplemented with a combination of postbiotic and inulin. Through the study, it showed that such combination could lower the FCR compared to the group without adding any feed additive. Another benefit of

postbiotic is shown in the ruminal fermentation and growth performance of lambs (Izuddin et al. 2018; Izuddin et al. 2019a; Izuddin et al. 2019b). Majority of the research on postbiotics in poultry have established their positive impact on growth performance.

7.4 Implications of Postbiotic Supplementation on Gut Microbiota and pH

The gut microbiota in poultry chickens is vital for general health and productivity (Yang et al. 2019; Shang et al. 2018). The beneficial effects of postbiotic supplementation on the gut microbiota have been determined in several studies (Thanh et al. 2009; Choe et al. 2012; Thu et al. 2011; Loh et al. 2014; Kareem et al. 2016b). In poultry, such studies assess the population of pathogenic and non-pathogenic microorganisms following postbiotic supplementation in feeds (Thanh et al. 2009; Choe et al. 2012; Loh et al. 2014). Broilers supplemented with combinations of basal diet, inulin, and varying concentration of postbiotic *L. plantarum* RG14 promoted the proliferation of total caecal bacteria and *Bifidobacterium* compared to the negative control group (Kareem et al. 2016b). Also, the non-treatment group had greater counts of *E. coli* and *Enterobacteriaceae*, whereas no effect of diet on *Lactiplantibacillus*, *Enterococcus* (ENT), and *Salmonella* population in broilers fed postbiotic with prebiotic. Similar findings were reported following the supplementation of broiler feed with the combination of various postbiotics and inulin (a prebiotic) (Kareem et al. 2016b). Thanh et al. (2009) observed increased faecal LAB population after supplementing broilers feed with different strains of *L. plantarum* derived metabolites. The LAB counts and mesophilic microbial population increased significantly following dietary supplementation with combined fermentative products of LAB (bacteriocins and organic acids) in Ross broilers (Fajardo et al. 2012). A similar result was reported using the postbiotics in layer hens (Choe et al. 2012). These works reinstate that intestinal microbiota maturation index could serve as an important parameter when comparing the efficacy of feed additives on poultry microecology.

The feeding of *L. plantarum* postbiotic to livestock has been proven to shift the gut microbiome towards the proliferation of good bacteria. Kareem (2016) revealed that supplementation of *L. plantarum* RG14 combined with inulin enhanced the colonization of *Bifidobacterium* while lowered the population of *E. coli* and *Enterobacteriaceae* compared to control groups. Similarly, broiler and layer birds fed with a combination of *L. plantarum* postbiotics had a higher faecal LAB population (Thanh et al. 2009; Choe et al. 2012). Humam et al. (2019) reported that the supplementation of postbiotic to broiler chicken reared under heat stress environment recorded higher counts of caecum total bacteria, *Lactiplantibacillus* and *Bifidobacterium* but with a significantly lower population of pathogenic bacteria such as *Enterobacteriaceae*, *E. coli*, and *Salmonella* compared to the control groups. It also has been shown that caecal pH correlates with the bacteria counts. The presence of various organic acids in the postbiotic lowers the pH of the caecum.

Subsequently, this inhibits the growth of the low acidic tolerant pathogenic bacteria such as *Enterobacteriaceae*, *E. coli*, and *Salmonella* and stimulates the proliferation of beneficial bacteria such as *Lactiplantibacillus* and *Bifidobacterium*. In lambs, the inclusion of *L. plantarum* postbiotics in feed improved fibre degrading bacteria but with a reduction in total protozoa and methanogens in the rumen (Izuddin et al. 2019b).

7.5 Implications of Postbiotic Supplementation on Gut Morphology and Immune Response

Maintenance of the integrity of the GIT is a prerequisite for optimal physiological function. Such maintenance enables a stable microbial population and conditions to protect against offending substances (Yang et al. 2009; Adedokun and Olojede 2019; Dudek-Wicher et al. 2018). Majority of the studies investigate the relationship between postbiotics and gut morphology by focussing on the height and depth of the intestinal villi and crypts, respectively, since they are the portals for the absorption of nutrients (Choe et al. 2012; Gao et al. 2019). Accordingly, gut health can be assessed based on the condition of the villus height and crypt depth (Uni et al. 1995).

Postbiotic supplementation in laying hens was reported to improve nutrient digestibility based on the maintenance of villus height and crypt depth of mucosal architecture (Choe et al. 2012). Increment in villi height and reduced crypt depth are optimal for efficient nutrients absorption to take place across the intestine into the systemic circulation (Markovi et al. 2009). The addition of a combination of postbiotics obtained from *L. plantarum* strains also increased small intestinal villus height in broilers (Loh et al. 2010; Thanh et al. 2009; Kareem et al. 2016a) and pigs (Loh et al. 2013; Thu et al. 2011). Likewise, the addition of six per cent liquid metabolites obtained from the same bacteria showed enhancement on villus height in layers (Choe et al. 2012). Moreover, Izuddin et al. (2019a) reported that addition of postbiotic postweaning lamb feed had increased the villus height. Improvement was also detected in the small intestine morphology (higher villi height and lower crypt depth) when the broiler chickens were supplemented with postbiotic (Humam et al. 2019). Based on the information generated by Markovi et al. (2009) the positive effect of probiotic supplementation on intestinal villi and crypt depth could be one of the reasons for better health and growth in broiler chickens when supplemented with postbiotic.

It is assumed that associations between postbiotic supplementation and improved health and productivity, as shown in several studies, are connected to underlying mechanisms that activate a protective immune response against offending pathogens. Many studies have reported that inclusion of postbiotic in the diets improves the immune response in the broilers (Kareem et al. 2016b) and lambs (Izuddin et al. 2019a) and the gut health for animals.

7.6 Implications of Postbiotic Supplementation on Meat Quality

There is limited published data on the meat quality of broiler chickens fed with postbiotics. However, one study showed that broiler chickens fed a combination of postbiotics and inulin showed reduction of drip loss and better breast muscle lightness (Kareem et al. 2015). Other parameters, such as shear force, cooking loss, and related bone attributes, were not affected by the in-feed supplementation of the combination, as mentioned earlier (Kareem et al. 2015). Another study conducted by Humam et al. (2020) revealed that when postbiotic was added to the feed of heat-stressed broiler chickens, there was an increased of breast meat pH but decreased in the shear force, lightness, drip loss, cooking loss, and yellowness. The prevention of pH drop might contribute to the results, improved antioxidant activity and reduced corticoid hormone levels (Sato et al. 2010; Hao and Gu 2014; Zaboli et al. 2019).

7.7 Implications of Postbiotic Supplementation and Gene Expression Related to the Gut Barrier Function and Immunity

Exploring expression of gene information regarding postbiotic supplementation could assist in better understanding of the mechanisms underlining their effect in poultry birds. The gene expression includes immune response and reactions relating to the impacts on the gut microbiota and barrier function, as well as processes involved in arresting pathogenic bacteria. Another study conducted by Kareem et al. (2016a) evaluated the ileal cytokine expression in birds fed with postbiotic (RG14) and prebiotic (inulin). The birds fed with diet not containing the metabolites had higher expression of interferon (IFN) and the tumour necrosis factor alpha (TNF- α) when compared with all the other treatment groups. Also, the mRNA expression of IL-6 (interleukin-6) had significantly higher expression in the group fed various percentages of the metabolite combination than the basal diet and antibiotic-treated groups. In another study, the liver of broilers fed with various postbiotics (metabolites from the LAB) combined with inulin had significantly up-regulated the IGF-1 expression compared to other treatments groups (Kareem et al. 2016b). Moreover, the group fed RG14 and inulin had greater GHR mRNA expression compared to other treatments. Izuddin et al. (2019b) found out the addition of in feed postbiotic of postweaning lambs led to an increase in the IL-6 mRNA and decrease of IL-1 β , IL-10, TNF gene expression. Postbiotics increased the gene expression of IGF-1 in the liver and MCT-1 in the rumen of the postweaning lambs (Izuddin et al. 2019b).

There are intrinsic associations between gut microbiota and IGF-1 production as established in experiments conducted in mice (Yan et al. 2016). Accordingly, mice supplemented with short-chain fatty acids (SCFA) recorded increased secretion of IGF-1 in both the adipose and liver. This effect (increased SCFA production) was

successfully found in broiler chickens following the combined dietary supplementation using *L. plantarum* metabolites and prebiotics (Kareem et al. 2016a) and heat stress broiler chickens (Humam et al. 2019).

The effects on antioxidant enzyme-related gene expression due to supplementation of *L. plantarum* postbiotics can be detected in postweaning lambs. The study carried out by Izuddin et al. (2020) showed that the postweaning lambs fed with postbiotics had up-regulated the expression of hepatic glutathione peroxidase (GPX1 and GPX4) and Cu/ZN SOD genes. Besides, the same group of lambs received postbiotic supplementation affected the gene expression of TJPI, OCLD, CLDN1, and CLDN 4 in the rumen and zonula occludin-1 in broiler chickens under heat stress (Humam et al. 2020). As mucin secretion affects the gut permeability, immune status, and nutrient absorption in the intestine, the postbiotic of *L. plantarum* has been proven to improve the expression of intestinal mucin in livestock. Humam et al. (2020) showed that postbiotic RI11 up-regulated the expression of MUC2 with the increased inclusion level in feed.

7.8 Implications of Postbiotic Supplementation on Antioxidant Activities

During heat stress condition, there is an increased production of reactive oxygen species such as hydroxyl free radical and superoxide anions which posed harmfully and even damaging effect on the animal tissues (Akbarian et al. 2016; Altan et al. 2003). In poultry, antioxidants are substances synthesized by related enzymes such as superoxide dismutase, glutathione peroxidase, and catalase as defensive products to mitigate the effects of reactive oxygen species by making them non-toxic (Surai 2015). Humam et al. (2020) revealed that postbiotic supplementation RI11 improved the activity of total-antioxidant capacity, catalase, and glutathione while lowered the level of alpha-1-acid-glycoprotein and ceruloplasmin in the blood plasma when the broiler chickens were raised under heat stress condition. However, no significant changes were observed in plasma corticosterone and heat shock protein 70 between all the treatments. On the other hand, Izuddin et al. (2020) revealed that the glutathione peroxidase and thiobarbituric acid reactive substance activities in the blood serum were affected due to the supplementation of postbiotic.

7.9 Conclusions

A good and efficient gastrointestinal tract is essential for nutrient digestion and absorption besides protecting the animals from various infections and stress by secreting immune-related compounds. The feed additives such as antibiotics were included since a long time in broilers to enhance the gut health and boilers productivity. However, excessive usage of antibiotics contributed to the emergence of antibiotic-resistant bacteria and residual effects in the ecosystem and food product, which could have a harmful influence on both broiler and human health. Several

alternatives to antibiotics such as ascorbic acid and probiotics were used to promote the broilers health and productivity. However, some probiotics own antimicrobial resistance genes which can be transferred to other living organisms. Therefore, this limitation may compromise the expected health consequences exhibited by the probiotic. For these consequences, it becomes necessary to find safe and effective alternatives to antibiotics and probiotic. Postbiotics are the metabolites produced by probiotic and exert antimicrobial activity due to the presence of antimicrobial compounds, for example, bacteriocins and organic acids. This characteristic leads to better gut health. Postbiotics have been documented to enhance gut health and growth performance and production in livestock such as poultry, lambs, and pigs.

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Probiotics Application: Implications for Sustainable Aquaculture

8

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Abstract

Probiotics, known as beneficial microorganisms, are being proposed as an effective and eco-friendly alternative to antibiotics. They were first applied in aquaculture species more than three decades ago, but considerable attention had been given only in the early 2000s. Probiotics defined as live, dead, or a component of the microorganisms which act under different modes of action in conferring beneficial effects to the host or its environment. Several probiotics have been characterized and applied in fish, and a number of them are of host origin. Unlike some disease control alternatives being adopted and proposed in aquaculture where actions are unilateral, the immense potential of probiotics lies on their multiple mechanisms in conferring benefits to the host fish and the rearing environment. The staggering number of probiotics papers in aquaculture highlights the multitude of advantages from these microorganisms and conspicuously position them in the dynamic search for health-promoting alternatives for cultured fish. The present review provides an update on the use of probiotics in finfish aquaculture, mainly focusing on their modes of action. It explores the contemporary understanding of their spatial and nutritional competitiveness, inhibitory metabolites, environmental modification capability, immunomodulatory potential, and stress-alleviating mechanism.

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191

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KeywordsProbiotics · Fish · Shellfish aquaculture · Positive effects · Antibiotic resistance

8.1 Introduction

The aquaculture industry is rapidly growing and is now considered a significant contributor to global food production. According to the United Nations Food and Agriculture Organization, the growth of the aquaculture sector is higher than any other types of animal food production systems (www.fao.org). To meet the global demand, aquaculture production practices have been intensified to a greater extent both in technological and practical measures (Tuan et al. 2013; Dawood et al. 2020a). However, the growth of the aquaculture industry is hampered by unpredictable mortalities which are caused by pathogenic microorganisms. Bacterial diseases have been attributed as biological production bottlenecks in intensive aquaculture, hence necessitating the use of chemicals such as drugs and antibiotics in health management strategies (Newaj-Fyzul and Austin 2014; Ringø 2020). The antibiotic application had been an effective strategy in the beginning, but the residuals remaining in the rearing environment exerted selective pressure for long periods and became a big challenge (Lakshmi et al. 2013; Soltani et al. 2019). The indiscriminate use resulted in the emergence of antibiotic-resistant bacteria in aquaculture environments, in the increase of antibiotic resistance in fish pathogens, in the transfer of these resistance determinants to bacteria of land animals and human pathogens, and in alterations of the bacterial flora both in sediments and in the water column (Dawood et al. 2018). These alarming disadvantages prompted the aquaculture industry to explore and develop strategies that are as equally effective as antibiotics, eco- and consumer-friendly, and most importantly sustainable (Standen et al. 2013; Lazado et al. 2015a, b).

Probiotics are one of the identified alternatives that can lessen the dependence of the aquaculture industry to antibiotics (Verschuere et al. 2000; Nayak 2010; Lazado and Caipang 2014a, b; Akhter et al. 2015). Probiotics have several mechanisms in conferring their benefits to the host fish (Fig. 8.1). Such a feature makes probiotic research in aquatic animals a very dynamic field. The results demonstrating the multitude of ways in delivering benefits to the host have immensely expanded the traditional understanding of probiotics as a modifier of the microbial community in the host. This paper discusses the immense potential of probiotics as a health-promoting alternative through the identified different modes of action of probiotics following their application in finfish aquaculture. It focuses more on how they improve the quality of the rearing environment, protect fish from biological hazards, and modulate physiological processes that eventually promote the health and welfare status of fish in culture. The synthesis provided here collates our current understanding of how probiotics are beneficial to fish and how we can utilize these microorganisms in fostering a more sustainable aquaculture practice.

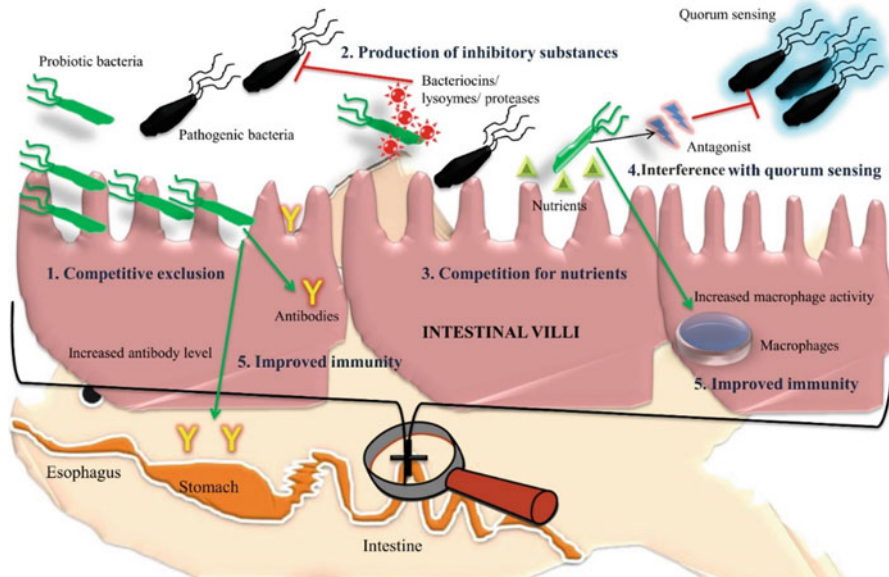


Fig. 8.1 General mechanism of action of probiotics. 1. Competitive exclusion—probiotic organism colonizes the gut, thereby inhibiting colonization of pathogenic bacteria. 2. Probiotic organisms produce certain inhibitory substances which hinder pathogenic organism. 3. Competition for nutrients—probiotic body utilizes the nutrients causing unavailability of nutrients to the pathogens. 4. Substances produced by probiotics act as an antagonist for quorum sensing mechanism. 5. Improved immunity—increase macrophage activity and antibody level

8.2 Probiotic Definition

Several definitions of probiotics have been put forward since the first definition was given by Lilly and Stillwell (1965), but the most widely used is the definition by World Health Organisation's (WHO); "live microorganisms that when administrated in adequate amounts, confer a health benefit to the host." The word probiotic originated from the Greece words "pro" and "bios" which collectively mean "for life," hence being widely regarded as beneficial microorganisms. For some time, Fuller's definition of probiotics as "a live microbial feed supplement which beneficially affects the host animal by improving microbial balance" was the adapted understanding of the probiotic concept in many cultured animals (Fuller 1989). Interestingly, the results of probiotics research in aquaculture have opened numerous possibilities on the benefits of this group of microorganisms. Recently, Lazado and Caipang (2014a, b) proposed that probiotics under an aquaculture understanding be defined as "alive or dead, or even a component of the microorganisms that act under different modes of action in conferring beneficial effects to the host or its environment." This contemporary definition reflects all the advances in probiotics research in aquaculture for over three decades since its first application.

8.3 Regular Probiotics in Aquaculture

In the last three decades, several probiotic microorganisms have been identified, characterized, and applied in aquaculture. These beneficial microorganisms can be of host or non-host origin (Lazado et al. 2015a; Lazado and Caipang 2014b). In a recent review paper, it was highlighted that host-associated microorganisms offer a great prospect as a source of probiotics with diverse biochemical features (Dawood and Koshio 2016; Lazado et al. 2015a). Bacteria obtained from intestine of aquatic as well as terrestrial animals are commonly used as probiotics in aquaculture (Hai and Fotedar 2010). Several bacterial species such as *Vibrio* and *Pseudomonas* spp. isolated from marine fishes are being proposed as probiotics. Different species of probiotics used in aquaculture and their beneficial effects are enumerated in Table 8.1. There is no united stand as to what the best source of probiotics is to be applied for fish. Probiotics from the terrestrial environment have been documented conferring numerous benefits to the cultured animals. On the other hand, probiotics of host origin offer several advantages as well, uniquely leverage in some biotechnical concerns (i.e. temperature, salinity, the familiarity of the environment).

Various factors impose a decisive role in the selection of a suitable probiotic for aquatic species. Different features like the type of probiotic (i.e. bacteria, fungi or algae), host from which they are derived (i.e. host or non-host), single strain probiotic or multi-strain, viable or non-viable organisms as probiotic and also use of spore formers or non-spore formers (Nayak 2010; Dawood et al. 2019). These are some of the reasons why having probiotics of universal application seem impractical.

The most commonly used probiotic species include genera *Lactobacillus*, *Bifidobacterium*, *Aeromonas*, *Plesiomonas*, *Bacteroides*, *Fusobacterium*, *Alteromonas*, *Carnobacterium* and *Eubacterium* and strains of *Bacillus*, *Enterococcus*, *Bacteroides*, *Clostridium*, *Agrobacterium*, *Pseudomonas*, *Paenibacillus*, *Brevibacterium*, *Microbacterium*, *Staphylococcus*, *Streptomyces*, *Micrococcus*, *Vibrio*, *Psychrobacter*, *Carnobacterium*, *Phaeobacter*, *Pediococcus*, *Pseudoalteromonas*, *Rhodospiridium*, *Saccharomyces*, *Debaryomyces*, *Aeromonas*, *Tetraselmis*, *Roseobacter*, *Weissella* and *Aspergillus* (Balcazar et al. 2006; Nayak 2010; Lakshmi et al. 2013; Tuan et al. 2013; Lazado et al. 2015b; Zorriehzahra et al. 2016; Dawood et al. 2019; Ringø 2020).

8.4 Modes of Action

8.4.1 Competition for Space

Many of the pathogenic bacteria require attachment to the mucosal layer of the host gastrointestinal tract to initiate the development of a disease (Zorriehzahra et al. 2016). An essential mechanism of action in probiotic bacteria is competition for adhesion sites, also known as “competitive exclusion” (Boaventura et al. 2012). The ability of bacteria to colonize the gut and adhere to the epithelial surface and

Table 8.1 The application of different species of probiotics in aquaculture

Probiotics	Species	Positive effects	References
<i>Aeromonas hydrophila</i>	Rainbow trout (<i>Oncorhynchus mykiss</i>)	<i>Aeromonas salmonicida</i> infection reduced	Irianto and Austin (2002a, b)
<i>Aeromonas media</i> A199	<i>Crassostrea gigas</i> (Pacific oyster)	Reduced <i>Vibrio tubiashii</i> infection	Gibson (1999)
<i>Aeromonas sobria</i> GC2	Rainbow trout	Protection against <i>Lactococcus garvieae</i> and <i>Streptococcus iniae</i>	Pieters et al. (2008); Brunt and Austin (2005)
<i>Agarivorans albus</i> F1-UMA	<i>Haliotis rufescens</i> (abalone)	Survivability increased	Silva-Aciaries et al. (2011)
<i>Alteromonas</i> CA2	Pacific oyster	Survivability increased	Douillet and Langdon (1994)
<i>Alteromonas macleodii</i> 0444	<i>Perna canaliculus</i> (Greenshell mussel)	Controls <i>Vibrio splendidus</i> infection	Kesarcodi-Watson et al. (2010); Kesarcodi-Watson et al. (2012)
	<i>Pecten maximus</i> (scallop)	Controls <i>Vibrio coralliilyticus</i> and <i>V. splendidus</i>	
<i>Burkholderia cepacia</i> Y021	<i>Crassostrea corteziensis</i> (Cortez oyster), <i>Nodipecten subnodosus</i> (lions-pay scallop)	Increased growth and survival	Granados-Amores et al. (2012)
<i>Enterobacter amnigenus</i>	Rainbow trout	Increased resistance towards <i>Flavobacterium psychrophilum</i>	Burbank et al. (2011)
<i>Neptunomonas</i> 0536	<i>Perna P. canaliculus</i> (Greenshell mussel)	<i>V. splendidus</i> infection controlled	Kesarcodi-Watson et al. (2010, 2012)
<i>Pseudomonas aeruginosa</i> , <i>P. synxantha</i>	<i>Penaeus latisulcatus</i> (Western king prawns)	General health and immune status improved	Hai et al. (2009)
<i>Pseudomonas</i> sp. (GP21) and <i>Psychrobacter</i> sp.	Atlantic cod (<i>Gadus morhua</i>)	Immune response	Lazado and Caipang (2014b)
<i>Shewanella putrefaciens</i>	<i>Sparus aurata</i> L., (Gilthead Sea bream)		De la Banda et al. (2012)
<i>Gordonia bronchialis</i>	Rainbow trout (<i>Oncorhynchus mykiss</i>)	Growth performance, intestinal histology and biochemical parameters	Shabanzadeh et al. (2016)
<i>Arthrobacter</i> XE-7	<i>L. vannamei</i> (Pacific white shrimp)	Alters intestinal microbes	Li et al. (2008)
<i>Bacillus circulans</i> PB7	<i>Labeo rohita</i> (Rohu)	Act as immune stimulant and protects against <i>A. hydrophila</i>	Ghosh et al. (2003); Bandyopadhyay and Das

(continued)

Table 8.1 (continued)

Probiotics	Species	Positive effects	References
			Mohapatra (2009)
<i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i>	Rainbow trout	Protects against <i>Yersinia ruckeri</i> , FCR and growth improved	Raida et al. (2003)
<i>Bacillus coagulans</i>	Pacific white shrimp	Stress tolerance and disease resistance	Cai et al. (2019)
<i>Bacillus subtilis</i>	<i>Labeo rohita</i> (Indian major carp)	Controls <i>A. hydrophila</i>	Kumar et al. (2006)
	White shrimp	Immunity increased and resistance against <i>V. harveyi</i> increased	Zokaiefar et al. (2012)
	<i>Ictalurus punctatus</i> (channel cat fish) and <i>Pangasianodon hypophthalmus</i> (striped cat fish)	Decreased mortality rate due to <i>Edwardsiella ictaluri</i>	Ran et al. (2012)
<i>Bacillus subtilis</i> UTM 126	<i>Litopenaeus vannamei</i> (White shrimp)	Protection against vibriosis	Das et al. (2006)
<i>Bacillus subtilis</i> E20	<i>Litopenaeus vannamei</i> (White shrimp)	Growth improved; mortality reduced	Liu et al. (2010); Tsai et al. (2019)
<i>Bacillus megaterium</i>	Shrimp	Immunity improved, intestinal microbes altered and resistant to white spot syndrome virus	Li et al. (2009)
<i>Bacillus pumilus</i>	<i>P. japonicus</i>	Improved larval survival	El-Sersy et al. (2006)
	<i>O. niloticus</i> (Tilapia)	Immunity increased and survivability increased against <i>A. hydrophila</i> challenge	Aly et al. (2008a)
<i>Bacillus</i> P64	<i>L. vannamei</i> (white shrimp)	Immunostimulant	Gullian et al. (2004)
<i>Bacillus</i> 48	<i>Centropomus undecimalis</i> (common snook)	Growth improved	Kennedy et al. (1998)
<i>Brevibacillus brevis</i>	<i>Dicentrarchus labrax</i> (sea bass)	Prevent vibriosis and improve growth	Mahdhi et al. (2012)
<i>Brochothrix thermosphacta</i> BA211	Rainbow trout	Protect against <i>A. Bestiarum</i>	Pieters et al. (2008)
<i>Clostridium butyricum</i>	Rainbow trout	Protect against vibriosis and also from <i>A. hydrophila</i> and <i>V. anguillarum</i> infections	Sakai et al. (1995)
	<i>Miichthys miiuy</i> (Chinese drum)	Increased immunity and disease resistance	Pan et al. (2008)

(continued)

Table 8.1 (continued)

Probiotics	Species	Positive effects	References
<i>Carnobacterium divergens</i>	<i>Gadus morhua</i> (Atlantic cod), Atlantic salmon (<i>Salmo salar</i>) and rainbow trout	Protects against <i>V. anguillarum</i> infection	Gildberg et al. (1997); Robertson et al. (2000)
<i>Enterococcus faecium</i> SF 68	<i>Anguilla Anguilla</i> (European eel)	Prevents against Edwardsiellosis	Chang and Liu (2002)
<i>E. faecium</i> MC13	<i>P. monodon</i> (shrimp)	Protects against <i>V. harveyi</i> and <i>V. parahaemolyticus</i>	Swain et al. (2009)
<i>Enterococcus faecalis</i>	<i>P. monodon</i> (shrimp)	Improved growth performance and levels of glutathione peroxidase (GPs)	Guzmán-Villanueva et al. (2020)
<i>Enterococcus casseliflavus</i>	Rainbow trout (<i>Oncorhynchus mykiss</i>)	Improved resistance against <i>Streptococcus iniae</i> infection	Safari et al. (2016)
<i>Kocuria</i> SM1	Rainbow trout	Protects against <i>V. anguillarum</i> and <i>V. ordalii</i>	Sharifuzzaman and Austin (2010)
<i>Lactobacillus acidophilus</i>	Nile tilapia	Immunity increased and protects against <i>P. fluorescens</i> and <i>S. iniae</i>	Aly et al. (2008b)
<i>Lactobacillus acidophilus</i>	<i>Clarias gariepinus</i> (African catfish)	Growth performance, haematological parameters and immunoglobulin concentration	Al-Dohail et al. (2009)
<i>Lactobacillus paracasei</i> spp. <i>paracasei</i> (06TCa22)	Japanese pufferfish (<i>Takifugu rubripes</i>)	Disease resistance	Biswas et al. (2013)
<i>Lactobacillus rhamnosus</i> ATCC 53101	Rainbow trout	Reduction in mortality caused by <i>A. salmonicida</i>	Nikoskelainen et al. (2001)
<i>L. rhamnosus</i>	<i>O. niloticus</i>	Protects against <i>E. tarda</i> infection	Pirarat et al. 2006
<i>Lactobacillus fructivorans</i> and <i>L. plantarum</i>	<i>S. aurata</i> (sea bream)	Increase in production of HSP70 thereby increasing heat tolerance	Carnevali et al. (2004); Rollo et al. (2006)
<i>Lactococcus lactis</i>	<i>Litopenaeus vannamei</i>	Improved growth and immunity	Adel et al. (2017b)
<i>Lactococcus lactis</i> AR21	Rotifers	Improved growth and protects against <i>V. anguillarum</i> infection	Harzevili et al. (1998)

(continued)

Table 8.1 (continued)

Probiotics	Species	Positive effects	References
<i>Lactobacillus sporogenes</i>	<i>Macrobrachium rosenbergii</i> (freshwater prawn)	Boosts the survival, growth and levels of biochemical constituents	Seenivasan et al. (2012)
<i>Leuconostoc mesenteroides</i> CLFP 196 and <i>L. plantarum</i> CLFP 238	Rainbow trout	Mortality due to <i>L. garvieae</i> was reduced	Vendrell et al. (2008)
<i>Lactobacillus brevis</i>	<i>Macrobrachium rosenbergii</i>	Growth promotion	Karthik and Bhavan (2018).
<i>Micrococcus luteus</i>	<i>O. mykiss</i> (rainbow trout)	Infection due to <i>A. salmonicida</i> was reduced	Irianto and Austin (2002a)
<i>Micrococcus</i> MCCB 104	<i>M. rosenbergii</i> (fresh water prawn)	Different bacteria inhibited	Jayaprakash et al. (2005)
<i>Pediococcus pentosaceus</i>	Red sea bream (<i>Pagrus major</i>)	Growth performance, feed utilisation and blood characteristics	Dawood et al. (2016a, b, c)
<i>Pediococcus pentosaceus</i>	White shrimp (<i>Litopenaeus vannamei</i>)	Increase the amylase, protease and lipase activities	Adel et al. (2017a)
<i>Pediococcus acidilactici</i>	Rainbow trout fry	Vertebral column compression syndrome (VCCS) was reduced	Aubin et al. (2005)
<i>Rhodococcus</i> SM2	Rainbow trout	Immunity improved and protection against <i>V. anguillarum</i>	Sharifuzzaman et al. (2011)
<i>Streptococcus phocae</i> P180	<i>P. monodon</i>	Growth increased and protects against <i>V. harveyi</i> infection	Swain et al. (2009)
<i>Streptococcus faecium</i>	<i>Oreochromis niloticus</i> (Nile tilapia)	As growth promoters	Lara-Flores et al. (2003)
<i>Streptococcus faecium</i>	<i>Cyprinus carpio</i> (carp)	Improves growth and intestinal micro flora	Bogut et al. (1998)
<i>Streptomyces</i>	<i>P. monodon</i>	Growth improved and water quality was also increased	Das et al. (2006); Newaj-Fyzul et al. (2014).
<i>Vagococcus fluvialis</i>	Sea bass	Protection against <i>V. anguillarum</i> infection	Sorroza et al. (2012)
<i>Weissella hellenica</i> DS-12	–	Protects against several fish pathogens	Byun et al. (1997); Cai et al. (1998)
Phages of family Myoviridae and Podoviridae	<i>Plecoglossus altivelis</i>	Protection against <i>Pseudomonas plecoglossicida</i>	Park et al. (2000)

(continued)

Table 8.1 (continued)

Probiotics	Species	Positive effects	References
Microaglae <i>Tetraselmis suecica</i>	Penaeids	Protection against bacterial pathogen	Austin and Day (1990)
<i>Dunaliella tertiolecta</i>	<i>Artemia</i>	Protection against <i>Vibrio campbellii</i> and <i>V. proteolyticus</i>	Marques et al. (2006)
<i>Phaffia rhodozyma</i> , <i>Saccharomyces cerevisiae</i> and <i>Saccharomyces exiguous</i>)	Penaeids	Protection against vibriosis	Scholz et al. (1999)
<i>Vibrionaceae 51M6 and Pdp11</i>	Rainbow trout (<i>Oncorhynchus mykiss</i>)	Immune responses	Choi and Yoon (2008)

consequently interfere with the adhesion of pathogens is a desirable criterion in the selection of probiotics (Lazado et al. 2011; Balcazar et al. 2006). Non-pathogenic intestinal microbes such as *Lactobacilli* compete with the pathogens for adhesion sites on the intestinal surfaces, particularly on intestinal villus and enterocytes (Brown 2011).

Probiotic addition is being suggested as an early stage husbandry practice in larviculture because the feature of competitive exclusion for attachment sites could provide favourable rearing conditions (Irianto and Austin 2002a). Attachment of probiotics may be non-specific based on the physicochemical agents or specific based on the adhesion of the probiotics on the surface of the adherent bacteria and receptor molecules on the epithelial cells (Salminen et al. 1996; Lazado et al. 2015a).

8.4.2 Production of Inhibitory Substances

Probiotic bacteria produce substances with bactericidal or bacteriostatic effects such as bacteriocins, hydrogen peroxide, siderophores, lysozymes, and proteases (Panigrahi and Azad 2007; Servin 2004; Tinh et al. 2007). Besides, some bacteria produce organic acid and volatile fatty acids (e.g. lactic, acetic, butyric, and propionic acids) that can result into the reduction of pH in the gastrointestinal lumen, thus preventing the growth of opportunistic pathogenic microorganisms (Tinh et al. 2007; Boaventura et al. 2012).

Recently, a compound called indole (s,3-benzopyrrole) with potent inhibitory activity against pathogens was identified in some bacteria known to have anti-bacterial and anti-fungal activities (Gibson 1999; Lategan et al. 2006).

8.5 Probiotics vs. Antibiotics

One of the most vulnerable points of aquaculture is the fish's mortality related to infectious diseases (10–20% of total mortality). Infectious diseases are often a consequence of stress conditions as an excessive density of fish in tank or basin, hypoxia, high nitrite, ammonia concentrations, etc. So, antibiotics are used in the aquaculture industry to prevent or treat bacterial diseases in farmed fish and shellfish (Adel et al. 2018).

Today, with the increasing population, access to healthy food resources has become one of the main concerns for human beings (Zaineldin et al. 2018). Protein from different sources and especially red and white meats plays a vital role in human daily nutrition. However, due to the prevalence of various cardiovascular diseases in today's society, which occurs following the excessive consumption of unhealthy foods, including red meat, consumers are increasingly inclined to white meat consumption like seafood. On the other hand, natural fish and shellfish products are restricted, and therefore aquaculture tries to meet this demand. But intensive and highly intensive aquaculture has caused many infectious diseases and force the farmers to use antibiotics and chemical compounds (Dawood et al. 2016c). The presence of drug residues in fish and fish products threatens public health. Moreover, antibiotic misuse and overuse can promote antibiotic resistance.

The use of healthy or pathogen-free fish, balanced diet, high water quality, biosecurity plans in managing fish farms can substantially prevent disease entrance and transmission into the farm. Despite the above points, antibiotics are widely used to reduce the complications and symptoms of diseases. In some countries, antibiotics are widely used as a routine procedure for treating different types of diseases in aquaculture. Therefore, residues of antibiotics in fish meat and roe will have harmful and destructive impacts on the health of consumers. Studies have shown that antibiotic residues can change the resistance of normal microbial flora in the human body to a specific group according to the antibiotics type. Also, it may cause resistance to the antibiotics used in the treatment of humans and other animals, which is why attempts are now being made to use alternatives to antibiotics.

8.5.1 Antibiotics Action

The antibiotics mechanism of action seems to be based on the selective action on intestinal bacteria (Fig. 8.2). Antibiotics are used in the aquaculture industry to accelerate the growth performance, treat diseases, reduce mortality, increase meat production, increase the absorption of nutrient in the gastrointestinal tract, and increase the neutralization of toxins produced by harmful intestinal bacteria. For optimal effectiveness of antibiotics, they should be available in high concentrations in the body for a few days.

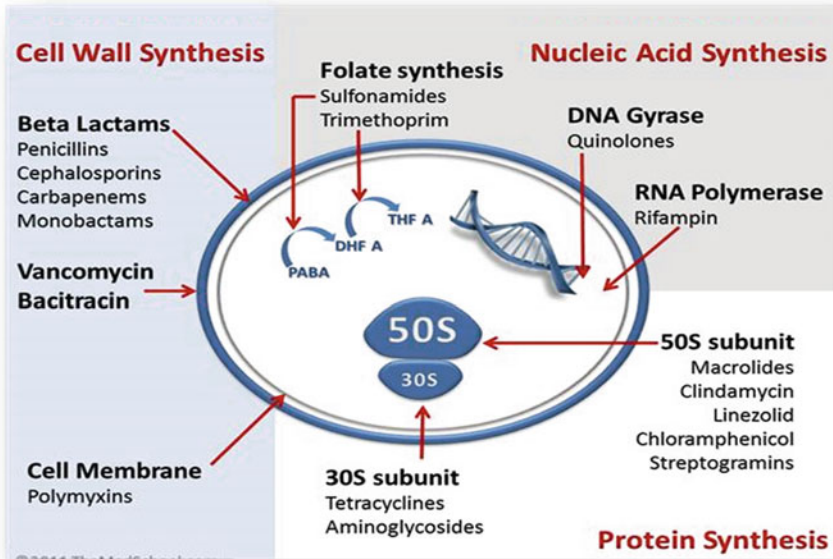


Fig. 8.2 Mechanism of action of antibiotic

8.6 Overview of the Effect of Probiotic on Aquatic Animals

8.6.1 Antibacterial Activity

Several probiotics in aquaculture have been documented possessing antibacterial activity against known pathogens. For example, probiotic *L. lactis* RQ516 that is being used in tilapia (*Oreochromis niloticus*) exhibited inhibitory activity against *A. hydrophila* (Zhou et al. 2010). It was also shown by Balcázar et al. (2008) that probiotic *L. lactis* had antibacterial activity towards two fish pathogens, namely, *A. salmonicida* and *Yersinia ruckeri*.

Zapata and Lara-Flores (2013) found that *Leuconostoc mesenteroides* was able to inhibit the growth of pathogenic fish bacteria in Nile tilapia (*O. niloticus*). Ghosh et al. (2008) found that *B. subtilis* significantly reduced the amount of motile *Aeromonads*, presumptive *Pseudomonads*, and total Coliforms in ornamental fishes (Newaj-Fyzul and Austin 2014). Moosavi-Nasab et al. (2014) also reported that lactic acid bacteria (*Lactobacillus buchneri*, *Lactococcus lactis*, *Lactobacillus acidophilus*, *Lactobacillus fermentum*, and *Streptococcus salivarius*) isolated from the intestine of Spanish mackerel (*Scomberomorus commerson*) were able to inhibit the growth of *Listeria innocua*. Dhanasekaran et al. (2008) reported that several *Lactobacilli* isolated from the intestine of catfish (*Clarias orientalis*), Hari fish (*Anguilla* sp.), Rohu fish (*Labeo rohita*), Jilabe fish (*Oreochromis* sp.), and

Gende fish (*Puntius carnaticus*) showed remarkable antibacterial activity against *Aeromonas* and *Vibrio* sp.

The potential of probiotics including *Lactobacillus plantarum* (LP1, LP2), *Saccharomyces cerevisiae* (SC3), *Candida glabrata* (CG2), *Lactococcus lactis* subsp. *lactis* (LL2), and *Staphylococcus arlettae* (SA) isolated from an indigenous fish sauce in Malaysia showed high inhibitory activity on *Staphylococcus aureus* and *Listeria monocytogenes*.

8.6.2 Antiviral Activity

The knowledge of the antiviral activity of probiotics has been raised in recent years (Lakshmi et al. 2013). For example, *Pseudomonas*, *Vibrio*, *Aeromonas* spp., and *Coryneforms* had antiviral activity against infectious hematopoietic necrosis virus (IHNV) (Kamei et al. 1988). Li et al. (2009) demonstrated that feeding with a *B. megaterium* strain increased the resistance to white spot syndrome virus (WSSV) in the shrimp *Litopenaeus vannamei*. It was documented that probiotics, like *Bacillus* and *Vibrio* sp., positively protect shrimp *Litopenaeus vannamei* against WSSV (Balcazar 2003). Application of *Lactobacillus* probiotics as a single strain or mixed with Sporlac improved disease resistance against lymphocystis viral disease in olive flounder (*Paralichthys olivaceus*) (Harikrishnan et al. 2010).

8.6.3 Antifungal Activity

There are few studies regarding the antifungal effect of probiotics. Lategan et al. (2004) isolated *Aeromonas media* (strain A199) from eel (*Anguilla australis*) culture water and was observed to have a strong inhibitory activity against *Saprolegnia* sp. In a separate study, *Pseudomonas* sp. M162, *Pseudomonas* sp. M174, and *Janthinobacterium* sp. M169 enhanced immunity against saprolegniasis in rainbow trout (Heikkinen 2013). Atira et al. (2012) demonstrated that *Lactobacillus plantarum* FNCC 226 exhibited inhibitory activity against *Saprolegnia parasitica* A3 in catfish (*Pangasius hypophthalmus*).

8.6.4 Competition for Chemicals or Available Energy

The existence of any microbial population depends on its ability to compete for chemicals and available energy with the other microbes in the same environment (Verschuere et al. 2000). Many microorganisms, including the known probiotic group lactic acid bacteria, consume the nutrients that are essential for the growth of several pathogens (Dawood et al. 2016a, b; Brown 2011).

For example, siderophores are low-molecular-weight ferric iron chelating agents that can dissolve precipitated iron or extract it from iron complexes, then making it available for bacterial growth (Neilands 1981). Siderophore-producing bacteria can

be used as probiotics because they can sequester ferric iron in an iron-low environment, hence making it unavailable for the growth of pathogenic bacteria (Tinh et al. 2007). Gram et al. (1999) showed that a culture supernatant of *Pseudomonas fluorescens*, grown in iron-limited conditions, inhibited growth of *Vibrio anguillarum*. It has been revealed that *P. fluorescens* can competitively inhibit the growth of the fish pathogen *Aeromonas salmonicida*, by competing for free iron (Smith and Davey 1993; Gram et al. 1999). It was also revealed that GP12 and GP21, candidate probiotics from Atlantic cod, are capable of releasing siderophores, and this ability had been implicated for their beneficial use (Lazado et al. 2011).

