Application of Potential Microbial Biotechnology for Sustainable Human Health

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Neha Rani Bhagat, Younis Ahmed, Rajesh Kumar, and Arup Giri

Abstract

In the present era, the most important concern is food security for providing stability and sustainability to the growing population throughout the world. Therefore, there is an urgent need for the development of sustainable methods for the augmentation of agricultural products. This chapter discusses some microbiological aspects of sustainable agriculture that can help us to maintain human civilization in changing climatic conditions. In this aspect, an emphasis has been laid upon significance of microbiotechnology in agriculture and human sustainability along with microbial bio-fertilizers, growth-promoting rhizobacteria (PGPR) in plants, and microbial biopesticides for sustainable agriculture. It has been found that a lot of bacteria may act as PGPR for higher agricultural yields. Microplastics are a great hindrance to reducing agricultural products. Therefore, the role of microbiotechnology in the detection of pollution has been discussed. However, waste management strategies, especially for plastic waste, industrial wastewater treatment, attenuation of textile industry based dyes, and microbial strategies for the biotransformation of food waste into useful resources, have been elaborated. In the agro-animal sector, microbes play a great role in maintaining normal animal physiology for optimum production,

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N. R. Bhagat
DRDO-Defence Institute of High Altitude Research (DIHAR), Ladakh, India

Y. Ahmed
Department of Life Sciences and Allied Health Sciences, Sant Baba Bhag Singh University, Jalandhar, Punjab, India

R. Kumar
Department of Biosciences, Himachal Pradesh University, Shimla, Himachal Pradesh, India

A. Giri (✉)
Department of Zoology, Baba Mastnath University, Rohtak, Haryana, India

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like the flourishing of the aquaculture sector, the livestock industry, and especially the poultry industry. Microbiotechnology has a great impact on the maintenance of normal human physiology after improvement in biomedical sector activity. This technology has the potential for the generation of electricity and may act as the main source of omega-3 fatty acids as well as the required protein for future sustainability.

6.1 Introduction

Global agricultural production is growing day by day for the feeding of growing population (Köhler and Triebskorn 2013). There are a lot of methods to increase the plant and animal based product yield. The higher yield will provide the sustainability of human race. Meanwhile, among all those methods, microbial biotechnology is flourishing day by day for better agricultural management and yield.

Meanwhile, biotic and abiotic factors causes the stressful environment to plants (Tewari and Mishra 2018; Farooq et al. 2009; Gowtham et al. 2020; Tevini 2004; Sharma et al. 2017; Bharti and Barnawal 2019; Awasthi et al. 2015; Khan et al. 2017; Hameed et al. 2016; Ghori et al. 2019; Dubois et al. 2018). Therefore, agricultural yield reduced throughout the world (Vurukonda et al. 2016). It has been reported that due to abiotic stress, the yield has been reduced to 50–82% (Wang et al. 2003) (Fig. 6.1). It has been found that all the accumulated stress

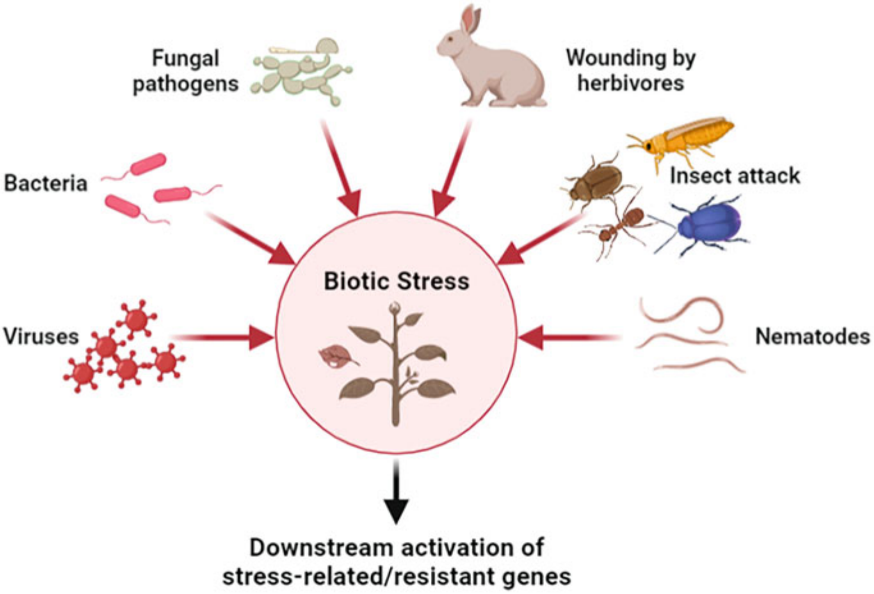

Fig. 6.1 Different types of stress that affects plant growth and development

caused reduction in plant growth and development after induction of reactive oxygen species formation in plants (Huang et al. 2019; Sharma et al. 2012).