8.6.5 Positive Effects on Rearing Water Quality

Interactive effects between aquaculture environment and aquatic species have been confirmed for sustainable aquaculture (Dawood et al. 2019). Application of Gram-positive bacteria, such as *Bacillus* spp., is beneficial in improving the quality of the water system. *Bacillus* spp. have a more efficient ability in converting organic matter into carbon dioxide in comparison to the Gram-negative bacteria, which converts a higher proportion of organic matter into bacterial biomass or slime (Mohapatra et al. 2012; Balcazar et al. 2006). Certain probiotic bacteria possess significant algicidal effect as well, particularly on several species of microalgae (Fukami et al. 1997). Ammonia and nitrite toxicity can be eliminated by the application of nitrifying cultures into the fish environment (Mohapatra et al. 2012). Besides, probiotics are beneficial as they can increase microbial species' composition in the water and modify its quality (Elsabagh et al. 2018; Mohapatra et al. 2012). The temperature, pH, dissolved oxygen, NH₃, and H₂S in rearing water were found to be of higher quality when probiotics were added, hence maintaining a positive, healthy environment for shrimp and prawn larval in green water system (Aguirre-Guzman et al. 2012; Banerjee et al. 2010; Dawood et al. 2020b). Dalmin et al. (2001) reported that the using of an indigenous *Bacillus* spp. in the rearing water of giant tiger prawn was able to maintain optimum transparency and low organic carbon of the pond. Mohamed et al. (2013) approved that applications of commercial probiotics to saline tilapia (*Oreochromis mossambicus*) could improve the growth performance, phytoplankton production, and water quality.

8.6.6 Nutrients and Enzymatic Contribution

Some microorganisms have a positive effect on the digestive processes of aquatic animals (Dawood et al. 2017; Balcazar et al. 2006). It has been shown that some bacteria contribute to the digestion process by producing extracellular enzymes, such as proteases, lipases, as well as growth-promoting factors (Wang et al. 2000).

Reports are demonstrating that some probiotics, especially from *Bacteroides* and *Clostridium* sp., are capable of supplying vitamins, fatty acids, and essential amino acids to the host (Balcazar et al. 2006; Tinh et al. 2007). Gnotobiotic oyster larvae

(*Crassostrea gigas*), fed with auxenic algae (*Isochrysis galbana*) supplemented with a bacterial strain CA2, showed not only improved growth performance but efficient nutrient utilization as well (Douillet and Langdon 1994). Yeasts are well known in animal nutrition because they can produce polyamines, which enhance intestinal maturation. Besides bacterial probiotics, many strains of yeast have been used as dietary supplements in several fish species (Tinh et al. 2007).

8.6.7 Interference of Quorum Sensing

Quorum sensing is defined as the regulation of gene expression in response to fluctuations in cell-population density. Many bacteria are using this system to communicate and regulate a diverse array of physiological activities (Miller and Bassler 2001). The disruption of quorum sensing (QS) is considered a potential anti-infective strategy in aquaculture (Defoirdt et al. 2004).

Halogenated furanones, which are produced by the marine red alga *Delisea pulchra* (Manefield et al. 1999), have been investigated as a promising QS antagonist. These compounds, added at adequate concentrations, protected *Brachionus*, *Artemia*, and rainbow trout from the harmful effects of pathogenic *Vibrios* (Rasch et al. 2004; Defoirdt et al. 2006; Tinh et al. 2007). Also, some probiotic bacteria such as *Lactobacillus*, *Bifidobacterium*, and *B. cereus* strains degrade the signal molecules of pathogenic bacteria by enzymatic secretion or production of autoinducer antagonists (Brown 2011). It was demonstrated by Medellin-Pena et al. (2007) that *L. acidophilus* secretes a molecule that inhibits the QS or interacts with a bacterial transcription of *E. coli* O157 gene.

8.6.8 Immunostimulants

8.6.8.1 Fish

Probiotics by stimulation of immune system of hosts, including the stimulation of pro-inflammatory cytokines on the activity of immune cells, increasing the phagocytic activity of leucocytes (Pirarat et al. 2006), increasing the levels of antibodies, acid phosphatase, lysozymes (Lara-Flores and Aguirre-Guzman 2009), complement (Balcazar et al. 2007), cytokines (interleukin-1 (IL-1), IL-6, IL-12, tumor necrosis factor α (TNF- α), gamma interferon (IFN- γ), IL-10 and transforming growth factor b) (Nayak 2010) and antimicrobial peptides (Mohapatra et al. 2012), and also by improving the intestinal microbial balance, inhibition of the colonization of fish pathogens in the digestive tract, production of inhibitory compounds such as bacteriocins, siderophores, lysozymes, proteases, hydrogen peroxides (Saurabh et al. 2005), increasing the digestive enzymes activity (amylase, protease and lipase) (Ringø 2020) and production of fatty acids, vitamins (Sakata 1990) and essential amino acids that are useful for lactic acid bacteria (Ringø and Gatesoupe 1998) could improve the growth performance, immune system and increased resistance on common pathogens in fish (Fig. 8.3) and shrimp (Lakshmi et al. 2013).

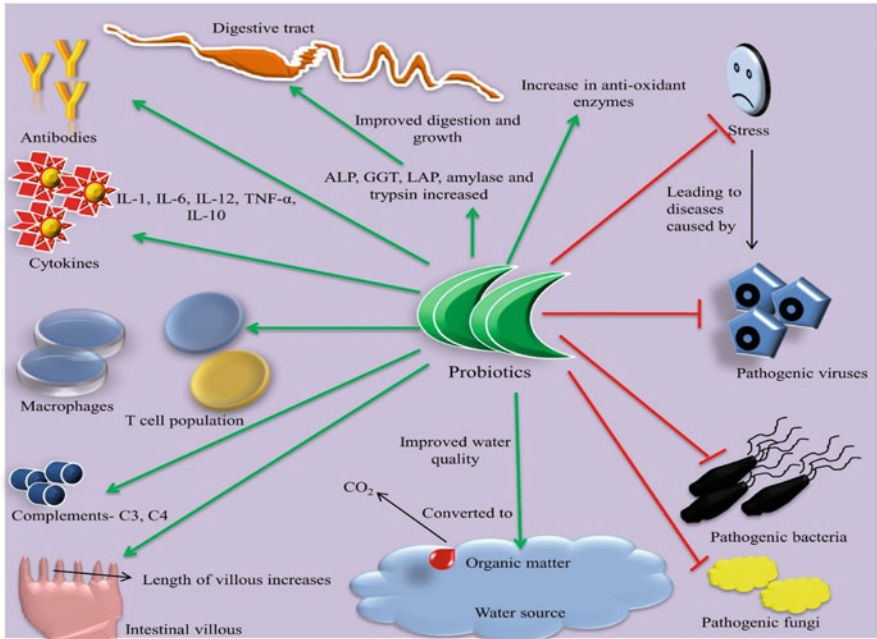


Fig. 8.3 Overall beneficial effects of probiotics in aquaculture. The green arrow indicates additive effects. Red lines indicate inhibitory effect

The administration of probiotics in tilapia (*Oreochromis niloticus*) caused an increase in lysozyme activity, neutrophil migration, bactericidal action, and finally enhanced resistance of fish to infection of *Edwardsiella tarda* (Taoka et al. 2006b). Also, Gomez et al. (2007) used *Vibrio alginolyticus* strains as probiotics in white shrimp (*Litopenaeus vannamei*) and observed increased survival and growth in shrimp (Zhou et al. 2009).

Harikrishnan et al. (2011a) reported that administration of probiotics (*Lactobacillus sakei* BK19) with herb (*Scutellaria baicalensis*) in tilapia (*O. fasciatus*) reduces the mortality, altered haematological parameters, and enhances innate immunity against *Edwardsiella tarda*. The same researchers repeated this experiment in olive flounder (*Paralichthys olivaceus*) against *Streptococcus parauberis* and found growth, blood biochemical constituents, and non-specific immunity improved in the groups treated with probiotics and herbals mixture supplementation diet (Harikrishnan et al. 2011b). Irianto and Austin (2002a) reported that feeding with Gram-positive and Gram-negative probiotics resulted in the stimulation of cellular rather than humoral (serum of mucus antibodies) immunity. There was an increase in the number of erythrocytes, macrophages, and lymphocytes, and enhanced lysozyme activity during feeding with probiotics. Feeding with diets containing single or mixed isolated probiotic bacteria for *O. niloticus* showed different results in survival rates and highest with fish fed diets supplemented with

B. pumilus, followed by a mixture of probiotics (*B. firmus*, *B. pumilus*, and *C. freundii*), and then *C. freundii*.

Avella et al. (2010) used a mixture of *Bacillus* probiotic bacteria including *B. subtilis*, *B. licheniformis* and *B. pumilus* in the diet of the gilthead seabream (*Sparus aurata*) larviculture and observed apparent effects on survival, growth, and general welfare.

Assessment of mRNA levels of several immune parameters like cytokine IL-8 in the intestine of the control and *L. plantarum* groups by using real-time PCR showed that IL-8 gene expression was significantly up-regulated by *L. plantarum* after *Lactococcus garvieae* infection (Pérez-Sánchez et al. 2011). Standen et al. (2013) evaluated the probiotic effect of *Pediococcus acidilactici* on Nile tilapia (*Oreochromis niloticus*) and suggested that the probiotic treatment may cause up-regulation of the gene expression of the proinflammatory cytokine TNF- α in the probiotic fed fish. Presence of *Bacillus subtilis* C-3102 in the diets of hybrid tilapia juvenile (*O. niloticus* \times *O. aureus*) caused up-regulation of cytokines such as IL-1 β , TGF- β , and TNF- α in the intestine of fish (He et al. 2013). *Lactobacillus delbrueckii* ssp. *delbrueckii* (AS13B) added in diet of gilthead sea bream resulted in lower transcription of proinflammatory cytokine genes such as IL1 β , IL10, cox2, and TGF- β in the intestine of treated group (Picchietti et al. 2009).

8.6.8.2 Shrimp

Use of probiotics in different species of shrimps has improved the innate immunity (natural or non-specific immunity) (Fig. 8.4). Several studies have demonstrated that by using probiotics the production of cellular components such as phagocytosis, encapsulation, the formation of nodules and humoral components including

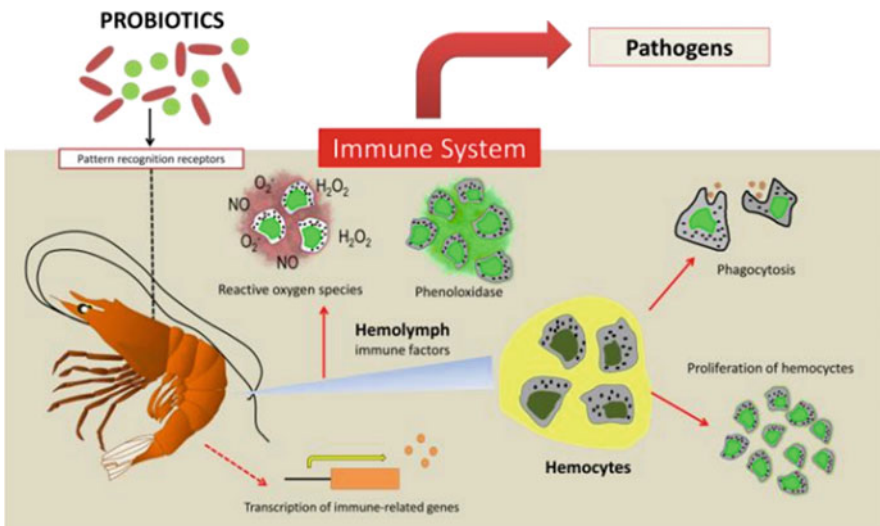


Fig. 8.4 Model of immunomodulation in shrimp by probiotics (Lazado et al. 2015b)

anticoagulant proteins, agglutinins, phenoloxidase enzyme (Lakshmi et al. 2013; Song et al. 2014), antimicrobial peptides (defensins and chemokines), an antiapoptotic protein, free radicals, bacteriocins, siderophores, monostatin, lysozymes, proteases, hydrogen peroxide, gramicidin, polymyxin, tyrotricin, competitive exclusion and organic acid was increased. The transcription of several immune-related genes can also be modulated by probiotic treatment (Antony et al. 2011). These stimulated immune defences to play a crucial role in the responses and eventual protection during pathogen exposure. Probiotics have an essential role in enhancing the resistance of shrimps against common diseases such as vibriosis, white spot disease and *Aeromonas hydrophila* infection (Ahilan et al. 2004; Ma et al. 2007; Harikrishnan et al. 2009; Liu et al. 2010; Zokaefar et al. 2014).

It was also confirmed by RNA interference (RNAi) assay that the immunity of shrimps was increased against viral diseases using probiotics (Kawai and Akira 2006). Rangpipat et al. (2000) showed that *Bacillus* sp. (strain S11) protected against infection by activating the *Penaeus monodon* immune system.

8.6.8.3 Immunomodulation of the Gut Immune System

The immune system of the gut is related to gut-associated lymphoid tissue (GALT) (Nayak 2010; Lazado and Caipang 2014a, b), and there are some differences in respect of Peyer's patches, secretory IgA, and antigen-transporting M cells in the intestine of piscine and mammal gut immune system (Nayak 2010). Although lymphoid cells, macrophages, granulocytes, and mucus IgM were observed in the intestine of fish (Bakke-McKellep et al. 2007).

There is limited knowledge about the application of probiotics and their ability in stimulating the piscine gut immune system (Nayak 2010; Lazado and Caipang 2014a, b; Mamun et al. 2019). The present knowledge is mostly associated with humans and terrestrial vertebrates (Lazado and Caipang 2014a, b). However, studies indicated that probiotics could stimulate the piscine gut immune system, increasing the number of Ig⁺-cells and acidophilic granulocytes (AGs) (Picchiatti et al. 2007, 2008, 2009; Salinas et al. 2008). For example, it has been reported that the supplementation of LAB (*Lactobacillus rhamnosus* GG, human origin) in the diet of tilapia, *Oreochromis niloticus* could modulate the population of the intestinal immune cells. Also, the amount of intraepithelial lymphocytes and acidophilic granulocytes (AGs) enhanced significantly in the probiotic-fed group (Pirarat et al. 2011). Addition of probiotic-containing *Lactobacillus fructivorans* (host origin) and *Lactobacillus plantarum* (human origin) to the diet of larval gilthead sea bream, *Sparus aurata* by live vectors affected the extent of Ig⁺-cells and acidophilic granulocytes mostly the MAb G7(+) phagocytic population in the gut (Picchiatti et al. 2007).

Picchiatti et al. (2009) used rotifers and artemia in the administration of *Lactobacillus delbrueckii* ssp. *delbrueckii* (AS13B) as the live vectors to the larval sea bass, *Dicentrarchus labrax*. They observed that the population of T cells and acidophilic granulocytes in the intestinal mucosa significantly increased in probiotic-fed fish.

In a study, rainbow trout (*Oncorhynchus mykiss*) were fed by diets supplemented with probiotics such as *L. Lactis* spp. *lactis*, *L. mesenteroides*, and *L. sakei*. In the

end, an enhancement was observed in the phagocytic activity of mucosal leucocytes by the LAB group (Balcazar et al. 2006). *Pediococcus acidilactici* was used by Standen et al. (2013) in the feeding of Nile tilapia (*Oreochromis niloticus*).

8.7 Amelioration of the Effects of Stress

Stress might be regarded as a physical or chemical agent, causing reactions that may result in disease and death (Rottmann et al. 1992). Any change in water parameters may have a side effect on the physiological and behavioural aspect of aquatic animals (Dawood 2021). Different types of stress that may have adverse effects on fish include thermal (Das et al. 2005; Logan and Somero 2011), nutritional, high density (Lupatsch et al. 2010), anoxia, hypoxia, chemical, and toxins (DeMicco et al. 2010). Many harmful agents for fish exist in their environments like the water, soil, air, or even their own body (Smith et al. 2012). In intensive systems of aquaculture where the high density is an essential factor for the outbreak, in stressful conditions, aquatic animals are more susceptible than wild fishes. Application of probiotic bacteria, both as a feed supplement and water quality, can prevent stressful conditions, enhancing the immune system and therefore reducing the harmful effects of various stressors (Taoka et al. 2006a).

Any situation that enhances reactive oxygen species (ROS) concentration is called oxidative stress that can lead to disturbing cellular metabolism and its regulation, thereby damaging cellular constituents (Jia et al. 2011; Lushchak 2011). ROS production is nearly related to antioxidant responses (Lesser 2006; Bidhan et al. 2014). The alterations of temperature and other environmental parameters can severely affect the physiological activities of aquatic animals (Wabete et al. 2008). Also, a wide range of contaminants (xenobiotics), UV-radiation, hypoxia, and other environmental physicochemical parameters may cause oxidative stress in the animal (Mohapatra et al. 2012). Feeding with probiotics may ameliorate the effects of these oxidative stress factors by increasing the antioxidant status (Mohapatra et al. 2012).

Blood glucose, cortisol, and the RNA/DNA ratio of the different tissues is used as valid biochemical stress indicators to study the fish stresses, growth, and health status (Sivaraman et al. 2012). Another way to assess stress tolerance in fish involves subjecting them to heat shock (Cruz et al. 2012).

Taoka et al. (2006a) grew flounder (*Paralichthys olivaceus*) under stress conditions and evaluated the effects of probiotics on growth, stress tolerance, and non-specific immune response in fish. Plasma lysozyme activity in the probiotic diet group and the water supply group was significantly higher than in the control group. In heat shock stress tests, flounder in the probiotics-treated groups showed higher heat tolerance. Koninkx and Malago (2008) demonstrated that under stress conditions, normal intestinal microflora taken as probiotics were able to enhance the defence system by increasing specifically the putative heat shock protein (HSP).

Some probiotic bacteria have been found to decrease several biochemical stress indicators. There is a report regarding the decrease in cortisol level on supplementation of *Lactobacillus delbrueckii* ssp. *delbrueckii* in the diet of European sea bass

(*Dicentrarchus labrax*) compared to the controls during temperature stress (Carnevali et al. 2006).

Gomes et al. (2008, 2009) found that administration of *Bacillus* spp. during transport reduced handling stress by influencing the cortisol level. Varela et al. (2010) carried out probiotic administration studies on gilthead seabream (*Sparus auratus*) and concluded that there was improved tolerance to stress with this treatment under high stocking density. Castex et al. (2009) evaluated the antioxidative effect of *Pediococcus acidilactici* MA 18/5 in shrimp, *Litopenaeus stylirostris*. Results showed the modulation of the activities of antioxidant enzymes such as superoxide dismutase and catalase. It has been reported that administration of *Lactobacillus plantarum* could enhance the antioxidant state in shrimp *Litopenaeus vannamei* and consequently improve resistance to *V. alginolyticus* infection (Chiu et al. 2007).

Chai et al. (2016) investigated the effects of *Bacillus* bacteria isolated from the intestine of healthy, wild shrimps on the growth of Pacific white shrimp and showed that probiotics reduced shrimp culture risks from stressful conditions.

8.8 Side Effects

Probiotics are generally considered safe and well tolerated (Boyle et al. 2006). One theoretical concern associated with probiotics includes the potential for these viable organisms to move from the gastrointestinal tract and cause systemic infections (Snydman 2008). Another theoretical risk associated with probiotics involves the possible transfer of antibiotic resistance from probiotic strains to pathogenic bacteria; however, this has not yet been observed (Martin et al. 2013). Also, the possibilities of change in intestinal microflora, emerging diseases, mutagenesis, or recombination of DNA of bacteria may result into systemic infections and economical losses in fish farms (Ringø et al. 2010).

8.9 Maximizing the Benefit of Probiotics

To maximize the competitive advantage of probiotics, early delivery notably before first feeding improved the chances of producing persistent fish population (Ringo et al. 1997). Choosing the right probiotic, appropriate concentrations of probiotic, sufficient feeding time, and feeding status are several important parameters that are necessary for maximizing the benefit of probiotics.

8.10 Conclusion Remarks and Future Consequences

Despite doing many studies about efficiency and mechanisms of probiotics, many questions are not yet clear. Additional and future studies can be directed to transcriptome and proteome profiling of gut microbiota, host/microbe interactions,

interactions between gut microbes, the intestinal epithelium, gut immune system, antioxidant status, lipid level of hosts, antagonistic and synergist activity or probably side effects of probiotics.

Use of probiotics is a useful alternative sustainable source of beneficial microbes with bactericidal or bacteriostatic effect on pathogenic bacteria, with anti-bacterial, anti-viral and anti-fungal activity, immunomodulatory capabilities of promoting health and welfare to improve the growth performance, augment the immune system, disruption of quorum sensing (QS) as a new anti-infective strategy, ameliorate the harmful effects of oxidative stress factors and increased resistance for common pathogens in fishes for controlling potential fish pathogens. An interactive approach among academicians, scientists, producers and fish sector owners is required to focus and explore the specific aspects of bacterial host interactions conferring the possible favourable changes in diverse immune responses elicited by different bacterial strains to propose clinically useful, bacteria-based strategies to promote the health, production and economic growth of the aquaculture industry.

In future studies on probiotics in shellfish aquaculture, bio-floc culture system using probiotics should be investigated on growth performance, immune response, gut microbiome and disease resistance as only some information are available on this topic. Also, more studies are needed to investigate the fate of probiotic organisms in the environment and the shellfish.

The probiotic formulation should be viable on a large scale at low operational cost. They should not be treated as “elixir of life”; instead they should be used as a supplement to balance the diet to avail and maintain the sound health free of infections and disease-causing microorganisms.

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Honeybee Gut: Reservoir of Probiotic Bacteria

9

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Abstract

Honeybees are the most important crop pollinators that contribute significantly to agricultural productivity and profitability worldwide. Microbiota accounts for up to 1–10% of the insect's biomass. The intestine of European Honeybees, *Apis mellifera*, have diverse microbiota and are known to be occupied by approximately 70% Gram-negative bacteria, 27% Gram-positive bacteria, and 1% yeast. The native microbiota of the honeybees is known to contribute to their nutrition, growth, digestion, pathogens defense, and insecticide resistance. As with other humans and animals, intestinal dysbiosis might greatly influence these insects' health status posing a threat to their safe existence. Lactic acid bacteria (LAB) have been discovered in abundance in the honeybee gut and are believed to be of great importance to the honeybee health. Among several symbiotic LAB species isolated from the digestive tract of honeybees, it is found that some of them have the potential to be developed as probiotics. One of the most important health benefits of probiotic LAB in honeybees is their ability to protect against several bee pathogens and contribute to honey's antimicrobial properties. Hence, the use of probiotics in beekeeping could prevent diseases, enhance bee health, and consequently increase honey production. Although probiotic bacteria isolated from different sources could be used for honeybees, using the host bacteria, i.e., the bacteria from the honeybees' gut microbiome community would be more desirable for their own health. In this review study, we discuss the important aspects related to *Apis mellifera* gut microbiome such as composition, perturbation, fermentation, and most important of all, the probiotic bacterial community, mainly LAB species residing in the gut of these insects.

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221

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Apis mellifera · Gut microbiome · Lactic acid bacteria · Probiotic · Dysbiosis

9.1 Introduction

Apis mellifera (*A. mellifera*) or European honeybee could colonize virtually all habitable biomes on Earth and adapt to diverse bioclimatic conditions. *A. mellifera* has been classified as a member of the order Hymenoptera and the superfamily Apoidea (Alatawy et al. 2020). They have been divided into six evolutionary lineages including A lineage (Africa), M lineage (western and northern Europe), C lineage (southern and eastern Europe), O lineage (Caucasus, Turkey, Middle East, Cyprus, Crete), Y lineage (Ethiopia), and S lineage (Syria and Lebanon) (Tihelka et al. 2020). As *A. mellifera* is an essential pollinator species for natural ecosystems and agricultural production, its health status and, consequently, continuous existence is of great importance.

As obvious from numerous research reports, *Apis mellifera* depends on its gut microbiome to perform its basic functions and survival. Bacterial communities living in symbiosis with their hosts, also known as probiotics, are essential factors in maintaining host health (Zeinali et al. 2020). Additionally, a close association between Honeybee colony productivity and increased bacterial diversity was discovered recently. Hence, an improved understanding of the honeybees' gut microbiome can help manage modern challenges to these insects' health and production.

The gut of the honeybee is a continuous tube starting from mouth to anus and demarcated into foregut (stomodeum), midgut (mesenteron), and the hindgut (proctodeum). In many insects, the hindgut is the gut region bearing the largest microbial populations. In particular, the ileum (the region between the proximal pylorus and distal rectum) is a relatively benign environment, in that it lacks the digestive enzymes of the midgut and, for many terrestrial insects, the desiccation stress of the distal hindgut, where water is actively resorbed from the lumen into insect tissues. Microbial function and growth may also be favored by the ions and metabolites delivered to the hindgut in the filtrate from the Malpighian tubules (Huang et al. 2010). On the contrary, due to midgut epithelium actively secreting immunologically active enzymes as well as several antimicrobial peptides, the midgut shows a hostile environment for microorganisms. Besides, the midgut also contains a region of pH < 3 that mediate many microbial cells degradation (Engel and Moran 2013; Shanbhag and Tripathi 2009).

9.2 Gut Microbiome Composition

In the last couple of years, marked deterioration in honeybee hives' colony health has been reported that has raised worldwide concerns (Meixner 2010). One of the major reasons for such depurations of honeybee colonies is due to the effect of several honeybee diseases (Genersch et al. 2010). In this context, the honeybee gut's microbial ecosystem has known to play an essential role in maintaining their health and survival. Thus, understanding the microbial community residing in the gut of different honeybee species could lead us to better health management of the bees that would consequently result in enhanced agriculture productivity and human well-being.

The bee gut microbial community is far simpler than the mammalian microbiota and contains a distinctive community of bacterial species. The composition of the gut bacterial communities of these social insect insects has been shaped by coevolution. These insects' social behavior provides favorable conditions for the exchange of the symbiont microbes, and a number of these microorganisms are efficiently transmitted between bee colony members and their different generations (Engel and Moran 2013).

The composition of microbial communities in the honeybee gut varies enormously within and between species. Honeybees acquire gut microorganisms from the natural environment via foods, such as nectar, pollen, and water. Hence, honeybees' gut flora varies according to seasonal or geographical differences in food sources, even among individual honeybees from the same colony (Mohr and Tebbe 2006; Moran et al. 2012).

A. mellifera gut microbiota is dominated by only nine bacterial species clusters that are specific to bees and are transmitted through social interactions between individuals (Fig. 9.1). According to available information, there are five main bacterial groups in the honeybees gut including (i) Gram-negative bacteria group (*Snodgrassella alvi* and *Gilliamella apicola*), (ii) phylum Proteobacteria to Gram-positive bacteria, Firmicutes (*Lactobacillus Firm-4* and *Lactobacillus Firm 5* groups), (iii) phylum Actinobacteria (*Bifidobacterium asteroides*), (iv) a small number of Proteobacteria species (*Frischella perrara*, *Bartonella apis*, *Parasaccharibacter apium*), and (v) Gluconobacter-related species group designated Alpha2.1 (Bottacini et al. 2012; Kwong and Moran 2016).

As seen in Table 9.1, honeybee microbiota occupies distinct metabolic niches in the *A. mellifera* gut. According to reports, the abundance of *Snodgrassella alvi*, *Frischella perrara*, *Gilliamella apicola*, and *Bartonella apis* is seen in the ileum while *Lactobacillus Firm-4*, *Lactobacillus Firm-5*, as well as *Bifidobacterium* predominantly reside in the rectum (Kwong and Moran 2016).

Many factors are known to affect the gut microbiota composition and profile of the honeybees, including the age and physiological condition of honeybees. Martinson and Moran in 2012 reported that newly emerged honeybee workers have no or very few gut bacteria, while they uptake bacteria later via contact with the collected honey and bee bread and through trophallactic exchange with nestmates (Martinson et al. 2012). In other research findings, it was stated that

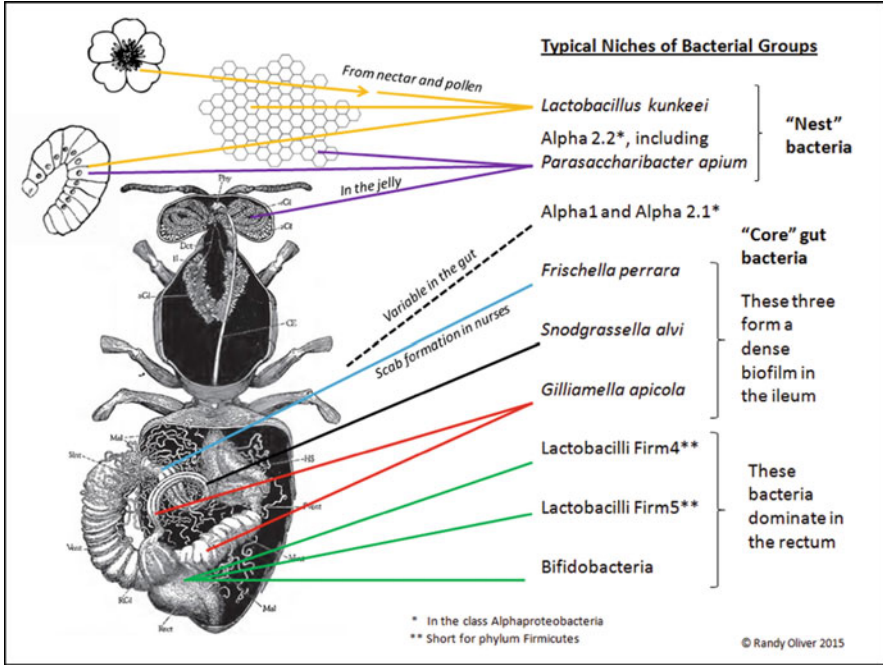


Fig. 9.1 Bacterial groups present in honeybees

larvae's gut microbial composition differs vastly due to the differences in the bee bread microbial communities (Martinson et al. 2012; Mohr and Tebbe 2006). The observation that certain gut bacteria are maintained in all of the developmental stages of an adult bee, irrespective of differences between species, colonies, and individuals, suggests that distinctive gut bacteria are transferred between generations by eusocial behaviors, such as food exchange between the honeybee populations in a hive (Martinson et al. 2011; Martinson et al. 2012; Vásquez et al. 2012).

Zhi-Xiang Dong and his colleagues, through the use of 16 s rRNA gene sequencing analysis, found that 0-day postemergence (dpe) did not harbor core gut flora in the gut, and the critical points for colonization of the core gut flora were around 1–3 dpe. For example, colonization of *Frischella*, *Gilliamella*, and *Snodgrassella* occurred at 1dpe, while *Bifidobacterium*, *Commensalibacter*, and *Lactobacillus* colonization were significantly detected at 3 dpe (Dong et al. 2020). It is worth mentioning that type of overwintering sugar also influences honeybee gut microbiota. Wang et al. in 2020 via 16 s rRNA sequencing determined bacterial communities in honeybee midguts and hindguts before winter and after bees were fed honey, sucrose, and high-fructose syrup as winter-food. In the midgut, the sucrose group's microbial diversity was higher than that of the honey and high-fructose syrup groups, but in the hindgut, the microbial diversity of the honey and high-fructose groups was higher than that in the sucrose group. Sucrose increased the relative abundance of Actinobacteria (*Bifidobacteriales*) and

Table 9.1 *A. mellifera* gut microbiome composition and their main functions

<i>A. mellifera</i> microbiome composition	Location	Main function	Reference
<i>Snodgrassella alvi</i>	Ileum	Activation of the innate immune system	Horak et al. (2020)
<i>Gilliamella apicola</i>	Ileum	Degradation of pectin	Kwong and Moran (2016)
<i>Lactobacillus Firm-4</i>	Rectum	Degradation of pectin	Lee et al. (2018)
<i>Lactobacillus Firm-5</i>	Rectum	Degradation of pectin	Lee et al. (2018)
<i>Bifidobacterium asteroides</i>	Rectum	Through glycosidase and pectinesterase could degrade pollen	Lee et al. (2018)
<i>Frischella perrara</i>	Ileum	Activation of the innate immune system	Emery et al. (2017)
<i>Bartonella apis</i>	Ileum	Positive effects on disease resistance	(Corman et al. (2012)
<i>Parasaccharibacter apium</i> and a Gluconobacter- related species group designated Alpha2.1	Rectum	Oxidative fermentation/perform gluconeogenesis	Bonilla-Rosso et al. (2019)

Alphaproteobacteria of honeybee midgut, and honey enriched the Bacteroidetes and Gammaproteobacteria in honeybee hindgut. High-fructose syrup increased the relative abundance of Betaproteobacteria of the midgut. Furthermore, they introduce sucrose as an appropriate overwintering food for honeybee. In this manner, the relative abundance of the dominant microbiota significantly altered with the different sugar types and seasons (Wang et al. 2020).

In another research report, Christina Geldert et al. investigated the effect of phytochemical supplementations on the microbiome diversity and abundance of *A. mellifera*. They disclosed that phytochemical supplementations are able to enhance gut microbial diversity and significantly increase the abundance of the most represented bacterial genera such as *Snodgrassella* spp. and *Lactobacillus* spp. (Geldert et al. 2020).

9.3 Gut Microbiome Perturbation

Exposure to an environmental stressor, including antibiotics as well as the herbicide, is one of the major sources of perturbation to the microbiome that has a detrimental effect on *A. mellifera* health. Antibiotic treatment of bee colonies has been widely used for over 50 years to prevent bee larvae's bacterial disease. Some of the most frequently used antibiotics by beekeepers include tetracycline, fumagillin, and tylosin (Genersch et al. 2010). However, these chemical drugs are known to have

many side effects, including the emergence of antibiotic resistance. Hence, more attention has been paid to evaluate the effect of antibiotics on the survival and growth of honeybees to identify and pinpoint the main disadvantages of these drugs on honeybee and their environment's health. Raymann et al., in 2017, assessed the relationship between tetracycline exposure and the size and composition of honeybee gut communities. Their results showed that treatment with tetracycline greatly influenced both the honeybee gut microbiome's composition and size. According to their observations, tetracycline induced dysbiosis in these insects, which resulted in increased susceptibility to opportunistic pathogens and subsequently led to a significant reduction in bee survival rate (Raymann et al. 2017).

Apart from antibiotics, some agrochemicals such as herbicides can perturb the honeybee gut microbiota and therefore compromise bee health. Shikimate pathway that is found in the bacterial community residing in the bee gut, such as in *Snodgrassella alvi*, *Gilliamella* spp., and *Bifidobacterium* spp., is known to play a key role in the production of essential aromatic compounds such as the amino acids phenylalanine, tryptophan, and tyrosine. In this context, glyphosate, the primary herbicide, inhibits 5-enolpyruvyl-shikimate-3-phosphate synthase (EPSPS) in the shikimate pathway (Motta et al. 2018). Thus, glyphosate via shikimate pathway inhibition and subsequently essential nutrients depletion play a crucial role in bacterial death and reducing beneficial bacteria in bee gut.

Propolis is another critical factor involved in honeybee gut microbiome consistency. In this context, Saelao et al. investigate the association between propolis and microbial community consistency in the honeybee microbiome. They disclosed that propolis insufficiency contributes to significant perturbation in the abundance of several key gut microbiota members. These authors proposed that propolis, via restricting alterations in the microbial community, play a key role in honeybee colony microbial health (Saelao et al. 2020).

9.4 Probiotic Potential of Honeybee Gut-Associated Bacteria

Inappropriate and misuse of antibiotics has led to a rise in antibacterial resistance and diminished the efficacy of these once considered miracle drugs. Since the alarming rise of antibiotic resistance, many strategies and investigations have been carried out to explore other safer ways to treat human ailments without harming the natural immunity of the host, and replacing or augmenting these antibiotics.

In the late nineteenth century, microbiologists identified microflora in healthy individuals' gastrointestinal tracts that differed from those found in diseased individuals. The beneficial microflora found in the gastrointestinal tract was termed probiotics. FAO and WHO experts defined the term probiotics as "Live microorganisms which when administered in adequate amounts confer a health benefit on the host" (Joint 2002). In other words, probiotics are living microorganisms used to restore gut health by maintaining the intestinal microbiota (Manzanares et al. 2016). Similar to humans and animals, the gut-associated bacterial flora in honeybees has been reported to have the ability to provide health

benefits, most important of all, which is the capability to protect them from several honeybee diseases (Li et al. 2017; Schwarz et al. 2016).

Below we discuss some of the beneficial functions carried out by the gut microbiome of honeybees.

9.4.1 Antimicrobial Effects of Honeybee Gut-Associated Bacteria

As stated earlier, the gut microbial community in honeybee *A. mellifera* protects the host from infection. Schwarz et al. provide experimental support linking parasite susceptibility of honeybee to dysbiosis of their core microbiota. They disclosed that honeybee, in a dysbiosis state, lose their ability to control encounter protozoan *Lotmaria passim* and lead to *L. passim* infection in these insects (Schwarz et al. 2016). *Nosema ceranae* is a gut intracellular parasite of honeybees that destroys epithelial cells and gut tissue integrity. In this context, Jiang Hong Li in 2017 revealed that disruption of bacteria in the honeybee by antibiotic treatment mediates honeybee's susceptibility to *Nosema* infection (Li et al. 2017).

Moreover, Huang and Evans in 2020 investigated the effect of *Nosema* on the gut microbiome via suppression of *N. ceranae* with specific siRNAs. They found that suppressing *N. ceranae* led to significant positive effects on gut microbial abundance. These researchers concluded that *N. ceranae* is negatively correlated with the abundance of 15 identified bacteria (Huang and Evans 2020). In a study conducted by a group of researchers, it was found that the members of the gut microbiome, by lowering the local intestinal pH with the production of lactic acid, antimicrobial metabolites, as well as induction of innate immunity, interfere with the growth of *Nosema* infection (El Khoury et al. 2018). Furthermore, Streptomycin is an aminoglycoside antibiotic function in protein synthesis inhibition in Gram-negative bacteria. In 2015, through a metagenomics approach, Saraiva identified genes involved in streptomycin biosynthesis in *A. mellifera* microbiome. The presence of such genes raises the hypothesis about the possible role of normal microbiota in protecting *Apis mellifera* against pathogenic bacteria and in maintaining the healthy status of the hive (Saraiva et al. 2015).

Paenibacillus larvae, a Gram-positive sporulated bacterium that causes the American foulbrood disease, is an extremely contagious and dangerous pathogen of honeybees. In 2009, Sabate et al. aimed to explore the biological control capability of *Bacillus* strains associated with the bee intestine and evaluate their influence against *P. larvae*. They found that *Bacillus* strains through surfactin synthesis inhibit the growth of *P. larvae* (Sabaté et al. 2009). These novel findings collectively emphasize the importance of *A. mellifera* gut bacteria in modulating honeybees' susceptibility to various infections.

9.4.2 Gut Microbiome Role in Immune Function

Various predators, including parasites, parasitoids, and pathogens, threaten insect health during their life cycle. A complex immune system has evolved in insects for protection against these threats. Several studies have illustrated that gut bacteria are key mediators in immune modulation and are essential for a healthy immune system (Kaltenpoth and Engl 2014). Hemocyte (immune cells), as a crucial element in the innate immune system through phagocytosis, plays a key role in hemolymph pathogen clearance. Vitellogenin (Vg) is a protein engaged in honeybee worker's stress tolerance, and behavior. Vg is the main zinc carrier in honeybee workers, and zinc deficiency is associated with hemocyte pycnosis (cell death). Thereby, Vg is considered a critical mediator in honeybee immunity and lead to a longer life span. In an experimental investigation by Zheng et al. in 2017, it was found that normal microbiota compared to germ-free bees increase vitellogenin expression almost fivefold (Kaltenpoth and Engl 2014; Zheng et al. 2017). Overall, based on these findings, we can consider the gut microbiome as a major contributing factor for honeybee immune activation.

Furthermore, the Scab phenotype as a prominent immune response factor is triggered by reminiscent of melanization and develops 5–7 days after adult worker bees have emerged. Scab phenotype is characterized by a dark brown to black deposit forming a localized thin band in the pylorus at the midgut-hindgut boundary, in close proximity to the Malpighian tubules of the honeybees. Emery et al. identified significant host gene expression alteration in the pylorus region following *Frischella perrara* colonization compared to non-colonized bee. Using gene ontology (GO) enrichment analysis, they disclosed that immune-related genes, including *irp30*, *cdc2c*, *abaecin*, *apid73*, *b-guc2*, and *def-1*, were increased in the pylorus region of the screened honeybees. In this manner, *Frischella perrara* via colonization in a restricted region in the pylorus, as well as immune-related genes activation, play a key role in scab phenotype induction (Emery et al. 2017). Additionally, Horak and his research team investigate the beneficial effect of symbiont *Snodgrassella alvi* on honeybee immune gene expression. They illustrate that *Snodgrassella alvi* via expression of host antimicrobial peptides as well as Toll pathway upregulation aid in the clearance of opportunistic pathogen *Serratia marcescens* from the honeybees gut (Horak et al. 2020).

9.4.3 Gut Microbiome Role in Food Fermentation

Fermentation products such as short-chain fatty acids (SCFAs) are highly beneficial for host energy metabolism. In the fermentation process, *A. mellifera* gut microbiota members play an important role in breaking saccharides into an array of alcohols, SCFAs, gases, and other organic acids such as acetate and lactate. Acetate kinase (*ackA*) and L-lactate dehydrogenase (*ldh*) are the main enzymes responsible for acetate and lactate production, respectively. In turn, acetate production and lactate through increased sucrose sensitivity play a crucial role in honeybee weight gaining

(Lee et al. 2018; Zheng et al. 2017). Therefore, *A. mellifera* gut microbiota through organic acid production plays an important role in honeybee weight gain.

9.4.4 Gut Microbiome Role in Detoxification

Gut microbiota strongly promotes the expression of key enzymes of the honeybee xenobiotic detoxification pathway. Three important enzymes responsible for insect detoxification, including carboxylesterases (COEs), Cytochrome P450 monooxygenases (CYPs, also called P450s), and glutathione S-transferases (GSTs), have been identified recently. Thereby, honeybee gut microbiota enhance host detoxification capability and manipulate host metabolism (Wu et al. 2020). Furthermore, some monosaccharide sugars, including xylose, mannose, rhamnose, and arabinose, have been reported to endorse toxic effects on *A. mellifera* and decrease their life span. Recently, genes responsible for mannose metabolism, including phosphotransferase systems (PTSs) and mannose-6-phosphate isomerase (MPI), were identified in the *Gilliamella apicola* genome. Additionally, several genes associated with catabolism of rhamnose, xylose, and arabinose have also been detected in the genome of *Gilliamella apicola*. Hence, it is concluded that *Gilliamella apicola* is able to metabolize xylose, mannose, rhamnose, and arabinose and subsequently boost *A. mellifera* life span (Zheng et al. 2016).

9.4.5 Probiotic Properties of Honeybee-Specific Lactic Acid Bacteria

Lactic acid bacteria (LAB) are a group of Gram-positive lactic acid-producing bacteria present in diverse habitats. LAB belongs to phylum Firmicutes with low G + C in the genome. These bacteria are well known for their role in food fermentation, and a wide variety of strains are routinely employed as starter cultures in the manufacture of dairy, meat, vegetable, and bakery products. Additionally, they have a significant role as starter cultures for cheese and yogurts. One of the factors that make LAB of high importance, especially for human and animal use, is their “generally recognized as safe” (GRAS) status that make these food-grade microorganisms to be employed as probiotics (Åvall-Jääskeläinen and Palva 2005; Choi et al. 2005). While the European Food Safety Authority (EFSA) proclaimed the LAB strain to have QPS (Qualified presumption of safety) status (EFSA 2008). In several findings, the presence of LAB in the gut of honeybees has been reported, where they are shown to provide beneficial effects to their host, and thereby they are potential probiotic candidates.

Majority of honeybee-specific LAB has found significant importance owing to their probiotic potentials. Up to date, thirteen genetically distinct lactic acid-producing bacteria have been identified from the honeybee crop, of which nine are Lactobacilli and four are Bifidobacteria (Olofsson et al. 2014; Olofsson and Vásquez 2008).

Table 9.2 Lactic acid bacteria isolated from different species of honeybees

Honeybee species	LAB isolated	Country of isolation	Reference
<i>Apis mellifera</i>	<i>Micrococcus</i> , <i>Bifidobacterium asteroides</i> , <i>Fructobacillus fructosus</i>	Iran	Sharifpour et al. (2016)
	<i>Lactobacillus johnsonii</i> , <i>Enterococcus faecium</i> , <i>Lactobacillus kunkeei</i>	Argentina, Egypt	Audisio et al. (2011), Elzeini et al. (2020)
	<i>Lactobacillus brevis</i> , <i>Lactobacillus casei</i>	Egypt	Elzeini et al. (2020)
	<i>L. melliventris</i> , <i>L. kimbladii</i> , <i>L. mellis</i> , <i>L. apinorum</i> , <i>L. kullabergensis</i> , <i>L. helsingborgensis</i>	Sweden	Olofsson et al. (2014)
<i>Apis mellifera jemenitica</i>	<i>L. kunkeei</i> , <i>Lact. Lactis</i> , <i>Enterococcus faecalis</i>	Saudi Arabia	Khan et al. (2017)
<i>Apis cerena</i>	<i>Bifidobacterium indicum</i> , <i>Bifidobacterium asteroides</i> , <i>Fructobacillus fructosus</i> , <i>L. apinorum</i> , <i>L. apis</i> , <i>L. helsingborgensis</i> , <i>L. kimbladii</i> , <i>L. kullabergensis</i> , <i>L. kunkeei</i>	Vietnam	Duong et al. (2020)
<i>Apis dorsata</i>	<i>Bifidobacterium indicum</i> , <i>Lactobacillus kunkeei</i> , <i>Lactobacillus vermiform</i> , <i>Lactobacillus sp.</i>	Malaysia, Indonesia	
<i>Apis florea fabricius</i>	<i>L. kunkeei</i> , <i>L. plantarum</i> , <i>L. apis</i>	Iran	Parichehreh et al. (2018)

Lactic acid bacteria has been isolated from the gut of several honeybee species, including *Apis mellifera*, *A. dorsata*, *A. florea*, *A. nigrocincta*, *Apis nuluenis*, *Apis laboriosa*, *A. cerana indica*, *Melipona beecheii*, *Meliponula bacandei*, and *Trigona* sp. (Mathialagan et al. 2018; Niode et al. 2020; Vásquez et al. 2012). *Lactobacillus* is one of the most important genera within the LAB, which at present includes 175 listed species (Euzéby 1997). Among this group of bacteria, genus *Lactobacillus* is the most frequent Gram-positive bacteria isolated from different honeybee species' gut. While *Lactobacillus kunkeei* has been reported to be one of the most dominant species of this genus residing in their gut (Niode et al. 2020). Table 9.2 depicts a variety of LAB species isolated from different honeybee species around the world.

9.4.6 Antimicrobial Effect of Honeybee Gut-Associated LAB Against Honeybee Diseases

LAB comprises a group of Gram-positive, catalase-negative, non-motile, non-spore-forming facultative anaerobic bacteria that are commonly found as both exogenous and endogenous microbes in healthy individuals. Similar to the LAB found within humans and animals, the honeybee-specific LAB defends their hosts from invasion and colonization of several pathogenic bacteria via the production of a variety of

antimicrobial metabolites and modulation of the host immune response (Huang and Evans 2020; Mathialagan et al. 2018; Niode et al. 2020). Hence, honeybee-specific LAB can also provide protection against several honeybee diseases by production of these metabolites.

The antimicrobial effects exerted by these bacteria are owing to their metabolite-producing abilities. These metabolites, also referred to as postbiotic metabolites, includes organic acids (lactic acid, acetate acid, and formic acid) (Olofsson et al. 2016), extracellular proteins, benzoate, bacteriocins, hydrogen peroxide (H₂O₂), lipopolysaccharides, and lipoteichoic acid volatile compounds (Butler et al. 2013; Olofsson et al. 2016; Olofsson and Vásquez 2008) etc.

Hence, due to the stated health-promoting functions of LAB in honeybees, they are considered safe alternative therapeutic strategy for the control of a number of honeybee diseases, including *Paenibacillus larvae* (infective bacterial agent of American foulbrood disease), *Melissococcus pluton* (infective bacterial agent of European foulbrood), Nosemosis, and varroosis (Audisio 2017; Forsgren et al. 2010). In a study conducted by a group of researchers, an organic acid-producing *L. johnsonii* was shown to inhibit the growth of *Nosema ceranae* and harbored fumigillin activity (60).

Paratransgenesis has come to mean a Trojan horse strategy, where endogenous microorganisms via effector molecules production inhibit pathogen development. Candidate microorganisms to being practical in honeybee, they should possess several criteria including (1) candidate microorganism should be genetically modifiable for effector molecules expression; (2) ideally the candidate microorganism must be ecologically and functionally fit with other nonpathogenic bee-associated microorganisms, and (3) following reintroduction the modified organism should have no negative impact on honeybee health. In this context, Rangberg et al. investigated *L. kunkeei* potency in honeybee paratransgenesis. They concluded that *L. kunkeei* complies with the three criteria required for being a suitable paratransgenic candidate (Rangberg et al. 2015). Similar to these findings, Maddaloni and his co-investigators demonstrated that *Fructobacillus fructosus* can be used as a powerful tool for honeybee paratransgenesis to control diseases and expand nutrition repertoire (Maddaloni et al. 2014).

9.5 Commonly Used Methods for Microbiome Analysis

Researcher frequently utilizes full-length 16S rRNA gene sequences with nine hypervariable regions (V1–V9) to infer phylogenetic relationship among the microbiome. Therefore, a full-length 16S rRNA amplicon sequencing approach with high accuracy and efficiency can be used for microbial diversity detection in various biological samples. Nanopore DNA sequencer (MinION) containing several significant advantages including rapid library construction, low cost, real-time detection and small size that made it a suitable tool for identifying microbiome composition at the species levels (Shin et al. 2016). However, it was disclosed that bacteria with almost identical 16S rRNA sequences could exhibit high sequence

divergence levels at other loci and very different gene repertoires. Thereby, it is difficult to gain insight into intraspecific diversification of bacterial lineages in the gut with 16S rRNA sequencing. Single-cell genomics and transcriptomics can provide reliable context for assembled genome fragments and gene expression activity on the level of individual prokaryotic genomes. In this manner single cell genomics, through allowing direct access to information from individual microorganisms, has the potential to elucidate processes of bacterial diversification (Engel et al. 2014). However, low DNA and mRNA content restrict the yield of reasonable amounts of genetic material for sequencing analysis from a single cell.

Furthermore, the lack of polyadenylation of bacterial mRNA limits its separation from rRNA. Additionally, cell walls and membranes diversity induce a challenge to consistent lysis or permeabilization required for single-cell RNA sequencing (scRNA-seq). These problems impede the characterization of microbes by traditional single-cell sequencing methods (Sharma and Thaiss 2020).

9.6 Microbiome Engineering as a Future Perspective

Engineering of microbiomes is used to modify structures of the microbiota and restore ecological balance. Synthetic biology and engineering principles are frequently applied in microbiome engineering to improve microbiome function. Thereby, microbiome engineering could lead to a breakthrough in agriculture and medicine. In medicine, microbiome engineering enables exploring individual microbes' contribution and generating potential therapies against metabolic (e.g., phenylketonuria and chronic kidney disease), inflammatory, and immunological diseases, among others. In the case of honeybee, due to their agricultural importance as well as the simple gut microbiome, they are a promising testbed for the nascent field of microbiome engineering (Foo et al. 2017; Leonard 2020). There are several approaches to honeybee microbiome engineering. A plasmid toolkit by combining a broad-host-range (BHR) replicon with a set of modular genetic parts can be applied to bacteria from the *A. mellifera* gut microbiome. It was disclosed that plasmids constructed using bee microbiome toolkit (BTK) act faithfully in various species of Proteobacteria detected in the *A. mellifera* gut microbiome. The BTK can be used to express heterologous genes or to repress or disrupt genes in the bacterial chromosome (Leonard 2020). Consequently, microbiome engineering could be employed as a powerful tool for improving *A. mellifera* health and subsequently agricultural productivity.

9.7 Conclusions

The economic value of commercial honeybee pollination is estimated at over US \$220 billion worldwide. Any damage to these insects leads to detrimental consequences not only to our agriculture and production values that ultimately would result in economic losses but might also threaten and endanger our lives on

the planet. Hence, intensive research has been done and is still ongoing to find solutions to prevent colony losses and find ways to increase their survival and control the pathogens from harming their viability.

A.mellifera digestive tract is a reservoir of a diverse variety of bacterial communities that play a significant role in these insects' growth and survival. Recent studies with gut microbiome disclosed the honeybee gut-associated microbial in immune system activation, carbohydrate fermentation, and inhibition of disease in the host. This suggests that the gut bacterial community structure may be considered as an indicator of honeybee health. Since related microbiotas are found across bee species, it strongly suggests a close evolutionary relationship between bacteria and hosts, as well as underscoring the importance of LAB symbionts for bees. Not only are LAB symbionts involved in honeybee food production and preservation, but they are also of importance in host defense against pathogen and transient microbes intercepted during foraging. Hence preserving the balance of these gut bacteria is crucial for maintaining honeybee health and vigor. Tools to engineer a microbial member of these honeybees might play a significant role in beekeeping management issues such as increased colony survival.

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Role of Probiotic Bacteria on Bioavailability of Functional Ingredients Under Fermentation Process 10

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Abstract

Consumer attention to consume healthier foods has been significantly encouraged the food industry to formulate new products within the area of so-called functional foods. Functional foods are defined as whole foods, enriched, enhanced, and fortified foods or dietary compounds that in addition to traditional nutrient contents possess healthy and physiological benefits. Food products containing probiotics comprise the majority of functional food market worldwide. This chapter focuses on the bioactive compounds produced in different probiotic fermented food matrices and investigates how these metabolites and fermentation conditions affect the bioavailability of different compounds in foods.

Keywords

Probiotic · Functional foods · Bioactive compounds · Postbiotics · Dairy products

10.1 Introduction

Probiotics are defined as live microorganisms which when ingested in adequate numbers (at least 10^6 – 10^7 CFU/ml) impart health benefits to the host and include mainly *Lactobacillus* and *Bifidobacterium* genera but some other bacteria and yeast species are also considered as probiotics (de Melo Pereira et al. 2018; George Kerry et al. 2018; Meira et al. 2015; Morton 2015) (Table 10.1). Probiotics have

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237

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Table 10.1 List of some important probiotic microorganisms (Morton 2015)

Category and genus	Species
Bacteria	
<i>Lactobacillus</i>	<i>Lb. acidophilus</i> , <i>Lb. amylovorus</i> , <i>Lb. brevis</i> , <i>Lb. casei</i> , <i>Lb. curvatus</i> , <i>Lb. crispatus</i> , <i>Lb. delbrueckii</i> subsp. <i>bulgaricus</i> , <i>Lb. fermentum</i> , <i>Lb. helveticus</i> , <i>Lb. gasseri</i> , <i>Lb. johnsonii</i> , <i>Lb. reuteri</i> , <i>Lb. rhamnosus</i> , <i>Lb. salivarius</i> , <i>Lb. paracasei</i> , <i>Lb. plantarum</i>
<i>Bifidobacterium</i>	<i>B. adolescentis</i> , <i>B. animalis</i> , <i>B. bifidum</i> , <i>B. lactis</i> , <i>B. breve</i> , <i>B. infantis</i> , <i>B. longum</i> , <i>B. thermophilum</i> , <i>B. essensis</i> , <i>B. laterosporus</i>
<i>Streptococcus</i>	<i>S. cremoris</i> , <i>S. diacetylactis</i> , <i>S. intermedius</i> , <i>S. salivarius</i>
<i>Propionibacterium</i>	<i>P. freudenreichii</i> , <i>P. freudenreichii</i> subsp. <i>shermanii</i> , <i>P. jensenii</i>
<i>Enterococcus</i>	<i>E. faecalis</i> , <i>E. faecium</i>
<i>Lactococcus</i>	<i>L. lactis</i> subsp. <i>cremoris</i> , <i>L. lactis</i> subsp. <i>lactis</i>
Other bacteria	<i>Pediococcus acidilactici</i> , <i>Leuconostoc mesenteroides</i> , <i>Bacillus cereus</i> , <i>Clostridium butyricum</i> , <i>Escherichia coli</i> Nissle 1917
Yeast	<i>Kluyveromyces lactis</i> , <i>Saccharomyces boulardii</i> , <i>Saccharomyces cerevisiae</i>

anticarcinogenic antimutagenic activities and are able to suppress cholesterol level and blood pressure. They improve digestive system function, epithelial homeostasis, nutrient uptake, intestinal barrier function, immune modulation, and antagonism action against pathogens (Liptáková et al. 2017; Marhaida et al. 2015).

Traditionally, the effectiveness of probiotics was assumed to be related to cell viability. Apart from probiotic cells, bacterial products may have similar benefits to the host. These products are characterized as postbiotics which have biological activity in the host cell (George Kerry et al. 2018; Wegh et al. 2019). Postbiotics are generally regarded as functional fermentation products and include a wide range of metabolites such as bacteriocins, enzymes, vitamins, amino acids, oligosaccharides, exopolysaccharides, short-chain fatty acids, and immunomodulatory compounds (George Kerry et al. 2018; Zielińska and Kolożyn-Krajewska 2018).

In other words, the functionality of probiotics in fermented foods is accomplished in different ways which eventually affect the nutritional quality of foods which include: 1) increase of nutrient density, mostly due to a decrease of sugar content, 2) hydrolysis of polymers from the raw material and bioactive compounds content, 3) biosynthesis of bioactive molecules, 4) degradation of toxic or anti-nutritional factors, and 5) synthesis of promoters for absorption and uptake (Septembre-Malaterre et al. 2018; Tamang et al. 2016).

10.2 Probiotic Fermentation of Foods

Food fermentation is considered as one of the oldest ways of food processing and preservation. Fermentation results in the enhancement of the flavor and nutritional quality of food and extending its shelf life (Beena Divya et al. 2012). Fermentation is microbe-driven process in which the low value substrates are converted to added-value products (Hussain et al. 2016; Sadh et al. 2018). According to scientific data, both nutritive and non-nutritive components are in fermented foods which could potentially implement specific target functions in the body relevant to well-being and health of the consumers (Tamang et al. 2016). Probiotic bacteria as functional microorganisms, in fermentation process, convert the chemical constituents of raw materials of plant/animal sources leading to the enhancement of the bioavailability of nutrients, enrichment of sensory quality of the food, improvement of food safety, degradation of toxic components and anti-nutritive factors, production of antioxidant and antimicrobial compounds, stimulation of the probiotic functions, and fortification with some health-promoting bioactive compounds (Homayoonfal et al. 2018; Mousavi and Mousavi 2019; Rollán et al. 2019). In fact, the probiotic microorganisms promote beneficial effects in a host which are due to the production of bioactive compounds (Indira et al. 2019).

These bioactive compounds play an important role in bio-preservation of fermented food products including dairy, fish, seaweeds, microalgae, beverages, and fruits and vegetables (Mousavi and Mousavi 2019). Additionally, they show antimicrobial activities against food pathogens such as *Listeria monocytogenes*, *Staphylococcus aureus* and *Enterococcus faecalis*. In addition to their antimicrobial properties, these metabolites can be aromatic which can influence the sensory and organoleptic features of food products. Some peptides with health benefits are also produced as bioactive compound in fermentation of and prevent diseases associated with metabolic syndrome (Indira et al. 2019; Ojha and Tiwari 2016) (Table 10.1).

10.3 Production and Modification of Bioactive Compounds Over Probiotic Fermentation

Bioactive compounds as result of probiotic fermentation have two major sources. The first source is direct synthesis of the compound by the probiotic such as bacteriocins, exopolysaccharides (EPS), or enzymes and they can be found in either supplements or foods. The second source of bioactive is a compound that only appears as a result of the modification of the food matrix itself by the probiotic culture fermentation (Champagne et al. 2018). The following section will discuss the bioactive compounds produced during probiotic fermentation and their effect on food bioavailability.

10.3.1 Bioactive Peptides

Bioactive peptides are short sequences of amino acids generally consisting from 2 and 20 amino acids. Such sequences stay intact and inactive when present in the parental protein, but can be released after protein hydrolysis during gastrointestinal digestion (GID), *in vitro* enzymatic hydrolysis, or microbial fermentation. These peptides have biological activities that may influence human health in addition to basic human nutrition (Erdmann et al. 2008). Cardioprotective functions, modulation of immune system, anti-atherosclerosis, antioxidant, mental health, and general well-being functions are associated with bioactive peptides (Ojha and Tiwari 2016; Septembre-Malaterre et al. 2018). According to various researches, it is concluded that microbial fermentation could be regarded as an appropriate approach improving protein bioavailability and digestibility in different food products (Chi and Cho 2016; Hur et al. 2014; Limon et al. 2015; Wu et al. 2015).

10.3.1.1 Dairy Products

Milk-proteins and associated bioactive peptides released during microbial or enzymatic fermentation of milk offer a broad spectrum of new functional properties, for instance antihypertensive, antimicrobial, antioxidative, immunomodulatory, opioid, and mineral-binding properties (Beermann and Hartung 2013).

Calcium casein phosphopeptides (CCP) are phosphorylated bioactive peptides derived from calcium-sensitive caseins (α s1, α s2, and β caseins). These peptides are inactive fragments entrapped in the sequence of precursor protein, and exhibit biological action after its release during the passage through the gastrointestinal tract. In addition, they are also produced *in vitro* by the action of specific enzymes during fermentation of a number of dairy-based products such as cheese, yogurts, and fermented milks (Ledesma-Martínez et al. 2019; Mohanty et al. 2016). The main activities of CCP include anticancer, body fat reduction, prevention of cardiovascular diseases through the reduction of atherosclerosis lesions and levels of cholesterol and triacylglycerides, anti-inflammatory, and antioxidant. A great number of studies approved the role of CCP on calcium, iron, and zinc (Ledesma-Martínez et al. 2019).

The effect of peptidases activity of *Lactobacillus delbrueckii* ssp. *bulgaricus* and *Streptococcus thermophiles* on milk proteins resulted in the production of antimicrobial and hypotensive peptides. These small biological peptides can be used as food supplements to improve the health-promoting qualities of liquid and semisolid dairy foods prepared by the yogurt fermentation process (Paul and Somkuti 2009).

Investigations revealed that probiotic LAB such as *Lactobacillus helveticus* produces bioactive peptide like, proline-containing peptides isoleucyl-prolyl-proline (IPP) and valyl-prolyl-proline (VPP) which may induce greater availability of calcium (Dubey and Patel 2018). The study on the level of level of calcium, magnesium, phosphorus, and zinc absorption in a series of fermented goat and cow milk showed that the bioavailability of minerals was significantly higher compared with non-fermented milks (Bergillos-Meca et al. 2013).

Oxidative damage caused by various free radicals which are by-products of physiological reactions within human body can be protected by antioxidants. It has

been found that yogurt and fermented milks have a higher antioxidant activity than milk. In fermented milks, bioactive peptides are released following the proteolysis of milk proteins, especially lactalbumin, lactoglobulin, and casein (Melini et al. 2019). Yogurt produced with camel milk by fermentation with *Lactobacillus rhamnosus* strain PTCC 1637 has a higher antioxidant activity than cow milk, because of the higher proline content in camel milk caseins. The presence and position of the amino acids tryptophan, tyrosine, and methionine in the peptides are claimed responsible for the antioxidant activity of fermented milks as well.

10.3.1.2 Fruits, Vegetables, Legumes, and Grains

Various studies showed that probiotic fermentation of nondairy foods including vegetables, fruits, legumes, and grains could enhance the level of protein, peptides, and amino acid in these products (Septembre-Malaterre et al. 2018). Bioactive peptides have been mainly studied from milk or whey hydrolysis during lactic fermentation. However, different studies on fermented soybeans, grapes, and cereal flours also showed a significant increase in their bioactive contents (Septembre-Malaterre et al. 2018). Probiotic LAB are naturally present in legume grains; they have also been traditionally used for legume fermentation. Evidences showed that fermentation of legumes with *Lactobacillus* genera can encourage the production of bioactive compounds, improving health benefits beyond basic nutrition. Fermentation of cowpeas with *Lactobacillus plantarum* resulted in the modification of phenolic compounds and improvement of antioxidant activity (Dueñas et al. 2005; Limon et al. 2015).

L. plantarum B1-6 has been studied for its potential proteolysis effect on mung bean protein during fermentation. Electrophoresis profiles revealed that *L. plantarum* B1-6 degraded Mung bean proteins with the hydrolysis percentages between 49 and 64%. In addition, reverse phase high-performance liquid chromatography (RP-HPLC) analysis showed that larger/more hydrophobic peptide contents decrease the amount of smaller/more hydrophilic peptides has substantially augmented after fermentation (Wu et al. 2015). In addition, the degradation of gluten could render the final product to be suitable for celiac consumers (Heredia-Sandoval et al. 2016; Houben et al. 2012; Poutanen et al. 2009; Verni et al. 2019). Cereals are in general good sources of proteins. The proportions of essential amino acids and their digestibility mainly determine protein nutritional quality. Peptidase enzymes produced by LAB convert peptides to amino acids. Specific products of these enzymes are responsible for the aroma and taste of final products (Pessione and Cirrincione 2016; Verni et al. 2019).

Solid-state fermentation of whole soybeans by *Lactobacillus plantarum* P-8 mixed with *B. subtilis natto* also resulted in an intensive protein degradation and generation of hydrophilic peptides during fermentation (Pessione and Cirrincione 2016; Zhang et al. 2014).

Various scientific reports stated that hydrolyzed peptides produced by probiotics during fermentation can act as antioxidants (Coda et al. 2012; Raveschot et al. 2018; Taha et al. 2017). Rapeseed proteins are hydrolyzed to amino acids and peptides by proteases produced by probiotic *Bacillus subtilis* during fermentation (Rong et al.

2012). Hydrolysis of peptide bonds enhances the levels of free amino and carboxyl groups, resulting in increased solubility. This enhanced solubility may improve the antioxidant activity of the peptide (Karami and Akbari-Adergani 2019; Sohaib et al. 2017). Low-molecular-weight peptides have been reported to exhibit better radical-scavenging activities than their high-molecular-weight counterparts (Xie et al. 2008). Thus, increasing the low-molecular-weight peptides by enzymatic hydrolysis may influence the antioxidative activity during fermentation. Metal-chelating amino acid residues, such as methionine, glutamic acid, glutamine, lysine or arginine, within the sequences of these peptides contributed to the superior Fe²⁺-chelating ability of the antioxidant peptides (Hur et al. 2014).

According to different studies, proteolytic activity of probiotic LAB could enhance the level of bioactive peptides in fermented cereals. Antihypertensive properties are attributed to these bioactive peptides. In addition, thanks to the production of flavoring free amino acids and other amino acid derivatives during fermentation which convey tastiness to fermented cereals such as bread, it is possible to decrease salt content in the final product (Melini et al. 2019).

10.3.1.3 Fish

Large quantity of liquid and solid waste generated by fish industry can be regarded as a potential resource for valuable products. Due to their high protein contents, fish waste could be used as a suitable medium for culturing probiotic bacteria. Fermentation of fish waste can partially degrade the protein contents, which could help the absorption from the gut and influence its bioactive properties through the production of bioactive peptides (Venegas-Ortega et al. 2019).

10.4 Digestible Saccharides

10.4.1 Fruits and Vegetables

Fruits and vegetables are a rich source of sugars. During fermentation of fruits and vegetables, monosaccharide are significantly consumed by probiotic bacteria specially LAB species. However, with the help of glucosidases and glycosyl hydrolases produced from the cells, hydrolysis of polysaccharides occurs, which release monomers of sugars. Release of monomers contributes to the increase in nutrient density of the fermented products (Ojha and Tiwari 2016).

10.4.2 Cereals

Lactobacillus species are the predominant organisms involved in the fermentation of cereal-based foods and beverages in African countries (Richard and Jooste 2012). A multiple of researches showed that cereal fermentation is considered as a significant potential in improvement and design of the nutritional quality and health effects of foods and ingredients (Rollán et al. 2019). Cereal grains are primarily a source of

carbohydrates, and thus a good source of energy. However, a high proportion of starch in cereals is in the form of amylopectin, which is not completely digested and absorbed in the small intestine. Digestible polysaccharides are produced as a result of probiotic lactic acid fermentation of cereal, which are more accessible to gut microbiota. (Liptáková et al. 2017).

10.5 Exopolysaccharides (EPS)

EPS are secondary metabolites with long chain of homo or hetero-polysaccharides containing repeated units of sugars or sugar derivatives. These polysaccharides are produced outside of the cell. Depending on the carbon source, LAB belonging to the genera *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, and *Weissella* are able of producing a variety of EPS (Zeidan et al. 2017).

10.5.1 Dairy

In dairy-based foods, extracellular polysaccharides (EPS) are produced from rropy probiotic cultures (*Streptococci*, *lactobacilli*, and *lactococci* strains) (Prasanna et al. 2012). These EPS could improve physicochemical and rheological properties of foods. In addition, they may also protect cells to against phage attack, desiccation, and osmotic stress, thus behaving as prebiotics and improve immunity to fight against pathogenic organisms (Ruas-Madiedo et al. 2002). In addition, blood cholesterol-lowering, immunostimulatory, antitumoral, and antiulcer activity have been also attributed to EPS produced in fermented probiotic dairy products (Madhuri and Prabhakar 2014; Shao et al. 2014).

10.6 Galacto-Oligosaccharides (GOS)

GOS are non-digestible carbohydrates and comprise a chain of galactose units usually with a terminal glucose unit. They are derived from lactose by the action of β -galactosidase enzyme in a trans-galactosylation reaction that occurs simultaneously with the hydrolysis. These bioactive compounds can be synthesized by probiotic microorganisms in fermented products during processing (Otiemo 2010). In the case of use of probiotics as enzyme sources for GOS synthesis, they could provide the double advantage as probiotics as well as in prebiotic. GOS are fermented by the beneficial gut microflora of the large intestine resulting in the inhibition of pathogenic and putrefactive bacteria growth. Therefore, the level of toxic metabolites is significantly decreased which could prevent diarrhea, constipation relief, and lactose tolerance. Also, metabolism of GOS results in the production of short-chain fatty acids which could assist in increased calcium and magnesium absorption, control of serum lipid and cholesterol level, and reduction of cancer risk (Davani-Davari et al. 2019).

10.6.1 Dairy

Milk sugar (lactose) is a component of dairy by-products especially from whey which is half consumed by human and animals and the remaining is generally discarded. Various reports used different probiotic strains specially *Lactobacillus* and *Bifidobacterium* species to produce GOS from milk, cheese, whey, and yogurt which can be used as a suitable substrate for GOS synthesis. Therefore, fermented dairy-based foods could be considered as the main carrier of GOS (Lappa et al. 2019; Sabater et al. 2018; Song et al. 2013). There are many parameters affecting the synthesis of these compounds such as β -galactosidase enzyme source and concentration, type and counts of microorganisms, concentration of substrate (lactose), composition of food matrix, conditions of fermentation and storage, and time/temperature of hydrolysis/transgalactosylation (Morton 2015).

10.7 Conjugated Linoleic Acid (CLA)

CLA is a collective term used to describe a heterogeneous mixture of positional and geometric isomers of octadecadienoic acid or linoleic acid (c9,c12-C18:2) in which double bonds are conjugated (cis-, trans-, or mixed configurations). Biological and biochemical roles attributed to CLA include anticancer, body fat reduction, prevention of cardiovascular diseases through the reduction of atherosclerosis lesions and levels of cholesterol and triacylglycerides, anti-inflammatory and antioxidant. Linoleate isomerase (LAI) enzyme is responsible of CLA synthesis, which is bond to the cell membrane of microorganisms. CLAs exert various health benefits and their effectiveness depends on CLA isomer form. Studies demonstrated that trans-9, trans-11 C18:2 has a much higher inhibitory and antiproliferative effect on the growth of the human colon and breast cancer cells, than cis-9, trans-11 CLA isomer (Beppu et al. 2007; El Roz et al. 2013; Park 2009).

In contrast, the results of other studies showed that cis-9, trans-11 CLA has extra beneficial effects, such as anti-inflammatory and antiatherogenic effects (Tricon et al. 2006). However, the mixture of the two CLA isomers (cis-9, trans-11 and trans-9, trans-11 CLA) had a synergistic anti-proliferation effect on a human colorectal carcinoma cell line (Zhong et al. 2012).

10.7.1 Meat Products

CLA is a compound found mainly in the meat of ruminants that is recently the subject of many researches due its health-promoting properties, i.e., antiatherogenic, cancer inhibition, anti-diabetic, obesity lowering, and improved immunity (Mulvihill 2002). In a detoxification mechanism, some probiotic bacteria of *Lactobacillus* and *Bifidobacterium* types are able to change fatty acid profile in meat sausages by converting polyunsaturated fatty acids into CLA through isomerization, hydrogenation, and dehydration (Galgano et al. 2015).

10.7.2 Dairy

In some countries, liquid milk, powdered milk, fermented milk, yogurt, and cheese enriched in CLA are marketed. On the other hand, the known fact that several strains of bacteria possess the ability to synthesize CLA *in vitro* in the presence of precursor substrate raised the possibility for increasing the production of CLA *in situ* during manufacture of fermented dairy foods. The co-culture of *L. rhamnosus* and yogurt starter in the presence of hydrolyzed soy oil as the lipid source showed that CLA contents significantly increased in the final fermented (Xu et al. 2005). A study performed by Ribeiro et al. (2017) showed that *Lactobacillus plantarum* isolated from Pico cheese exhibited probiotic properties and presented the highest production of both cis-9, trans-11 and trans-9, trans-11 CLA isomers, exhibiting a great potential for application in health-promoting food product.

10.8 Short-Chain Fatty Acids (SCFA)

SCFA such as butyrate, acetate, propionate, and lactate are secondary metabolites released from the hydrolysis of food fiber and non-digestible carbohydrates in gut by probiotic bacteria and are used as a source of energy for colon cells. In humans, 10% of the daily caloric requirement is from short-chain fatty acids produced in large intestine. Among all short-chain fatty acids, 60–70% of the energy is from butyrate produced in colonocytes. SCFAs, particularly butyrate, have a therapeutic effect in various diseases such as inflammatory bowel disease, antibiotic-associated diarrhea, colon cancer, and heart diseases (Indira et al. 2019; Septembre-Malaterre et al. 2018).

According to different researches, the increase of Ca bioavailability by probiotics would definitely satisfy the bone health. The mechanism behind the increase in Ca bioavailability and ensure the bone health is that the probiotics produce short-chain fatty acids, which increase the solubility of available calcium. Simultaneously, the level of the para-thyroid hormone level (increased PTH level causes the Bone resorption by stimulating the osteoclasts) decreases and minimizes the bone loss (Dubey and Patel 2018).

10.9 Vitamins

Vitamins play an important role in regulating the intestinal metabolism and absorption of minerals. Calcium absorption is enhanced in the presence of Folate and vitamin C, D, and K (Kiela and Ghishan 2016). Probiotics are associated with the synthesis of vitamins and increase the metabolism and absorption of available calcium (Parvaneh et al. 2014; Whisner and Castillo 2018). Therefore, food fermentation with probiotic bacteria could result in an increased vitamin content of the final product (Richard and Jooste 2012). Probiotic LAB are able of producing B vitamins

including niacin (B3), panthothenic acid (B5), folic acid (B9), and also vitamins B1, B2, B6, and B12 (Capozzi et al. 2012; Septembre-Malaterre et al. 2018).

10.9.1 Fruits and Vegetables

Vitamin B12 deficiencies in plant based-diet forced researchers to investigate potential ways to fortify plant-based foods with vitamin B12 (Chamlagain 2016; Melini et al. 2019) Cereal-based products such as Ogi, Mageu, and Kenkey, which are considered as traditional fermented products in Africa, have been reported to have an improved B-vitamin content. Beside probiotic LAB benefits in the enrichment of foods with vitamins, they may lower production costs by eliminating the need to add synthetic vitamins (Rollán et al. 2019). A study performed by Varmanen et al. (2016) showed that *L. reuteri* can be used for vitamin B12 fortification in soy-yogurt.

10.9.2 Dairy

Folate, as an essential vitamin, plays an important role in human life for the synthesis of nucleotides, vitamins, and some amino acids. However, this vitamin could not be synthesized by human and have to be taken by daily diet. Dairy products, especially yogurt, are an appropriate choice for bio-fortification of folate as they contain folate-binding protein which improves folate bioavailability. It is reported that the use of folate-producing probiotic bacteria in combination with *S. thermophilus* and/or *L. bulgaricus* provides the largest increase in folate during the fermentation process of probiotic yogurt compared to original milk and conventional fermented milk (Rad et al. 2016). The level of vitamin B12 is significant in dairy products. This vitamin is necessary for the maintenance of the nervous system and the formation of blood cells. Fermentation by probiotic bacteria could increase its content up to 10-folds (Melini et al. 2019).

10.10 Enzymes: Anti-Nutrient Degradation

Food fermentation is considered as an important part in food detoxification. Probiotics LAB are able to metabolize anti-nutrient compounds including phytates, trypsin inhibitors, saponins, tannins, cyanogens, or phenolic compounds in foods. This effect can be associated with modification of minerals bioavailability (Septembre-Malaterre et al. 2018).

10.10.1 Phytates

According to clinical investigations, it has been found that vegetarians may suffer from nutritional deficiencies and, specially, they have an impaired absorption of

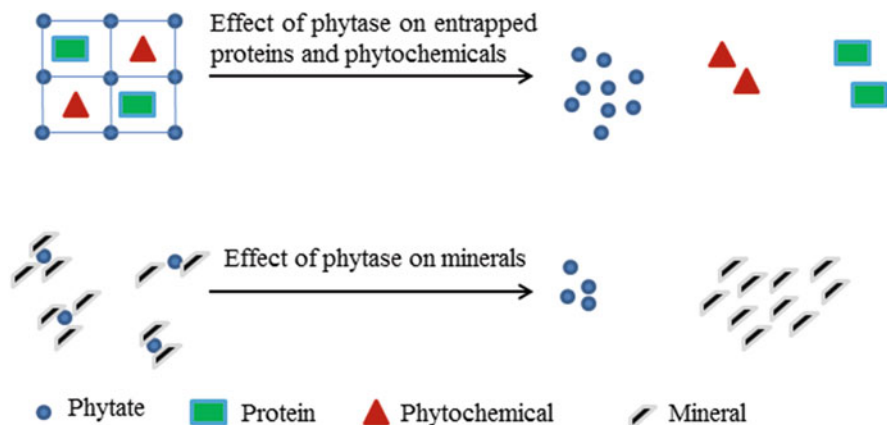


Fig. 10.1 Effect of fermentation on minerals, phytochemicals, and proteins bioavailability of foods

trace minerals, such as zinc, iron, and calcium, proteins, vitamin B₁₂, and folate (Bergillos-Meca et al. 2013; Masum Akond et al. 2011; Popova and Mihaylova 2019; Rekha and Vijayalakshmi 2010). This malabsorption syndrome may cause severe health-threatening diseases ranging from anemia to neurological disorders and immune deficiency (Hunt 2003). It is postulated that this intestinal malabsorption of minerals is due to the high content of phytate in cereals, nuts, legumes, and oilseeds. Furthermore, it accounts from 60% to 90% of total phosphorus content in cereals and is, therefore, the major storage compound for phosphorus (Gupta et al. 2015). Phytate is able of chelating nutritionally important cations such as Ca²⁺, Mg²⁺, Fe²⁺, and Zn²⁺, thus decreasing the dietary bioavailability of these nutrients.

Intestinal microfloras, especially LAB, are an important source of phytase with high activity. The consequence of phytate hydrolysis by LAB in gut is the release of phosphate, other metal ions and proteins through the degradation of complexes formed by phytate (Dubey and Patel 2018; Famularo et al. 2005) (Fig. 10.1). Various studies have approved an improvement in mineral bioavailability by different probiotic microorganisms used in the fermentation process (Bergillos-Meca et al. 2013). Daily diet enriched with probiotic lactic acid bacteria could minimize phytate or phytic acid in plants. The fermentation of bran with probiotic LAB could provide optimal pH conditions for enzymatic degradation of anti-nutritional factors induced by the degradation of phytate (up to 90%). This results in better bioavailability of minerals (Lopez et al. 2001; Rollán et al. 2019). According to researches, Ca absorption is related to pH in the colon (Diaz de Barboza et al. 2015; Rekha and Vijayalakshmi 2010). Calcium is a divalent cation which salt form is available in food. The soluble and ionized form of Ca is absorbed. Phytate and oxalate in a diet form insoluble salts with calcium and inhibit the calcium absorption (Dubey and Patel 2018). Fermentation of soymilk with five strains of probiotic lactic-acid bacteria (*L. acidophilus* B4496, *L. bulgaricus* CFR 2028, *L. casei* B1922,

L. plantarum B4495, and *L. fermentum* B4655) with the yeast *Saccharomyces boulardii* made Ca more soluble (Parvaneh et al. 2014; Ramsubeik et al. 2014; Rekha and Vijayalakshmi 2010). In a study performed by Lorusso et al. (2017), evaluations showed that the minerals bioavailability in quinoa-based pasta flour fermented by selected LAB with phytase activity substantially augmented. A similar study (Rizzello et al. 2016) reported that phytase activity of quinoa sourdough has increased 2.75 times after fermentation with autochthonous LAB (*L. plantarum* T6B10 and *L. rossiae* T0A16).

10.10.2 Phenolic Compounds

Phenolic compounds as secondary metabolites produced by plants are widely used as dietary supplements and have numerous biological and pharmacological effects such as anticancer, antioxidative, antiviral, anti-inflammatory, and antiatherogenic activities (de Souza et al. 2019; Hur et al. 2014; Rollán et al. 2019). Many phenolic compounds occur in food as esters, glycoconjugates, or polymers, which are not directly bioavailable (Rossi et al. 2013). According to estimations, as little as 5–10% of total ingested phenolic compounds can be absorbed in the small intestine, whereas 90–95% reach the colon because of insufficient gastric residence time, low permeability or solubility in the intestine (de Souza et al. 2019). The evidences showed that the gut microbiota are major responsible of polyphenols biotransformation into more biologically active components (de Souza et al. 2019; Pereira-Caro et al. 2018). Enzymatic activity of intestinal bacteria able to catabolize phenolics could results in the production of various compounds with different bioavailability and biological functions to their parent compounds (Dudonné et al. 2015) As oligo- and polysaccharides bounded to phenolic compounds are the major carbon sources for saccharolytic fermentative bacteria, in the first step of phenolic degradation, aglycones are released from glycol-conjugated forms of polyphenols by microbial enzymes including glycosidases, glucuronidases, and sulfatases (Rossi et al. 2013). These aglycones are further degraded through several functional groups cleavages reactions (dehydroxylation, demethylation, and decarboxylation) and ring-fission. Therefore, the produced microbial metabolites are absorbed from the colon and are also subjected to liver metabolism, resulting in their conjugated derivatives. This intensive microbial metabolism ultimately reduces the structural diversity of native phenolic compounds to a limited number of smaller phenolic acids and derivatives of phenylpropionic and phenyl acetic acids metabolites. Biological activities of phenolic compounds have mostly been attributed to their microbial metabolites, present in higher quantities in circulation than the native compounds (Marín et al. 2015).

Modulating the activity of gut microbiota by the incorporation of appropriate probiotics into daily diet can enhance bioavailability and/or biological activity of these phenolic compounds. In a study performed by Rekha and Vijayalakshmi (2010), investigations showed that soymilk fermentation with LAB in combination with probiotic yeast *Saccharomyces boulardii* could increase the bioactive aglycones form of soy isoflavone (Rekha and Vijayalakshmi 2010). Investigations

showed that glucoside conjugates of isoflavones exist principally in soya foods which is poorly absorbed in the body and their biological effect are mainly attributed to their glycosides form (Rekha and Vijayalakshmi 2010; Zubik and Meydani 2003).

Various studies revealed an increase in total phenols after fermentation of different foods, and observed that the increase in antioxidative activity may be due to the increase in the total phenolic compounds (Călinoiu et al. 2019; Hur et al. 2014; Zou et al. 2017). Probiotic LAB are naturally present in legume grains; they have also been traditionally used for legume fermentation. Evidences showed that fermentation of legumes with *Lactobacillus* genera can encourage the production of bioactive compounds, improving health benefits beyond basic nutrition. Fermentation of cowpeas with *Lactobacillus plantarum* resulted in the modification of phenolic compounds and improvement of antioxidant activity (Dueñas et al. 2005; Limon et al. 2015).