Therefore, there is need of antidote development against different stress to plants. In these terms, growth-promoting rhizobacteria in plants has great role to improve the soil fertility and to maintain the soil environment so that optimum plant growth, development, and yield occur (Yang et al. 2009; Glick 2012; Vejan et al. 2016; Vurukonda et al. 2016; Gowtham et al. 2020).

This discussion covers various aspects of microbiotechnology in agriculture, including the use of microbial bio-fertilizers, plant growth-promoting rhizobacteria (PGPR), microbial biopesticides, and microbiotechnology's role in developing pollution detection and mitigation methods for agricultural and human sustainability.

6.2 Microbiotechnology in Agriculture and Human Sustainability

6.2.1 Plant Growth-Promoting Rhizobacteria for Sustainable Agriculture

6.2.1.1 Importance of PGPR

"Plant growth-promoting rhizobacteria (PGPR)" are population of rhizospheric bacteria which promote plant growth and development after rhizosphere engineering, nitrogen fixation, siderophore production, etc. (Bhattacharyya and Jha 2012) (Fig. 6.2).

Bacillus, Rhizobium, Azotobacter, Azospirillum, Frankia, Gluconacetobacter, Burkholderia, Azorhizobium, Beijerinckia, Cyanobacteria increased the nitrogen fixation and soil fertility (Zahran 2001; Govindasamy et al. 2010; Bhattacharyya and Jha 2012; Merzaeva and Shirokikh 2006; Jang et al. 2017; Islam et al. 2016; Ahmad et al. 2011). "*Arthrobacter, Burkholderia, Enterobacter, Microbacterium Pseudomonas, Bacillus, Erwinia, Rhizobium, Mesorhizobium, Flavobacterium, Rhodococcus, Serratia"* increase the phosphate solubilization in soil (Podile and Kishore 2007; Oteino et al. 2015). Siderophore production in soil is caused by *Pseudomonas, Bacillus, Rhizobium, Azotobacter, Enterobacter, Serratia* (Ansari et al. 2017). Different types of phytohormones are produced by *Bradyrhizobium*, *Burkholderia*, *Xanthomonas*, *Mesorhizobium*, *Bacillus*, *Rhizobium*, *Pantoea*, *Enterobacter*, *Agrobacterium*, *Azospirillum, and Arthrobacter Pseudomonas* (Egamberdieva et al. 2017; Tsukanova et al. 2017; Kalam et al. 2020; Cassán et al. 2001; Tahir et al. 2017; Barnawal et al. 2017). *Pseudomonas species, Bacillus species, Burkholderia, Brevibacterium, Streptomyces* help in antibiotic production (Jayaprakashvel and Mathivanan 2011; Zhou et al. 2019). Volatile metabolites which help in plant development may be produced by *Bacillus, Pseudomonas, Agrobacterium, Burkholderia, Xanthomonas,* and *Paenibacillus polymyxa* (Sharifi et al. 2018). However, *Bacillus*, and *Pseudomonas* species are responsible for lytic enzyme production (Mabood et al. 2014). Incorporation of *Pseudomonas*, *Bacillus*, *Pantoea*, *Burkholderia*, *Rhizobium* reduced stress tolerance (Jha and Subramanian

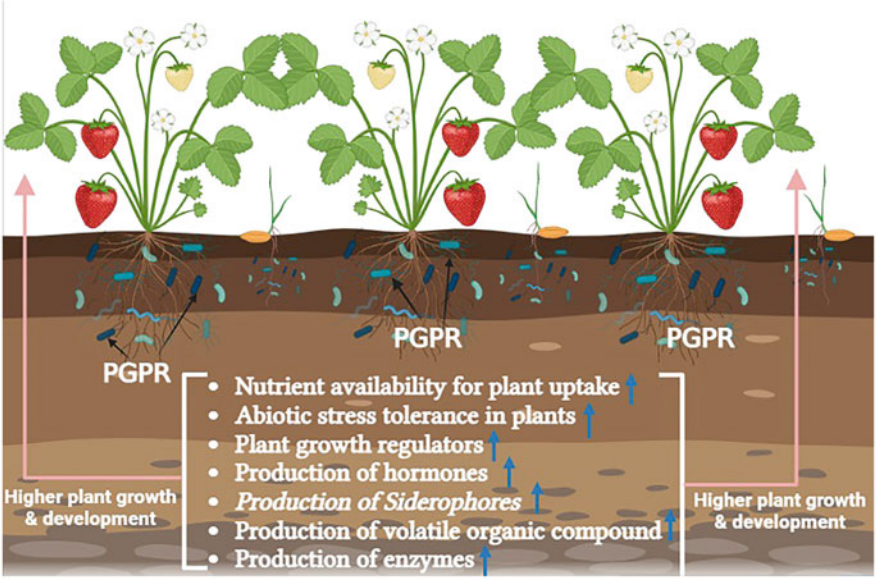

Fig. 6.2 Role of plant growth-promoting rhizobacteria (PGPR) for plant growth and development