A research showed that complex polyphenols were hydrolyzed to simpler and more biologically active compounds during fermentation of cowpea flour, and the concentration of phenolic compounds in fermented has significantly increased (Dueñas et al. 2005). In humans, isoflavones bioavailability depends on the relative ability of gut microflora to degrade these compounds. Variation in the intestinal bacterial community as a result of illnesses, diet, or age could significantly influence isoflavones bioavailability (Rekha and Vijayalakshmi 2010; van der Velpen et al. 2014). A research carried out by Dudonné et al. (2015) consumption of showed that cranberry extract co-supplemented with probiotic *Bacillus subtilis* CUI resulted in the significant change in the composition of gut microbial communities of high-fat fed diet mice through the inhibition of pathogenic bacteria and stimulation of beneficial bacteria (de Souza et al. 2019). According to a study performed by Parkar et al. (2014), anthocyanin-rich blackcurrant juice stimulated the in vitro growth and adhesion properties of *L. rhamnosus* 299. In contrast, it suppressed the growth and adhesion properties of *Salmonella Typhimurium* 450.

It has been reported that fermentation can significantly improve total phenolic content and antioxidant activity of cereals and pseudocereals, which is highly dependent on the species of microorganism, on the grains types, fermentation conditions, particularly time, temperature, and pH values (Hur et al. 2014; Rollán et al. 2019). The enzymes involved in the phenolic metabolism by LAB are mainly decarboxylases (PAD), reductases (PAR), esterases, and/or glycosidases (Rollán et al. 2019). Fermentation of cowpeas with *Lactobacillus plantarum* resulted in the modification of phenolic compounds and improvement of antioxidant activity (Dueñas et al. 2005; Limon et al. 2015) (Fig. 10.1).

Catabolic products of orange juice flavanones identified by HPLC–HR–MS showed that probiotication of orange juice by *Bifidobacterium longum* R0175 could significantly enhance the aglycone form of flavanones in orange juice which could eventually augment the bioavailability of orange juice flavanones, and, therefore, their potential beneficial effects on health. A study on the effect of probiotic fermentation of pomegranate juice revealed that fermentation of the juice using *L. plantarum* and *L. acidophilus* as probiotic starter organisms increased the antioxidant activity significantly (Mousavi et al. 2013). In a similar study, investigations

showed that fermentation of liquorice root extract could effectively improve the antioxidant activity of the extract from 53% to a maximum level of 73% (Mousavi and Mousavi 2019).

10.10.3 Allergens

Hydrolysis of proteins into smaller peptide fragments during lactic acid fermentation by probiotics could also suppress the potential allergenicity of parent proteins in different foods (Verhoeckx et al. 2015; Xiang et al. 2019). For instance, despite the high protein content, balanced amino acid composition, and high level of lysine in comparison with other vegetable protein sources, soybean meals contain anti-nutritional factors (ANFs) and allergens, which cause decrease in protein digestibility and absorption in animals (Gu et al. 2010). The soybean is one of the “Big 8” food allergens. The allergen proteins account for 65–80% of total protein content in the soybean and approximately 30% in soybean. The major allergen proteins are beta conglycinin, the 30-kDa allergen (GlymBd 30), and glycinin. In human subjects, these allergens can induce symptoms ranging from skin, gastrointestinal, or respiratory reactions to anaphylaxis. They also cause hypersensitivity in weaned piglets, with the primary adverse effect being diarrhea (Adachi et al. 2009).

Lactobacillus kefirifaciens M1 isolated from Kefir grains has an anti-allergic effect. Digestion of caseins during maturation of fermented milk products has shown to facilitate loss of allergenic reactivity (Chen et al. 2012).

Fermentation of soybean meal enhanced the bioavailability of nutritious components and decreased the incidence of diarrhea in weaned pigs due to the degradation of allergens into peptides (Chi and Cho 2016). The absorption of peptides was significantly improved by the animal. In addition, soybean protein hydrolysate also exhibited antioxidative, metal-chelating activity and lipid peroxidation inhibitory activity attributed mainly to the low-molecular-weight (3 kDa) peptide (Chi and Cho 2016).

The probiotic *B. coagulans* GBI-30, 6086 has the capacity to produce enzymes degrading proteins and a wide of carbohydrates. These enzymes can increase the amount of digested milk protein available for absorption. *B. coagulans* GBI-30, 6086 could be exploited to improve protein quality in plant protein sources with lower essential amino acid such as Leucine (Jager et al. 2018).

10.10.4 Cyanogenic Glucosides

Galactosidase is recognized to metabolize cyanogenic glucosides present in some vegetal matrixes such as cassava roots, bitter almonds, or whole sorghum. Cyanogenic glycoside linamarin and lotaustralin in cassava tubers can be detoxified by species of *Leuconostoc*, *Lactobacillus*, and *Streptococcus* during traditional method to Gari and Fufu productions to yield hydrocyanic acid (HCN). This compound is

volatile and can escape from the dewatered pulp during toasting rendering the product safe for human consumption (Tamang et al. 2016).

10.10.5 Tannins

Tannins are polyphenols widely available in cereals and legumes. They can easily bind to proteins making indigestible complexes with reduced bioaccessibility of nutrients. Various probiotic *Lactobacillus* species such as *L. plantarum*, *L. paraplantarum*, and *L. pentosus* have been confirmed to have tannase activity (Osawa et al. 2000). Therefore, the exploitation of these bacteria in the fermentation of plant-based foods rich in tannins can cleave the protein-tannin complexes rendering protein more available to the cells (Nkhata et al. 2018).

10.11 Conclusion

During food fermentation with probiotic bacteria, a number of chemical changes occur in the structure of components of the raw matrix, which thus results in the improvement of the functional properties of foods. This improvement is resulted from several mechanisms such as the elimination of anti-nutritional factors, production of metabolites with a positive effect (bioactive peptides, exopolysaccharides), improvement of the bioavailability through biopolymers hydrolysis (esters of phenolic compounds), and increased vitamin, mineral, and phenolic compounds, leading to an increase in the antioxidant capacity of the final product.

A higher bioactive molecule content and an improved antioxidant activity were found in fermented milks, cereals, fruit and vegetables, meat and fish. Antihypertensive peptides were detected in fermented milk and cereals. Changes in vitamin content were mainly observed in fermented milk and fruits. The imparted health benefits of probiotic fermentation to consumers make this category of foods worthy of recommending for regular dietary guidelines. However, it seems that molecular mechanisms behind the bioavailability and the potential health effects of the newly formed compounds by probiotic fermentation are not deeply investigated yet. Therefore, development of molecular tool analysis such as metabolomics, proteomics, and transcriptomics would considerably help in that respect. Analysis of food composition and enzyme activity evaluation in the gastrointestinal tract would be helpful to evaluate the extent of molecular changes at each stage. Eventually, clinical trials would be useful to measure the health effect of probiotic-fermented foods on different groups of the population.

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Quality and Health Aspects of Dairy Foods as Affected by Probiotic Bacteria and Their Metabolites

11

Mahdieh Iranmanesh

Abstract

With the growing demand for healthy food products, there has been increasing scientific and commercial interests for developing foods that besides providing the nutritive values could also improve the overall health status of the consumer. In this context, the probiotic dairy products are of immense interest to both consumers and researchers who are searching for healthy food products with increased health benefits. Administration of live bacteria especially lactic acid bacteria (LAB) to ferment and non-fermented dairy food products are considered a health-promoting strategy that could bestow health benefits on the consumer. Probiotics are mixture of friendly bacteria capable of maintaining and improving intestinal balance and hence boosting immune system effectiveness. Mounting evidence are present on the role of probiotic strains acting as adjuncts to antibiotic therapy by reducing adverse effects, improving antibacterial function and enhancing mucosal immunity. Apart from probiotic bacteria, their nonviable counterparts (paraprobiotics) and the metabolites produced by probiotic bacteria (postbiotic metabolites) are also known to provide physiological health benefits to the consumers, and demonstrate therapeutic actions that are comparable to the actions of probiotics. In this review these concepts will be approached, as well as their potential applications in dairy products, highlighting the functional and technological advantages compared to the use of probiotics.

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257

Keywords

Probiotics · Postbiotics · Paraprobiotics · Dairy food · Fermented milk · Non-fermented milk

11.1 Introduction

With the rise in healthy living and integrative medicine, the importance of beneficial bacteria has become prominent and the use of products known as probiotics is becoming more and more common among ordinary people. The importance of probiotic foods especially dairy foods has been emphasized by many researchers in last decades (FAO/WHO 2001, 2002; Gardiner et al. 2002; Moeller and de Vrese 2004; Malcata et al. 2005; Sharma and Ghosh 2006; Shah 2007; Shiby and Mishra 2013; Sharma and Devi 2014; Santiago Lopez et al. 2015; Tunick and van Hekken 2015). The word Probiotic is derived from a Greek word that means “for life” (Kollath 1953). As stated in FAO/WHO reports (2001), Probiotics are “*live microorganisms which when administered in adequate amounts confer a health benefit on the host.*” The most widely used probiotic species includes species from the Genus *Lactobacillus* and *Bifidobacterium*, while some species of *Streptococcus*, *Lactococcus* and *Enterococcus* has also been used. Apart from these, some yeast like *Saccharomyces boulardii* and *Kluyveromyces lactis* are also used as a probiotics (Kumura et al. 2004; Kumar et al. 2015). The health benefit of probiotics and their metabolites has been observed in many probiotic food products. Among different category of food products, fermented dairy products are considered as the most important vehicle for delivering probiotic organisms (Tamime et al. 1995), and many research reports have highlighted their therapeutic effects (Granato et al. 2010; Parmjit 2011; Sánchez et al. 2017). In addition, the postbiotic metabolites produced by these added probiotic bacteria can affect the microbiological and sensory qualities of dairy products (Guzel-Seydim et al. 2005; Hekmat and Reid 2006; Sobrino-López and Martín-Belloso 2008; Allgeyer et al. 2010). In this chapter, the effect of probiotic bacteria and their metabolite on quality of dairy products and the health benefits of consumption of these kinds of products will be reviewed.

11.2 Probiotic, Paraprobiotic, and Postbiotic

Probiotics in fermented dairy products impose beneficial health effects on the host by several mechanisms (Fig. 11.1). According to Oelschlaeger (2010) these effects can be divided into three groups based on their mode of action: (1) modulating hosts defenses through the mucosal barrier function by decreasing the apoptosis of epithelial cells and increasing mucin production (Mattar et al. 2002; Gaudier et al. 2005; Yan and Polk 2006; Caballero-Franco et al. 2007; Gogineni et al. 2013; Saad et al. 2013), (2) direct effect on pathogenic microorganisms by producing antimicrobial substances such as bacteriocins (Alakomi et al. 2000; Penner et al.



Fig. 11.1 Health benefits of fermented dairy products

2005; Liévin-Le Moal and Servin 2006; Sharma and Devi 2014) and antimicrobial peptides (Schlee et al. 2008; Kelsall 2008; Mondel et al. 2009), and (3) effect on microbial products such as toxins.

Most of the functions performed by probiotic bacteria have been reported to depend on their viability (Sanders 2009), and it was considered essential for a probiotic bacterium to retain its viability at concentrations of approximately 10^9 cfu/mL to be effective. However, recent studies have suggested that bacterial viability is not an imperative factor for these beneficial microbes to show their health effects, and dead probiotic bacterial cells are also able to show significant health benefits. The nonviable counterpart of the probiotic bacteria was termed paraprobiotic.

Paraprobiotic or nonviable probiotic can be defined as “inactivated microbial cells or cell fractions that confer health benefits to the consumer” (Taverniti and Guglielmetti 2011). Paraprobiotics include the cell wall components including peptidoglycans, surface proteins, cell wall polysaccharides, etc. (Shin et al. 2010).

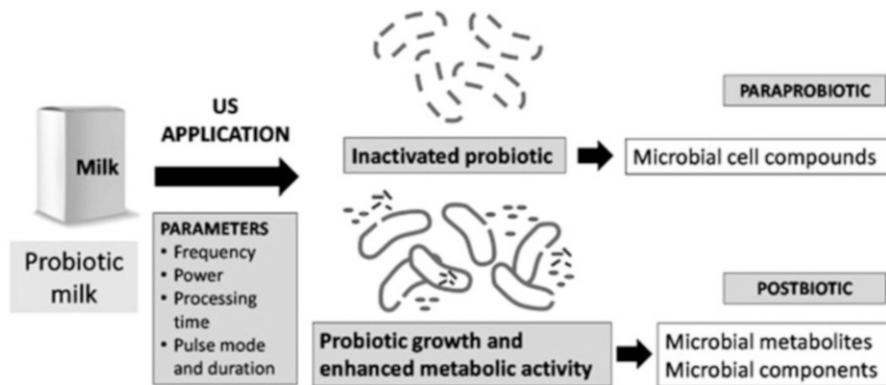


Fig 11.2 High-intensity ultrasound in the development of paraprobiotics and postbiotics (Guimarães et al. 2019)

Various methods like heat, high pressure, sonication, UV irradiation, and other methods such as dehydration, pulsed electric field (PEF), and ohmic heating have been used for inactivating bacterial cells (de Almada et al. 2016). These kinds of methods are also used in dairy products manufactured with probiotics in order to improve the functional activities. Guimarães and his colleagues (2019) used high-intensity ultrasound (HIUS) as a mild preservation technology in dairy products (Fig. 11.2). These researchers concluded that HIUS technology could shorten the processing time, improve probiotic viability, and could be utilized for development of paraprobiotics and improving the production of postbiotics with health effects.

Postbiotic or probiotic metabolic, biogenics, or simply metabolites/CFS (cell-free supernatants) refers to soluble fractions (products or metabolic byproducts) secreted by live probiotic bacteria or released after bacterial lysis (Tsilingiri and Rescigno 2013). Postbiotics are classified differently based on the data available in the literature. As on these reports, postbiotics can be categorized depending on their elemental composition like lipids (e.g., butyrate, propionate, dimethyl acetyl-derived plasmalogen), proteins (e.g., lactocepin, p40 molecule), carbohydrates (e.g., galactose-rich polysaccharides, and teichoic acids), vitamins/cofactors (e.g., B-group vitamins), organic acids (e.g., propionic and 3-phenyllactic acid) enzymes, bacteriocins, and complex molecules such as peptidoglycan-derived muropeptides and lipoteichoic acids (Kostantinov et al. 2013; Tsilingiri and Rescigno 2013). In another words, postbiotics include extracellular and intracellular bacterial cell fractions. The extracellular cell wall components include exopolysaccharide and peptidoglycans, while the intracellular metabolites are organic acids, short-chain fatty acids, and bacteriocins like acidophilin, bifidin, reuterin, peptides, etc. (Matsuguchi et al. 2003). Besides, postbiotics can be divided into different groups according to their function such as immunomodulation, anti-inflammatory, hypocholesterolemic, antiobesogenic, antihypertensive, antiproliferative, and anti-oxidant effects (Nakamura et al. 2016; Shin et al. 2010; Sawada et al. 1990).

11.3 Dairy Products

With increasing consumer demands, there is surge for safe and nutritive foods that would not only provide the required energy and the nutrients for the human, but might also improve the overall health status of the consumer including their physiological and psychological status (Young 2000; Mollet and Rowland 2002). These food products are referred to as functional foods and are known for their ability to improve the general health of the consumers (Stanton et al. 2005). Functional foods enriched with probiotics are termed probiotic functional foods.

Dairy products are an important source of energy as well as micro- and macronutrients and among the highly consumed food product worldwide. Among these dairy products yogurts, fermented dairy products, LAB drinks and mixture of probiotic (fermented) milks and fruit juices are highly reputed for their dietary health benefits and are considered a rich source of beneficial bacteria including lactic acid bacteria. It is a well-known fact that milk and dairy products are a powerful tool and significant vectors for creating probiotic dairy foods (Fig. 11.3).

11.4 Classification of Probiotic Dairy Products

This category of dairy products includes raw milk (fermented and unfermented), cheese, ice cream, and dried dairy products (infant formula and dairy base dried products). Below we discuss the importance of some of these probiotic products.

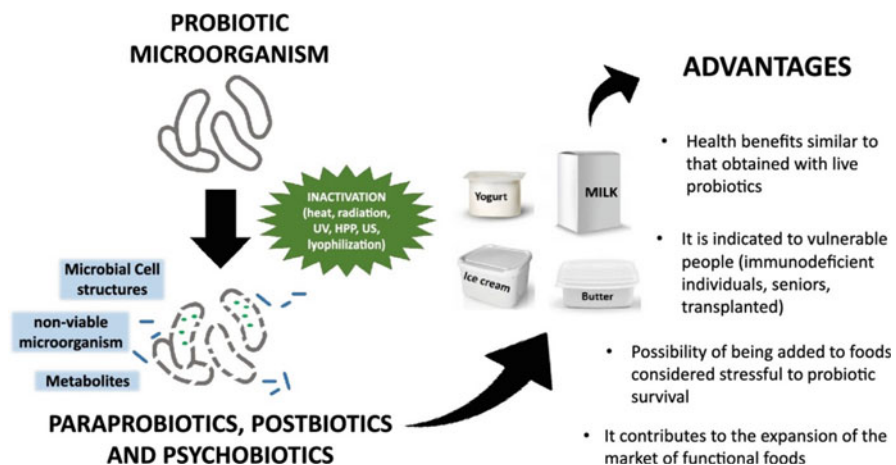


Fig. 11.3 Advantages of probiotics, paraprobiotics, and postbiotics in dairy products (Barros et al. 2020)

11.4.1 Probiotic Fermented Milks

Fermented milk is a dairy product that is produced by fermentation of milk with abundant number of viable and active microorganism that are safe for use (García-Burgos et al. 2020). This milk has been produced in many countries for centuries, and is considered one of the oldest methods for extending the shelf life of milk and also helps to produce various products from milk. Fermented milk products offer vast array of nutritional and health benefits due to the presence of abundant LAB and their metabolites which are produced during the process of fermentation (Granier et al. 2013). These products are produced from different mammal milk like cow, sheep, goat, buffalo, and camel (Tamime 2002), and are a good source of calcium which is vital for bone formation and mineralization (Baba et al. 2014). Fermented milk products are recognized as suitable carrier for probiotic microorganisms.

According to Robinson and Tamime (1990) fermented milks can be classified into three groups based on the dominant microorganisms in the products as follows:

- A. Lactic fermentations: (i) mesophilic type like cultured buttermilk, (ii) thermophilic type such as yogurt, Bulgarian buttermilk, zabadi, dahi; and (iii) therapeutic or probiotic type including acidophilus milk
- B. Yeast—lactic fermentations like kefir and koumiss
- C. Mold—lactic fermentations such as viili

In addition to these groups, we discussed other probiotic dairy product in this section as shown in Fig. 11.4.

Lactic fermentations could be divided into mesophilic probiotic fermented milks and thermophilic probiotic fermented milks.

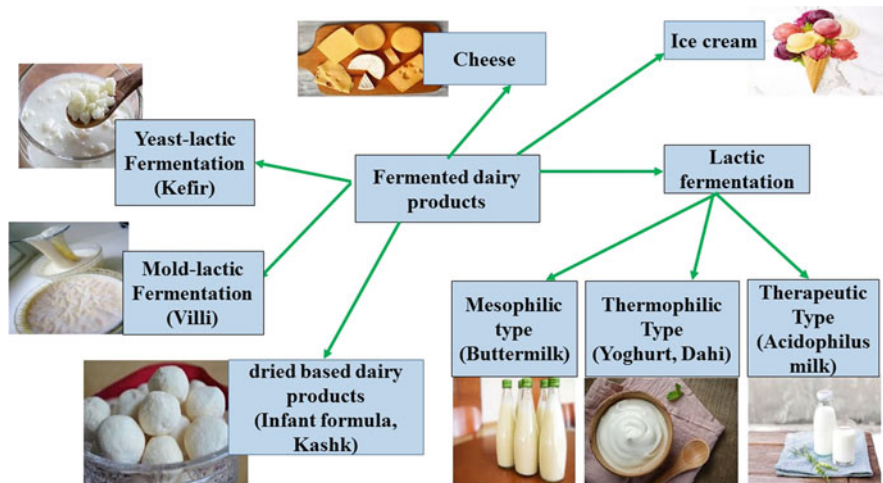


Fig. 11.4 Classification of fermented dairy products

Mesophilic cultures are widely used in fermented dairy products, like in sour creams, cultured buttermilk, kefir, etc. The primary mesophilic starter cultures used in these fermented dairy products belongs to the Genus *Lactobacillus*, *Lactococcus*, and *Leuconostoc* spp. These species are known to produce a variety of biogenic metabolites including proteins, peptides, oligosaccharides, vitamins, and fatty acids (Ebringer et al. 2008). The production of some fatty acids such as pyruvic, acetic, propionic, and especially lactic acid in cultured buttermilk produced during the fermentation by *Lc. lactis* and *Leu. citrovorum* was evaluated by Marsili 1981. According to the results, the content of acetaldehyde was shown to increase initially and then a decline was observed followed by formation of ethanol, whereas the content of acetone and uric acid remained constant during fermentation. In our previous study, some probiotic LAB species like *Lb. brevis*, *Lb. pentosus*, *Ped. acidilactici*, and *Lb. paracasei* were isolated from a traditional buttermilk in Iran (Iranmanesh et al. 2012). The paraprobiotic of the isolates also showed interesting health characteristics and were able to lower the cholesterol concentrations *in vitro*. Among the tested species, *L. brevis* demonstrated the highest level of cholesterol removal (Iranmanesh et al. 2014). Our results also showed that *Lb. pentosus*, *Lc. lactis*, *Lb. paracasei*, and *Ped. acidilactici* were able to produce protein metabolite (bacteriocins) that inhibited the growth of *L. monocytogenes* and *S. aureus*. The bacteriocin produced by the mentioned species was produced in the culture medium in the early logarithmic phase and continued to the end of exponential phase (Iranmanesh et al. 2015). Similar to our results, *Lc. lactis* subsp. *Hordniae* and *Lc. lactis* subsp. *Lactis* isolated from homemade buttermilk was shown to produce a bacteriocin that was active against *Staphylococcus aureus* MTCC96 and *Pseudomonas aeruginosa* MTCC741 (Barman et al. 2018).

Thermophilic cultures used in fermentation of milk include *Lb. delbrueckii* subsp. *bulgaricus*, *Lb. helveticus*, *Lb. acidophilus*, *Lb. paracasei* subsp. *paracasei*, Bifidobacterium species, and *Streptococcus thermophilus*. These cultures are mainly used for the production of yogurt, Bulgarian buttermilk, etc. Below we describe the beneficial health effects of some fermented dairy products having probiotic bacteria, beside the thermophilic starter cultures.

11.4.2 Yogurt

The popularity of yogurt as one of the most consumed fermented dairy products has increased in recent years due to its high nutritional-physiological values (Lourens-Hattingh and Viljoen 2001). The nutritional aspects of probiotic yogurt are mainly due to the presence of the beneficial bacteria with health-benefiting potentials. Some of the health benefits of thermophilic probiotic fermented milks are summarized as below.

Cancers are results of lethal cellular damage caused by free radicals, while antioxidant compounds prevent generation of these free radicals and consequently could prevent cancer generation (Urso and Clarkson 2003). The antioxidant property of probiotic yogurt that contained *Lb. bulgaricus*, *S. thermophiles*, *B. lactis* Bb12,

and *Lb. acidophilus* La5 was evaluated in 30- to 60-year-old patients with type 2 diabetes (Ejtahed et al. 2012). These patients consumed 300 g/day probiotic yogurt for 6 weeks. The results showed that consumption of probiotic yogurt increased erythrocyte superoxide dismutase and glutathione peroxidase activities as well as total antioxidant status, significantly ($P < 0.05$), compared to the control group. Furthermore, the level of insulin was not significantly different in comparison with the healthy control group, while the content of serum malondialdehyde significantly decreased.

Some bioactive peptides have shown to possess antioxidant activity. Sah et al. (2014) showed that peptides separated from probiotic yogurt had antioxidant and antimutagenicity activity. These researchers showed that the IC₅₀ of two peptides including 1,1-diphenyl-2-picrylhydrazyl and 2,20-azino-bis (3ethylbenzothiazoline-6-sulphonic acid) were 1.51 and 1.63 mg/mL, respectively.

The effect of metabolites produced by probiotic starter cultures on the texture and other sensory properties of the fermented milk products has been assessed. A number of bacterial species such as *S. thermophilus*, *Lb. kefiranoferiens*, *Lb. helveticus*, *Lb. sake*, *Lb. delbrueckii* subsp. *bulgaricus*, *Lc. lactis* subsp. *cremoris*, *B. longum*, and *B. infantis* are known to produce exopolysaccharide (EPS) (Surono and Hosono 2011). EPS plays an important role in the rheology, texture, and mouthfeel of fermented milks, and are found in yogurt, kefir, viili, and some other fermented dairy products. In a study, Hess and his co-investigators (1997), studied the effect of exopolysaccharide (EPS) produced by *Lb. delbrueckii* ssp. *bulgaricus* strain C1 and *S. thermophilus* strain B1 on the texture of the produced yogurt. They found that the susceptibility to syneresis was decreased, whereas the ropiness or extensibility was increased significantly. In addition, the shear stress of yogurt with EPS was increased from 0.1 to 0.3 s⁻¹ and then a steady increase as shear rate was increased from 0.3 to 100 s⁻¹. Similar findings were reported by Guzel-Seydim et al. (2005), who stated that whey separation was decreased in probiotic yogurt with ropy polysaccharide-producing culture. These results also indicated increase in the contents of lactic acid, volatile fatty acids, and tyrosine whereas the acetaldehyde concentration and pH values were decreased. In another research, the effect of EPS on the texture of inulin-containing probiotic yogurt during 21 days of storage showed that the firmness in the texture of yogurt was not influenced by EPS significantly (Ramchandran and Shah 2010). Whereas the influence of EPS on yield stress (Pa), consistency index (Pa s), and thixotropic behavior (Pa/s) was observable only after day 7. In addition, the use of the EPS from *Lb. fermentum* Lf2, as an additive, in yogurt augmented hardness and improved the water holding capacity of the product (Ale et al. 2016). The sensory properties of non-fat yogurts with 300 and 600 mg EPS/L showed that 600 mg/L of EPS extract had the highest values of consistency after 3 days of storage, while this property was not detected at the end of the shelf life. Similar to other results, the EPS333 produced by *S. thermophilus* strain AR333 in yogurts could increase the viscosity and water holding capacity which resulted in improved quality of yogurt (Zhang et al. 2018). These exopolysaccharides are composed of galactose, glucose, and galactosamine in a molar ratio of 3:2:1.

The immunostimulatory effects of EPS produced from *Lb. delbrueckii* ssp. *bulgaricus* OLL1073R-1 was described by Makino et al. (2016). They found that the oral administration of EPS or yogurt fermented with OLL1073R and *S. thermophilus* OLS305 to mice models, increased natural killer cell activity and also the production of IFN- γ production in spleen cells of mice after 3 weeks.

Another metabolite produced by probiotic bacteria includes folate which is B-group vitamin that is not synthesized in humans. Hence, humans require this vitamin which they receive through exogenous source such as food. Crittenden et al. (2003) showed that *S. thermophiles*, *bifidobacteria*, and *E. faecium* can produce folate. Based on his results, *S. thermophiles* produced higher content of folate than the other tested strains. In another research study, combination of *B. lactis*, *L. acidophilus*, and *S. thermophilus* used in the production of probiotic yogurts was shown to demonstrate higher content of folate than yogurts produced by traditional starter cultures (*Lb. delbrueckii* subsp. *Bulgaricus* and *S. thermophiles*). Similar findings were reported by Laiño et al. (2012), who showed that *Lb. delbrueckii* subsp. *bulgaricus* CRL 863 isolated from artisanal Argentinean yogurts could produce folate. This strain produced both intracellular and extracellular folate after 6 h of growth in folate-free culture medium and then decreased after 10 h, while extracellular folates remained constant up to 24 h but intracellular forms reduced slightly. Besides, the content of folate in milk fermented by *Lb. delbrueckii* subsp. *bulgaricus* CRL 863 was shown to increase after 24 h of incubation at 37 °C.

The effect of fermented milk like yogurt on cholesterol has been investigated widely. Ataie-Jafari et al. (2009) had shown that consumption of probiotic yogurt was able to reduce total cholesterol levels in the serum of 14 healthy subjects. The subjects in study were given 300 g of ordinary yogurt or probiotic yogurt for 6 weeks, after a 4-week washout period, the study continued for another 6 weeks. In this study, probiotic yogurts were fermented by *S. thermophilus* and *Lb. delbrueckii* subsp. *Bulgaricus*, *Lb. acidophilus* and *B. lactis*. They concluded that the two probiotic strains *Lb. acidophilus* or *B. lactis* had important role on the observed hypocholesterolemia effects. Similarly, Baroutkoub et al. (2010) showed that total cholesterol and LDL (low-density lipoprotein) levels were decreased, while HDL (high-density lipoprotein) increased by consumption of probiotic yogurt. Furthermore, consumption of 300 g of probiotic yogurt containing *Lb. acidophilus* La5 and *B. lactis* Bb12 for 6 weeks in people with type 2 diabetes also showed that the total cholesterol and LDL-C were decreased 4.54% and 7.45%, respectively (Ejtahed et al. 2011). The total cholesterol:HDL-C ratio and LDL-C:HDL-C was also significantly decreased.

Some major antibacterial metabolites produced by probiotic bacteria include bacteriocin and other antimicrobial compounds like organic acid, hydrogen peroxide, and low-molecular-weight substances like Reuterin (Ammor et al. 2006). In a study, *S. thermophile* was shown to produce a bacteriocin which could decrease *L. monocytogenes* counts below detectable levels (Benkerroum et al. 2002). Zaeim et al. (2014) identified bacteriocin from *Lb. bulgaricus* isolated from local yogurt samples. This bacteriocin had activity against Gram-positive bacteria like

L. monocytogenes and *Bacillus cereus* and Gram-negative bacteria such as *E. coli* O157:H7 and *Proteus vulgaris*.

11.4.3 Dahi

Dahi is another fermented dairy product belonging to yogurt group, which is produced in India for long time. It is prepared by buffalo milk fermented by lactic acid bacteria. This product has been reported to be highly nutritious and possess therapeutic effects, and hence can be used as a functional food (Abbas and Jaffri 1992; Sinha and Sinha 2000). The effect of probiotic dahi fermented by *Lb. acidophilus* and *Lb. casei* in rats with type 2 diabetes showed that HDL levels were reduced slightly and the thiobarbituric acid-reactive substances were lower than control group (Yadav et al. 2007a).

Kaushal and Kansal (2012) also evaluated the activity of antioxidant enzymes in dahi prepared from buffalo milk with different bacteria. Based on the type of bacteria used in the preparations of dahi, they divided this product into 2 groups: 1. *Lc. lactis* ssp. *cremoris* NCDC-86 and *Lc. lactis* ssp. *lactis biovar diacetylactis* NCDC60 along with selected strain of *Lb. acidophilus* LaVK2 (La-Dahi) and 2. *Lb. acidophilus* and *B. bifidum* BbVK3 (LaBb-Dahi). The activity of antioxidant enzymes was evaluated in mice fed with 5 g/day dahi for 4 months. The results showed the content of oxidation products, thiobarbituric acid-reactive substances (TBARS) and protein carbonyls, in red blood corpuscles (RBCs), heart tissues, liver and kidney was increased. Moreover, the level of superoxide dismutase (SOD) activity in RBCs and hepatic tissues during aging of mice was increased in both groups, while the CAT activity increased in RBCs and heart tissue of only LaBb-Dahi group.

In another study, the EPS-producing non-ropy strain of *Leuconostoc* sp. CFR 2181 isolated from dahi (Vijayendra et al. 2008) was evaluated. This EPS consisted mostly of glucose (91%), and hamnose and arabinose (1.8% each) and its molecular weight was in the range of 1.0×10^4 to 1.5×10^6 Da. The EPS produced from *Lb. fermentum* in low-fat dahi improved the rheological quality by lesser whey separation, higher viscosity, increased adhesiveness, and stickiness (Behare et al. 2013). Similar results were shown that demonstrated that some LAB like *Lb. fermentum* and *Lb. plantarum* isolated from traditional dahi could produce EPS (Patel et al. 2014) that could have beneficial effects when used in dairy products.

The production of free fatty acids (FFAs) and conjugated linoleic acid (CLA) in probiotic dahi containing *Lb. acidophilus* and *Lb. casei* during storage at 4°C for 10 days indicated an increase in butyric acids, linoleic acids, and also CLA content in probiotic dahi (Yadav et al. 2007b).

Immunomodulatory effects of bacteria isolated from dahi have also been reported. In a study conducted by Jain and his colleagues (2009), the ability of dahi containing probiotic *Lb. casei* to modulate immune response against *Salmonella enteritidis* infection in mice was evaluated. They found that the levels of the secretory immunoglobulin A (sIgA) and proliferation of spleen lymphocytes rate were significantly increased. In addition, interleukin (IL) IL-2, IL-6, and IFN- γ

increased, but IL-4 reduced. Mitra et al. (2007) showed that the bacteriocin produced by *Lb. lactis* isolated from homemade dahi had activity against *B. cereus*, *L. monocytogenes*, *C. perfringens*, *E. faecalis*, and *St. aureus*. Similarly, the bacteriocin produced by *Lb. acidophilus* isolated from dahi was investigated by Mahmood et al. (2014). The bacteriocin showed activity against *E. coli*, *S. aureus*, *P. aeruginosa*, and *L. monocytogenes* and had antibacterial activity of 5369.13 AU/mg.

11.4.4 Zabadi

Zabadi is another traditional dairy product recognized as Egyptian yogurt. Zabadi is mostly made from cow milk and is produced at a local level by boiling, then cooling the milk and inoculation with a day-old previous batch of zabadi (serves as starter). Later, the milk is inoculated with starter cultures (*S. thermophilus* and *Lb. bulgaricus*), and incubated at temperature ranging ~30–38 °C for 12–15 h. This product can be consumed as a fresh product or stored in a refrigerator. Zabadi (plain full-fat yogurt) has a smooth consistency and a thin body and is not solid like manufactured yogurt (Eissa et al. 2011). According to reports, increased production of polysaccharides at low-temperature fermentations could contribute to a smoother perceived texture of this traditional yogurt (Driessen 1984).

11.4.4.1 Therapeutic or Probiotic Fermented Milk Product

Food matrices are known to play significant role in the beneficial health effects of probiotic bacteria in the host (do Espírito Santo et al. 2011). Acidophilus milk is one of the well-known probiotic dairy foods that is recognized as a functional food and is made by the addition of *Lb. acidophilus*. Some potential benefits of acidophilus milk were reviewed by Gilliland (1989). These beneficial effects include antibacterial activity against pathogens, cholesterol lowering, and anticarcinogenic activity.

Yeast: Lactic Fermentations

Kefir and koumiss are categorized in this group. Kefir is a fermented drink traditionally made by adding kefir grains to cow or goat milk. These grains with cauliflower like appearance are a mixture of bacteria (*Lb. caucasicus*) and yeasts (*Saccharomyces kefir* and *Torula kefir*). Kefir drink is thought to aid in digestion and calm upset stomachs (Hertzler and Clancy 2003). The role of LAB bacteria in kefir is to ferment lactose to lactic acid and provides the tangy flavor, while the yeasts ferment the available fermentable sugars in milk to yield small amounts of alcohol and CO₂, which gives kefir its fizz and effervescence.

Immunomodulatory properties of some yeasts of the kefir like *Kluyveromyces marxianus* B0399 have also been reported. This yeast has the ability to adhere to Caco-2 cells and cause a reduction in the secretion of IL-10, IL-12, IL-8, and IFN- γ . In addition, *K. marxianus* B0399 caused a reduction in the secretion of proinflammatory cytokines TNF- α , IL-6, and MIP1 α in peripheral blood mononuclear cells stimulated with lipopolysaccharide (Maccaferri et al. 2012). Another yeast

strain that is of probiotic potential is *S. boulardii*. This yeast has been known for its ability to improve diarrhea symptoms caused by *Clostridium difficile* (Bourrie et al. 2016). The antioxidant activity of 28 *Saccharomyces cerevisiae* isolates from kefir has been described by de Lima et al. (2017), and antioxidant activity was higher than 90. In addition, all strains showed intracellular β -galactosidase activity.

Functional properties of kumis were evaluated by several research (Ohashi et al. 2000; Osorio et al. 2011; Chaves-López et al. 2012), but research on probiotic metabolites has been very limited. Furthermore, Chaves-López et al. (2012) isolated ninety-three yeast strains from Colombian Kumis with Angiotensin I-converting enzyme (ACE) inhibitory activity. *Clavispora lusitaniae* KL4A, *Galactomyces geotrichum* KL20B and *Pichia kudriavzevii* KL52 showed the higher level of ACE peptide production while *Torulasporea delbrueckii* KL66A had the lowest.

Mold: Lactic Fermentations Such as Viili

Viili is a traditional fermented milk from Scandinavia, which is produced from LAB and the mold *Geotrichum candidum* (Kahala et al. 2008; Wang et al. 2008). Kahala et al. (2008) isolated *Lc. lactis* subsp. *lactis* biovar *diacetylactis* and *Leu. mesenteroides* subsp. *cremoris* *Lc. lactis* subsp. *cremoris* from Viili.

11.5 Probiotic Non-fermented Milks

There is limited data available regarding probiotic milk from different livestock and most available data is related to cow milk. The angiotensin-converting enzyme inhibitory (ACEI) activity of two peptides of milk containing *Enterococcus faecalis* CECT 5727 named β -casein *f* (133–138) (LHLPLP) and β -casein *f* (58–76) (LVYFPFGPIPNSLPQNIPP) demonstrated (IC₅₀) values as low as 5 mM in rat (Quirós et al. 2007). Although T β -casein *f* (58–76) peptides showed lower antihypertensive activity in spontaneously hypertensive rats compared with LHLPLP. In another research, the impact of unfermented milk containing *Lb. fermentum* MTCC 5898 on immunity system, antioxidant capacity, and severity of pathogenic infection in aging mice was evaluated by Sharma et al. (2014). They found that the activity of some antioxidant enzymes like Catalase and glutathione peroxidase were increased significantly ($P < 0.05$); followed by activity of these enzymes, immune system improved due to enhanced free radical clearance system. While there was no significant difference in IgG2a compared with control group in mice. The pathogen colonization in the intestine, liver, and spleen was also decreased significantly ($P < 0.05$). Balakrishnan and Agrawal (2014) compared the antioxidant activity of fermented cow, goat, and camel milk with *Ped. pentosaceus*. They found that the activity was the highest in goat milk followed by camel and cow milk. In another study, the different function of postbiotics in camel milk and bovine milk probiotic strain *Lc. lactis* KX881782 in vitro was investigated by Ayyash et al. (2018). The fermented camel milk showed grater inhibitions of α -amylase than bovine milk. Whereas, the inhibition of α -glucosidase was not significantly different in both milk. This inhibition resulted in decrease carbohydrate

hydrolysis, so reduces the possibility of sugars being absorbed by the human intestine. Furthermore, the proliferation of Caco-2, MCF-7, and HELA cells were more inhibited by fermented camel milk. In contrast the 1,1-diphenyl-2-picrylhydrazyl (DPPH) antioxidant capacity in camel milk was lower than bovine milk.

Fatty acids particularly conjugated linoleic acid (CLA) is another metabolite of probiotics. The content of CLA in fermented milk containing only *S. thermophilus* and *Lb. bulgaricus* was the highest among 10 commercial fermented cow milk products (Manzo et al. 2015). The fatty acid profiles of fermented cow, goat, and camel milk with *Ped. pentosaceus* indicated that oleic acid was higher in camel milk and also the content of linoleic and linolenic acids was low in all fermented milk (Balakrishnan and Agrawal 2014).

Some strains isolated from raw milk showed antimicrobial activity by producing bacteriocin. *Lb. plantarum* isolated from raw cow's milk samples produced bacteriocin with molecular weight approximately 9.5 kDa and could tolerate high temperature up to 121 °C (Sankar et al. 2012). Another strains of lactobacillus, *Lb. sakei* GM3 isolated from goat milk produced bacteriocin which had antimicrobial activity against *C. albicans*, *C. tropicalis*, *S. aureus*, *P. aeruginosa*, *S. enterica*, and *L. monocytogenes* (Avaiyarasi et al. 2016). The Molecular weight of this bacteriocin was 4.811 kDa and could withstand heat treating at 100 °C for 20 min. Furthermore, bacteriocin produced from various lactobacillus strains which isolated from raw cow, buffalo, and goat milk showed activity against some mastitis pathogens such as *S. aureus*, *E. coli*, *Y. enterocolitica*, *S. uberis*, and *S. xylosus* (Eid et al. 2016).

11.6 Probiotic Cheeses

Cheeses can be divided into different groups like very hard and hard (≤ 38 g 100 g⁻¹ moisture), semi-hard (averages ~ 40 g 100 g⁻¹ moisture), Brined cheeses (50–55 g 100 g⁻¹ moisture), soft cheeses, and other kinds of cheese (Tamime and Thomas 2018). However, we categorize different cheeses based on the metabolite produced by the probiotic bacteria.

Cottage cheeses prepared with *Lb. casei*, *Lb. rhamnosus* GG and Himalayan cheese (Kalari) prepared by different probiotic strains (*Lb. casei*, *Lb. plantarum*, and *Lb. brevis*) showed higher antioxidant activity due to higher concentration of bioactive peptides (Abadía-García et al. 2013; Mushtaq et al. 2016). This may be related to the proteolysis occurred by these bacteria. Additionally, probiotic Minas Frescal cheese added with *Lb. casei* 01 showed higher ACEI (antioxidant and angiotensin I-converting enzyme inhibitory) activity compared to conventional cheese (Sperry et al. 2018).

ACEI peptides that are produced by a number of probiotic bacteria in many fermented dairy products have antihypertensive properties. Also adding probiotic bacteria like *Lb. casei* and *Lb. plantarum* to Cheddar cheese showed higher DPPH (2,2-diphenyl-picrylhydrazyl) and antioxidant activity during the ripening time at 16th weeks compared to the control samples (Chen et al. 2019). The DPPH reached

its maximum at 16th weeks while other properties of probiotic cheese like texture and sensory analysis was not affected by probiotics.

The EPS-producing probiotic *Lb. plantarum* used in low-fat akawi cheese showed higher antioxidant activities and angiotensin-converting enzyme (ACE) inhibition in comparison with cheese made with non-EPS producers (Ayyash et al. 2012). In addition, the antioxidant activity increased when the storage time was prolonged. Donkor et al. (2012) also showed that inhibition of α -amylase in cheese with EPS-producing culture was higher, while the α -glucosidase inhibition was not significantly increased. The inhibition of α -amylase and α -glucosidase resulted in controlling diabetes and reducing carbohydrate hydrolase. This inhibition might be due to the presence of bioactive peptides.

In another study, it was shown that the content of free fatty acids (FFA) increased in cheeses inoculated either with *Lb. casei* and *B. lactis* at 60 days of ripening (Rodrigues et al. 2012). In addition, three conjugated linoleic acids (CLA) isomers (i.e., *cis*-9, *trans*-11-C18:2, CLA1; *trans*-10, *cis*-12-C18:2, CLA2; *trans*-9, *trans*-12-C18:2, CLA3), α -linolenic acid (ALA) and γ -linolenic acid (GLA) were increased during ripening in 15 days that raised up to 60 days. The content of CLA (*cis*-9, *trans*-11-octadecadienoic acid) from different probiotic white cheese showed that *B. longum* cheese and *E. faecium* cheese had the highest and lowest CLA, respectively (Gursoy et al. 2012). Moreover, linoleic acid has been shown to increase in cheese samples prepared with *Lb. paracasei* and *Lb. acidophilus*. Besides, reports showed that addition of *Lb. casei* 01 to Minas Frescal cheeses showed higher level of medium- and long-chain fatty acids (Sperry et al. 2018). In addition, monounsaturated fatty acid such as oleic acid was higher than conventional cheese.

Nine strains of *E. faecium* isolated from Tafi Cheese (a homemade traditional cheese from Tucuman, Argentina) showed cholesterol reduction in vitro (Saavedra et al. 2003). All these strains had bile salts hydrolase activity (BSH), while some strains with negative BSH activity could not reduce cholesterol levels. Similar to these studies, it was shown that *Lb. plantarum* and *Lb. paracasei* isolated from Italian Castelmagno PDO cheese could reduce cholesterol levels in vitro (Belviso et al. 2009). While some research also showed in vivo cholesterol lowering effects of the cheese that harbored probiotic bacteria. The fresh Brazilian cheese containing *Lb. acidophilus* LA14 and *B. longum* BL05 fed for 2 weeks to rats, probiotic cheddar cheese with *L. plantarum* K25 in mice for 4 weeks could decrease total cholesterol and LDL cholesterol, while HDL cholesterol increased compared to control groups (Lollo et al. 2012; Zhang et al. 2013; Lollo et al. 2015).

The effect of probiotic Minas Frescal cheese on hypertension parameters in spontaneously hypertensive rats indicated that the systolic, diastolic, and mean blood pressure over 15 days decreased significantly ($P < 0.05$) compared to the control groups (Lollo et al. 2015). In addition, cheese containing LGG and *Lb. rhamnosus* LC 705 could reduce salivary microbial counts in young adults (Ahola et al. 2002). The subjects ate 5×15 g cheese per day for 3 weeks and the result showed that *S. mutans* and yeast counts decreased in 20% and 27%, respectively, in all the subjects.

The bacteriocinogenic *Lb. paraplantarum* FT259 isolated from Brazilian semi-hard Minas cheese was evaluated by Tulini et al. (2013). This bacterium produced bacteriocin against *L. monocytogenes*, *L. innocua*, and *L. sakei*, while no activity against Gram-negative bacteria was reported. Furthermore, *E. faecium* AQ71 isolated from Azerbaijani Motal cheese produced bacteriocin named enterocins P which had activity against *L. monocytogenes* and *B. cereus* (Ahmadova et al. 2013).

In another study, the inhibitory effects of the probiotics *Lb. acidophilus*, *Lb. casei* subsp. *paracasei*, and *B. lactis* in a Brazilian semi-hard goat cheese (coalho) was reported, during storage time (de Oliveira et al. 2014). The *Lb. casei* subsp. *paracasei* showed the highest inhibitory activity against *L. monocytogenes* and *S. aureus* on the 14th and 21st days of storage, respectively. While, *B. lactis* had activity against *S. aureus* on the 1st (16.32%), 14th (10.12%), and 21st (3.67%) days of storage, and only on 1st day of storage they had activity against *L. monocytogenes*. *Lb. plantarum* isolated from Traditional Iranian Cheese (Kouzeh) showed high activity against *S. aureus* and *S. epidermidis* (Jabbari et al. 2017). Furthermore, *Kluyveromyces marxianus* S-2-05 and *Kluyveromyces lactis* S-3-05 isolated from a traditional French cheese had inhibitory activity against *Salmonella typhimurium*, *Salmonella enteritidis*, and *Salmonella paratyphi* B (Ceugniesz et al. 2017).

The availability of some minerals is significantly affected by probiotic bacteria in the different cheeses. As demonstrated by Aljewicz and Cichosz (2015), addition of *Lb. rhamnosus* increased in calcium availability in Dutch-type cheese. However, the availability of magnesium and phosphorus decreased in Swiss Dutch-type cheese after 6 weeks of ripening, respectively. In addition, the zinc availability Dutch-type cheese was increased and the availability of potassium lowered in Swiss-type cheese.

11.7 Probiotic Ice Cream

Probiotic ice cream containing 1×10^6 CFU of bacterial strains *B. lactis* Bb-12 and *Lb. acidophilus* La-5 per gram could reduce levels of salivary *S. mutans* in school children after 10 days (Singh et al. 2011). In addition, the goat's milk ice cream with *B. animalis* subsp. *Lactis* showed good sensory characteristics, while other physico-chemical properties such as overrun and melting behavior were not affected by adding probiotic (Da Silva et al. 2015).

11.8 Dried Probiotic Dairy Products

Drying milk is one of the ways to extend the shelf life and decrease the loss of milk in long chain between farmer and consumer. Dried products include milk powder, whey powder, whey protein concentrate, yogurt powder, and infant formula. The methods of drying can be divided into two groups, thermal and non-thermal (Aadinath et al. 2017). In dried probiotic dairy product, some factors play essential role for maintaining the viability of probiotic microorganisms, such as the methods of drying, the type and size of packaging used, condition of storage like temperature

and humidity, quality of powder, the process of rehydration and handling of rehydration product, etc. (Gilliland 2001). One of the most widely used dried dairy products of this group is infant formula which is described below.

11.8.1 Infant Formula

The effect of probiotic supplemented infant formula on plasma lipid of infant was described by Kankaanpää et al. (2002). The *Bifidobacterium* Bb-12 supplemented formula could increase the α -linolenic acid in phospholipids, while the *Lb.* GG had no effect on this fatty acid. In addition, both probiotics were able to increase the percentage of the total monounsaturated fatty acids (MUFA).

Saavedra et al. (2004) showed that probiotic supplemented formula could lower the frequency of reported colic or irritability. According to their results, consumption of formulas containing *B. lactis* and *S. thermophiles* for long time resulted in reduction of colic, irritability and reduced the frequent use of antibiotics. Similar to these findings, it was reported that *B. lactis* (BB-12) and *Lb. reuteri* in infant formula could reduce infections in healthy 4- to 10-month-old infants after 4 weeks (Weizman et al. 2005). The control group had more diarrheas with longer duration, whereas *Lb. reuteri* group, compared to BB-12, had fewer days of diarrhea and lower visits to the clinic or child care unit. In addition, the effect of supplemented formula with *Lb.johnsonii* La1 on fecal microbiota composition of infants was evaluated by Brunser et al. (2006). Ninety infants close to 4 months of age were divided into various groups and received probiotic supplemented infant formula for 13 weeks. The results showed that the fecal *Lactobacillus* count was higher than controls, while the count of *Clostridium*, *Bacteroides*, or *Enterococcus* were not significantly difference between the groups.

The safety of a prebiotic-containing starter formula supplemented with *Lb. paracasei* ssp. *paracasei* and *B. animalis* ssp. *lactis* for first 3 month in 126 newborns and then continued in 80 infants for 6 month was evaluated by Vlieger et al. (2009). The growth, clinical outcomes like crying and sleeping hours, number of gastrointestinal or upper respiratory tract infections, the amount of antibiotics used and visits to the general practitioner were not significantly difference compared to the control group.

11.8.2 Dairy-Based Dried Products

The traditional dairy-based dried products like Kashk, Tarhana, and Kurut are produced for many centuries. The most data about these kinds of products were related to isolation lactic acid bacteria, while the probiotic characteristics were not assessed. In addition, some nutrition value of these products was evaluated by researcher. The Kashk is produced under various names in different countries, Kishk (Lebanon, Syria), Zhum (Yemen), Kushuk (Iraq) (Tamime and O'connor 1995). These traditional dairy-based products are a good source of endogenous

probiotics. The dried Kashk has been produced in a wide geographical region especially in rural parts of Iran for many years. Dried Kashk is produced from cow's and/or sheep's milk which is boiled and then cooled and inoculated with traditional yogurt made earlier as starter culture. The butter is isolated from sour yogurt and the remaining sour buttermilk is boiled followed by sieving by cloth bag. Finally, the thick whitish semi-solid part of buttermilk, which is sieved, is shaped in the form of conic or cubic balls and then sun-dried for 3–4 days (Iranmanesh et al. 2018). Ebrahimi et al. (2011) isolated *Lb. agilis* from Kashk which had the ability to assimilate cholesterol *in vitro* conditions. The Kishk samples containing *Lb. casei* (10^8 – 10^9 CFU mL⁻¹) showed antimicrobial activity against *E.coli* O157:H7 and reduced its count during storage at 4 °C after 20 days (Sadrizadeh et al. 2018).

Tarhana is another traditional fermented cereal dairy product produced in Turkey. It is made from cereal flours, yogurt, and different vegetables, and after fermentation it is sun dried and used as soap (Ozdemir et al. 2007). Sengun et al. (2009) isolated various LAB from Tarhana such as *S. thermophilus*, *L. fermentum*, *E. faecium*, *Ped. pentosaceus*, *Leu. pseudomesenteroides*, *Weissella cibaria*, *Lb. plantarum*, *Lb. delbrueckii* spp. *bulgaricus*, *Leu. citreum*, *Lb. paraplantarum*, and *Lb. casei*.

Kurut is traditional foods of Tibetan people. Kurut is prepared by natural fermentation of yak milk in a custom-made specially treated Tung made big jar, at ambient temperatures for 7–8 days. Kurut like kefir and koumiss have both alcohol and lactic acid. Kurut is almost known to all regions of Qinghai (Zhang et al. 2008). Sun et al. (2010) isolated *Lb. helveticus*, *Lb. suntoryeus*, *Lb. fermentum*, *Lb. plantarum*, and *Lb. delbrueckii* subsp. *bulgaricus* from Kurut. Furthermore, other cocci isolates were identified as *Lc. lactis* subsp. *lactis*, *Lc. lactis* subsp. *cremoris*, *Leu. lactis*, *Leu. mesenteroides* subsp. *mesenteroides*, and *S. thermophiles*. Luo et al. (2011) showed that some LAB strains isolated from Kurut had antimicrobial activity. Among the isolates, *Lb. casei*, *Lc. lactis* and *Leu lactis*, possessed bacteriocin-producing ability that could inhibit both *S. aureus* and *E. aerogenes*. The probiotic *Lb. helveticus* H9 isolated from Kurut was shown to produce antihypertensive peptides during milk fermentation (Chen et al. 2015).

11.9 Conclusions

It is evident that in last decades probiotic bacteria have been used in various dairy products due to their valuable health effects. Not only can probiotic be added to dairy products, but some traditional dairy products already are enriched with abundant of LAB species which show significant probiotic potential. These probiotic bacteria are able to add nutritious values to the milk and their products, as well as producing a number of metabolic products during fermentation they show therapeutic properties. Probiotic bacteria and their postbiotics (secretory metabolic compounds) can affect the quality of the dairy products by showing health benefits and might also improve the flavor, texture, and other sensory properties of the product. Furthermore, probiotic strains reveal other properties such as cholesterol lowering and immunomodulatory properties, anticancer and antioxidant activity. Besides, the consumption of

fermented dairy products can simulate the immunity system. Further research studies are required that investigate the role of probiotic metabolite in some dairy products especially traditional dairy products that have intrinsic probiotic microbes. Consequently, these studies could lead to development of more nutritious and safe foods with proven therapeutic potential.

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Encountering the Antibiotic Resistance by Bioactive Components and Therapies: Probiotics, Phytochemicals and Phages 12

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Abstract

Improper antimicrobial practices expedite the evolution of antibiotic-resistant and super-drug-resistant bacteria, and result in varied and elevated antibiotic resistance throughout the world. The dominant problem with antibiotic therapy is the antibiotic resistance acquisition in bacteria. Therefore, it is important to use non-antibiotic agents which could prevent the microbial propagation and control their virulence. The agents like probiotics, phytochemicals and bacteriophages have been found to tackle drug-resistant bacteria. The application of probiotics in medicines, agriculture and food industry is becoming influential to contain drug-resistant and virulent bacteria. The probiotic bacteria (Lactobacilli, Bifidobacteria, etc.) directly and indirectly by their products (bacteriocins, organic acids, short-chain fatty acids, polysaccharides, etc.) can counter or evade the entero-virulent, pathogenic and drug-resistant bacteria such as *Salmonella typhi*, *Clostridium difficile*, MRSA, Carbapenem-resistant representatives of enterobacteriaceae, *H. pylori*, *E. coli* O157:H7, etc. Intestinal probiotic bacteria (Lactobacilli) can also help to reduce diarrhoea, post-antibiotic therapy complications and inflammatory bowel disease. Phytochemicals offer strong antimicrobial action against virulent and resistant bacteria. These substances unaccompanied or accompanied with antibiotics can enhance antibacterial effect. Several plant procured compounds (Alkaloids, Phenolics, Coumarins, Terpenes

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283

and Sulphur-compounds) have been observed to carry antimicrobial effects with a vast variety of mechanisms. Bacteriophages and the related enzymes (endolysins and virion-associated peptidoglycan hydrolases) having antimicrobial effect are also considered as therapeutic candidates to encounter drug-resistant bugs. Based on the literature review, probiotics, plant procured compounds and phages in solo or in combo with antibiotics can be the favourable and valuable therapeutic options.

Keywords

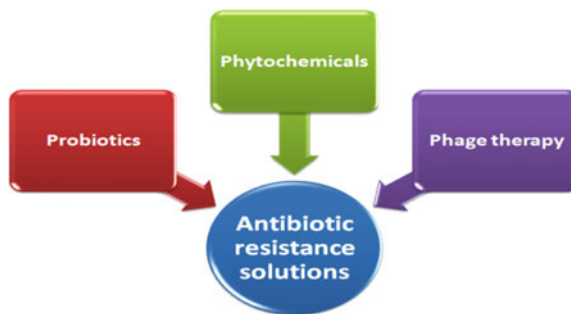
Antibiotics · Drug resistance · Probiotics · Bacteriophages · Phytochemicals

12.1 Introduction

Extraordinary expansion in the occurrence and predominance of antibiotic resistance has been witnessed after the administration and extensive application of antibiotics. This resistance is considered to have prevailed much before antibiotic consumption by humans (Broaders et al. 2013; Rasool et al. 2019a). Several ecological interaction-based studies have proved that microorganisms produce antimicrobials in microbial communities to ensure their survival (Samuels et al. 2013; Cawoy et al. 2014; Téllez et al. 2015). During natural selection events, the microbes which are able to accommodate and withstand antimicrobial stress can produce resistant microbial populations; therefore, antibiotic resistance is recognized as an innate aspect (Sherpa et al. 2015; Imperial and Ibana 2016; Rasool et al. 2019b). After knowing the antibiosis phenomena, antimicrobials were welcomed in chemotherapy of infectious diseases (Scanlon et al. 2014; Sherpa et al. 2015). Moreover, antibiotics are employed in agriculture and livestock (animals) for the enhancement of their yield and growth ratio, and treatment of animals' infections (Allen and Stanton 2014; Xiao et al. 2015). Nevertheless, unchecked and unrestrained antimicrobial practices accelerate the evolution of resistant and super-resistant bugs and lead to varied and heightened antibiotic resistance resulted in response to discriminative antibiotic stress on microbes (Rosander et al. 2008; Verraes et al. 2013; Hu et al. 2014; Card et al. 2015). The ratio of emerging resistant bugs is more rapid than the revelation of novel antibiotics (Sherpa et al. 2015). There are about 23,317 genes responsible for targeting 249 antibiotics (Hu et al. 2013). The microbial ecology considerably influences the existence of antibiotic resistance genes (Gibson et al. 2015). Further, vertical transmission of resistance genes through mobile genetic elements (MGEs) supports the prosperity of resistant microorganisms in the presence of antibiotics (Penders et al. 2013; Fouhy et al. 2014). Antibiotic resistance genes (with the help of plasmids) can travel between virulent and normal bacterial flora of humans (Broaders et al. 2013; Imperial and Ibana 2016).

The major issue of antibiotic therapy is the development and acquisition of antibiotic resistance in bacteria through various systems; drug inactivation, antibiotic target alteration, advancement of outer membrane permeability and efflux pumps,

Fig. 12.1 Possible solutions for antibiotic resistance



circumvention of biochemical pathways, mutagenesis and horizontal gene transmission (Walsh 2000; Wright 2005; Naderi et al. 2014). Since, it is almost impossible to revert the resistance phenomena, the prevention of pathogenic microbial propagation, microbial killing, and subverting their virulence factors may be targeted by non-antibiotic agents; probiotics, phytochemicals and bacteriophages (Fig. 12.1). Due to growing antibiotic resistance dilemma, there is an urgent demand to recognize the performance of probiotics and normal microbiota or commensal microorganisms in subverting antimicrobial resistance and virulence (Liévin-Le Moal and Servin 2014).

12.2 The Probiotics: Significance in Agriculture and Human Health

Apart from antibiotic resistance issue, symbiotic tie up of microorganisms with gastrointestinal tract (GIT) of livestock animals facilitates fermentation. Fermentation of complicated polysaccharides by GIT normal microbial flora provides 70% energy required by farm animals and about 30% energy for monogastric herbivores (Téllez et al. 2015). Several researches have indicated that probiotics can be the alternatives of antibiotics in growth enhancement and restricting diseases in farm animals (Muñoz-Atienza et al. 2013; Téllez et al. 2015). The probiotics prevent turkeys and chickens from infections of *Salmonella* spp. by colonizing GIT as normal microflora. Moreover, probiotics can lower the severity of diarrhoea of unknown cause in turkeys. Extensive trials of suitable probiotics use in turkeys and chickens witnessed the decrease in complete production cost and boosted the performance. Livestock animals excrete *Escherichia coli* O157:H7 in their faeces which can be transmitted to humans (and produce bloody diarrhoea). The use of various bacterial probiotic blends can diminish the faecal discharge of *Escherichia coli* O157:H7 by sheep and cattle, and hence can reduce the chances of human infection (Téllez et al. 2015). Antimicrobial action of probiotics has also been determined against fish pathogenic Gram positive and Gram negative bacteria (Muñoz-Atienza et al. 2013).

Probiotics are prominent for the improvement of human health in general. Probiotic bacteria are being incorporated in several commercial foods to maintain GIT microbial flora (Songisepp et al. 2012). They are involved in various important functions like controlling lipid storage, inflammatory bowel disease (IBD), GIT epithelial growth, and inflammatory reactions (Collins and Gibson 1999; Ventura et al. 2009). Probiotics are medically verified to adjust baby's GIT normal flora upset after antibiotic therapy (Collado et al. 2012). Antibiotic treatment is harmful for gut normal flora of neonates resulting in killing the gut flora leading to diarrhoea (Varankovich et al. 2015). The application of probiotics before and after birth of baby has been found to avoid the onset of hypersensitivities (e.g. asthma) and GIT infections (Luoto et al. 2010). In adults, regular oral probiotics consumption has shown to cure intermittent diarrhoea inflicted by *Clostridium difficile* which is offered by post extended antibiotic therapy. Such antibiotic treatment approach kills GIT normal flora, which can enhance the *Clostridium difficile* growth (Ursell et al. 2013; Varankovich et al. 2015).

The application of probiotics in medicines and agriculture is becoming common since the evolution of drug-resistant microbial strains (Muñoz-Atienza et al. 2013; D'Orazio et al. 2015; Téllez et al. 2015; Varankovich et al. 2015). Reducing the antibiotics usage and employment of probiotics instead of antibiotics may assist in lowering the proportion of flourishing resistant microbial strains (Muñoz-Atienza et al. 2013; Varankovich et al. 2015). Probiotics application is the adoption of active advantageous microorganisms to get required consequences, for example, inhibiting ailments and promoting health in living beings (Collins and Gibson 1999). Prior to employment of probiotics, it is necessary to check probiotics for the presence of antibiotic resistance genes (Sanders et al. 2010). An important step in screening of antibiotic resistance is to differentiate between acquired or transmissible resistance and inherent resistance of probiotic bacteria (Chang et al. 2009; Hammad and Shimamoto 2010).

12.3 Probiotic Bacteria, Their Anti-Pathogen Products and Potentials

Probiotic bacteria are well established because they can control pathogens by producing organic acids and lowering the clustering and production of adhesins. Further, they are normal microbial flora of humans and animals and produce bacteriocins (Reid 1999; Ennahar et al. 2000; McAuliffe et al. 2001; Anas et al. 2008). They promote gut microbial habitat by attachment with mucous of intestine, and therefore prohibit the adherence of pathogenic microorganisms and also challenge pathogens for nutrient acquisition and provoke immunity in intestine. They are hostile to a wide variety of urinary and GI tract associated pathogenic bacteria (Gilliland and Walker 1990; Hutt et al. 2006). Interestingly, repression of virulence factor genes in *E. coli* O157:H7 is carried out by biologically active compounds released by probiotic bacteria. Probiotics may also reduce the attachment of *E. coli* O127:H6 and *E. coli* O157:H7 to the epithelial cells. Cell-free supernatants of

B. longum, *L. plantarum*, *L. rhamnosus* and *L. helveticus* were observed to possess anti-biofilm effect against MDR-*E. coli* (Abdelhamid et al. 2018).

The most familiar probiotics reside in the lactic acid bacteria (LAB) group, which involves various species of Lactobacilli and Enterococci (Tompkins et al. 2008; Chang et al. 2009; Nueno-Palop and Narbad 2011; Songisepp et al. 2012; Gueimonde et al. 2013; Devi et al. 2015; Senan et al. 2015). In addition to other health benefits in animals and humans, lactobacilli can destroy *Helicobacter pylori* (responsible for peptic ulcer, gastric cancer and gastritis) (Télez et al. 2015; Varankovich et al. 2015). Enterococci as probiotic quickly heal diarrhoea (Vankerckhoven et al. 2008; Varankovich et al. 2015). According to studies, a few lactic acid bacterial species have inherent resistance to beta-lactams, teicoplanin, bacitracin, vancomycin and kanamycin. Such resistance is advantageous when combine therapy (probiotic with antibiotic) is required (Hammad and Shimamoto 2010; Varankovich et al. 2015).

The dominant probiotic, bifidobacteria are crucial component of the human and animal GIT normal microbial flora. They are capable of preventing the attachment of *C. difficile*, enterotoxigenic and enteropathogenic *E. coli* with the cells of gut epithelia. A combo of bifidobacteria and lactobacilli is responsible to reduce the adverse effects of anti-*H. pylori* therapy. Furthermore, some strains of bifidobacteria down-regulate the genes in human epithelia, inflicted by *H. pylori*, and mitigate inflammatory bowel disease (IBD) and diarrhoea (Varankovich et al. 2015). The other frequently employed probiotics in medicines, agriculture and food involve Streptococcus, Lactobacillus, Bacillus, Lactococcus, Enterococcus, Bifidobacterium, Pseudomonas, Pediococcus, Bacteroides, Trichoderma, yeast and Aspergillus, etc. Many food supplements have Lactobacillus (*L. rhamnosus*, *L. acidophilus*, *L. plantarum*, *L. farciminis*, *L. casei*), Bacillus (*B. subtilis*, *B. licheniformis*, *B. cereus var. toyoi*), *Escherichia coli* Nissle 1917, Enterococcus (*E. faecium*), Streptococcus (*S. infantarius*), Pediococcus (*P. acidilactici*) and a few fungi like *Kluyveromyces*, *Saccharomyces cerevisiae* and *Saccharomyces boulardii* (Anadon et al. 2005; Cheng et al. 2014).

Important characteristics: avirulent, acid and bile stable, adherence and propagation in GIT, antimicrobial activity and production of valuable metabolites are needed to be a good probiotic (Fijan 2016). Many research trials have shown antibacterial potential of various probiotic strains against virulent and drug-resistant strains of *P. aeruginosa*, *K. pneumoniae*, *E. coli*, *Salmonella* spp., *E. fecalis* and *S. aureus* and also have antifungal action on *C. albicans* (Manzoor et al. 2016; Prabhurajeshwar and Chandrakanth 2017). Both in vivo and in vitro *L. acidophilus* (isolate of human stool) was found antagonistic against *H. pylori* (Coconnier et al. 1998). While human milk-isolated lactobacilli displayed antibacterial action over *S. typhi*, *S. flexneri*, *B. cereus* and *P. aeruginosa*, the lactobacilli of neonatal stool origin are antagonistic for enterotoxigenic *E. coli* (ETEC) (Tsai et al. 2008; Sharma et al. 2017). Moreover, antiparasitic action of *L. acidophilus* was also witnessed against *Trichomonas vaginalis* (Valadkhani et al. 2016). The vaginal lactobacilli are effective against anaerobic Gram negatives (*Mobiluncus* spp., *Prevotella bivia* and *Gardnerella vaginalis*), and Herpes Simplex Virus (HSV-2). Antimicrobial effect

of probiotics is peculiar to the pathogenic strains (Matu et al. 2010; Ranjbar et al. 2015; Saud et al. 2020).

12.4 Bacteriocins

The production of bacteriocins by Gram positive probiotic bacteria (normal intestinal inhabitants) has killing and suppression effect on very similar relevant bacteria (Dobson et al. 2012; O'Shea et al. 2012; Cotter et al. 2013). Many bacteriocins target cell wall of the bacteria and some can alter gene expression (McAuliffe et al. 2001). Another conventional mode of action of bacteriocin is the formation of pores and channels in bacterial cell membrane which results in outflow of cellular contents. Additionally, normal *E. coli* (normal inhabitant of intestine) also yield plasmid-borne bacteriocins, specifically of low molecular mass (microcins) (Gordon and O'Brien 2006; Duquesne et al. 2007; O'Shea et al. 2012) and of greater size (colicins) (Cascales et al. 2007). Microcins upset various essential mechanisms in the focused bacterial cell like activity of DNA gyrase and ATP synthase. Colicins kill bacteria by forming pore, prohibiting the activity of nucleases and murein biosynthesis. In LAB, formation of bacteriocins is regulated by quorum sensing (QS) mechanism which is controlled by quorum sensing molecules or pheromones (bacteriocin like peptide) (Eijsink et al. 2002; Risoen et al. 2000; Sturme et al. 2007). These quorum sensing molecules get stimulated during infection (Moslehi-Jenabian et al. 2011). Numerous clinical studies express metabolites based antimicrobial activities of Lactobacillus that could serve as a substitute to antibiotics (Liévin-Le Moal and Servin 2014). Assorted bacteriocins are being applied as preservatives in foodstuff to prevent the growth of food-related pathogenic bacteria (Dobson et al. 2012; Cotter et al. 2013). Usually, it is considered that bacteriocins of lactobacilli origin are less effective against Gram negative bacteria, but it has been noticed that various bacteriocin-mimicking molecules and bacteriocins have hostile effect on entero-virulent Gram negatives (Campylobacter, EHEC, Salmonella, *H. pylori* and Shigella) (Zamfir et al. 1999; Kim et al. 2003; Han et al. 2007; Pascual et al. 2008; Messaoudi et al. 2012). Anti-*H. pylori* bacteriocins have been recognized in *L. casei* Shirota and *L. johnsonii* NCC 533 (Morency et al. 2001; Kim et al. 2003; Ryan et al. 2009; Simova et al. 2009).

12.5 Probiotics Potential Against Drug Resistance

Multidrug-resistant (MDR) bacteria are responsible for diverse global health dilemma. Oral introduction of lactobacilli can prevent many MDR-bacterial infections by producing hydrogen peroxide, lactic acid and other metabolites which discourage growth of pathogens (Jamalifar et al. 2011). Several prebiotics (products of probiotics) consist of polysols, polysaccharides, oligosaccharides [(mannanoligosaccharide (MOS), fructooligosaccharide (FOS)], hydrolysates of proteins, etc. Prebiotics can discriminatively propagate gut bacterial flora, improve

immunity and offer antiviral activity. On the other hand, synbiotics, combination of pre- and probiotics, can improve immunity and decrease diarrhoea-related illness and fatality in piglets (Andersson et al. 2001; Gaggia et al. 2010).

Currently, carbapenem-resistant Enterobacteriaceae (CRE) is an important threat associated with illness and deaths because of the availability of narrow treatment options (Rodriguez-Bano et al. 2018; Chi-Chung Chen et al. 2019). Lactobacilli synthesize lactic acid, formic acid, acetic acid, etc. to lower the pH of intestine which results in antimicrobial effect. Various antimicrobials of lactobacilli like bacteriocins, fatty acids, ethanol and hydrogen peroxide employ antimicrobial action (Inglin et al. 2015). Such antimicrobials are accountable for the inhibition of pathogens, *P. aeruginosa*, *S. aureus*, *Streptococcus mutans*, *E. coli*, *Shigella* spp., and *C. difficile* (Jamalifar et al. 2011; McFarland 2015; Kumar et al. 2016; Kang et al. 2017; Ahn et al. 2018). Another notorious pathogen methicillin-resistant *Staphylococcus aureus* (MRSA) causes high mortality and morbidity and has few therapeutic options (Drew 2007; Raygada and Levine 2009). Specific probiotic therapy can solve this multidrug resistance problem (Tagg and Dierksen 2003; Roghmann and McGrail 2006). Many LAB on the basis of their antimicrobial metabolites can stop the growth of antibiotic-resistant bacteria (Petrova et al. 2009). Much pronounced antimicrobial activity was observed when cell lysate and entire broth of 3 LAB mix (1:1:1 ratio) was employed. This assay displayed 85% suppression of MDR-*S. aureus* (Bhola and Bhadekar 2019).

Propionibacterium is mostly recruited from farm cattle milk and the products obtained from milk (Rossi and Dellaglio 2007; Quigley et al. 2013). They are immobile, Gram positive probiotic bacteria which yield short-chain fatty acids and more metabolic products in gut (Huang and Adams 2004). *Propionibacterium freudenreichii* is popular as probiotic, in food and dairy industry and for the production of cheese and vitamins (Falentin et al. 2010; Thierry et al. 2011; Cousin et al. 2012; Ganan et al. 2013; Yuksekdogan et al. 2014; Rabah et al. 2017). They are categorized in Qualified Presumption of Safety (QPS) and Generally Recognized as Safe (GRAS) for the application in food products (EFSA 2013; FDA 2014). Anti-virulence activity of *P. freudenreichii* subsp. *shermanii* (PS) and *P. freudenreichii* subsp. *freudenreichii* (PF) has been noted against multi-drug-resistant (MDR) *Salmonella* (Nair and Kollanoor-Johny 2017). Dairy recruited *L. helveticus* R0052 and *L. rhamnosus* R0011 have been proved to harbour activities against MDR bacterial infections clinically (Hagen et al. 2010; Foster et al. 2011; Tompkins et al. 2012; Nair and Kollanoor-Johny 2018).

12.6 The Antimicrobial Role of Gut-Related Microbiota or Probiotics

The probiotic bacteria in gut produce metabolites of low molecular mass which move towards systemic circulation and heal diseases. These metabolites establish metabolome which include polyamines and short-chain fatty acids (Matsumoto et al. 2012). It is important to note that antibiotic therapy leads to changes in the content of

intestinal microbiota or probiotics which influence the intestinal metabolome and homeostasis (Antunes et al. 2011). The probiotics also cooperate in the anatomical and functional development of epithelial cell linings, hence improving immunity of the intestine (Kamada and Nunez 2013). Several gut probiotics or microflora prohibit the encroachment and virulence factors mediated damaging responses of pathogens by offering challenge for nutrient acquisition, enhancing gut immunity, release of organic acids and antimicrobial chemicals (Brown et al. 2013; Buffie and Pamer 2013). Moreover, they regulate and activate receptors on innate immune cells (Kinnebrew and Pamer 2012).

12.7 Human Intestinal Lactobacillus Strains

In many clinical analyses, lactobacilli as probiotics have been found effective against rotaviruses and gastroentero-virulent pathogens. The antibacterial action is based on metabolites: non-bacteriocin components (proteolytic enzymes), lactic acid and non-protein molecules. These antibacterial components directly kill bacteria, repress virulence genes and minimize detrimental response of virulence factors on intestinal cells (Kleerebezem et al. 2010; Lebeer et al. 2010; Bron et al. 2012; Dobson et al. 2012; Cotter et al. 2013; van Baarlen et al. 2013). Probiotic-stimulated immunomodulatory activities have been noticed in in vitro studies (Sanchez et al. 2008; Sanchez et al. 2010). Six strains of lactobacilli in randomized controlled trials (RCTs) proved to have antirotaviral and antimicrobial activities. These include *L. casei* strain Shirota YIT9029, *L. casei* DN-114 001, *L. acidophilus* strain LB (rearranged as *L. fermentum* LB-f), *L. jhonsonii* NCC 533, *L. rhamnosus* GG (ATCC 53103) and *L. reuteri* DSM17938 (Rosander et al. 2008; Liévin-Le Moal and Servin 2014).

Killing effect on entero-virulent bacteria (Gram negative and Gram positive) of lactobacilli cultures directly has been investigated. But in a few studies cell free spent culture supernatants (CFCs) explored for bactericidal response. It is noteworthy that bactericidal response causes >3-log decline of living bacterial cell number after incubating the target bacterial culture for specified time and under controlled conditions. A fall in *Shigella* growth till 4-log CFU/mL was noticed that was caused by 4 h exposure of *L. reuteri* ATCC 55730, *L. jhonsonii* NCC 533, *L. acidophilus* LB and *L. rhamnosus* GG (Bernet-Camard et al. 1997; Hutt et al. 2006; Spinler et al. 2008; Zhang et al. 2011). Similar findings can be seen for other entero-virulent bacteria (Table 12.1).

L. reuteri ATCC 55730 behaves unfriendly with *Vibrio cholerae*. It is necessary to treat entero-virulent bacteria before their entrance in gut cells. Gut concerned antibiotic treatment often failed by entero-invasive bacteria because of their internalization by host gut cells in a vacuole. Interestingly, metabolites of *L. acidophilus* LB can efficiently kill *S. Typhimurium* nested in intracellular vesicle of enterocyte Caco-2/TC7 (Coconnier et al. 2000). Destructive effect of *L. acidophilus* LB, *L. jhonsonii* NCC 533, *L. casei* DN-114 001, *L. casei* Shirota, and *L. rhamnosus* GG on entero-virulent bacteria is due to the presence of their metabolites or

Table 12.1 Decline in growth (log CFU/mL) of entero-virulent bacteria in 4 h after direct exposure to various lactobacilli strains

Targeted entero-pathogens	Direct exposure of lactobacilli strains	Decline in log CFU/mL	References
Entero-virulent <i>E. coli</i>	<i>L. acidophilus</i> LB <i>L. casei</i> Shirota <i>L. rhamnosus</i> GG <i>L. reuteri</i> ATCC 55730	3–4	Ogawa et al. (2001), Spinler et al. (2008), Zhang et al. (2011), Liévin-Le Moal and Servin (2014)
Listeria	<i>L. johnsonii</i> NCC 533, <i>L. acidophilus</i> LB	3–4	Bernet-Camard et al. (1997), Liévin-Le Moal and Servin (2014)
Shigella	<i>L. reuteri</i> ATCC 55730, <i>L. johnsonii</i> NCC 533 <i>L. acidophilus</i> LB <i>L. rhamnosus</i> GG	4	Bernet-Camard et al. (1997), Spinler et al. (2008), Liévin-Le Moal and Servin (2014)
<i>S. Typhimurium</i>	<i>L. rhamnosus</i> GG, <i>L. johnsonii</i> NCC 533, <i>L. casei</i> Shirota, <i>L. casei</i> DN-114 001 <i>L. reuteri</i> ATCC 55730, <i>L. acidophilus</i> LB	5	Bernet-Camard et al. 1997, Coconnier et al. (2000), Coconnier-Polter et al. (2005), Fayol-Messaoudi et al. (2005), Hutt et al. (2006), Makras et al. (2006), Vizoso Pinto et al. (2006), Fayol-Messaoudi et al. (2007), Pridmore et al. (2008), Spinler et al. (2008), Burkholder and Bhunia 2009, Atassi and Servin (2010), Marianelli et al. (2010), Asahara et al. 2011, Zhang et al. (2011), Liévin-Le Moal and Servin (2014)

compounds in CFCs. These metabolites act either cooperatively or in solo (Fayol-Messaoudi et al. 2005; Makras et al. 2006). Bactericidal activity is also offered by low pH. Lactobacilli produce lactic acid through fermentation which lowers the intracellular pH of pathogens and makes cell membrane more pervious resulting in death. The killing effect of lactic acid over *S. Typhimurium* rises linearly as its concentration increases (Makras et al. 2006; Zhang et al. 2011). This effect is further supported by production of H₂O₂ (Pridmore et al. 2008; Atassi and Servin 2010). Several emitted compounds (non-proteinaceous) in CFCs of *L. acidophilus* LB, *L. rhamnosus* GG and *L. johnsonii* NCC 533 screened for susceptibility of *S. Typhimurium* and found bactericidal. Few of these antibacterial compounds are thermo-stable and are effective at low pH (De Keersmaecker et al. 2006). Furthermore, some heat stable small peptides are active against *Salmonella typhi* and entero-aggregative *E. coli* (EAEC) (Lu et al. 2009). Lactobacilli have bactericidal potential over *H. pylori* straight forwardly and indirectly. CFCs of *L. casei* Shirota have low pH-based killing effect on *H. pylori* (Sgouras et al. 2005). In the same manner, exposure of CFCs of *L. acidophilus* LB and *L. johnsonii* NCC 533 leads to quick decline of *H. pylori* growth (6 log CFU/mL) (Michetti et al. 1999).

12.8 Effects of Probiotics on the Expression and Functionality of Virulence Factors

L. rhamnosus GG is capable of lowering the *stx2A* mRNA (shiga toxin mRNA) content in *E. coli* O157:H7 (Carey et al. 2008). Mobility of *S. Typhimurium* is adversely affected when it is treated with CFCSs of *L. casei* Shirota and *L. acidophilus* LB. This destruction of motility is due to the depolarization of cell membrane that disturbs the performance of flagella (Lievin-Le Moal et al. 2011; Lievin-Le Moal et al. 2013). Lactobacilli treatment can also adversely affect the morphology of *H. pylori*. Accordingly, a switch from spiral form to coccoid was observed (Sgouras et al. 2005). These forms are less virulent than the spiral form (Sisto et al. 2000).

Urease activity is crucial for the survival of *H. pylori* under acidic environment of stomach. Functionality of urease is diminished by *L. casei* Shirota and *L. acidophilus* LB (Coconnier et al. 1998; Sgouras et al. 2005). In addition to spiral form, motility of *H. pylori* is important for colonization. Non-proteinaceous substances (1000 Da) released by *L. johnsonii* NCC 533 are capable to hinder the *H. pylori* motility (Lertsethtakarn et al. 2011; Isobe et al. 2012). Similarly, motility and spiral form are irreversibly affected by CFCS of *L. casei* Shirota (Lievin-Le Moal et al. 2013).

12.9 Findings of Probiotics Antimicrobial Potential by Various Methods

Various researchers proved the antimicrobial potential of numerous probiotic strains. Choi and Chang planned the strategy to check the antimicrobial effect of *Lactobacillus plantarum* EM by applying spot-on-lawn procedure against serious pathogens including *S. aureus* ATCC 29123, *E. coli* O157:H7 ATCC 43895, *M. luteus* ATCC 1530, *P. aeruginosa* ATCC 27853, *B. cereus* KCTC 3624, *S. enterica* serovar Typhi ATCC 19430 and *V. parahaemolyticus* ATCC 17802. Most powerful bacterial-foe effect was noted against *V. parahaemolyticus* ATCC 17802 and the very low effect was found against *S. aureus* ATCC 29123. The researcher concluded that *Lactobacillus plantarum* EM bears vast antibacterial spectrum, and hence executed the advantageous need of probiotics (Choi and Chang 2015; Chan et al. 2018). In another study, *Lactobacillus plantarum* KL-1 was observed to generate bacteriocins of broad antibacterial potential. The examination of bacteriocins activity was carried out by spot-on lawn procedure. These bacteriocins were able to produce zones of inhibition against various Gram positives but, highest activity was noted against closely relevant *L. sakei* (Pilasombut et al. 2015). Various strains of lactobacilli were recorded antibacterial against *Pseudomonas aeruginosa*, *Shigella* spp., *S. aureus*, *S. typhi*, *E. faecalis*, *E. coli*, and *K. pneumonia* by altered agar well method. The most efficient probiotic strains displayed the area of inhibition against aforementioned pathogens varies from 19 to 33 mm (Prabhurajeshwar and Chandrakanth 2019).

Cell-less supernatants of lactobacilli and bifidobacteria species were investigated for probiotic potential against *E. coli* and *S. aureus* by applying agar well diffusion

protocol. Effectiveness of supernatants was measured by the expansion of one of inhibition. Interestingly, supernatants were less active against *E. coli* comparatively (Ali et al. 2013). By the same technique, Naderi and colleagues evaluated the antibacterial activity of *L. rhamnosus*, *L. casei* and *L. acidophilus* against uropathogens (*Enterobacter* spp., *Enterococcus* spp., *Klebsiella pneumoniae* and *E. coli*). Accordingly, *L. casei* was the most competent probiotic against MDR-*E. coli* (Naderi et al. 2014). A spot-on-lawn and agar diffusion-based study was conducted in Iran in which child faecal isolate *Lactobacillus acidophilus* presented powerful effect against MDR-*P. aeruginosa*. But the commercial *Lactobacillus acidophilus* and *Lactobacillus reuteri* indicated comparatively weak activity (Jamalifar et al. 2011). Co-culturing of multi-species probiotics (species of Lactobacilli, Bifidobacterium and Enterococcus) with pathogenic *P. aeruginosa* has resulted in decline in *P. aeruginosa* growth from 9.2 log/mL (without probiotics) to 5.2 log/mL (with probiotics) (Koning et al. 2010; Fijan 2016). PCR and gene sequencing-based detection of bacteriocins genes (*plnA* to G, *plnI* to K, and *plnN*) was reported in yogurt-isolated Lactobacilli strains by Qian et al. (2020).