2014; Egamberdieva et al. 2019). However, *Pseudomonas*, *Bacillus*, *Trichoderma* act as biocontrol agents (Saraf et al. 2014; Meena and Swapnil 2019). Drought stress in plants has been reduced by *Bacillus subtilis, Pseudomonas fluorescens DR11, Enterobacter hormaechei DR16, Rhizobium tropici, Phyllobacterium brassicacearum, Pseudomonas migulae DR35, Achromobacter piechaudii ARV8, Paenibacillus polymyxa,* and *Azospirillum brasilense* (Niu et al. 2018; de Lima et al. 2019; Bresson et al. 2013; Figueiredo et al. 2008; Yang et al. 2009; Ilyas et al. 2020). Salinity related stress to plants gets reduced by *Bacillus pumilus, Exiguobacterium oxidotolerans, Bacillus megaterium, Azospirillum* sp., *Achromobacter piechaudii, Enterobacter* sp. *PR14* (Mayak et al. 2004; Bharti et al. 2013; Marulanda et al. 2010; Fasciglione et al. 2015; Sagar et al. 2020). Different types of biotic stress to plants are reduced by *Paenibacillus xylanexedens, Bacillus amyloliquefaciens, Streptomyces* sp., *Ochrobactrum intermedium, Paenibacillus lentimorbus, Pseudomonas* spp. (Verma et al. 2016; Srivastava et al. 2016; de Vasconcellos and Cardoso 2009; Gowtham et al. 2016; Khan et al. 2012; Reshma et al. 2018). Meanwhile, nutrient absorption to plants increases by *Pantoea* sp. *S32, Paenibacillus polymyxa* (Chen and Liu 2019; Pii et al. 2015; Castillo-Aguilar et al. 2017). It has been found that seed germination also increases due to the presence of *Pseudomonas putida, Serratia marcescens, Bacillus subtilis, Pseudomonas fluorescens, Azospirillum lipoferum, Providencia* sp., *Brevundimonas diminuta* (Almaghrabi et al. 2014; Nezarat and Gholami 2009; Rana et al. 2011). Bioremediation in terms of lowering the heavy metals and other pollutants level is done by "*Ochrobactrum* sp., *Bacillus* spp., *Pseudomonas* spp., *Pseudomonas fluorescens, Bacillus cereus, Alcaligenes faecalis*

RZS2, Pseudomonas aeruginosa RZS3, Enterobacter sp. *RZS5"* (Pandey et al. 2013; Khan and Bano 2016; Das and Kumar 2016; Kalam et al. 2020; Patel et al. 2016; Sayyed et al. 2015).

6.2.1.2 Mechanism of Action

PGPR helps in different dimensions as stated above so that the agricultural environment is changed to most suitable condition. They are doing all these activities in two diverse ways: direct and indirect effects. In direct effects, plant growth augmentation happens due to higher nutrient acquisition to plants, which is helping plants to resist against different pathogens. This pathway mainly depends upon the bio-fertilization and phyto-stimulation. Conversely, in indirect effects, PGPR helps to reduce the completion effects from nearby plants and increase the antibiosis against adverse pathogens. Therefore, ultimately, PGPR mainly increased the pathogen resistance to plants (Mustafa et al. 2019).

6.2.1.3 Limitations of PGPR

Apart from all the usefulness of PGPR, some limitations also existed. Sometimes, PGRP is not suitable for a specific plant variety. In different climatic conditions and soil ecosystems, it may not act at optimum level. However, the algorithm on the plant–PGPR relation may reduce the limitation of PGPR use in different geographical conditions in different doses.

6.2.2 Microbial Biopesticides

Pesticides are used for higher production by reducing the pest attack—causes the reduction of 45% crop yield per annum (Mundt 2014; Yadav et al. 2015). Synthetic pesticides have great concern on soil health after long term use, higher ecotoxicity, reduced fungal activity in soil, reduction of rhizospheric bacteria, etc. (Bowles et al. 2014; Fenner et al. 2013; Kumar et al. 2017). Therefore, in the recent decades, "biopesticides are being used for pest management."

Bacillus thuringiensis (Bt) is used as biopesticide due to the presence of δ-endotoxins against insect. These δ-endotoxins secreted after the activation of cry genes (Kumar et al. 2021). Carbendazim is utilized to combat various plant diseases due to its properties as a benzimidazole fungicide (Yang et al. 2014; Zhang et al. 2009). There are a lot of bacterial strains which have significant impact as biopesticide (Table 6.1).

Some studies indicated that biopesticide may impact soil health. But it has been recorded that low dose of biopesticide reduces those bad impact on soil health (Czaja et al. 2015; Leahy et al. 2014).

Table 6.1 Different microbial biopesticides and their role (Kumar et al. 2019; Brownbridge and Buitenhuis 2019)

Types of microbes	Name of microbes	Activity against different pests
Bacteria	*Bacillus thuringiensis* (Bt) kurstaki and aizawai	Reduce caterpillar pests like tortricid leafrollers, *European corn borer*, etc.
Bacteria	*Bt galleriae* and *Bt tenebrionis*	Leaf beetle of potatoes, tomatoes
Bacteria	*Bt israelensis* (Bti) and *Lysinibacillus sphaericus*	Larvae of different insects like mosquito, blackfly
Bacteria	*Paenibacillus popilliae*	Caused milky disease in Japanese beetle
Bacteria	*Actinomycetales*	Thrips, caterpillars, and many other pests
Bacteria	*Burkholderia rinojensis* strain A396, *Chromobacterium subtsugae* strain PRAA4-1	Pest in aquatic environments
Bacteria	*Bacillus firmus* and *Pasteuria* spp.	Nematodes lives on plants
Fungi	*Beauveria bassiana*	Reduce the number of foliar pests
Fungi	*Metarhizium brunneum*	Weevils, mites, whiteflies, and thrips in different vegetables and ornamental plants
Fungi	*Isaria fumosorosea*	Aphids, mites, whiteflies, and thrips in different vegetables and ornamental plants
Fungi	*Purpureocillium lilacinum* and *Myrothecium verrucaria*	Nematodes living on plants
Fungi	*Paranosema locustae*	Mormon crickets and grasshopper in agricultural field as well as domestic premices
Fungi	Baculoviruses	Act against Lepidoptera larvae found in different vegetables in greenhouse gas condition
Fungi	Nucleopolyhedroviruses (NPV)	Beet armyworm, corn earworm, *Spodoptera exigua*, etc.
Fungi	Granuloviruses (GV)	Moth found in apple orchard
Virus	*Autographa californica* NPV	*Trichoplusia ni*
Nematode	*Steinernema feltiae*	Western flower thrips

6.3 Role of Microbiotechnology in Waste Management and Human Sustainability

The interaction between humans and the environment is a complex phenomenon. It's not solely dependent on meeting basic food needs but is also influenced by factors such as resource consumption levels, waste generation, and the use of various technologies across different applications (Selvam and Wong 2016). However, the continuous discharge of hazardous wastes such as plastic, industrial, food, household waste, into the environment poses the greatest threat to mankind in the long run, raising enormous concerns about environmental and human sustainability (Mondal and Palit 2019). Given the broad and intricate nature of sustainability goals and their various components, microbial technology can play a significant role in helping to achieve sustainability, as elaborated below (Timmis et al. 2017).

6.3.1 Microbiotechnology Against Plastic Waste

Plastics are employed in a wide variety of industries across the globe, including the medical, transportation, manufacturing, sanitation, food packaging, storage, and petroleum-based feedstock industries, worldwide. Plastics viz. polyhydroxybutyrate/polyhydroxybutyrate-*co*-valerate (PHB/PHBV), polyethylene (PE), poly(ε-caprolactone) "(PCL), poly(lactic acid) (PLA), polyester/poly(butylene succinate) (PES/PBS), Poly(ethylene terephthalate) (PET), Low-density polyethylene (LDPE), high-density polyethylene (HDPE), poly(vinyl alcohol)-linear low-density polyethylene)" (PVA-LLDPE), poly butyl succinate, etc. comprise 80% of plastic usage and has contributed significantly to the expansion of the global economy as well as employment for over 60 million people (Urbanek et al. 2018; Mazhandu et al. 2020).

Plastic offers numerous advantages, but its production, consumption, and disposal have led to the depletion of non-renewable resources. These patterns also contribute to environmental degradation, negatively impacting the sustainability of both humans and animals (Mazhandu et al. 2020). Besides these concerns, the rapidly growing demand and production of plastics in the past few decades give rise to huge generation of plastic waste in the environment that accounts for 54% of the total anthropogenic waste (Satti and Shah 2020). In terms of the numbers that are currently available, there is a persistent rise in plastics usage and has led to an increase in the generation of plastics waste. Furthermore, this waste is considered to be one of the most pervasive forms of pollution, and it has significant negative effects on the environment as a result of its composition and the presence of hazardous chemicals. These chemicals are known to cause cancer, chronic respiratory disorders, neurological disorders, and reproductive anomalies in humans and animals (Rajmohan et al. 2019; Satti and Shah 2020).

Efforts have been made to reduce plastic waste through methods like reuse, recycling, incineration, or landfilling. However, approximately 8300 million tonnes of plastic still end up in the environment, including landfills, oceans, and terrestrial areas (Mohanan et al. 2020). These plastics exhibit high resistance to natural biodegradation and can endure for many years. As a result, alternative methods such as photo-, bio-, or thermo-oxidative depolymerization and friction methods can be employed for plastic waste management (Mohanan et al. 2020). However, with growing concerns about environmental friendliness and economic effectiveness, microorganisms or their byproduct-based degradation has emerged as a potential option in recent years (Mohanan et al. 2020). Hence, several studies related to microorganisms capable of degrading synthetic plastics are discussed in Table 6.2.