12.10 Plant Procured Chemicals (Phytochemicals)

Due to the incidences of drug resistance evolution the currently used antibacterial drugs have been unsuccessful (WHO 2014; Baym et al. 2016). One of the approved approaches is to include the combo of additional molecules (non-antibiotic or phytochemicals) with unsuccessful antibiotic in order to bring back its antibacterial potential and generate the chances for advanced treatment options (Brown 2015; Vandeveldel et al. 2016; Rana et al. 2018). Hereof, phytochemicals present strong antimicrobial action while numerous scientists have employed plant-oriented natural substances against bacterial drug resistance (Cowan 1999; Khameneh et al. 2016; Fazly Bazzaz et al. 2018; Shakeri et al. 2018). These substances or compounds, unaccompanied or accompanied with antibiotics, can boost antibacterial effect up to extended spectrum (Fazly Bazzaz et al. 2010; Betts and Wareham 2014; Fazly Bazzaz et al. 2016; Fazly Bazzaz et al. 2018). The bacterial-foe effect of phytochemicals and other antibacterial compounds is chiefly connected with two processes: chemically obstruction of production and activity of integral constituents of bacteria and/or bypassing the typical antibacterial resistance systems. Many targets have been observed to be encountered by antibacterial compounds; (1) demolition of plasma membrane (2) bio-formation of cell wall (3) polypeptide synthesis (4) DNA restoration and bio-formation and (5) metabolism pathway hindrance. In response bacteria may offer resistance to antibacterial compounds by an array of processes (Khameneh et al. 2019).

Despite that microbes-foe artificial compounds have been authorized in various countries, the application of natural agents obtained from animals or plants and microbes captivates the concentration of numerous scientists (Gyawali and Ibrahim 2014; Moloney 2016). These agents displayed encouraging results in defeating bacterial antibiotic resistance (Rossiter et al. 2017). A wide variety of antibacterial,

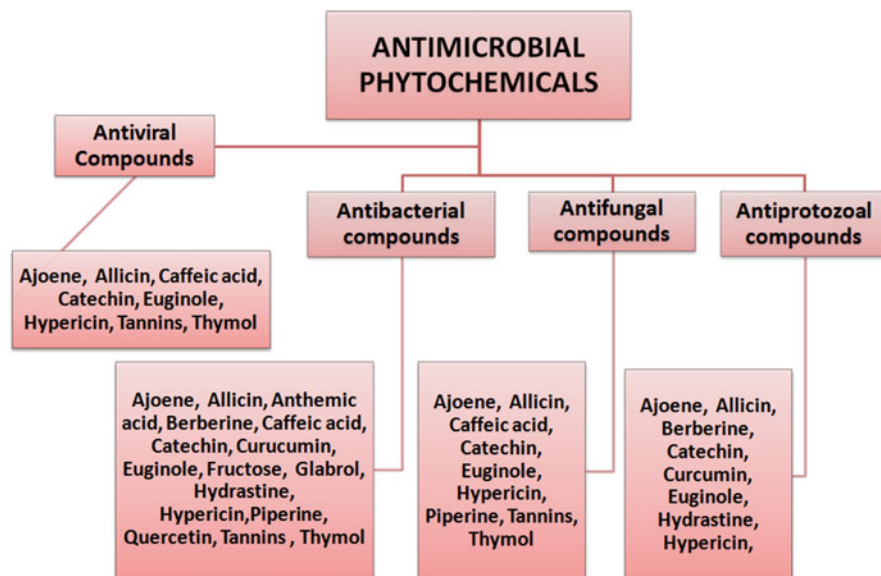


Fig. 12.2 Plant procured potentially antimicrobial compounds

antioxidant, anti-protozoan, antiviral and antifungal chemical compounds are derived from plants (Fig. 12.2). They can improve clinical utilization of earlier antibiotics by enhancing their potential of evading the resistance emergence (Barbieri et al. 2017).

The antimicrobially active plant chemicals can be categorized into various large groups depending upon their chemical configuration consisting of terpenoids, alkaloids, polyphenols and sulphur-bearing chemicals. These substances bear various potent strategies to encounter pathogenic microbes (Fig. 12.3) (Khameneh et al. 2019).

12.11 Terpenes or Terpenoids

Terpenes (isoprenoids) are acknowledged as divergent group of natural products and found in plants and in cell structures (Paduch et al. 2007; Oldfield and Lin 2012). Comparatively, Gram positives are more vulnerable to terpenes than Gram positives. Monoterpenes are inclined to decrease the density and raise the permeability of plasma membrane by changing the shape of its proteins and disrupt the respiratory pathway (Paduch et al. 2007). Alcoholic compounds of terpene (phytol, linalool, geranylgeraniol, geraniol, farnesol, plaunotol and nerolidol) suppress the propagation of *S. aureus*. Only nerolidol and farnesol could exhibit the bactericidal action relied on the damage to cell membrane (Togashi et al. 2010). Dehydroabietic acid (resin acid) and its derivatives (especially Carvone) were recorded efficient

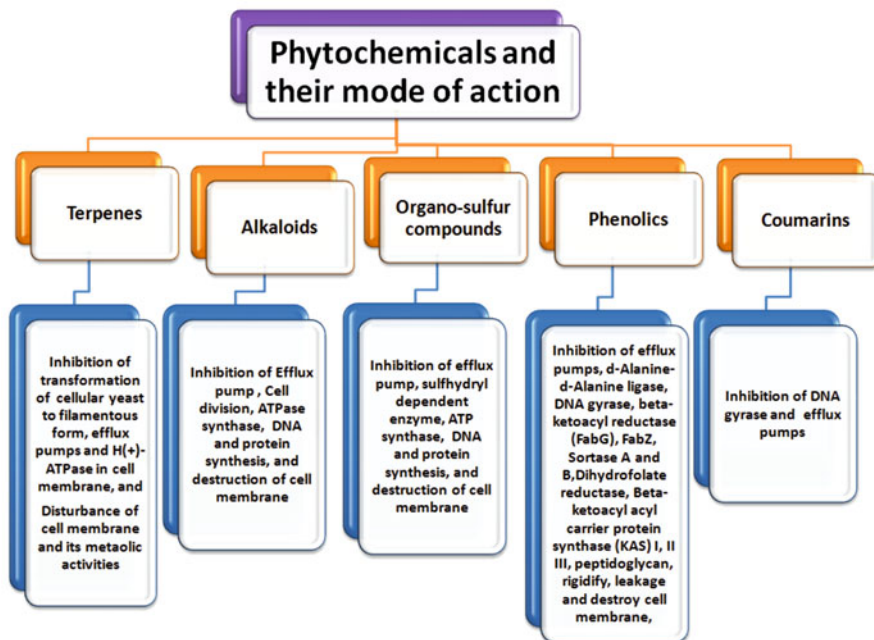


Fig. 12.3 Groups of plant-oriented compounds and their modes of antimicrobial action

antibacterial to *Campylobacter jejuni*, *S. aureus*, *E. coli*, *L. monocytogenes*, *E. faecium* and *C. albicans* (De Carvalho and Da Fonseca 2006; Savluchinske-Feio et al. 2006; Paduch et al. 2007). Furthermore, an antifungal, antibacterial and antiviral agent, Thymol has expressed dynamic effect over *Candida krusei*, *Candida glabrata* and *C. albicans* in solo and together with fluconazole (Sharifzadeh et al. 2018). Because of their extensive antifungal effect, thymol, menthol, eugenol and carvacrol are applied in food industries against food decomposing fungi (*Aspergillus* spp., *Penicillium* spp., *Rhizopus oryzae*, *Botrytis cinerea*, *Fusarium oxysporum* and *Alternaria alternata*) (Abbaszadeh et al. 2014). In addition to antifungal potential, thymol and carvacrol have efflux pump (EP) inactivation ability, anti-biofilm effect, and disintegration of plasma membrane and are bactericidal to *P. aeruginosa*, *E. coli*, *S. aureus* and *Enterobacter aerogenes* (Chauhan and Kang 2014; Amaral et al. 2015; Miladi et al. 2016). Eugenol presents anti-biofilm action against *S. aureus*, disruption of plasma membrane, and down-regulation of enterotoxin and biofilm genes. Finally, several terpenes have anti-mycobacterial effect (Yadav et al. 2015).

12.12 Alkaloids

They belong to heterocyclic compounds of nitrogen and have been verified for antibacterial effectiveness and infectious disease therapy (Cushnie et al. 2014). Many alkaloids work as efflux pumps inhibitor (EPI) that is an important process of most antibacterials. The extracts of *Piper longum* and *Piper nigrum* (Piperine), i.e. piperidine-like alkaloid, when used with Ciprofloxacin prevents the propagation of resistant *S. aureus* and lowers MICs for *S. aureus* (Khan et al. 2006). Similarly, co-application of gentamicin and Piperine was potent against methicillin-resistant *S. aureus* (MRSA) ailments (Khameneh et al. 2015). Additionally, its anti-NorA efflux pump activity has been noted in MRSA and non-MRSA (Kumar et al. 2008; Khameneh et al. 2015). Berberine (applied as traditional medicine) is recognized as alkaloid of isoquinoline and is present in bark and roots of Berberis species and other plants. This agent is anti-protozoan and antibacterial by intercalating within DNA, inhibiting topoisomerase IV, RNA polymerase and gyrase, and restriction of cell division (Iwasa et al. 2001; Yi et al. 2007; Domadia et al. 2008). Cell division restriction is linked with the inactivation of protein FtsZ needed for cell division (Boberek et al. 2010). Berberine has emerged as a vigorous bacteria-foe compound aimed to replace antibiotics and to defeat resistance.

Ungeremine is the alkaloid of iso-quinoline acquired from *Panacratium illyricum* which also has bacterial-foe activity. It is responsible for the DNA breaking as it inactivates topoisomerase IA (Casu et al. 2011; Schrader et al. 2013). Alkaloids of quinolone (maculine, dictamine, and kokusagine) have shown antibacterial activity and are separated from *Teclea afzelii*. They hinder the DNA biosynthesis by targeting topoisomerase II (Heeb et al. 2011). Reduction in oxygen utilization in bacteria has been observed when they are treated with Alkyl methyl quinolones (respiratory inhibitors) (Tominaga et al. 2002). Alkaloid of indole (Reserpine) acquired from *Rauwolfia serpentina* and has an excellent EPI effect (Abdelfatah and Efferth 2015). It improves the antibiotic effect against *Micrococcus* spp., *Staphylococcus* spp. and *Streptococcus* spp. when co-employed with antibiotics (Sridevi et al. 2017). Furthermore, it boosts the sensitivity of MDR-A. *baumannii* to antibiotics. Reduction in EP-based resistance to flouroquinolones in *Stenotrophomonas maltophilia* is noticed with the use of reserpine (Jia et al. 2015). It acts as EPI against Gram negative and positive bacteria (Sun et al. 2017). Extracts of *Macleaya cordata*, *Chelidonium majus* and *Sanguinaria canadensis* consist of Sanguinarine which is found as anti-MRSA. It is responsible for the discharge of autolytic enzyme and causes the disruption of MRSA. It also modifies altogether the process of septa development during cell division of MRSA (Obiang-Obounou et al. 2011). In addition to anti-MRSA effect, it has been reported as anti-mycobacterial against few species of Mycobacteria (Newton et al. 2002). Berberine and Sanguinarine both are vigorous transcriptional and DNA biosynthesis inhibitors (Al-Ani et al. 2015). Steroidal alkaloid (Tomatidine) are produced in eggplant, tomato and potato plant. In combo with aminoglycoside or in solo, it has demonstrated the killing activity against *S. aureus* (Mitchell et al. 2012; Jiang et al. 2016). It is an antibiotic enhancer which can synergistically improve the effects

of Cefepime, Ampicillin, Gentamicin and Ciprofloxacin against *P. aeruginosa*, *S. aureus* and *E. fecalis* (Soltani et al. 2017). Another steroidal alkaloid (conessine) is obtained from *Holarrhena antidysenterica* and has broad spectrum bacterial-foe potential, EPI against AdeIJK efflux pump of *A. baumannii* and synergistic effect with antibiotics (Kumar et al. 2007; Damier-Piolle et al. 2008; Siddiqui et al. 2012; Siriyong et al. 2016; Zhou et al. 2017). Tricyclic ergot alkaloid (Chanoclavine) procured from *Ipomoea muricata* was noted effective against MDR-*E. coli* when delivered together with Tetracycline. Its antibacterial act is EPI (Dwivedi et al. 2019).

12.13 Sulphur-Containing Compounds or Organosulphur Compounds

The vast spectrum bacterial-foe effects of plant procured sulphur-containing compounds (isothiocyanates, allicin, *S*-allyl-mercaptocystein, ajoene, dialkyl sulphides, *S*-allyl cysteine and diakyl) have been observed (Sobolewska et al. 2015; Barbieri et al. 2017). Allicin (diallylthiosulphinat) is derived from garlic and is potentially effective against *P. aeruginosa*, *S. epidermidis*, MRSA and *Streptococcus agalactiae* (Reiter et al. 2017). Its co-acting anti-*P. aeruginosa* effect has been realized concomitantly with Ciprofloxacin, Cefoperazone and Tobramycin (Cai et al. 2008). The antimicrobial mode of action of allicin is because of blocking sulfhydryl-reliant enzymes (RNA polymerase, alcohol dehydrogenase and thioredoxinreductase), protein and DNA biosynthesis (Lanzotti et al. 2014). Ajoene is also present in garlic mainly as *E*- and *Z*-stereoisomers which strive extended spectrum antimicrobial effect (Gram negative and Gram positive bacteria, protozoa, fungi and viruses). It has similar bacterial-foe mode of action as that of allicin (Rehman and Mairaj 2013).

The volatile sulphur-containing compounds like isothiocyanates (ITCs) are derived through plant glucosinolates after interaction with myrosinase. These are considerable antibacterial contenders against *H. pylori* by lowering the urease activity (Fahey et al. 2013; Park et al. 2013). These agents probably bind with proteins or enzymes, bearing sulfhydryl groups and block various biochemical systems (Dufour et al. 2015). They intrude in ATP linking sites of *E. coli* ATPase by targeting cysteine. A novel Sulforaphane belongs to ITCs and has bacterial-foe behaviour for *H. pylori*, *Listeria monocytogenes* and *S. aureus* (Benzekri et al. 2016). Allyl ITCs (AITCs) are present in the *Eutrema japonicum* and *Armoracia rusticana* and are effective against *S. aureus* and *E. coli*. They also lower synergistically Erythromycin MICs against *Streptococcus pyogenes* and Streptomycin MICs against *P. aeruginosa* and *E. coli* (Palaniappan and Holley 2010; Saavedra et al. 2010; Lu et al. 2016). Their antibacterial effect is mediated by cell wall disruption, pore formation in cell membrane and oxidative breakage of disulphide linkage (Luciano and Holley 2009; Nedorostova et al. 2009). Phenethyl isothiocyanate (PEITC) is an efficient antimicrobial (anti-Gram positives and antifungal) chemical (Aires et al. 2009). Its antifungal effect is due to the accretion of reactive oxygen

species (ROS) resulting in damage to mitochondria (Calmes et al. 2015). Benzyl ITCs (BITCs) have bactericidal response towards MRSA and act on plasma membrane as cationic protein (Sofrata et al. 2011; Dias et al. 2014).

12.14 Phenol-Containing Plant Compounds

These chemicals involve an extensive spectrum of natural substances which are broadly employed for medical objectives and intensify the antibiotic effect against resistant microorganisms by many mechanisms. They have indicated varied modes of action and synergistic effect through targeting cell membrane, EPs inactivation, and several vital enzymes like dihydrofolate reductase, urease and sortase A inactivation. The following noticed activities of phenol-containing compounds are impressive which make them marvellous candidates for clinical application (Farhadi et al. 2019a, b; Górniak et al. 2019).

They are expert in inhibiting efflux pumps, e.g. CmeABC of *C. jejuni* (Lechner et al. 2008; Klančnik et al. 2017). In addition to EPI effect, resveratrol causes the accretion of Ethidium bromide in *Arcobacter cryaerophilus* and *Arcobacter butzleri* (Ferreira et al. 2014). Baicalein can extraordinarily bring back the performance of Ciprofloxacin, Tetracycline and Beta-lactams against MRSA through inactivation of NorA efflux pumps (Chan et al. 2011). It also acts synergistically with Tetracycline in order to inactivate *E. coli* efflux pump (Fujita et al. 2005). Similar to Baicalein, Biochanin A (isoflavon) can also subvert the MRSA efflux pump (NorA) (Zou et al. 2014). It has growth-preventive response towards *Chlamydia* spp. and is a dominant EPI of Mycobacterium (Lechner et al. 2008; Cannalire et al. 2017). Isoflavonoid, flavonolignans (synergistic with Norfloxacin and Berberin) and many other flavonoids (flavones) like Chrysopenetin and Chrysosplenol-D (synergistic with Berberin) also restrict NorA activity (Stermitz et al. 2001; Morel et al. 2003; Stermitz et al. 2003). For the decline of EP efficiency, concentration of scientists has been captivated towards flavonoid-antibiotic hybridization. Studies have proved the intracellular aggregation of antibiotics and extraordinarily heightened effect of co-molecule (flavonoid-antibiotic hybrid) that validate required double action (Xiao et al. 2014). Kaempferol (flavonoid) is an impressive antimicrobial against *C. albicans* (Fluconazole resisted) and MRSA (Randhawa et al. 2016; Shao et al. 2016). Its anti-MRSA effect is due to the NorA EPI activity (Holler et al. 2012). Chalcones can impede NorA EP activity and lower erythromycin MICs (0.4–0.1 µg/mL) (Belofsky et al. 2004). Phenol-containing Catechin gallates like Epigallocatechin gallate (EGCG) can efficiently eradicate MRSA. They can attach themselves at ATP adhesive site on DNA gyrase, leading to the blockage of DNA gyrase activity (Gibbons et al. 2004).

Antimicrobial potential of plant-oriented phenols is not restricted to EPI effect however; other mechanisms are also known (Farhadi et al. 2019a, b). Green tea procured Tannins/polyphenols (anthraquinones and chebulinic acid) have been found to have anti-DNA gyrase effect (Patel et al. 2015). Semisynthetic Haloemodins (of natural anthraquinone) are the vital inhibitors of DNA gyrase in

Enterococcus faecium (vancomycin resistant) and MRSA (Duan et al. 2014). A novel plasma membrane destructive, 3-*p-trans*-coumaroyl-2-hydroxyquinic acid (CHQA) has been found effective against food-related pathogens (Wu et al. 2016). Compounds of phenol bind with essential enzyme β -Ketoacyl acyl synthase (KAS), responsible for the linking process of FabZ, FabL and FabG (fatty acid) biosynthesis. These fatty acids are the precursors of the cell membrane formation in bacteria. Curcumin (Turmeric derivative) can destroy *E. coli* and *S. aureus* by disrupting their plasma membrane (Tyagi et al. 2015). Cell wall formation can be interrupted by Apigenin and Quercetin (flavonoids) as they inactivate *d*-alanine:*d*-alanine ligase, an essential enzyme for cell wall formation (Wu et al. 2008). However, there are few other compounds like Sophoraflavanone B that can also target peptidoglycan elongation in MRSA (Mun et al. 2014). Other mechanisms for microbial enzymes inhibition by phenolic compounds have been studied such as inactivation of sortase, dihydrofolate reductase and urease (Navarro-Martínez et al. 2005; Maresso and Schneewind 2008; Xiao et al. 2013). EGCG have indicated anti-dihydrofolate reductase activity in *Stenotrophomonas maltophilia* (Navarro-Martínez et al. 2005). Sortase A enzyme of *S. aureus* can be targeted by Curcumin and Morin (Park et al. 2005). The functionality of urease of *H. pylori* is hindered by acetohydroxamic acid 4',7,8-trihydroxyl-2-isoflavene (Xiao et al. 2013).

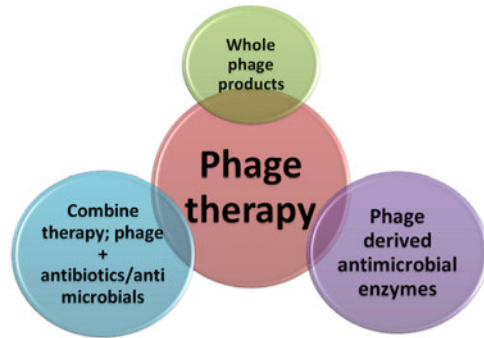
12.15 Coumarins

These compounds are not only obtained from plants but also from microbes (Smyth et al. 2009). They can inhibit DNA gyrase, inactivate EP and abolish quorum sensing resulting in reduction of biofilm and virulence components synthesis (Gutiérrez-Barranquero et al. 2015; D'Almeida et al. 2017; Reen et al. 2018; Zhang et al. 2018). The various derivatives Pyranocoumarins and Coumarins (Aegelinol benzoate, Agasyllin and Grandivittin) exert antioxidant and widened spectrum antibacterial effects. Mainly, agasyllin and aegelinol have more bactericidal effects against *S. aureus*, *Salmonella typhi* and *Enterobacter* spp., and *H. pylori* (Melliou et al. 2005; Basile et al. 2009). However, other compounds of Coumarins (osthole and 4'-senecioloxyosthol) have exhibited bactericidal activity against *Klebsiella pneumoniae* and *S. aureus* (Tan et al. 2017). Reduction in norfloxacin MIC against MRSA has been witnessed when Coumarins are used concomitantly with Norfloxacin (Roy et al. 2013).

12.16 Bacteriophages

The earliest analysis on the application of phage (phage therapy) was carried out by Bruynoghe and Maisin in Belgium, 1921. They cutaneously infused phage suspension peculiar to *S. aureus* in order to cure carbuncle and fruncle. In 1940s, phages were first launched commercially by the companies of France and United States (O'Flaherty et al., 2009). The dilemma of antibiotic resistance and the demand of

Fig. 12.4 Targeting drug-resistant and virulent bacteria by the application of phages and their enzymes



novel antimicrobials have provoked the attention of the researchers towards non-clinical and clinical utilization of bacteriophages (phages) and their procured enzymes having antimicrobial effect (Van Boeckel et al. 2014; Van Boeckel et al. 2015; Webber et al. 2015; Soumet et al. 2016). Phages in comparison with antibiotics also occupy therapeutic benefits. The undistinguishing antimicrobial effects of antibiotic treatment lead to the loss of microflora. On the other hand, therapeutic employment of phages can diminish this loss (Meader et al. 2013; Faber et al. 2016; Zhao et al. 2017).

Various infections are being dealt in Europe with phage treatment, taking the benefit of whole phage having lytic style of replication (Abedon et al. 2011; Viertel et al. 2014). A few food products containing whole phage are employed in Western countries, while phage procured enzymes are introduced in man and animal medicines (Sulakvelidze 2013; Cooper 2016; Totté et al. 2017; Cooper et al. 2018). Phage-oriented proteins of therapeutic interest are usually endolysins, needed for the release of freshly formed phages (Briers and Lavigne 2015; Rodríguez-Rubio et al. 2016). Nevertheless, some phage-oriented enzymes (e.g. spanins and holins) bearing antimicrobial response have also been explored (Roach, 2015; Song et al. 2016). Various phage therapeutic strategies have been adopted: (1) whole-phage occupying treatments consisting of various preferred phages of desired properties and selective antimicrobial effect in a blend (Gill and Hyman 2010; Weber-Dabrowska et al. 2016), (2) mix therapy (Phages together with antibiotics) has been found to kill drug-resistant bacteria, efficiently (Ryan et al. 2012; Daikos et al. 2014) and (3) synergistic effect has been noted with various blends of antibiotics and endolysins and endolysins alone against Gram negatives and Gram positives (Fig. 12.4) (Becker et al. 2008; García et al. 2010; Schuch et al. 2014).

Phages have been found antibacterial to popular entero-virulent bacteria like *Campylobacter*, *Salmonella* and *E. coli* O157:H7 (Huff et al. 2005; Johnson et al. 2008). US-FDA accepted LMP-102TM phage cocktail having six different types of phages in 2006, for targeting *Listeria* in meat. United States Department of Agriculture (USDA) in 2007 endorsed a phage therapeutic product for the eradication of *E. coli* from cattle. However, various phage products are under investigation for

therapeutic scope. Phages reproduced in targeted bacteria and give rise to numerous fresh lytic phages, and also produce mutations in pathogens (Cheng et al. 2014).

12.17 Phage-Originated Antibacterial Enzymes

Some phage-oriented enzymes (e.g. endolysins and hydrolases) bearing antimicrobial response have also been explored (Roach and Donovan 2015; Song et al. 2016). Phage-oriented proteins of therapeutic interest are usually endolysins, needed for the release of freshly build-up phages (Briers and Lavigne 2015; Rodríguez-Rubio et al. 2016). Some of these enzymes are discussed below.

12.18 Endolysins

During late stage of lytic cycle several endolysins (transglycosylase, glucosidase, endopeptidase and amidase) are produced and are capable of deteriorating mucopeptide/murein of bacterial cell wall, in order to promote the new phages discharge. During 1950s, these enzymes were first time detected and found antibacterial to *Clostridium butyricum*, Staphylococcus, *L. monocytogenes* and *Bacillus anthracis* (Low et al. 2005). They are found effective in sepsis and bacterial infections of Group B Streptococcus, *Enterococcus faecalis* and *C. perfringens* (Fenton et al. 2010). Endolysin PAL has the capability to destroy Group-A Streptococci. Together with Endopeptidase Cpl-1 and Amidase PAL can lower the occurrence of pneumonia (both systemic and localized) (Fischetti 2005). Phage K originated Endolysin LysK can destroy MRSA (O'Flaherty et al. 2005). Similarly, PlyV12 Endolysin expresses excellent lytic action on Vancomycin-resistant-*E. faecium* and *E. faecalis* (Yoong et al. 2004). The phage phi3626 based endolysins can successfully cure Clostridium related ailments (Courchesne et al. 2009). Endolysins have exclusive Gram positive antibacterial spectrum and lead to very rapid bacterial lysis by targeting their murein of cell wall (Loeffler et al. 2003). So, that there is no chance for bacteria to evolve into resistant forms. But they are of little or no worth for targeting Gram negatives (Fischetti 2005).

12.19 Virion-Associated Peptidoglycan Hydrolases (VAPGHs)

They are a sort of lyases which break down murein or peptidoglycan to facilitate phage entrance in bacteria (Rodríguez-Rubio et al. 2013). Various viron-associated peptidoglycan hydrolases (VAPGHs) have been identified and their antimicrobial potential has been verified. For example, HydH5 (phiPLA88 phage origin), protein gp61 (produced by phiMR11 phage) and Protein 17 (produced by P68 phage) were found remarkably antibacterial (at exponential growth phase) against MRSA and non-MRSA (Takac and Blasi 2005; Rashel et al. 2008; Rodríguez et al. 2011). Similarly, P5 protein produced by phage 6 bears antibacterial efficiency against

Proteus vulgaris, *Pseudomonas*, *S. Typhimurium* and *E. coli*. In addition to aforementioned Gram negatives, gp181 (produced by KZ phage) have shown lytic effect against *Yersinia* and *Ralstonia solanacearum*. Gp36 (produced by bacteriophage KMV) is heat stable and impressive against *E. coli* and *P. aeruginosa* (Lavigne et al. 2004). VAPGHs produced by phages targeting Gram negatives are of extensively antibacterial spectrum while, VAPGHs generated by phages of Gram positives are effective against only limited bacteria. They can also efficiently encounter drug-resistant pathogenic bacteria by lowering the expression of efflux system (Paul et al. 2001). Most of VAPGHs can tolerate and remain effective at high temperature, hence can be employed in food industry (Rodriguez-Rubio et al. 2013). We salute to the scientists (working in above referred domains) whose efforts are indeed laudable.

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Probiotic Bacteria as a Functional Delivery Vehicle for the Development of Live Oral Vaccines

13

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Abstract

Probiotics improve the immune system and help to fight with different infection. The LAB ability in eliciting the immune response against foreign antigens has led to their use as candidate vectors for mucosal vaccines. Here, the use of LAB as oral vaccine carriers and various expression systems intended to the production of heterologous proteins are reviewed and discussed. *Lactococcus lactis*, *Lactobacillus* strains, and *Streptococcus gordonii* are lactic acid bacteria (LAB) currently being advocated for use as live antigen delivery vehicles to mucosal sites. Since these vehicles differ in their life span and mode of antigen delivery within the **small intestine**, in this chapter we tried to determine the promising LAB candidates for the development of oral vaccines.

Keywords

Probiotics · *Lactococcus lactis* · *Streptococcus gordonii* · Lactobacillus strains · Vaccine

13.1 Introduction

The development of effective mucosal vaccines could have several advantages in modern vaccinology. Due to high cost, storage and delivery condition of vaccines, further improvements in the vaccination coverage are actively demanded in developing world. The development of a new generation of vaccines which could be

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319

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applied orally, with the ability to stimulate both mucosal and systemic immune responses, offers promising perspectives for the eradication of infection diseases in many regions worldwide. For this purpose, over the last decade probiotic lactic acid bacteria (LAB) have been extensively studied for their potential use in the development of new generation of oral vaccines (Mojgani et al. 2020). Probiotic bacteria are known as profitable bacteria that can be easily stored, delivered, and relatively inexpensive to produce (Dadar et al. 2017; Mojgani et al. 2020). Another important advantage of these bacterial vectors is their ability to deliver immune-protective antigens at the mucosal surfaces, leading to cell and/or humoral-mediated responses. The induction of targeted and specific local immune responses in the mucosa-associated lymphoid tissue (MALT) can be most effectively achieved by the direct application of the vaccine antigen to the mucosal surface by bacterial vectors. In this regard, a number of LAB that are commonly found in the intestine of animals and humans appeared to be promising candidates (Jandhyala et al. 2015; Boersma et al. 2000). Some strains of *Lactobacillus* and *Lactococcus* spp. are termed as biotherapeutic agents due to their immune regulatory responses. The main immune effects of probiotic LAB could be summarized in their immune modulatory features that have been reported in the treatment of many disorders such as autoimmune diseases and different cancers as well as their anti-inflammatory, immunogenic, and immuno-adjuvant properties favoring their use as live vaccine delivery system (Kassayova et al. 2014). Some randomized, placebo-controlled clinical trials (RCTs) highlighted the promising and effectiveness of probiotics as delivery vehicle able to promote both parenterally and mucosally administered vaccine-specific immune responses (Amdekar et al. 2010). Particularly, *Lactobacilli* were found to increase the performance of several candidate mucosal vaccines for infantile diarrhea, HIV, and malaria in preclinical studies involving experimental animals. One of the most important advantages of probiotics is the ease of its administration (Licciardi and Tang 2011), while stimulating the immune responses against the vaccine antigen. These outstanding properties could help to provide effective protection against infectious diseases particularly in regions with low vaccination coverage. In this chapter we will highlight different aspects of promising probiotics species, effective transformation systems, and putative live oral vaccines. The promising results achieved with a number of these beneficial constructs will be discussed.

13.2 Probiotics and Their Safety Status

The profitable live microorganisms colonizing our digestive tract have been named “probiotics” (Morelli and Capurso 2012). They preserve gut health by induction of immunomodulatory impacts to maintain the intestinal homeostasis and by modulation of the gastrointestinal microbiota (Adel et al. 2017; Azcárate-Peril et al. 2011; Kałużna-Czaplińska et al. 2017; Mojgani et al. 2020). Lilly and Stillwell introduced the term “probiotic” to explore components released by protozoa, which improved the growth of other organisms (Lilly and Stillwell 1965). Several investigation

supported the effective role of probiotic strains as promising supplements to improve mucosal immunity while having limited side effects (Rolfe 2000; Van Doan et al. 2020). It is now well documented that probiotics help to preserve healthy digestion (Cremon et al. 2018). Very limited reports of any adverse effects of probiotics have been reported. However, the safety of probiotic strains is highly associated with specific health claims and their purported advantages (Pradhan et al. 2020). Furthermore, probiotic can provide benefits to multiple parts of the body, where other supplements commonly focus on specific organs (Reid et al. 2003; Varankovich et al. 2015; Bisanz et al. 2015). The beneficial effects of probiotics have been reported on improving the bioavailability of essential nutrients (Pandey et al. 2015), gastrointestinal health (Varankovich et al. 2015), ameliorating the adaptive and innate immune response (Galdeano et al. 2019), decreasing common symptoms of food intolerance (Oak and Jha 2019), preventing the onset of certain cancers (Sharma 2019), and preventing atopic sensitization among susceptible subjects (Allen et al. 2014). Probiotics also clearly benefit patients who have had broad-spectrum antibiotic therapy by restoring a healthy intestinal microbiota (Sartor 2004; Peterson et al. 2015; Sánchez et al. 2017). Probiotics also appeared to be effective in the stimulation of both mucosal and systemic antigen-specific immune responses throughout the nasal and oral route (Anand et al. 2019; Neto et al. 2018; Cervin 2018; Mercenier et al. 2000).

13.3 Probiotics as Delivery Vehicles for Vaccine

Probiotics are described as live microorganisms that live in the gastrointestinal (GI) tract and, when administered in acceptable amounts, may confer a health benefit to the host (Tang 2009). About 100 years ago, Elie Metchnikoff discovered the health properties of probiotics and attributed the long life of Bulgarian peasants to their consumption of *Lactobacillus* probiotic bacteria (Rizzardini et al. 2012; Youngster et al. 2011). More recently, many reports pointed out the beneficial effects of probiotics on adaptive and innate immune responses in vivo and in vitro (Adel et al. 2017; Mojgani et al. 2020; Safari et al. 2016; Van Doan et al. 2020). Probiotics can regulate immunological responses directly by their interaction with epithelial cells and intestinal immune cells and/or indirectly by regulation of the **intestinal microbiota** (Adel et al. 2017; Power et al. 2014). Moreover, the effective role of probiotics in health improvement appeared to be the consequence of their combined impacts on epithelial barrier integrity, immune modulation, and **gut microbiota** (Mojgani et al. 2020). It was shown that interactions between immune system and the microbiota are important for the safe and natural improvement of healthy immune responses. Several investigation have reported that intestinal dysbiosis can lead to chronic inflammatory conditions such as **inflammatory bowel disease** and allergic disease likely as a result of abnormal regulation of **immune** system (Johansson et al. 2011; Westerholm-Ormio et al. 2010). Immune effects of probiotics can vary according to the selected probiotic, indicating its effects are strain- and species-specific (Licciardi and Tang 2011). Nowadays, the most broadly

evaluated probiotic bacteria in clinical trials and animal models are the *Bifidobacteria* and *Lactobacilli* species (Licciardi and Tang 2011). The immunomodulatory effects of probiotic bacteria also have been described by the beneficial role of some probiotic strains such as *Lactococcus lactis* as a protein expression system (Singh et al. 2017; Wang et al. 2020). Both commensal and pathogenic intestinal bacteria could interact with the gastrointestinal mucosal lymphoid system (GALT) by Pathogen Recognition Receptors (PRR) expressed on specialized epithelial DCs and M cells, and antigen-presenting cells (APC) (Amdekar et al. 2010). These signaling pathways are important for the homeostasis of the intestinal immune response, preventing immune dysregulation by promoting tolerogenic responses as well as by stimulating the host protection against intestinal pathogens at the same time (Licciardi and Tang 2011). Furthermore, lactobacilli can be delivered orally, thereby providing a convenient presentation of antigens that can be applied on a large scale as an inexpensive option in less industrialized countries (Pouwels et al. 1998). Molecular-biological features such as efficient adhesion and colonization to human tissue surfaces play a major role in specific and nonspecific immune responses to LAB (Bermúdez-Humarán 2009). The role of the human microbiome as a regulator of both systemic and mucosal immunity is now well documented, and some probiotics appeared to be promising vaccine candidates (Ferreira et al. 2005; Vitetta et al. 2017). The applicable LAB for use as delivery vectors of vaccine commonly comprise multiple *Lactobacillus* species, *Lactococcus lactis*, and *Streptococcus gordonii*. Several comprehensive reviews of recombinant *L. lactis* vaccines describing the immune response of these recombinant bacteria against viral and bacterial antigens have been published (Bahey-El-Din et al. 2010; Pontes et al. 2011; Bermúdez-Humarán et al. 2011). However, because of the large number of published articles detailing *L. lactis*, *S. gordonii*, and lactobacilli as vaccine vectors, this chapter will particularly focus on the results of *in vivo* studies.

13.4 Bacteria Antigen Expressed by Probiotics

Numerous studies have introduced engineered LAB strains as delivery vehicles for bacterial antigens. The efficacy of *L. lactis*-based vaccine is associated with the route of administration and is related to the nature and amount of antigen produced. For example, it has been shown that oral immunization with recombinant *L. lactis* expressing the pneumococcal protective protein A (PppA) induced sufficient protection against respiratory pneumococcal infection (Villena et al. 2008). However, another study suggested that a better immunostimulation is achieved by intranasal (IN) administration of recombinant *L. lactis* strains expressing *Yersinia pseudotuberculosis* low-calcium response V (LcrV) antigen (Daniel et al. 2009). Furthermore, IN-vaccinated mice had developed protection against both oral and systemic infections with *Y. pseudotuberculosis*, although oral vaccination failed to protect against an oral challenge with *Y. pseudotuberculosis* and did not induce any specific immune response (Daniel et al. 2009). *L. lactis*-secreting listeriolysin O (LLO) induces specific CD8⁺ T cells and sufficient protection against *Listeria*

monocytogenes in a murine infection model (Bahey-El-Din et al. 2010). However, in vivo and in vitro characterization of DNA delivery by recombinant *L. lactis* secreting a mutated form of *L. monocytogenes* Internalin A (InIA) confirmed the production of the mutated InIA at the *L. lactis* surface and appeared to be a promising strategy for plasmid transfer (De Azevedo et al. 2012).

In another experiment, recombinant *L. lactis* MG1363 expressing urease subunit B (UreB) of *Helicobacter pylori* failed to produce a sufficient immune response through the different tested oral vaccination regimens against *H. pylori* challenge (Lee et al. 2001). In contrast, another study reported that oral vaccination with *L. lactis* MG1363 expressing the antigen CagL of *Helicobacter pylori* can be evaluated as a potentially live vaccine able to induce a significant immune response in mice (Aliramaei et al. 2020). Another study also confirmed the significant immunoreactivity of BALB/c mice to the *H. pylori* Lpp20 antigen expressed in an engineered *L. lactis* strain and administered orally (Zhang et al. 2016). Orally and intraperitoneally immunized mice with recombinant *L. lactis* producing Omp31 antigen of *Brucella melitensis* also promoted the production of serum IgM and IgG antibodies as well as IFN- γ and IL-10 (Shirdast et al. 2020). The successful cloning and expression of *B. melitensis* bp26 gene in *L. lactis* also confirmed the efficacy of this vector for the production of an oral vaccine conferring protection against brucellosis (Maghvan et al. 2019). Similarly, oral immunization using the recombinant probiotic *Lactobacillus casei* expressing the outer membrane protein OMP19, which is specific to *Brucella* species, induced strong mucosal immune responses in mice and protection against *Brucella abortus* (Mohammadi and Golchin 2020). A recombinant *Lactobacillus casei* expressing a flagellar antigen from *Salmonella enterica* also induced cell-mediated immune responses and offered an efficient mucosal protection (Kajikawa et al. 2007). Another important LAB vector that has been used in numerous studies is *S. gordonii*. The subcutaneous injection of *S. gordonii* cells expressing S1 subunit of pertussis from *Bordetella pertussis* on their surface efficiently immunized New Zealand white rabbits (Lee et al. 1999). Furthermore, nasal or oral immunization of dd-Y mice with recombinant *L. lactis* expressing surface protective antigen (SpaA) led to the production of antigen-specific fecal IgA and serum IgG protecting mice against a challenge with *Erysipelothrix rhusiopathia* (Cheun et al. 2004). However, there are several oral vaccinations with LAB-based vaccine vectors that are highly variable in immune responses and antibody production; therefore, further works are needed to improve the efficiency and delivery route of the live bacterial vector.

13.5 Viral Antigen Expressed by Probiotics

A number of viral antigens have been produced in LAB-based vectors. Remarkably Xin et al. reported the protective effect and immunogenicity of an orally administered recombinant *L. lactis* expressing surface-bound (Env) protein of human immunodeficiency virus type 1 (HIV-1), showing sufficient protection in mice challenged intraperitoneally with the virus (Xin et al. 2003). Another study also

confirmed that the construction of paired cell surface display of *Salmonella enterica* Serovar Typhimurium *FliC* and HIV-1 *Gag* in *Lactobacillus acidophilus* as mucosal vaccine vectors could induce an increase of Gag-specific IgA-secreting cells. Interestingly, the expression of *FliC* in LAB conferred an adjuvant impact on the local production of IgA (Kajikawa et al. 2012). The oral administration of the recombinant *L. acidophilus* expressing the membrane proximal external region (MPER) of HIV-1 within the major S-layer protein (SlpA) led to a Th1 and Th17 dominance in the immune responses (Kajikawa et al. 2015). The use of lactobacilli expressing HIV antigens was found to be an effective way to improve the systemic (serum IgG) and mucosal (IgA) immune responses against HIV proteins (Gag, MPER) in orally immunized mice (LeCureux and Dean 2018). The subcutaneous injection of a genetically modified *Lactobacillus casei* producing VLPs of human papillomavirus (HPV) by the L1 protein led to an increased expression of serum-specific IgG in BALB/c mice (Aires et al. 2006). Other studies performed on C57BL/6 mice have effectively used a recombinant *L. casei*, displaying on its surface the minor capsid protein L2 as well as the early oncoproteins E6 and E7 proteins of HPV, to induce T cell-regulated cellular immunity with antitumor impacts (Lee et al. 2010; Poo et al. 2006). In Balb/c mice, the oral utilization of the L2 protein of HPV-16 expressed in *L. casei* was able to stimulate mucosal and systematic cross-neutralizing responses (Yoon et al. 2012). Similarly, the oral administration of the genetically modified *L. casei* displaying E7 protein of HPV-16 promoted the generation of antigen-specific cytotoxic T lymphocytes against HPV16 in C57BL/6 mice (Adachi et al. 2010). The same approach was used to immunize C57BL/6 mice with the severe acute respiratory syndrome coronavirus (SARS-CoV)-spike protein expressed in *L. casei*. The nasal and oral inoculations of the recombinant *L. casei* displaying this protein generated high level of neutralizing-antibodies and an effective protection against the SARS-CoV (Lee et al. 2006). In this study, the authors also reported an elevated content of mucosal IgA in bronchoalveolar and intestinal lavage fluids of immunized C57BL/6 mice following the intranasal or oral immunization. The N protein of SARS-CoV expressed into the cytoplasm or secreted in the medium of *L. lactis* modified by genetic engineering was also able to stimulate the production of N-specific IgG as a promising mucosal vaccine candidate (Pei et al. 2005). *L. lactis* was also used for the production of a recombinant flaviviral E protein of Dengue virus and effectively promoted the humoral immune response to dengue infection in immunized mice (Crill et al. 2009).