Table 6.2 Various microbes and enzymes involved in biodegradation of different types of plastics

S. no.	Plastic	Microorganisms/enzymes	References
1.	Polyhydroxybutyrate/ polyhydroxybutyrate-*co*-valerate (PHB/PHBV)	**M/Os:** "*Bacillus megaterium N-18-25-9, Bacillus* sp. *AF3, Actinomadura* sp. *AF-555, Streptoverticillium kashmirense AF1, Streptomyces ascomycinicus, Streptomyces* sp. *AF-111," Catenibacterium thermophilum, Thermus thermophiles HB8 Paecilomyces* sp. *"1407; Penicillium* sp. *DS9701-D2; Aspergillus fumigatus NA 25; Emericellopsis minima W2"* **Enzymes:** PHA depolymerases	Satti and Shah (2020)
2.	Polyethylene (PE)	*Zalerion maritimum, Bacillus amylolyticus, Bacillus subtilis, "Enterobacter* sp. *D1, Pseudomonas alcaligenes, Pseudomonas fluorescens, Pseudomonas putida, Pseudomonas putida MTCC 2475, Streptomyces SSP2, Streptomyces SSP4, Streptomyces SSP14, Acinetobacter ursingii"*	Urbanek et al. (2018), Asiandu et al. (2021)
3.	Poly(ε-caprolactone) (PCL)	**M/Os:** "*Lactobacillus plantarum, Brevundimonas* sp. *Strain MRL-AN1 Streptomyces thermoviolaceus* subsp. *Thermoviolaceus 76T-2, Ralstonia* sp.*"* **Enzymes:** Lipase, esterase, protease, cutinase, catalase, glucosidases	Satti and Shah (2020), Urbanek et al. (2018)
4.	Poly(lactic acid) (PLA)	*"Sphingobacterium* sp. *S2, Chryseobacterium* sp. *S1, Pseudomonas aeruginosa strain S3 and S4, Amycolatopsis orientalis, Alcanivorax borkumensis ABO2449, Bordetella petrii PLA-3 Laceyella sacchari LP175"* **Enzymes:** Lipase, protease, cutinase	Satti and Shah (2020), Asiandu et al. (2021)
5.	Polyester/poly(butylene succinate) (PES/PBS)	"Bacillus pumilus strain KT1012, *Pseudomonas* sp. AKS2" *Microbispora rosea* subsp.	Satti and Shah (2020)

(continued)

Table 6.2 (continued)

S. no.	Plastic	Microorganisms/enzymes	References
		Taiwanensis *Aspergillus clavatus* NKCM1003	
		Enzymes: Lipase, esterase, cutinase	
6.	Poly(ethylene terephthalate) (PET)	*“Pseudomonas* sp. *AKS2, Ideonella sakaiensis 201-F6 Saccharomonospora viridis AHK190, Thermobifida fusca KW3, Thermobifida cellulosilytica, Penicillium” funiculosum, Rhizopus delemar; Phormidium, Lewinella, Stanieria, Pseudophormidium; Bacillus subtilis; Staphylococcus pyogenes; Staphylococcus aureus*	Satti and Shah (2020), Asiandu et al. (2021)
		Enzymes: Lipase, esterase, cutinase	
7.	Low-density polyethylene (LDPE)	*Aspergillus versicolor, Aspergillus* sp., *Arcobacter Colwellia* sp., *Bacillus vallismortis bt-dsce01, “Aspergillus oryzae strain A5, Bacillus cereus strain A5, Trichoderma viride RH03, Aspergillus nomius RH06; Bacillus* sp., *Paenibacillus* sp.*”*	Urbanek et al. (2018), Elahi et al. (2021), Asiandu et al. (2021)
8.	High-density polyethylene (HDPE)	*Ochrobactrum anthropic, Aspergillus flavus, Klebsiella pneumoniae CH001*	Urbanek et al. (2018), Elahi et al. (2021), Asiandu et al. (2021)
9.	“Poly (vinyl alcohol)-linear low-density polyethylene) (PVA-LLDPE)”	*Vibrio alginolyticus*, *Vibrio parahaemolyticus*	Urbanek et al. (2018)

6.3.2 Microbial Biotechnology for Industrial Wastewater Treatment

Industrial wastewater pollution has become more problematic over the world, when treatment and administration of industrial effluents are not being handled effectively. These industrial effluents comprise dangerous inorganic and organic contaminants that pollute water streams and the surrounding soil ecosystem, affecting entire living species (Maszenan et al. 2011; Rani et al. 2019). Effluent water and solid discharge constitute around one-third of total water pollution in India alone, and growing industrialization causes approximately “3.4 million people to suffer and die worldwide” (Rani et al. 2019). It is possibly harmful to the ecosystems and has garnered a lot of attention from research scientists for its management to maintain the environmental as well as human sustainability.