The oral immunization with recombinant porcine rotavirus VP4 and VP4-LTB expressed in *L. casei* stimulated neutralizing serum IgG and mucosal IgA antibody responses in female Balb/c mice (Qiao et al. 2009). An efficient protection was also achieved by using a recombinant *L. rhamnosus* GG expressing protein G of rotavirus in mouse model, decreasing the severity, prevalence, and duration of diarrhea-associated rotavirus infections (Günaydın et al. 2014). In a fish model, the oral administration of *L. casei* expressing protein antigens of the infectious pancreatic necrosis virus (IPNV)(Min et al. 2012; Li-Li et al. 2012), Koi herpesvirus (KHV) (Cui et al. 2015), spring viremia of carp virus (SVCV) (Cui et al. 2015; Dadar et al. 2018), and viral hemorrhagic septicemia (VHS) (Naderi-Samani et al. 2020)

significantly stimulated the generation of serum IgM and was found to be a promising vaccine vector candidate against viral disease in fish.

Different study also confirm the protective role of the oral administration of an *L. plantarum* strain expressing hemagglutinin (HA) gene of H9N2 and H5N1 avian influenza virus by increasing the production of serum IgG, fecal IgA, and bronchiolar IgA in BALB/c mice (Shi et al. 2014; Wang et al. 2012).

13.6 Protozoal Antigens Expressed by Probiotics

L. lactis have also been applied as a promising candidate for the delivery and expression of protozoal antigens. Oral immunization of BALB/c and C57BL/6 mice against rodent malaria with recombinant *L. lactis* expressing the C terminal fragment of the merozoite surface protein 1 (MSP-119) of *Plasmodium yoelii* provided protection at the asexual erythrocytic stage of malaria (Zhang et al. 2005). The oral administration of the *Giardia lamblia* cyst wall protein 2 (CWP2) displayed at the surface of *L. lactis* led to increased levels of mucosal anti-CWP2 IgA in the intestine of mice along with a significant decrease in fecal cyst shedding following challenge experiments with *Giardia muris* (Lee and Faubert 2006).

The protective effect of vaccine antigens expressed in LAB against parasite infection could be significantly affected by inoculation doses, the vaccination regimen used, the route of administration, its cellular expression in LAB strain utilize and nature and amount of the expressed antigen.

13.7 Immunomodulatory Responses of Probiotic Bacteria

It is now well documented that immune response could be directly or indirectly affected by the gut microbiota, influencing the pathways involved in both innate and adaptive immune responses (Frei et al. 2015; Hoseinifar et al. 2017). Therefore, it was suggested that the condition of many diseases could be improved by improving the gut microbiota. This hypothesis was supported by the weak performance of oral vaccines in developing countries because of a higher proportion of children with impaired or dysbiotic gut microbiota (Rosshart et al. 2017; Sánchez et al. 2017). The protective mechanisms of probiotic are commonly related to the interaction of probiotics with host cells or to the cross-talk of probiotics with other microbiota or pathogenic microorganisms (Taverniti and Guglielmetti 2011). Direct interaction of probiotic bacteria with the host cell can be regulated by the bacterial cells, independent of their viability and by the multitude of specific components or products released by bacteria as well as through their effects on specific human cells, such as those of the mucosa-associated lymphoid tissue (MALT, playing an important immunoregulatory role on the specific immunity (Adams 2010). Furthermore, the immunomodulatory effects of genomic DNA of probiotic bacteria have been reported on the human peripheral blood mononuclear cells (PBMC) responses through elevated IL-1 and IL-10 production (Lammers et al. 2003). The significant

differences in magnitude and kinetics of IL-10 and IL-1 β release in response to genomic DNA of probiotic revealed the influence of gut bacterial components on the intestinal response of the mucosal immune system (Delcenserie et al. 2008; Lammers et al. 2003).

Interestingly, a study demonstrated that heat-inactivated probiotics such as *Lactobacillus casei* Shirota were marginally less effective in stimulating some proinflammatory cytokines, including interleukin tumor necrosis factor (TNF)- α and (IL)-12, when compared to viable cells, while similar induction of IL-10 was reported for viable and inactivated cells. Moreover, live Gram-negative probiotic bacteria of *Escherichia coli* Nissle 1917 stimulated the release of a higher amount of IL-10 and proinflammatory cytokines by the murine monocyte/macrophage cell line (J774A) when compared to heat-killed bacteria (Cross et al. 2004). The immunogenic effects reported by probiotics are directly associated with their immunomodulating responses (production of IL-6 and IL-10) and their tumor-reducing activities (Reid et al. 2003; Van Hoang et al. 2018; Amdekar et al. 2010). However, species- and strain-specific effects have been attributed to different LAB based on their ability to promote particular patterns of mucosal cytokine expression (Mojgani et al. 2020). Through the oral route, probiotic bacteria enter the gut and may promote the induction of cytokines through mucosal lymphoid cells. The up or down modulation of the immune response could be affected by a broad range of immune cells such as endothelial cells, fibroblasts, and stromal cells which are responsible for the production of specific cytokines. Furthermore, the interaction between probiotic bacteria and the gut epithelial cells leads to the stimulation of a cascade of signals regulating the immune response (Amdekar et al. 2010; Galdeano and Perdigon 2006). The nonspecific immune response induced by probiotics mainly occurs through inflammatory pathways resulting in the activation of macrophages and phagocytic cells [polymorphonuclear (PMN)] (Mojgani et al. 2020; Perdigon et al. 1995). After arrival of probiotic bacteria to the colon, they are absorbed by the overlying M cells in the Peyer's patches or across the overlying normal epithelium in the lamina propria of the small intestine. The intact probiotics cells are then handled by phagocytizing cells including antigen-presenting cells (APC), the macrophages, B and T lymphocytes, and dendritic cells (Perdigon et al. 1995; Perdigón et al. 2001). The mucosal immune epithelial cells stimulated by probiotics could regulate the immune defense pathways by the release of IL-2, IL-6, and IL-10 that are able to modulate both nonspecific and specific immune mechanisms through their actions on immune cells. Probiotic bacteria could also affect B cells in axillary lymph nodes by pulses of IL-6 expression, which is known as an important B cell differentiation factor (Akira et al. 2001). Probiotics are also capable to stimulate the release of cytokines through the macrophages and T cells, leading to the regulation of the mucosal immune response (Kawashima et al. 2018; Galdeano et al. 2019). Furthermore, the release of luminal secretory IgA could be promoted by some probiotic bacteria, regulating both systemic and mucosal immunity (Perdigon et al. 1995, Perdigón et al. 2001). LAB also regulates the immune responses by stimulating the production of type 1 interferons (IFNs), which has a critical effect on the anti-viral immune response (Kawashima et al. 2018). Moreover, it was shown that the

absorption of particular LAB strains by DCs promotes the fractional maturation of dendritic cells implicated in the immune response to foreign- and self-antigens (Foligne et al. 2007).

13.8 The Design and Construct of Probiotic Bacteria as Putative Vaccines

A promising application of LAB is its administration for the improvement of live mucosal vaccines. Some LAB species such as *L. lactis* have been reported as promising vaccine vector candidates for a multitude of bacterial and viral antigens (Pouwels et al. 1998; Wells et al. 1996). Several delivery systems such as cell wall, extracellular or cytoplasm medium have been designed to target different heterologous proteins to a particular location of cell (Le Loir et al. 2005). For the construction of recombinant protein in LAB vehicles, several parts, including genes coding for heterologous proteins, and multiple cloning site (MCS) promoters and terminator (T) should be accurately designed (Yeng et al. 2009). Promoters commonly are species specific and originate from the bacteria used for protein expression. Moreover, several efficient expression systems have been designed to produce various heterologous proteins in LAB (Boersma et al. 2000; Villatoro-Hernández et al. 2012). The regulation of the expression of recombinant immunogenic proteins in LAB may be performed by strong or inducible constitutive promoters. The nisin-inducible promoter Pnis, acting as one of the key components in the nisin-inducible controlled expression (NICE) system, is now widely applied (Villatoro-Hernández et al. 2012). The NICE system is largely used to express heterologous proteins in *L. lactis* because of several advantages, including efficiently induced and tightly controlled expression leading to high yields of protein (Roshan and Souza 2012), large-scale production process, and easy use (Mierau and Kleerebezem 2005). Fermentation parameters, nisin amounts, and growth conditions have been optimized to increase the yield of recombinant proteins. In addition, another constitutive promoter that could not be controlled by any regulator or growth conditions are thought to be constitutive under laboratory growth conditions. The most generally used constitutive promoters originating from *L. lactis* genomic library include P21, P23, and P59 (strong promoters) as well as P32 and P44 (weak promoter). These strong and weak promoters have been used to express different heterologous proteins in *L. lactis* (Morello et al. 2008). Furthermore, the expression of proteins bearing an N-terminal signal peptide in the growth medium could be performed by the Sec pathway (Mierau and Kleerebezem 2005). However, multistep process and different factors localized in all cell compartments could impact on the protein secretion in Gram-positive bacteria. For example, intracellular targeting factors such as bacterial *ffh* genes which are contributed in protein folding and secretion and encode the protein elements of signal recognition particle (Tjalsma et al. 2004). The translocation machinery in *L. lactis* comprised of the ATPase-dependent motor, SecA, partly prepare the energy demanded for preprotein translocation, and integral membrane proteins, i.e., SecG, SecE, and SecY, produce the conducting channel via

the hydrophobic membrane environment. Moreover, signal peptide cleavage such as *SipL* in *L. lactis* strains is another factor that is removed by type I signal peptidase during or shortly after preprotein translocation across the membrane. Surface quality control proteins *PmpA* and *HtrA* in the *L. lactis* are other factors involved in the protein secretion of Gram-positive bacteria. These proteins are transported by the Sec machinery and involved several folding factors like folding catalysts and chaperones, and are directly involved in the degradation of misfolded/unfolded proteins through housekeeping proteases (Morello et al. 2008).

13.9 Advantage and Disadvantage of Probiotics as Delivery Vectors of Vaccine

To date, human vaccines are categorized under 4 main groups including (1) live attenuated vaccines, (2) recombinant, subunit, conjugate, and polysaccharide vaccines, (3) toxoid vaccines, and (4) whole inactivated vaccines (Tong 2019). Some live attenuated vaccines raised safety and quality concerns leading to the further development of subunit and or killed vaccines during the last decades (Mercenier et al. 2000; del Rio et al. 2018; Jiang et al. 2019). After several studies on the nonpathogenic and pathogenic microorganisms naturally found in food, some of them have been applied in the development of safer live bacterial vaccines that can induce efficient immune response to one or more expressed antigens has been proposed (Glenting et al. 2007; Detmer and Glenting 2006). In this regard, some probiotics like LAB were proposed as potential mucosal delivery vehicles for vaccine development. The use of LAB as vaccine vectors showed several attractive benefits such as the maintenance and acceptance of genetic modifications, noninvasive administration (usually intranasal or oral), simple, high safety levels, and low cost. LAB also tends to induce high levels of mucosal and systemic antibodies against the expressed foreign antigen and minimal immune responses directed against LAB cells themselves after uptake by the mucosal immune system.

The main advantages of LAB such as *L. lactis* comprised of their well-recognized status as safe (GRAS) microorganisms for a long time in fermented foods, the lack of endotoxin lipopolysaccharides (LPS) commonly found in Gram-negative bacteria, safety administration for human, the accessibility to full genome sequencing of LAB, fewer native exoproteins, and smaller genome size in comparison with Gram-negative bacteria. The production of recombinant antigens in LAB is exempted from the use of complex and multistep purification and refolding procedures which complicate the protein production and is ideal for the development of mucosal vaccines (Bahey-El-Din et al. 2010; Bermúdez-Humarán 2009). Also, the secretion of heterologous proteins produced in LAB bacterial hosts into the medium can be performed easily, thereby facilitating their purification (Morello et al. 2008). However, a major disadvantage of the mucosal route for the use of recombinant *L. lactis* as oral vaccine vectors is the huge amount of protein which is required to compensate the natural protein degradation occurring at the mucosal surfaces of the gastrointestinal tract (Bermúdez-Humarán 2009). Moreover, the low efficiency

of LAB transformation is a critical obstacle in the development of LAB vaccines and therefore the organization of effective transformation protocols is hotly demanded (Glenting et al. 2007; Tarahomjoo 2012). Thus, the development of novel vectors capable to minimize these limitations and optimize the delivery of immunogenic molecules to target tissues is a real challenge for future researches in the field.

13.10 Conclusions

LAB have been safely ingested by humans for several millenia. *L. lactis* appeared to be one of the most promising LAB in the production of oral vaccines and has been genetically engineered for the expression of a large variety of antigens and therapeutic proteins. This property has been used by scientists for the development of novel delivery vectors for immunogenic proteins into the mucosal tissues. New window for the administration of genetically engineered LAB as delivery vehicles has been opened by the successful Phase I clinical trial of a *L. lactis* strain with secretion of interleukin-10 for Crohn's disease. However, an improved potency of LAB-based delivery vehicles is required to elicit specific immune responses at lower doses. The capability of LAB vehicle carriers to stimulate effective protection against infective agents related to the antigen presentation mode (secreted, cell surface exposed or cytoplasmic), the sufficient delivery of antigen in vivo, immunization regimen (timing, dose and route), and development of LAB carrier's requirements for the most suitable LAB strains. Moreover, important steps for improvement of the vaccines efficiency is the coexpression of antigens with antigen-presenting cells targeting peptides and adjuvants in LAB vehicles along with the coadministration of immunoregulatory cytokines. The characterization of regulatory anchoring, and secretion signals from genome sequences could improve these features (Wells and Mercenier 2008). *L. lactis* provides a powerful genetic platform for the expression of different antigens which can be expressed and delivered mostly to the gut environment, often with very hopeful outcomes. The number of investigations involving lactobacilli and *L. lactis* has regularly increased over the last decade, smoothing the way for the development of a new generation of oral mucosal vaccines. In this regard, more works should be done to investigate the associated immune mechanisms within the mucosa, particularly the pathways of bacterial uptake into the immune inductive sites (DCs, M cells). The oral route for LAB administration also can have an impact on the immune response stimulated due to the diversity of mucosal inductive sites. The basic differences between the various location of antigen expression, including intracellular, surface display and secreted, as well as the properties specific to different LAB considerably influence the immune response, and therefore the selected strains should be properly assessed and used for specific antigens. However, the implementation of standardized model systems with emphasis on the most common mouse models (C57BL/6 and BALB/c), follow-up, experimental setup, and methodologies should be a valuable step forward the production and release of LAB-base vaccines.

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Promising Prospects of Probiotics and Postbiotics Derived from Lactic Acid Bacteria as Pharma Foods

14

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Abstract

The focus of food consumption has shifted from satisfaction to health-promoting impact. Consumers are becoming more aware of their health. Food and health care industries procure myriad functional foods that contain additional nutritional components. Lactic acid bacteria (LAB) play an essential role in various industries owing to their health-promoting effects. Cancer originates at the sites of chronic inflammation. Cancer is a severe public health problem which is considered as among the common cause of death globally. The incidence and mortality rate of cancer have been steadily growing worldwide. Many chemotherapy regimens are effectively used to treat cancer; however, cancer cells often acquire drug resistance that generally leads to relapse and worsening of prognosis. Therefore, continuing endless effort in finding a safer alternative or add-on treatment with lower or no side effects through the healthy dietary constituents as well as practical and appropriate supplements is prior necessary. The promising

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337

prospects of LAB probiotics and fermented products mediated by LAB have been extensively reported. Recently, there are numerous studies on LAB metabolites, postbiotics, a new preparation of non-viable supplement, exhibiting various health-promoting and beneficial physiological effects to the animal host by improving the mucosal gut barrier integrity and reducing the pathogen-induced inflammation. Therefore, a comparative review of the promising potential of probiotics and postbiotics as a functional food, ingredient or supplements and adjunctive therapeutic aids are revealed in this chapter.

Keywords

Postbiotic · Probiotic · Health impact · Anti-cancer · Anti-inflammation

14.1 Introduction

Natural herbs and foods have a long-standing tradition in many cultures to treat ailments. However, in recent years, “superfoods” have received tremendous attention. Interest is now rapidly expanding to foods with clinically enhanced properties. Currently, the health and life science sectors are undergoing significant change across all their industries. Both sectors are converged frequently to formulate medical nutrition products, having specific nutritional compositions for intervention in disease progression and symptom alleviation (Weenen et al. 2013). Hence, new markets and industries have emerged from the convergence of both health and life science sectors.

The core technology domain of medical nutrition industry is food. Nevertheless, technological development is mainly driven by pharmaceutical/pharmacological technologies. Hence, boundary-crossing developments are occurring between the food and pharmaceutical industries, particularly (Weenen et al. 2013). Pharma food products resulting from this convergence are known as Nutritional Supplements, Functional Foods and Medical Nutrition, which are food substances that are considered to improve health and exist between conventional foods and pharmaceuticals (Eussen et al. 2011; Henry 2010; Verhagen et al. 2010). Generally, pharma foods promote either in general or by specifically targeting a bodily function, such as improving digestion, bone density and so on. In the next decade, we can expect to see a shift from traditional “farmer foods” to more sophisticated pharma foods.

Cancer is a severe public health problem and it is considered as among the common cause of death globally. Throughout the past years, the incidence and mortality rate of cancer have been steadily growing worldwide. Based on the World Health Organization (WHO 2018), there were an estimated 17 million new cancer cases (excluding non-melanoma skin cancer) and 9.6 million deaths due to cancer in 2018 worldwide. In both sexes, lung cancer is the most diagnosed cancer incidence (11.6% of the total cases), followed by female breast cancer (11.6%) and colorectal cancer (10.2%). By mortality, the lung is also a leading cause of cancer death accounting for 18.4% of the total cancer deaths, followed by colorectal cancer

(9.2%) and stomach cancer (8.2%). However, women are mostly diagnosed with breast cancer and it is the leading cause of cancer death in women.

Approximately 70% of cancer deaths happened in low- and middle-income countries, mostly due to late detection of cancer and limited access to treatment. In Malaysia, cancer is the third leading cause of death. As of 2018, 43,837 cases were diagnosed and 26,395 death were reported due to cancer (GLOBOCAN 2019). Despite the advancement in cancer therapy, these treatments cause various side effects due to unspecific toxicity to normal cells (Zakuan et al. 2019). Furthermore, cancer cells often acquire drug resistance which leads to relapse and worsening of prognosis (Kovalchuk et al. 2008). The treatments of chemotherapy, radiotherapy and immunotherapy could cause weakness, fatigue, nausea, hair loss, vomiting, tissue damage and autoimmune diseases (Aslam et al. 2014; Kroschinsky et al. 2017). Exposure to chemotherapeutic drugs could result in the acquisition of multi-drug resistance (MDR).

MDR leads to significantly worse response to treatment. Conventional treatment with nanoparticles like titanium dioxide, silica, and gold complexes could also increase the risk of metastasis of cancer cells (Peng et al. 2019). Although the severity of some of these side effects are generally mild, life-threatening complications may also occur. Therefore, finding an alternative or adjunctive treatment which can reduce the side effects is necessary for the advancement of cancer treatment. Lactic acid bacteria (LAB) are Gram-positive, non-motile, non-sporulating rods and cocci (Bernardeau et al. 2008) bacteria. Probiotics are highly selected LAB, such as *Bifidobacterium* spp., *Lactobacillus* spp. and *Streptococcus* spp. (Rafter 2002) with emerging evidence as potential preventative and therapeutic agents for cancers (Zhong et al. 2014). Bioactive metabolites produced by probiotics, so-called postbiotic, confer various beneficial effects including anti-inflammatory, anti-cancer and anti-microbial. This chapter reveals the comparative beneficial impacts of different preparations of LAB.

14.2 Lactic Acid Bacteria

LAB are commonly classified as a group of facultative anaerobes that produce lactic acid as the main product during sugar metabolism. It consists of *Lactobacillus*, *Streptococcus*, *Enterococcus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, *Tetragenococcus*, *Weissella* and *Bifidobacterium* (Hutkins 2006; Masood et al. 2011). They are subdivided into rod and cocci based on their morphology. Homofermentative LAB produce mostly lactic acid and heterofermentative LAB produce acetic acid or alcohol in addition to lactic acid (Halász 2009). Phylogenetically, LAB are divided into two lines of descent. Gram-positive LAB with a DNA base composition of less than 53 mol % guanine and cytosine (G + C) are in the group of Clostridium branch. In contrast, DNA with higher base composition than 53 mol % G + C belongs to the Actinomycetes branch (Savadogo et al. 2007). The typical LAB, such as *Carnobacterium*, *Lactobacillus*, *Lactococcus*,

Leuconostoc, *Pediococcus* and *Streptococcus*, have a G + C content of less than 50 mol % and belong to the Clostridium branch (Schleifer and Ludwig 1995).

LAB are typically found as natural microbiota or microflora in animals and the human intestine. To date, LAB have been applied widely as a starter culture or co-culture of fermentation processes in food and alcoholic beverages industries in favour of producing natural and healthy products (Leroy and De Vuyst 2004). One of the core genera of LAB is *Lactobacillus*. It has been recently reclassified into 25 new genera based on the polyphasic approaches, which includes host-adapted LAB of *Lactobacillus delbrueckii* group, *Paralactobacillus* and 23 novel genera of *Acetilactobacillus*, *Agrilactobacillus*, *Amylolactobacillus*, *Apilactobacillus*, *Bombilactobacillus*, *Companilactobacillus*, *Dellaglio*, *Fructilactobacillus*, *Furfurilactobacillus*, *Holzapfelia*, *Lacticaseibacillus*, *Lactiplantibacillus*, *Latilactobacillus*, *Lapidilactobacillus*, *Lentilactobacillus*, *Levilactobacillus*, *Ligilactobacillus*, *Limosilactobacillus*, *Liquorilactobacillus*, *Loigolactobacillus*, *Paucilactobacillus*, *Schleiferilactobacillus* and *Secundilactobacillus* (Zheng et al. 2020). The name of *Lactiplantibacillus plantarum* was suggested for the plantarum-group lactobacilli.

Some LAB have been proven to be a vital probiotic bacteria, which are generally recognised as safe (GRAS) microorganisms by the Food and Drug Administration (FDA) of USA and they are also given “quantified presumption of safety” (QPS) status by the European Union. Hence, probiotic LAB play an essential role in various industries, particularly in the food industry and livestock industry (EFSA Panel on Biological Hazards (BIOHAZ) 2013). Furthermore, LAB can produce an array of compounds which contribute to the improvement of nutritional value, organoleptic, technological and shelf life of the end product (Ayad et al. 2004). The prolong of shelf life by LAB fermentation is mainly due to the rapid acidification of food attributed to the production of organic acids, primarily lactic acid. However, the production of other metabolites, such as acetic acid, ethanol, aroma compounds, bacteriocins, exopolysaccharides and several enzymes, is of importance (De Vuyst and Leroy 2007).

14.3 Health Impacts of Bacterial Probiotics

Probiotic was initially defined as a live microbial feed supplement which beneficially affects the host animal by improving its intestinal microbial balance (Fuller 1989). However, this definition is unsatisfactory and imprecise as more probiotics were demonstrated to confer other beneficial health impacts. Food and Agriculture Organization and World Health Organization define probiotic bacteria as “live microorganisms which, when administered in adequate amounts confer a health benefit on the host” (FAO/WHO Expert Consultation 2001). To be classified as a probiotic strain, several aspects of functionality must acquire: 1) tolerance to acid and human gastric juice, 2) bile tolerance (for survival in the small bowel), 3) adherence to epithelial surfaces and persistence in the human gastrointestinal tract (GIT), 4) immuno-stimulation, but no pro-inflammatory effect, 5) antagonistic

activity against pathogens and 6) antimutagenic and anticarcinogenic properties (Lee and Salminen 1995).

Probiotics are mainly associated with LAB. *Lactobacillus* and *Bifidobacterium* are the 2 genera of LAB that are mostly employed for various industrial applications due to their long history of safe applications (Linares et al. 2016). In addition, *Propionibacterium* and *Streptococcus* were also observed to possess beneficial properties and hence they are also vogue as probiotic microorganisms. Dairy propionibacteria promote bifidobacteria growth in the gut, enhance the use of nutrients, hypocholesterolemic and immunomodulation effects (Zárate 2012), while *Streptococcus thermophilus* produces a high amount of β -galactosidase in the GIT, which is essential for lactose hydrolysis, making it beneficial to improve lactose intolerance (Rul et al. 2011). However, other bacterial and yeast species have been suggested to be a potential probiotic strain. Recently, a few strains of short-chain fatty acids (SCFA) producing *Escherichia coli* isolated from adult human microbiota were proven to possess promising probiotic properties (Nakkarach et al. 2020).

In the past decade, more health impacts of LAB were demonstrated, such as enhanced immune response, colonic microbiota balance, vaccine adjuvant effect, reduction of faecal enzymes implicated in cancer initiation, treatment of diarrheal diseases, antibiotic therapy, control of rotavirus and *Clostridium difficile*, control of gastric ulcers, reduction of serum cholesterol, antagonism against food-borne pathogens and tooth decay organisms, and lactose intolerance and malabsorption (Masood et al. 2011). Disruptions of the balance of gastrointestinal microflora will disturb the homeostasis, leading to intestinal microbial dysbiosis and other diseases associated with an unhealthy gut. Goldenberg et al. (2017) reported that probiotics could reduce the risk of *Clostridium difficile*-Associated Diarrhoea (CDAD) incidence rate by 60% on average. Patients treated with *Lactobacillus acidophilus* and *Lactobacillus casei* demonstrated a lower incidence rate of CDAD and antibiotic-induced diarrhoea (Gao et al. 2010). Supplementation of probiotics in patients with gestational diabetes mellitus improved glycaemic control and decreased triglycerides and VLDL cholesterol concentrations (Karamali et al. 2016).

As for immunity responses, administration of probiotic could modulate both innate and adaptive immunity (Vitetta et al. 2017). Probiotics exert a positive effect on human immunological defence by stimulating macrophages, NK cells, antigen-specific cytotoxic T-lymphocytes, and the release of different cytokines (Ashraf and Shah 2014). Ferreira dos Santos et al. (2016) reported that *Lactobacillus plantarum* Lp62 decreased the IL-8 secretion by *Salmonella Typhi*-stimulated HT-29 cells and prevented the adhesion of pathogens to the epithelial cells. Moreover, *L. plantarum* Lp62 inhibited the inflammatory stimulation in epithelial cells and macrophages by secreting TNF- α , IL1- β , and IL-17, while increased IL-10 secretion by mononuclear cells. Supplementation of probiotic *Lactobacillus rhamnosus* GG during breastfeeding stimulates the maturation of humoral immune response by increasing the total number of immunoglobulin secreting cells, particularly, IgG, IgA and IgM (Rinne et al. 2005).

Beneficial bacteria may also stimulate wound healing. Recently, Han et al. (Han et al. 2019) studied the effect of probiotics on oral mesenchymal stem cells and wound healing. They revealed that the probiotic *Lactobacillus reuteri* could activate the potentials of gingival mesenchymal stem cells and enhanced the wound healing process by regulating the pathway of PI3K/AKT/ β -catenin/TGF β 1. As for the wound healing effect, Mohseni et al. (2018) reported that 12 weeks supplementation of probiotic decreased ulcer length, depth and width of a wound in patients with a diabetic foot ulcer. Orally administered yoghurt containing probiotic *Lactobacillus gasseri* has significantly accelerated the wound healing of acetic acid-induced gastric ulcer in rats (Uchida et al. 2010). Probiotic of *Lactobacilli*, *Bifidobacteria* and *Streptococcus* species accelerated the acetic acid-induced gastric ulcer in rats by expressing and production of angiogenesis promoting vascular endothelial growth factor (Dharmani et al. 2013).

Currently, emerging evidence that relates to gut microbiota and the function of the central nervous system (Tillisch 2014) are extensively reported. Daily administration of probiotic formulation consisting of *Lactobacillus helveticus* R0052 and *Bifidobacterium longum* R0175 could reduce anxiety-like behaviour in rats and alleviate psychological distress in human volunteers (Messauodi et al. 2011). Folate is a vitamin B that plays a vital role in the health and physiological functions of human and animals. Some LAB have the capability of producing folate extracellularly. Interestingly, *L. plantarum* I-UL4 was suggested to be employed for the enhancement of folate level in milk and dairy products since it produced the highest folate extracellularly in comparison to other LAB species (Nor et al. 2010). Kobyliak et al. (2018) demonstrated that a multi-strain probiotic containing *Bifidobacterium*, *Lactobacillus*, *Lactococcus* and *Propionibacterium* reduced liver fat, aminotransferase activity, TNF- α and IL-6 levels in non-alcoholic fatty liver disease patients.

The focus of food consumption today has shifted from satisfaction to health-promoting impact. Consumers are becoming more aware of their health and the food industry is going hand in hand with the production of so-called functional foods, containing additional nutritional components. LAB play an important role in food and beverages industries owing to its GRAS and QPS status, which provide health-promoting effects when consumed in addition to several other reasons. The growth of LAB increases carbohydrate content of the foods they ferment with reduced pH condition resulting from the production of lactic acid from carbohydrate fermentation (Solioz et al. 2011). Certain LAB may secrete bacteriocin extracellularly. Bacteriocins have been suggested as an alternative to replacing chemical preservatives and heat treatment, to preserve food more naturally and rich in organoleptic and nutritional properties (Gálvez et al. 2007). Application of bacteriocins as bio-preservatives in food preparation is safe for consumers as they are inactivated by pancreatic or gastric enzymes (Liu et al. 2011). The combined action of both low pH and bacteriocins secretion is essential in the food industry to extend the shelf life by inhibiting the growth of food spoilage and pathogenic microorganisms (Gálvez et al. 2007). Bacteriocins are inhibitory peptide molecules that act against food-borne pathogens such as *Clostridium botulinum*, *Staphylococcus aureus* and *Listeria monocytogenes* (Nettles and Barefoot 1993).

L. plantarum IUL-4 is the first *L. plantarum* strain reported to harbour both class I *plw* and class II *plnEF* bacteriocin genes simultaneously (Tai et al. 2015). Both classes of plantaricin genes contributed to the broad anti-microbial activity against various pathogens such as *L. monocytogenes*, *Salmonella enterica*, *E. coli* and Vancomycin resistant *enterococci* (VRE) (Kareem et al. 2014). Several other LAB (*Lactococcus lactis* subsp. *lactis*, *Pediococcus pentosaceus*, *Leuconostoc mesenteroides* *Lactobacillus curvatus*, *Lactobacillus sakei* and *L. plantarum*) have also been documented for the secretion of bacteriocin (Todorov et al. 2006; Shin et al. 2008; Mataragas et al. 2003; Aasen et al. 2000; Kormin et al. 2001). Pediocin secretion from three *Pediococcus* species (*P. acidilactici* NCIM 2292, *P. pentosaceus* NCIM 2296 and *P. cervisiae* NCIM 2171) showed significant inhibition against *Bacillus cereus*, *L. monocytogenes*, and *S. aureus* but moderate against *E. coli* and *Pseudomonas* and less against *Clostridium perfringens* (Jamuna and Jeevaratnam 2004). The food acidification caused by LAB changes the texture due to the precipitation of some proteins (Solioz et al. 2011). Exopolysaccharides forming LAB such as *Streptococcus thermophilus* and *Lactobacillus delbrueckii* subsp. *bulgaricus* are used in the manufacturing of yoghurt to improve texture, avoid syneresis and increase the viscosity of products (Ruas-Madiedo et al. 2002). LAB produce aromas and flavours and accelerate the cheese's maturation through its proteolytic and lipolytic activities (Kongo 2013).

Applications of probiotics have been extended from human to agricultural applications, including animals and plants. In response to consumers' demands of natural product, probiotics have been widely used in agriculture as an alternative growth promoter to replace conventional antibiotic treatments and synthetic chemical feed (Fuller 1989), owing to the broad range of anti-microbial activity against pathogens. Several reports have demonstrated the beneficial effects of probiotic supplementations in animal feed. Corn-soybean meal supplemented with probiotic (*Pediococcus acidilactici*) increased villus height in duodenum and ileum while lowering the number of coliforms of the ileum and serum cholesterol level (Taheri et al. 2010). Probiotic supplementation showed lower oxidative spoilage in broiler breast meat over a 7-day post-mortem ageing, therefore increasing the shelf life of chicken meat (Abdulla et al. 2018).

Recently, probiotics isolated from Malaysian foods have been reported to produce various versatile extracellular hydrolytic enzymes (Mohamad Zabidi et al. 2020). *L. plantarum* that grow on palm kernel cake secreted a cocktail of multi extracellular hydrolytic enzymes (Lee et al. 2019). These enzymes degrade fibrous and crystalline cellulosic materials, thereby improving the nutritional value of fermented palm kernel cake substantially to be used as alternative feed ingredients to reduce the production cost of animals (Mohamad Zabidi et al. 2020; Lee et al. 2019). Alshelmani et al. (2016) suggested that inclusion of 15% fermented palm kernel cake could replace up to 30% of yellow maize in broiler diet, which can be reflected in the cost savings of feed for the poultry industry.

Furthermore, *Lactobacillus* and *Bifidobacterium* strains have also been found useful in the rapid removal of toxic metals such as cadmium and lead from the water as reported by Halttunen et al. (Halttunen et al. 2007). A similar study has also been

reported by Bhakta et al. (2012), whereby mud and sludge-isolated *Lactobacillus reuteri* Cd70–13 and Pb71–1 were used as a heavy metal sorbent to eliminate heavy metals in the ambience. Mechanisms such as complex formation, ion exchange, adsorption, chelation and microprecipitation have been proposed to be involved in metal biosorption (Ahalya et al. 2003).

14.4 Health Impacts of Postbiotic

Postbiotics are defined as non-viable soluble bioactive metabolites produced by probiotic LAB, which exerts a myriad beneficial effect on the host, directly or indirectly. Several terms have been proposed for postbiotic preparation, such as metabiotics, biogenics, metabolites or simply cell-free supernatants (CFS), soluble factors secreted by live probiotic, which when administered in adequate amount will confer beneficial effects (Tsilingiri et al. 2012). The composition of soluble bioactive components that present in postbiotics could vary substantially amongst the producer cells, attributing to the fermentation condition, such as growth medium and physical parameters of the fermentation process. The bioactive compounds of postbiotics include organic acid, bacteriocin, hydrogen peroxide, ethanol, fatty acids, diacetyl, acetaldehyde, acetone, reuterin, reutericyclin, SCFA, hydrolytic enzymes, peptides, teichoic acids, peptidoglycan-derived muropeptides, endo- and exo-polysaccharides, cell surface proteins, vitamins, [plasmalogens](#), bacteriocin-like compounds and other low molecular mass compounds with anti-microbial activities (Aguilar-Toalá et al. 2018; Konstantinov et al. 2013; Paul et al. 2018).

The bioactive compounds of postbiotic target the host-microbe-pathogen interface rescuing biotic and immune unbalances, as well as inflammation, thus providing new therapeutic opportunities (Puccetti et al. 2020). Postbiotics mimic the beneficial health effects of probiotics while avoiding the risk of administering live microorganisms. The supplementation of viable probiotics has been associated with systemic infections such as bacteraemia and fungemia, as well as transferring of antibiotic resistance gene and virulence factor, and risk of sepsis. The incidents of systemic infections by probiotics have been reported for premature infants, immunocompromised and impairment of epithelial barrier patients (Paul et al. 2018). Treatment with a combination of probiotics resulted in the death of 16% of acute pancreatitis patients, as compared to 6% in the placebo group (Besselink et al. 2018). Furthermore, consumption of live bacteria could also induce interaction with the compound of food matrix or ingredient which may cause bloating.

The growing evidence demonstrates that probiotic metabolites exert various beneficial health impacts, but not limited to, anti-microbial, antioxidant, and immunomodulatory in the same way as the parent-live probiotics over the last 10 years. Hypertension has been associated with gut microbiome dysbiosis. The manipulation of the gut microbiota can lead to the development of new antihypertensive therapies (Robles-Vera et al. 2017). The first evidence of SCFA that present in postbiotic metabolite could decrease blood pressure was reported in 1983, whereby hypotension was noted when acetate was added to haemodialysis lysate (Muralitharan et al.

2020). In addition, various *Lactobacillus* sp. have been identified to produce bioactive peptides, which are useful in promoting human health, including reducing the risk of hypertension (Raveschot et al. 2018).

Certain postbiotics may be a rich bacteriocin source for the inhibition of a wide range of pathogenic bacteria that are likely to reduce the occurrence of infection (Cicenia et al. 2014). Reuterin that produced by *Lactobacillus reuteri* is the first molecule identified with potent anti-pathogenic activity against a broad spectrum of microorganisms including *Escherichia*, *Salmonella*, *Shigella*, *Proteus*, *Pseudomonas*, *Clostridium*, *Staphylococcus*, fungi, and protozoa, many of which are pathogenic to humans (Talarico and Dobrogosz 1989). Six strains of *Lactiplantibacillus plantarum* (formerly was known as *Lactobacillus plantarum*) isolated from Malaysian foods exhibited antagonistic activity against *S. typhimurium*, *E. coli*, followed by *L. monocytogenes* and Vancomycin-resistant enterococci (Thanh et al. 2010).

Exopolysaccharides (EPS) produced by *Lactococcus lactis* F-mou showed high anti-microbial activity against *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *E. coli*, *L. monocytogenes*, *B. cereus*, *Proteus mirabilis*, *Acinetobacter baumannii*, *Enterobacter cloacae* and *Candida albicans* (Nehal et al. 2019). In addition, *L. lactis* F-mou also displayed potent beta-carotene bleaching inhibition and high radical scavenging activity (> 90%). EPS produced by *Lactobacillus reuteri* SHA101 and *Lactobacillus vaginalis* SHA110 isolated from the gut cecum of healthy hen showed potent radical scavenging activity of hydroxyl DPPH (2,2-diphenyl-1-picrylhydrazyl) and superoxide radicals and reducing power (Rajoka et al. 2019).

Antioxidant properties of postbiotics derived from *L. plantarum* were demonstrated in the study conducted by Izuddin et al. (2020), whereby an increase of hepatic antioxidant enzyme glutathione peroxidase (GPx) concentration in serum and ruminal fluid were observed. He et al. (2017) demonstrated a preventative effect against neonatal gut-derived *E. coli* K1 infection through promoting the maturation of neonatal intestinal defence. The addition of *L. casei* subsp. *rhamnosus* reduced the adherence of pathogenic bacteria, enteropathogenic and enterotoxigenic *E. coli* and *Klebsiella pneumoniae* to the tissue receptor of Caco-2 intestinal cells (Forestier et al. 2001). The CFS metabolites of four isolates of LAB isolated from the breast milk of healthy women demonstrated anti-viral activity (32% inhibition) against HIV-1 infection (Martín et al. 2010).

Postbiotics have also been reported to modulate inflammatory responses. CFS of *Lactobacillus fermentum* inhibited the pro-inflammatory response of HeLa 229 cells to *Yersinia enterocolitica* by inhibiting the production of IL8 (Frick et al. 2007). *Lactobacillus rhamnosus* and its CFS were evaluated for their immunomodulatory effects on human dendritic cells (DC) challenged with *E. coli* (Bermudez-Brito et al. 2014). The results showed that CFS was more effective than live probiotics in reducing the secretion of pro-inflammatory cytokines when DC was challenged with *E. coli*. Furthermore, in the presence of *E. coli*, both treatments induced the production of TGF-1 β , an inhibitor for the synthesis of pro-inflammatory cytokines, as well as an activator for the toll-death receptor signalling molecule to enhance the innate immunity. Therefore, cultured CFS is a safer alternative to live bacteria to

modulate immune responses of human DC. In another study, *L. casei* and its postbiotic reduced the mRNA level of (IL)-1 α , IL-6, IL-8 and increased the secretion of IL10 in ileal and colonic mucosa in post-infectious irritable bowel syndrome (PI-IBS) (Compare et al. 2017).

Recently, *E. coli* KUB-36 metabolite has been reported to reduce the production of pro-inflammatory cytokines IL-1 β , IL-6, IL-8 and TNF- α , but induced the secretion of IL-10 in lipopolysaccharide-induced THP-1 macrophage cells (Nakkarach et al. 2021). Postbiotics has also been shown to be a novel therapeutic agent for the prevention and treatment of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), due to their immunomodulatory properties (Mantziari et al. 2020). Gou et al. (Gou et al. 2020) suggested that intestinal microbiome and their metabolites can serve as a potential preventive/treatment target for intervention, particularly among those who are susceptible to the SARS-CoV-2 infection. However, more clinical trials should be performed to verify the suggestion.

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Nondairy Foods as Potential Carriers of Probiotic Bacteria and Postbiotics

15

Fereshteh Ansari and Hadi Pourjafar

Abstract

Dairy-based foods are suitable substrates as a carrier for probiotic microorganisms, nevertheless the great number of lactose intolerant people, their high fat content, and also by reason of the increasing vegetarianism the consumers are looking for substitutes. Consequently, studies have been extensively done on the possibility of probiotic microorganisms in nondairy-based carriers, for instance, vegetables, fruits, cereals, and meat products. This chapter reviews the utilization of probiotics in nondairy-based foodstuffs and some of the technical issues. These issues comprise the efficiency and viability of probiotic microorganisms in nondairy foods; sensory and acceptability of nondairy probiotic products, technological challenges and advancements of nondairy probiotic foods, and postbiotics and food applications of postbiotics.

Keywords

Nondairy foods · Probiotics · Carrier · Postbiotics

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351

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15.1 Introduction

Functional foods are nutrients that have possible positive impacts on healthiness beyond basic nourishment (Ansari et al. 2020b; Granato et al. 2020). The probiotic foodstuffs market is growing very quickly because of enlarged customer awareness about the influence of these functional foods on health and fitness, and currently probiotic products include 60–70% of the entire functional food market (Tripathi and Giri 2014). The universal market for probiotic products (foods and drinks) was about 24.8 billion € in 2011, over 31.1 billion € in 2015 and is predicted to reach about 43 billion € until 2020 (Aspri et al. 2020).