6.3.3 Microbial Biotechnology to Reduce the Textile Industry Based Dyes

The textile industry is accountable for the consumption of vast quantities of water, which is then released back into the atmosphere in the form of wastewater. This effluent consisting of textile-based colors (such as anthraquinone, azo dyes, and phthalocyanine), metals/metalloids, salts, and organic contaminants make it one of the most major contributors to the contamination of surface and groundwater bodies (Imran et al. 2015; Thanavel et al. 2019). In addition, in the years ahead, the annual growth rates of reactive dyes all over the world are going to expand as a direct result of the rising demand for items made of textiles. At the same time, the share of wastewater that is produced by the industry will also expand, “making it one of the principal sources for some of the most serious pollution problems in” recent times (Karim et al. 2018). Indeed, due to the carcinogenic and mutagenic properties of the dyeing agents, these dyes have become a severe hazard to all life (Thanavel et al. 2019). This has led to increased concerns over the removal of these dyes from the environment through the application of a variety of physicochemical and biological methods (Imran et al. 2015; Thanavel et al. 2019). Particularly, the biological strategies involving bacteria, yeasts, fungi, algae, and actinomycetes have drawn interest all over the world for their relative cost-effectiveness and environmentally friendly nature compared to the physicochemical methods (Thanavel et al. 2019). Subsequently, several microbial cultures and their microbial enzymes have been characterized and used for removal of dyes from simulated wastewater as discussed in Table 6.3.

6.3.4 Microbial Strategies for Bio-transforming Food Waste into Resources

As a result of shifting lifestyles and the rising urbanization round the globe, there is an increase in the amount of food that has been thrown away from a variety of industrial, agricultural, and domestic settings. Recently, “the Food and Agriculture Organization (FAO)” estimated that around one-third of all the food that is produced each year is lost or wasted. This raises significant concerns, not only because valuable resources are being wasted, but also because their disposal in the environment raises concerns. In fact, massive food waste disposal due to an increasing global population has prompted the hunt for sustainable food waste management systems to alleviate environmental issues. Traditional methods of food waste management, such as landfilling and incineration, pose substantial risks to both the environment and human health due to the generation of toxic fumes. Therefore, there is potential in utilizing microbial bioprocesses that offer economic and sustainable solutions for transforming food waste into high-value bioproducts. These strategies have appeared to be promising for a better human as well as environment sustainability (Ng et al. 2020). Thus, employing “biological methods for the treatment of” such waste offers a sustainable way for valorization (Sharma et al. 2020). In

Table 6.3 Microorganisms and their enzymes involved in treatment of textile industry based dyes

S. no.	Microorganisms	Most active enzyme	References
A. Bacteria			
1.	*Enterobacter* sp. GY-1	Azoreductase	Chen et al. (2011), Imran et al. (2015)
2.	*Pseudomonas putida* WLY	Azoreductase	Yang et al. (2011), Imran et al. (2015)
3.	*Bacillus* sp. VUS	"Lignin peroxidase, tyrosinase, NADH-DCIP reductase, azoreductase, and riboflavin reductase"	Dawkar et al. (2010), Imran et al. (2015)
4.	"*Lactobacillus casei* TISTR 1500"	Azoreductase	Seesuriyachan et al. (2007), Imran et al. (2015)
5.	*Galactomyces geotrichum* MTCC 1360	Lignin peroxidase and laccase activities	Jadhav et al. (2009), Imran et al. (2015)
6.	*Rhizobium radiobacter* MTCC 8161	"Azoreductase, lignin peroxidase, DCIP reductase, MG reductase, and aminopyrine *N*-demethylase"	Telke et al. (2008), Imran et al. (2015)
7.	*Bacillus cereus*	Azoreductase	Deng et al. (2008), Imran et al. (2015)
8.	*Basidiomycetous* isolate	Laccase	D'Souza et al. (2006), Imran et al. (2015)
9.	*Bacillus* sp.	Lignin peroxidase, laccase, and NADH–DCIP reductase	Dawkar et al. (2008), Imran et al. (2015)
10.	*Bacillus* sp.	–	Pourbabaee et al. (2006), Imran et al. (2015)
11.	*Bacillus* Mk-8	–	Cheunbarn et al. (2008), Imran et al. (2015)
B. Fungi			
1.	*Curvularia lunata* URM6179 and *Phanerochaete chrysosporium* URM 6181	"Laccase, lignin peroxidase, and Mn-peroxidase"	Imran et al. (2015)
2.	"Mixed culture consisting of *Pleurotus ostreatus* IBL-02 and *Coriolus versicolor* IBL-04"	"Laccase, lignin peroxidase, and Mn-peroxidase"	Asgher et al. (2010), Imran et al. (2015)
3.	*Bjerkandera adusta* (Willdenow) P. Karsten MUT 3060	–	Anastasi et al. (2011), Imran et al. (2015)
4.	*Ganoderma* sp. En3	Laccase	Zhuo et al. (2011), Imran et al. (2015)

(continued)

Table 6.3 (continued)

S. no.	Microorganisms	Most active enzyme	References
5.	*Penicillium ochrochloron* MTCC 517	Lignin peroxidase	Shedbalkar and Jadhav (2011), Imran et al. (2015), Abataneh et al. (2017)
6.	*“Myrothecium roridum IM 6482”*	Laccase, MG reductase	Jasińska et al. (2012, 2013), Abataneh et al. (2017)
7.	*Aspergillus lentulus*	–	Kaushik and Malik (2010), Imran et al. (2015)
8.	*Aspergillus niger*	–	Agarry and Ayobami (2011), Imran et al. (2015)
9.	*Ascomycetes*	–	Verma et al. (2010), Imran et al. (2015)
10.	*Basidiomycetous* fungus-PCK-3	–	Diwaniyan et al. (2010), Imran et al. (2015)
11.	*Ganoderma lucidum* IBL-05	–	Asgher et al. (2010), Imran et al. (2015)
12.	*Phanerochaete chrysosporium*	Lignolytic “enzymes such as lignin peroxidase and Mn-peroxidase”	Sedighi et al. (2009), Imran et al. (2015)
13.	*“Aspergillus fumigatus XC6”*	–	Jin et al. (2007), Imran et al. (2015)
14.	*Pleurotus florid*	–	Perumal et al. (2007), Imran et al. (2015)
15.	*Phanerochaete chrysosporium*	–	Cing et al. (2003), Imran et al. (2015)
16.	*Aspergillus niger*	–	Assadi and Jahangiri (2001), Imran et al. (2015)
C. Consortium			
1.	“*Providencia* sp. SDS and *Pseudomonas aeruginosa* strain BCH”	“Azoreductase, DCIP reductase, veratryl alcohol oxidase, and laccase enzymes”	Phugare et al. (2011), Imran et al. (2015)
2.	“*Sphingomonas paucimobilis*, *Bacillus* sp. and filamentous bacteria”	–	Ayed et al. (2011), Imran et al. (2015)
3.	*Pseudomonas* sp. SU-EBT	Intracellular laccase enzyme	Telke et al. (2010), Imran et al. (2015)
4.	*Pseudomonas* sp. SUK1, *Pseudomonas* sp. LBC2, and *Pseudomonas* sp. LBC3	Laccase and azoreductase	Jadhav et al. (2010), Imran et al. (2015)

(continued)

Table 6.3 (continued)

S. no.	Microorganisms	Most active enzyme	References
5.	*Sphingobacterium* sp. ATM, *Bacillus odysseyi* SUK3, and *Pseudomonas desmolyticum* NCIM 2112	"Laccase, veratryl alcohol oxidase, DCIP reductase, riboflavin reductase, and azoreductase"	Tamboli et al. (2010), Imran et al. (2015)
6.	*Proteus vulgaris* NCIM-2027 and *Micrococcus glutamicus* NCIM-2168	–	Saratale et al. (2010), Imran et al. (2015)
7.	*"B. subtilis strain NAP1, NAP2, NAP4"*	Peroxidases and dehydrogenases	Phulpoto et al. (2016), Abataneh et al. (2017)
8.	*Pycnoporus sanguineous, Phanerochaete chrysosporium, and Trametes trogii*	Laccase	Yan et al. (2014), Abataneh et al. (2017)
9.	*"Micrococcus luteus, Listeria denitrificans, and Nocardia atlantica"*	–	Hassan et al. (2013), Abataneh et al. (2017)
10.	*"Bacillus* spp. *ETL-2012, Pseudomonas aeruginosa, Bacillus pumilus HKG212"*	Azoreductase	Patel and Gupte (2016), Abataneh et al. (2017)
11.	*Exiguobacterium indicum, Exiguobacteriumaurantiacum, Bacillus cereus, and Acinetobacter baumannii*	–	Kumar et al. (2016), Abataneh et al. (2017)
12.	*"Bacillus firmus, Bacillus macerans, Staphylococcus aureus, and Klebsiella oxytoca"*	–	Adebajo et al. (2017)

this section, we provide a comprehensive discussion on the utilization of various food industry-generated wastes and the production of value-added bioactive compounds.

We also delve into the role of microorganisms in the eco-friendly biotransformation of food waste as a sustainable solution for its management (Table 6.4).