Dairy food products have been conventionally considered as the greatest carriers for probiotic microorganisms. Nevertheless, recently, alternative nondairy foodstuffs have been applied for the separation of possible probiotic isolates for the manufacture of innovative nondairy probiotic foods, and also on the other hand it is determined that nondairy probiotic products have been more appealing by reason of consumer demands (Aspri et al. 2020; Min et al. 2019). This chapter reviews the current knowledge concerning several nondairy probiotic products existing worldwide, for instance, vegetables, fruits, meat products, cereals, and confectionary products with the purpose of give a vision to the issue and to display a way advancing for the future.

15.2 Important Nondairy Probiotic Foods

Various probiotic products have been produced and marketed in different parts of the world, some of which are related to nondairy probiotic products. In the following, the most important nondairy probiotic foods are reviewed (see Table 15.1).

15.3 Fruits and Vegetables

The nutritional and biological potential of fruits and vegetables has led to the conversion of these foods into products with multiple properties in maintaining the balance of microorganisms. These beneficial effects cause the water of these products to be used to treat various diseases. Studies have shown that the presence of potassium salts, bioflavonoids, vitamins, and alkalis in fruit and vegetable and their lack of fat can have beneficial effects in the prevention and treatment of cardiovascular disease (DiRienzo 2014; Fernandez and Marette 2017). It has been shown that the beneficial effects of fruits and vegetables can be improved by a biological process such as lactic fermentation, so that today researchers are studying lactic fermentation of vegetables as a natural preservation method. In addition, some fruits and vegetables contain prebiotics that stimulate the growth of certain probiotics (Szutowska 2020).

Many studies have used probiotics in dairy products, but lactose intolerance and cholesterol levels of these products are the two main disadvantages that have led to

Table 15.1 Some selected publications related to nondairy probiotic products during the last 5 years

Probiotic product	Probiotic strains	Probiotic numbers (log/g or mL)	Reference
Carrot and orange juice	<i>L. plantarum</i>	~8 and 9	Valero-Cases et al. (2017)
Mango and guava juice	<i>L. casei</i> , <i>L. bulgaricus</i> , <i>Streptococcus thermophilus</i>	7–8	Maldonado et al. (2017)
Apricot juice	<i>B. lactis</i> Bb-12, <i>B. longum</i> Bb-46, <i>L. casei</i> 01, <i>L. acidophilus</i> La-5	~7	Bujna et al. (2018)
Tomato juice	<i>L. plantarum</i> , <i>L. casei</i>	–	Liu et al. (2018)
Sohiong juice	<i>L. plantarum</i> MCC 2974	10	Vivek et al. (2019)
Pomegranate juice	<i>L. plantarum</i> ATCC 14917	8.8	Mantzourani et al. (2019)
Banana, strawberry and juçara	<i>B. animalis</i> subsp. <i>Lactis</i> , <i>L. acidophilus</i> , <i>L. casei</i> , <i>L. plantarum</i>	~5 and 7	de Oliveira Ribeiro et al. (2020)
Cornelian cherry (<i>Cornus mas</i> L.) drink	<i>Saccharomyces cerevisiae</i> DDNd10, <i>Pichia kudriavzevii</i> DCNa, <i>Wickerhamomyces subpelliculosus</i> DFNb6	~8	Di Cagno et al. (2020)
Fermented beverage from maize and rice	<i>L. plantarum</i> , <i>L. acidophilus</i> , <i>Torulaspora delbrueckii</i>	7	Freire et al. (2017)
Fermented oat flour drink	<i>L. plantarum</i>	14	Gupta and Bajaj (2017)
maize-based substrate	<i>L. paracasei</i> LBC-81, <i>Saccharomyces cerevisiae</i> CCMA 0731, <i>Saccharomyces cerevisiae</i> CCMA 0732, <i>Pichia kluyveri</i> CCMA 0615	6	Menezes et al. (2018)
Legume sprouts	<i>L. plantarum</i> 299 V	9	Świeca et al. (2018)
Breadfruit flour drink	<i>L. plantarum</i> DPC 206, <i>L. acidophilus</i> , <i>L. casei</i> Shirota	7–8	Gao et al. (2019)
Wheat/rice cereal infant products	<i>B. animalis</i> subsp. <i>lactis</i> BB-12 [®]	6	Leboš-Pavunc et al. (2019)
Dry-fermented pork neck and sausage	<i>L. acidophilus</i> Bauer, <i>B. animalis</i> BB-12, <i>L. rhamnosus</i> LOCK900	~6–8	Wójciak et al. (2017)
Beef sausage	<i>L. plantarum</i> TN8, <i>Pediococcus acidilactici</i> MA18/5 M	~8	Slima et al. (2018)
Bovine Salami	<i>L. plantarum</i> 299v	7	Blaiotta et al. (2018)
Fermented sausage	<i>B. longum</i> KACC 91563	~3–6	Song et al. (2018)

(continued)

Table 15.1 (continued)

Probiotic product	Probiotic strains	Probiotic numbers (log/g or mL)	Reference
Dry fermented sausage	<i>L. paracasei</i> LPC02	~7–8	Coelho et al. (2019)
Fermented sausage	<i>L. paracasei</i> , <i>L. rhamnosus</i> GG	–	Bis-Souza et al. (2019b)
Dry-cured meat sausages	<i>L. plantarum</i>	~8	Sirini et al. (2020b)
Spanish Salchichón	<i>L. paracasei</i> , <i>L. rhamnosus</i> GG	~8	Bis-Souza et al. (2020)

their nonconsumption by some people. Therefore, the use of probiotics in fruit and vegetable foods can be a good alternative for a group of people with special needs (i.e., vegetarians and people with allergic reactions to milk proteins) (Aspri et al. 2020; Min et al. 2019).

Another important point to consider is the viability of probiotics in fruit and vegetable products. Due to the fact that the pH of fruits and vegetables is low (pH 2.5–3.7), and also bacteria are sensitive to acidic conditions, it is necessary to use strains that can survive in these conditions and make the product healthier and increase the shelf life. Therefore, the addition of probiotics to fruit and vegetable-based foods and beverages is more complex than dairy products because of the need to protect them from acidic environmental conditions (Min et al. 2019). It has been shown that in fruit juices (pH 3.7–4.3) Lactobacilli can resist and survive better than Bifidobacterial (Patel 2017). Nevertheless, some fruit juices may contain components that sustain the survivability of probiotic microorganisms like ascorbic acid, that declines O/R potential, organic acids or saccharides that may be used as a carbon source or cellulose that can guard these microorganisms throughout processing and storing (Martins et al. 2013).

Beetroot, cabbage, carrot, olive, oranges, pineapple, mango, strawberry, blueberry, cranberry, sweet lime, cashew apple, and grapes are some instances of vegetable and fruit juices employed as food substrates for the delivery of probiotic microorganisms. Various types of probiotic vegetable/fruit products have been technologically advanced and commercialized, including fermented, juices, deserts, and dried forms. Extensive variety of probiotic strains, mostly species of Bifidobacteria and Lactobacillus, for instance, *Bifidobacterium bifidum*, *B. longum*, *B. breve*, *Lactobacillus acidophilus*, *L. rhamnosus*, *L. casei*, *L. paracasei*, *L. plantarum*, and *L. fermentum* have been broadly used in the advance of several vegetable/fruit probiotic products (Aspri et al. 2020; Min et al. 2019).

Probiotic vegetable/fruit can be produced either with straight adding of the probiotic strain, for example, into the juice of them or via the fermentation with the probiotic microorganism. The fermentation is more valuable because probiotic strain grows into the vegetable/fruit texture or juice to a more adapted probiotic strain and a low-sugar product, which may perhaps develop its survival rates (Pereira

and Rodrigues 2018). Also, throughout the fermentation process, the metabolites of probiotics such as exopolysaccharides and bacteriocins can aid to improve the quality of the probiotic product and rise their shelf life through storing time (Aspri et al. 2020).

Newly, various studies focused on the manufacture of fermented probiotic and synbiotic vegetable/fruit, for instance pomegranate extracts, and Cornelian cherry drinks via delignified wheat bran (Kazakos et al. 2020; Liu et al. 2018; Valero-Cases et al. 2020), carrot-orange extracts and nectars with diverse inulin concentrations (Alizadeh et al. 2019; Lu et al. 2018), synbiotic apple juice or orange extract with oligofructose (Miranda et al. 2019; Pimentel et al. 2015; Zhu et al. 2020), blended drink of orange extract, hibiscus tea, and oligofructose (Miranda et al. 2019), and mixed red fruit drinks of papaya, blackberry, and strawberry added with three distinct prebiotics including inulin, galactooligosaccharides (GOS), and fructooligosaccharides (FOS) (Bernal-Castro et al. 2019).

Pereira et al. (2011) studied the production of probiotic cashew apple juice and they showed the cell counts of *L. casei* in the product after 6 weeks storage was about 8 log cfu/mL (Pereira et al. 2011). Similar results have been shown in melon juice (Fonteles et al. 2013) and pineapple juice (Sheehan et al. 2007).

Sheehan et al. (2007) described wide alterations relating to the acid resistance characteristic of *Bifidobacterium* and *Lactobacillus* in pineapple, orange, and cranberry juices. The survival rate of probiotics in pineapple and orange juices was higher than cranberry juice. The number of *L. rhamnosus*, *L. casei*, and *L. paracasei* was above 6 log cfu/mL in pineapple juice and over 7 log cfu/mL in orange juice for 12 weeks. In other study, a probiotic drink using coconut water was produced via fermenting it by means of *L. plantarum* (Prado et al. 2015).

It has been studied the suitability of beet juice (Yoon et al. 2005), cabbage juice (Ningrum et al. 2019; Yoon et al. 2006), and tomato (Dzandu 2019) by *L. casei*, *L. acidophilus*, *L. plantarum*, and *L. delbrueckii*, and the number of the viable cells the four probiotics in all fermented products ranged from 5–8 log cfu/mL after 4 weeks storing at 4 °C.

Kun et al. (2008) showed that carrot juice can promote the growth of *B. bifidum* B 3.2, *B. bifidum* B7, and *B. lactis* Bb-12. All probiotic strains displayed high primary cell counts of 10 log cfu/mL (Kun et al. 2008).

Mantzourani et al. (2018) applied *L. plantarum* ATCC 14917 in producing probiotic Cornelian cherry juice. Consequences of their study disclosed that the number of viable cells of *L. plantarum* ATCC 14917 was acceptable during cold storage time and no significant organoleptic changes were observed in both fermented and non-fermented samples (Mantzourani et al. 2018). Also, in another study, they produced and surveyed fermented pomegranate juice by use of the same strain (*L. plantarum* ATCC 14917) (Mantzourani et al. 2019).

Bujna et al. (2018) investigated mono- and mixed probiotic cultures for production of apricot juice as a new nondairy probiotic beverage. Fermentation process developed using probiotic bacteria individually disclosed cell numbers of, 7.06, 7.16, 7.2, and 7.25, log (cfu/mL h) *L. casei* 01, *L. acidophilus* La5, *B. lactis*

Bb-12, and *B. longum* Bb-46 strains, respectively, even though sample fermented via a mixed culture a higher cell numbers was detected (Bujna et al. 2018).

Li et al. (2019) demonstrated that using *L. plantarum* ATCC 14917 in apple juice can improve the phenolic composition of apple juice and promote its total antioxidant capacity. Also, Peng et al. (2020) assessed the fermentation performance of a combination of *Lactobacillus* spp. in cloudy apple juices from nine cultivars. The consequences disclosed that cultivar impacted most the characteristics of the fermented cloudy apple juice. The highest probiotic number (6.37×10^8 CFU/mL) and acetic acid contents (2.67 mg/mL) achieved from the fermented cloudy apple juices made from Changfu (Peng et al. 2020).

In another study by Zhu et al. (2020), survival rate of *L. sanfranciscensis* into three diverse nondairy carrier (apple, tomato, and orange) were investigated throughout 4 weeks storage at 4 °C. Results showed that the survivability of probiotics in all samples met the recommended level of $>6-7$ log cfu/mL at the end of storage time.

15.4 Cereals

Cereals are one of the most important sources of protein, carbohydrates, vitamins, minerals, and fiber for humans. They can be used as sources of indigestible carbohydrates and, with their water-soluble fiber such as beta-glucan, arabinoxylan, and oligosaccharides such as galacto and fructo oligosaccharides and resistant starch, as a prebiotic, can selectively stimulate the growth of *Lactobacilli* and *Bifidobacteria* in the colon. Whole grains are sources of phytochemicals such as phytosterols, phenolic compounds, antioxidants, phytic acid, and sterols (Lamsal and Faubion 2009; Ogunremi et al. 2020).

The nutritional quality of grains is sometimes lower than that of milk due to their lower protein content, deficiency of certain amino acids such as lysine, inability to digest starch, hard nature of grains, and the presence of anti-nutritional compounds such as phytic acid, tannins, and polyphenols. These compounds vary widely in chemical structure and function, so fermentation can reduce the levels of indigestible carbohydrates, poly and oligosaccharides, improve protein quality, and increase lysine levels. Some amino acids may also be synthesized and the availability of B vitamins may increase. Fermentation also provides the optimum pH for the enzymatic degradation of phytate and the release of minerals such as manganese (an important factor for the growth of lactic acid bacteria), iron, zinc, and calcium. Various strains of *Lactobacilli* and *Bifidobacteria* need fermentable carbohydrates, amino acids, B vitamins, nitrogen, and minerals to grow, and different types of cereals (like wheat, barley, millet, maize, oats, rye, and sorghum) are an inexpensive culture and good carrier for these probiotics (Charalampopoulos et al. 2002; Chavan et al. 2018; Kocková et al. 2013). Some instances of traditional cereal-based fermented beverages (like Mahewa, Bushera, Boza, Togwa, and Pozol) are described here.

Mahewu is a sour cereal-based probiotic beverage and it is made by means of a multi-grain combination which can contains millet, maize, malt, sorghum, and wheat

flour (Panghal et al. 2018). The natural fermentation process is made via the malt's microflora at about 25 °C. The chief bacteria isolated from Mahewu is *L. lactis* subsp. *lactis* (Blandino et al. 2003). Bushera is an old beverage made with millet or sorghum flour, and chiefly *L. brevis*, and another LAB like Enterococcus, Lactococcus, Leuconostoc, and Streptococcus were isolated from Bushera (Muyanja et al. 2003).

Boza is a traditional beverage from the natural fermentation of cereals like maize, wheat, millet, rye, and others that are mixed with sugar (Todorov et al. 2008). Boza displays a great variety of LAB and yeasts which contain *L. acidophilus*, *L. coprophilus*, *Lactobacillus brevis*, *L. plantarum*, *L. fermentum*, *Leuconostoc mesenteroides*, *Leuconostoc reffinolactis*, *Saccharomyces cerevisiae*, *Candida tropicalis*, *Candida glabrata*, *Geotrichum candidum*, and *Geotrichum penicillatum* (Heperkan et al. 2014). Togwa is another cereal-based fermented probiotic beverage from China and Japan. This traditional probiotic drink is produced via fermenting multi-grains like sorghum, finger millet, and maize flour with some probiotics, for instance Streptococcus and mainly *L. plantarum* (Mugula et al. 2003).

Various investigations have been done to promote cereal-based probiotic products and to assess the suitability of diverse cereal grains to improve probiotic microorganisms' growth and uphold their survivability into products during manufacturing and storage time and also throughout gastrointestinal conditions (in vitro and in vivo). Świeca et al. (2018) surveyed legume sprouts as a nondairy carrier for *L. plantarum* 299 V. The sprouts that have been supplemented with the probiotic, a lower mesophilic bacteria flora, particularly LAB, was detected in comparison with the control groups (without probiotic). The *L. plantarum* number was also steady throughout the cold storage period (Świeca et al. 2018).

In a study by Menezes et al. (2018), *L. paracasei* LBC-81 was employed lonely and in mix with *S. cerevisiae* CCMA0731, *S. cerevisiae* CCMA0732, and *Pichia kluyveri* CCMA0615 into maize-based substrate as a different functional food. Three out of the four strains displayed acceptable survivability with counts more than 6 log cfu/mL, which is the suggested for probiotic foodstuffs, excluding the *Pichia kluyveri* which reduced throughout fermentation and storage period (Menezes et al. 2018). Leboš-Pavunc et al. (2019) studied the effect of dehydrated wheat/rice media on probiotic activity of *B. animalis* ssp. *lactis* BB-12. The probiotic strain (*B. animalis* ssp. *lactis* BB-12) displayed the high survivability throughout the storage time of 106 weeks (Leboš-Pavunc et al. 2019). Gao et al. (2019) investigated the development of a probiotic beverage by means of breadfruit flour as a substrate, and *L. plantarum* DPC 206 and *L. acidophilus* as probiotic strains. The produced probiotic beverage was found to have adequate cell viability and also satisfactory sensory characteristic.

Soy milk is the main and well-known food in Asian countries that is now consumed all over the world. Soybean milk is a stable emulsion of oil, water, and protein which is prepared by soaking dried soybeans and grinding them. Soy milk is a rich source of high-quality plant protein, isoflavones and B vitamins that are free of milk sugar or lactose and is a good choice for people with lactose intolerance. Laboratory studies on probiotic microorganisms have shown that soy milk is a

good substrate for some probiotic bacteria, such as *L. casei*, *L. helveticus*, *L. fermentum*, *L. reuteri*, and *L. acidophilus* (Niamah et al. 2017; Shilpa et al. 2011; Shimakawa et al. 2003; Taghizadeh et al. 2018).

In a related study, Homayouni Rad et al. (2020) investigated soy ice cream (produced via the powder of soy milk) as a carrier for effective delivering of *L. casei*. The viability of mentioned probiotic bacteria was assessed over storage time (180-day, at -25°C). The results disclosed considerable changes in the count of *L. casei* in this product subsequently freezing and during storage time ($p < 0.05$). The most significant drop was perceived through the first 60 days approximately 1.83 logs after that the tendency of survival of *L. casei* leveled off over the next 120 days (Homayouni et al. 2020b). In similar study, Norouzi et al. (2019) surveyed the survival rate of probiotic *L. paracasei* ssp. *paracasei* into fermented and non-fermented frozen soy dessert during 180 days storage at -24°C . The results showed a considerable rise ($p < 0.05$) in overrun (42.57 ± 8.5) values in fermented probiotic frozen soy dessert compared to other samples. In contrast to non-fermented samples, there was no considerable ($p < 0.05$) reduction in cell numbers of *L. paracasei* throughout storage time. Both probiotic samples have capable potential for application as functional foods. Nevertheless, fermentation could rise the stability of *L. paracasei* in frozen soy dessert. Likewise, the organoleptic and physico-chemical properties of frozen soy dessert were enhanced via fermentation (Norouzi et al. 2019).

de Carvalho Marchesin et al. (2018) studied the impact of a soy-based probiotic drink as a carrier for *B. longum* ATCC 15707 and *Enterococcus faecium* CRL 183 on the fecal microbiota configuration, body weight and inflammatory parameters in diet-induced obese mice (de Carvalho Marchesin et al. 2018). In another study, Devanthi et al. (2018) investigated the impact of concurrent and consecutive inoculation of cultures (*Tetragenococcus halophilus* and *Zygosaccharomyces rouxii* as starter cultures) in moromi fermentation models, regarding survivability, physico-chemical variations, and volatiles formation (Devanthi et al. 2018). Lima Moraes Filho et al. (2019) studied creamy soy sauce as carrier for *L. plantarum* BG 112 (Moraes Filho et al. 2019).

Recently, Setta et al. (2020) reviewed potential of probiotics from fermented cereal-based beverages in enhancing healthiness of poor people in Africa. Also, several researches have exposed that traditional African fermented cereal-based drinks are possible probiotic carriers due to the probiotic bacteria (specially *Lactobacillus* and *Bifidobacterium* spp.) and yeasts which are involved in the fermentation of such foodstuffs. These probiotic products propose an occasion for the African cereal beverages to be used to deliver probiotic health advantages to the majority of populations. There are also other similar products in different countries that can replace the shortage of fermented dairy products and expensive probiotic foods (Setta et al. 2020).

15.5 Meat Products

The function of probiotics in dairy products is fully acceptable, while their function in meat products is still being studied. Fermented meat products are suitable for carrying probiotics because they are not heated at all during processing or receive very little heat and may improve the survival of probiotic bacteria in the gastrointestinal tract. In contrast, bacterial viability may be reduced due to high salt content and low water activity and low pH. Therefore, the results depend on the strain used. However, the combination of these microorganisms with fermented meat products can create some technological challenges. On the other hand, the acceptability of the new meat product for the consumer and the survival of sufficient probiotic microorganisms during the process is also among the issues under discussion (Kołóżyn-Krajewska and Dolatowski 2012). Probiotic bacterial strains have been used successfully in the production of dairy products and some fruit juices, but their use in the production of raw fermented meat products is not very suitable. It seems that it is possible to add strains of meat-derived probiotic bacteria in the process of producing fermented raw meat products, but research is needed to find out which probiotic species can grow in which meat products (De Vuyst et al. 2008; Kołóżyn-Krajewska and Dolatowski 2009).

Fermented sausages (as raw meat products) are auspicious target meat products with probiotic microorganisms, as such foodstuffs are treated without heat treatment and probiotic microorganisms can continue to be live in the final product (Aspri et al. 2020; Kumar et al. 2015). However, probiotics must maintain their stability under adverse conditions for the production of fermented sausages such as low pH (<4), nitrite (120 ppm), a_w (less than 0.85), and salt (1–3%) (Ordóñez et al. 1999; Vignolo et al. 2010). Probiotic cultures should be able to grow rapidly during fermentation and grow easily on industrial scales, be resistant to the freezing process, provide a longer shelf life, and also improve the sensory quality of the final product. In such fermented products, the addition of 3% sodium chloride and at least 120 ppm nitrite is mandatory to maintain the microbial safety of the product. Therefore, the use of salt-resistant medium is the first condition for the production of sausages with probiotic properties (Aspri et al. 2020; Papamanoli et al. 2003). Despite all the difficult conditions for the growth and survival of probiotics, fermented sausages are regarded suitable carriers for them due to the guard of the probiotic cells to bile salts and low pH which are applied from the fat molecules in the passageway over the GI zone and the motivation of probiotic growing by the existence of the prebiotic fibers (Bis-Souza et al. 2019a).

Important employed species of probiotic bacteria in fermented meat foods are *L. plantarum*, *L. casei*, *L. paracasei*, *L. sakei*, *L. acidophilus*, *L. rhamnosus*, *Pediococcus pentosaceus*, and *Pediococcus acidilactici*. The amalgamation of the probiotic microorganisms can be attained via substituting the traditional starter culture or via applying the traditional starter in association with the probiotic strain (Bis-Souza et al. 2019a). Various investigations reveal the effective utilization of probiotic strains into diverse fermented meat foods, for instance, different fermented

sausages, salami, dry cured pork loins, sturgeon fermented sausage, mutton fermented sausage, and Longaniza de Pascua (Aspri et al. 2020).

Rubio et al. (2014) studied nutritionally improved fermented sausages as a carrier for delivery of lactobacilli probiotics. They used *L. rhamnosus* CTC1679 as a probiotic for the making of Fuet (low acid fermented sausage). According to the results, *L. rhamnosus* CTC1679 was able to grow and reach numbers of 8 log cfu/g without disturbing the organoleptic characteristics of the product (Rubio et al. 2014). In another study, Wójciak et al. (2017) investigated technical aspect of *L. rhamnosus* LOCK900, *L. acidophilus* Bauer, and *B. animalis* BB-12 usage in dry fermented pork neck and sausage. They showed that *L. acidophilus* retained the quality of the product better than the *L. rhamnosus* and *B. animalis* (Wójciak et al. 2017). Slima et al. (2018) demonstrated that probiotic strains of *Pediococcus acidilactici* MA 18/5 M and *L. plantarum* TN8 could be employed to improve sensory properties and cooking yield and also extending sausage shelf life. In another study, Pavli et al. (2020) investigated the potential of dry-fermented pork sausages as a carrier for *L. plantarum* L125 strain. The results of their study disclosed that the viability rate of *L. plantarum* was suitable (>6 log cfu/g) during the storage time without considerable impacting on the technological and the organoleptic properties of the final product.

In similar study, de L Agüero et al. (2020) studied the technological characteristics of LAB as starter cultures for dry fermented sausages. Eight strains were evaluated properties counting the capability to grow, gas formation, lactic acid production, hydrogen peroxide production, salt tolerance, nitrate reductase activity, catalase activity, lipolytic activity, proteolytic activity, decarboxylation of amino acids, performance at low temperatures, and antimicrobial activity against pathogen microorganisms related to the product. According to the results, *L. rhamnosus* Lr-32, *L. rhamnosus* R0011, *L. casei* Shirota, *L. paracasei* Lpc-37, and *Enterococcus faecium* MXVK29 were suitable candidates for use as fermented sausages starters. *L. rhamnosus* Lr-32 was the best enduring the low pH, salt, and nitrate throughout the simulated phases of fermentation and maturing of sausage (de L Agüero et al. 2020). Sirini et al. (2020b) studied the effect of chestnut flour and probiotic microorganism on the functionality of dry-cured meat sausages. Adding the chestnut flour diminished pH and remaining nitrite in Longaniza de Pascua. The results of the study showed that Longaniza de Pascua is a good carrier for *L. plantarum* (Sirini et al. 2020b). The same authors reviewed the use of probiotic microorganisms in the formulation of healthy meat products (Sirini et al. 2020a).

15.6 Other Traditional Products

There are many traditional fermented products with different names in different parts of the world that can be the origin of different types of probiotic microorganisms and may not have been researched yet. These products can be suitable carriers of native probiotics and cause the transfer of probiotics into the consumer's GI tract. However, there are some products that have been extensively researched and their health

effects have been proven to be effective carriers of probiotic microorganisms, postbiotics, and other functional compounds. There are several non-dairy products that can be discussed in this regard, which in this section, we have explained two of these popular products; Kombucha and Chocolate.

One of the most famous of these products is Kombucha as a fermented beverage, with a history of some thousand years in the East. Kombucha drink has been claimed to be a nutritional supplement that consuming it supports the immune system and averts some diseases. Kombucha is a symbiotic evolution of acetic acid bacteria and osmophilic yeast species (SCOBY) which have to be cultivated in sweetened tea with glucose or sucrose. SCOBY includes some bacteria like *Acetobacter aceti* spp. *xylinum*, *Acetobacter xylinum*, *Corynebacterium glutamicum*, *Acetobacter pasteurianus*, and *Acetobacter xylinoides* and also some yeasts like *Saccharomyces bisporus*, *Saccharomyces cerevisiae*, *Saccharomyces ludwigii*, *Schizosaccharomyces pombe*, *Zygosaccharomyces bailii*, *Candida kefyer*, *Candia krusei*, *Pichia* sp., *Brettanomyces* sp., *Torulopsis* sp., and *Issatchenkia orientalis occidentalis*. Several complexes and postbiotics have been isolated from Kombucha including carbonic acid, glucuronic acid, gluconic acid, acetic acid, folic acid, butyric acid, oxalic acid, lactic acid, malic acid, nucleic acid, citric acid, carbon dioxide, ethanol, antibiotics, vitamins B including B1, B2, B6, and B12, and vitamin C (Ansari et al. 2017; Ansari et al. 2019; Chakravorty et al. 2016; Coelho et al. 2020; Villarreal-Soto et al. 2018).

Another product, as a functional food, not only does not unpleasantly impact healthiness, but also hinders some disorders such as cancer, osteoporosis, diabetes, and cardiovascular diseases. Cocoa is rich in proteins, minerals, carbohydrates, flavonoids, and polyphenolic antioxidants (Aspri et al. 2020). Several researchers have recommended that chocolate is a suitable substrate for probiotic microorganisms providing guard to probiotics throughout storing time and passage into GI lumen (dos Santos Filho et al. 2019; Kemsawasd et al. 2016; Konar et al. 2016). Klindt-Toldam et al. (2016) displayed that *B. lactis* HN019 and *L. acidophilus* NCFM combined into dark chocolate and milk chocolate remained viable throughout storage period and also during GI lumen (Klindt-Toldam et al. 2016). Zarić et al. (2016) showed that after 6 months of storage, the viability of *L. acidophilus* NCFM, *L. rhamnosus* HN001, and *B. lactis* HN01 was above 90%, with cell number of approximately 8 log cfu/g (Zarić et al. 2016). In another study, Mirković et al. (2018) studied the organoleptic quality and volatile profile of dark chocolate supplemented with microencapsulated probiotic *L. plantarum* 564 and *L. plantarum* 299v. The consequences disclosed suitable survival of both probiotic strains after manufacture and throughout storage period (8 log cfu/g in the first 60 days and over 6 log cfu/g up to 180 days) (Mirković et al. 2018). Cielecka-Piontek et al. (2020) studied survival of commercial probiotic strains and their effect on dark chocolate synbiotic snack with raspberry content during the storage and after simulated digestion. The results showed the cell count of probiotics was steady (8 log cfu/g) and moderately high through 6 months of storage time (Cielecka-Piontek et al. 2020).

15.7 Commercially Available Nondairy-Based Probiotic Products

Various nondairy probiotic foods are previously extant for consumers. The primary nondairy probiotic food was produced via a Swedish corporation Skane Dairy (1994-ProViva) (Aspri et al. 2020; Bansal et al. 2016). Oatmeal gruel being fermented via *L. plantarum* 299v was the base substrate and malted barley was supplemented to expand liquefaction of the product, and finally it has been mixed with diverse fruit extracts like strawberry, blueberry, or tropical fruits. This probiotic product comprised 5×10^{10} CFU/L of *L. plantarum* (Molin 2001). A comparable product GoodBelly was the primary nondairy probiotic beverage in the United States in 2006 (Aspri et al. 2020; Panghal et al. 2018). Furthermore, some cereal probiotic products have been available in some markets, for example, probiotic flakes (Muesli[®], Portugal), cereal bars (CornyActiv[®], Germany), whole wheat breakfast cereals (Weetaflakes[®], France), whole grain probiotic liquidR (Grainfields, Australia), whole grain oatmeal (United Kingdom), and snack bar (Goodness[®], United Kingdom) (Aspri et al. 2020; Dornblaser 2007).

15.8 Viability of Probiotics in Nondairy Foods

The survival rate of probiotics is one of the most important factors in the study of these microorganisms. Dairy/nondairy Foods containing probiotics fall within the “functional foods” class and these nutrients should comprise as a minimum 7 log cfu/g probiotics and consumed at levels higher than 100 g/day to have supportive impacts on healthiness (Abdolhosseinzadeh et al. 2018). However, there are still some complications related to the low survival of probiotic microorganisms in foods along with GI environments (Mirzaei et al. 2011; Suvarna et al. 2018). Various investigations have obviously showed that the kind of carrier foods could impact not only the survivability of probiotic microorganisms throughout production and storing period, but also on their functional characteristics, for instance vulnerability to harsh situations in the GI tract (low pH, bile salt, and several enzymes), ability to stick to enterocytes, and immunomodulation (Kedia et al. 2009; Marco and Tachon 2013; Ranadheera et al. 2012; Ranadheera et al. 2014).

Dairy foodstuffs (rich in milk fat) can enhance the viability of probiotics during manufacturing and GI tract. Nevertheless, the physical structure of nondairy foods, for instance fruits and vegetables, may offer protecting milieu for probiotic microorganisms and decrease their contact to strict GI circumstances too (Ansari et al. 2020a; Homayouni et al. 2020a; Homayouni et al. 2018). Fermented meats such as sausage structure have also revealed a possible in retaining the survivability of probiotic cells over GI transportation (Klingberg and Budde 2006; Rouhi et al. 2013). Various published articles are available on how to advance the viability of probiotic microorganisms in nondairy foods. The most striking and effective approaches are fortification via prebiotic ingredients (for instance dietary fiber, resistant starch, inulin, cellulose), adding antioxidants, refrigerated storing in

atmosphere improved carbon dioxide, and microencapsulation (Khosravi et al. 2021; Shah 2000; Tamime et al. 2005). In summary, the important point that has already been mentioned is to keep the number of probiotics in an acceptable range so that it can maintain its beneficial effects on the host, and this is very much affected by the type of food that carries these microorganisms.

15.9 Organoleptic/Sensory and Acceptability of Nondairy Probiotics

The organoleptic/sensory properties and acceptability of probiotic products are especially important in the case of nondairy products in terms of industrial and mass production. The organoleptic characteristics of nondairy probiotic foods can be impacted via interactions between diverse probiotics strains and food substrates, where taste, aroma, flavor, color, and textures may be improved via the creation of diverse metabolic ingredients, for instance, organic acids, exopolysaccharides, and other metabolites through processing and storage (Aspri et al. 2020; Panghal et al. 2018). Consequently, it is significant to assess not only the suitable probiotic viability, but also the organoleptic acceptance throughout manufacturing and storage time of probiotic nondairy foods. For example, in fruit products, depending on the type of fruit, processing and storing temperature, type of probiotic, and the addition of protectants and prebiotics, it can influence the organoleptic characteristics of the final product (Lebaka et al. 2018).

15.10 Summary of Technological Challenges and Advancements of Nondairy Probiotic Foods

The most investigated technologies which were involved in fermentation, rehydration, drying, microencapsulation, and storage have been advanced and effectively used to protect some probiotic microorganisms from environmental tensions related to several nondairy food media, nonetheless there are still various technological challenges in manufacturing and protecting probiotic foods. Certainly, the maintenance of adequate viable cells of probiotics is an important factor of quality. Merely applying any probiotic species such as *Lactobacillus* and *Bifidobacterium* does not assure high viable content in fermented foodstuffs after fermentation and throughout the storage period (Min et al. 2019).

Technological challenges such as manufacturing, handling out, temperature of production and storage, pH rate, oxygen content, O/R potential, a_w rate, relative humidity (RH), antimicrobial agents, and external stresses can affect the use of probiotic microorganisms in food products (Min et al. 2019; Vasudha and Mishra 2013). For example, several food components such as sugar and salts can bind water and cause low a_w and improve the viability of probiotics (Holck et al. 2011). Conversely, surplus a_w , for example, in fruit juice, can decrease the survival of probiotics throughout storage period (Vasudha and Mishra 2013).

Microencapsulation of the probiotic microorganisms is one of the modern and most effectual methods. Microencapsulation by means of emulsion and extrusion methods has been used for the protection of probiotics against harsh circumstances (Pourjafar et al. 2018, 2020). Some studies have shown that the addition of protectants (e.g., lactose, trehalose, cellobiose, and sucrose) to the probiotic media can advance survivability of probiotics in the nondairy foods (Min et al. 2019).

15.11 Postbiotics and Food Applications of Postbiotics

15.11.1 Classes of Postbiotics

Postbiotics can be secreted by live microbiota during its life cycle or may be released after bacterial lysis. These compounds are essential in regulating self-growth, development, reproduction and modulating the growth of other microorganisms and can also have an effect on the physiological responses of the host by modifying cellular processes and metabolic pathways (Aguilar-Toalá et al. 2018). In general, these postbiotics are classified either by their elemental composition or by their physiological function.

According to the first classification method there are seven main classes of postbiotics; (1) Cell-Free Supernatants including biologically active metabolites secreted by bacteria and yeast into the surrounding liquid. This kind of postbiotics is obtained directly from cell cultures. For this purpose, the microbial cells are separated from overnight grown whole culture broth by centrifugations, and the supernatant containing postbiotics is then filtered to ensure sterility. (2) Exopolysaccharides which are biopolymers with different chemical properties released outside the bacterial cell wall. These biopolymers form heterogeneous molecules called exopolysaccharides (EPSs). EPSs has recently gained a lot of attraction and are widely studied for their potential positive biological properties. (3) Enzymes that are a part of the defense mechanisms of the organism against harmful effects of reactive oxygen species (ROS) damaging lipids, proteins, carbohydrates, and nucleic acids. Antioxidant enzymes, such as glutathione peroxidase (GPx), peroxide dismutase (SOD), catalase, and NADH-oxidase are classified within this category. (4) Cell Wall Fragments such as bacterial lipoteichoic acid (LTA). These components are immunogenic and can elicit immune responses. They are proven to have anti-infectious, anti-inflammatory and anti-cancer effects. (5) Short-Chain Fatty Acids (SCFAs) produced by fermentation of plant polysaccharides by intestinal microbiota. Acetic, propionic, and butyric acids are from the most well-known SCFAs. Helping to renew intestinal epithelium, modulating gene expression, immunosuppressive effects, and metabolic and anti-inflammatory function are from the properties of SCFAs. (6) Bacterial Lysates (BLs) which are results of the chemical or mechanical degradation of Gram-positive and Gram-negative bacteria commonly found in the environment. They have specific immunological activities like activating T and B lymphocytes. The beneficial effects of BLs in the case of infections and allergic diseases have been observed in several

studies. (7) Metabolites Produced by Gut Microbiota including vitamins, phenolic-derived metabolites, and aromatic amino acids. These products have high bioavailability, antioxidative features, and signaling properties and are very important in host-microbiome crosstalk (Żólkiewicz et al. 2020).

According to the physiological function of the postbiotics they are grouped in categories such as immunomodulator, anti-inflammatory, hypocholesterolemic, anti-obesogenic, anti-hypertensive, anti-proliferative, and antioxidant (Aguilar-Toalá et al. 2018). These classifications lead to better understanding of the function of postbiotics and is used for the application of them for clinical and industrial purposes.

15.11.2 Manipulation of Postbiotic Composition for Food Application

To apply postbiotics in nondairy food products several issues should be considered. First of all, the susceptibility of postbiotics to manipulation processes such as pH alterations, heat treatment and exposure to NaCl and proteolytic enzymes which can severely change the postbiotic properties. For instance, it has been shown that antimicrobial activity of bacteriocinogenic *Lactococcus lactis* subsp. *lactis* CWBI-B1410 and *L. curvatus* CWBI-B28 was completely lost after 8 days storage at 10 °C in the neutralized pH solution. The second issue is the interaction of postbiotics with other food compounds. Food ingredients may contain several postbiotic inhibitory elements like enzymes, proteins, and carbohydrates which may limit the postbiotic properties. And the last but not the least is the effects of postbiotics on consumer's overall acceptance of the food (Moradi et al. 2020).

In the case of application postbiotics for each kind of food products all the above issues should be assessed. There are also some hurdle technologies to assist overcoming the mentioned concerns. For instance, postbiotics may be protected and released in their target sites through encapsulation processes. Moreover, application of nanocarriers for hydrophobic postbiotics like fat-soluble vitamins improves their resistance to the light, heat, and oxygen during storage and augments bioavailability of the postbiotics. They also increase transparency of the product, which is highly important in the case of postbiotic beverages (Homayouni Rad et al. 2020). However, we need more studies in this field to develop effective and applicable methods to protect postbiotics in the food matrix (Moradi et al. 2020).

15.11.3 Interaction Between Postbiotics and Food Ingredients

As it has been discussed previously, postbiotics have several kinds of properties, such as anti-cancer, anti-oxidant, and anti-microbial effects. All the ingredients of a food matrix have the potential to increase or decrease the specific effects of the added postbiotics. For instance, it has been shown that the postbiotic Nisin is rapidly inactivated in raw beef because of potential interaction with raw components like

proteases and glutathione. In this case heating the meat at 71 °C or application of liposome-encapsulated nisin was proposed for maintenance of the activity of nisin during processing and storage (Younes et al. 2017). Similarly, anti-microbial postbiotics may be applied to enhance the microbial safety of the food. Although the results of a research indicate that bacteriocins with strong inhibition on agar plates had only a reduced and transient inhibitory effect when applied in ground beef (Hartmann et al. 2011). Some metabolites like EPS can protect the pathogens from harsh environmental conditions, so their application in food products should be under specific cautions. Otherwise they may increase the proliferation of the bacteria and introduce a safety hazard for the consumers (Moradi et al. 2020).

On the other hand, some of the food ingredients lead to the production of valuable substances as postbiotics which are not normally produced by the bacterium. For example, some strains of *L. plantarum* produce 10-hydroxy-cis-12-octadecenoic acid (HYA) in the presence of linoleic acid. This substance is very beneficial for controlling colitis and diabetes (Moradi et al. 2020).

15.12 Conclusion

Nondairy food products (legumes, cereals, pseudocereals, fruits, and vegetables) provide a valuable opportunity for special groups of people such as people intolerant or allergic to milk proteins, those who are hypercholesterolemic, or those who are vegetarian to use the benefits of functional foods and specifically postbiotics. These products can be readily consumed by other groups, so they will have a wide market target. We need more in vitro and in vivo studies to address the growing international requirements for nondairy foods containing postbiotics.

The following research fields have been proposed for future studies:

- Developing products for consumers with certain dietary restrictions such as milk allergies, low cholesterol or fat content, diabetes, phenylketonuria, and lactose intolerance.
- Proposing novel products for specialized market segments such as children and chronically ill patients.
- Working on novel technologies for production of foods containing postbiotics.
- Evaluating the viability of postbiotics in different environmental conditions, in final product, and in gastrointestinal tube.
- Assessing Organoleptic and functional characteristics of the final product.
- Using encapsulation techniques for targeted delivery of postbiotics.
- Assurance of safety and effectivity of the final products.
- Developing international standards for products containing postbiotics.

The general plan for essential fields of future studies has been demonstrated in Fig. 15.1.

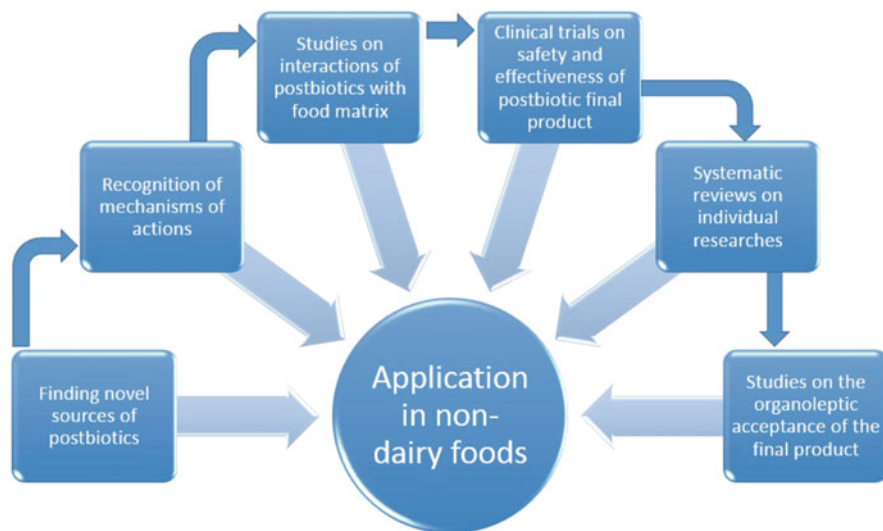


Fig. 15.1 Future perspectives of researches on the postbiotics in none dairy foods

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