6.4 Application of Microbiotechnology to Control Pollution

6.4.1 Microbiotechnology Derived Biosensors for Pollution Monitoring

Currently, due to the tight association "between environmental pollution and human health/socioeconomic" development, "environmental monitoring has become one of the" top objectives on a global scale. In this arena, biosensor technologies have emerged as an important area for numerous applications and are recognized as an

Table 6.4 Various food industry generated wastes and their related biotransformed value-added products

S. no.	Food industry	Waste	Value-added bioactive compounds	References
1.	"Fruits processing industry"	Pomace, peel, and seeds, rag, rind, skin, stem	Ethanol, dietary fiber, grape seed oil, pomace oil, oleanolic acid, polyphenols (catechin, epicatechin, gallic acid, and resveratrol), anthocyanins (enocyanin), procyanidins, tartates, malates, citric acid, single cell protein, pectin, lactic acid, citric acid, aroma compounds, biogas, ethanol, butanol, pectinases, essential oil (limonene), antioxidants, flavonoids, starch, fiber, sterols, tocopherols, tannins, xanthones, alkylresorcinols, lignin, cellulose, hemicelluloses, procyanidins, and flavanols, carotenoids, bromelain, dietary fiber, phytochemicals, biofertilizer	Galanakis (2017), Schieber (2017), Kiran et al. (2014), Matharu et al. (2016), Rohm et al. (2015), Sharma et al. (2021)
2.	Vegetable processing industry	Shell, peel, core, skin	"Lysine, protein (patatin), steroidal alkaloids, cellulolytic enzymes, adsorption dyes, biopolymer films, carotenoids, dietary fiber, pectin, fructans, phenolic compounds"	Kiran et al. (2014), Matharu et al. (2016), Schieber (2017), Sharma et al. (2021)
3.	Cereal and pulses industry	Husk, bran, lignocellulosic biomass	"Carbohydrates, oligosaccharides, phenolic compounds, lipid soluble vitamins, folic acid, phytosterols, amino acids, and peptides"	Schieber (2017), Kiran et al. (2014), Parate and Talib (2015)
			"Proteins, lipids, dietary fiber, minerals, and antioxidants (vitamin E and oryzanol)"	
			"Activated carbon, proteins, lipids, fatty acids, vitamins, minerals, and phenolic compounds"	
4.	Beverage industry	Wastewater	"Antioxidants, vitamins, enzymes, cellulose, starch, lipids, proteins, pigments, citric acid, gibberellic acid, ethanol, biogas, dyes, and dietary fibers (Murthy and Naidu 2012; Kiran et al. 2014) 46 (cellulose, hemicelluloses, lignin, pectin, gums) Caffeine, polyphenols, triacontanol, and saponins"	Murthy and Naidu (2012), Kiran et al. (2014), Sui et al. (2019)
5.	Dairy industry	Dairy effluent (cheese whey)	"Biodiesel, ethanol, whey protein, lactose, baker's yeast, and minerals"	Kiran et al. (2014), Parashar et al. (2016)

6.	Meat and seafood processing industry	Feathers, blood, heads, bones, skin, viscera, and sometimes whole fish and parsley	“Fertilizer, animal feed, blood meal, meat and bone meal, feather meal, lactic acid, and probiotics, chitosan, and glycosaminoglycans, nutraceuticals (Astaxanthin), chitin, and chitinase”	Kiran et al. (2014), Ning et al. (2018), Yaakob et al. (2019), Prameela et al. (2017), Kumar et al. (2018), Yan and Chen (2015), Sharma et al. (2021)
			“Chitin, calcium carbonate, and protein, meat protein”	
7.	Edible oil industry	Wastewater, organic wastes	“Biosurfactants like rhamnolipids and glycolipids, biodiesel, tocopherols, sterols, squalene, and single cell protein; phenolic compounds, polyphenols, carotenoids, phytosterols, squalene, and dietary fiber”	Henkel et al. (2012), Kiran et al. (2014), Schieber (2017)

analytical and self-sufficient device, appropriate for environmental assessment-cum-monitoring due to its rapid detection property, high sensitivity, and cost-effectiveness in regard to their sensing and monitoring qualities (Oldach and Zhang 2014; Ali and Singh 2020). These biosensors are categorized by the type of biological receptors viz. genetic material, aptamers, enzymes, antibodies, proteins, microbes, etc. or by physicochemical transducers viz. optical, electrochemical, visual, thermal, piezo-electrical, etc. employed for the detection of toxic environmental contaminants (Verma and Bhardwaj 2015; Ali and Singh 2020). Most biosensors used for environmental monitoring are traditionally microbe-based, immunosensors, or enzymatic-based. However, there has been a recent increase in the development of aptamer-based biosensors, driven by their advantageous characteristics, including ease of modification, stability, in vitro synthesis, and target specificity. Moreover, due to the rise of awareness about the detrimental impact of environmental contaminants (organic pollutants, pathogens, pesticides, toxic elements, etc.) on human health, more studies are being encouraged on the biosensor's development for a more sustainable society establishment. In fact, the efficiency of existing biosensors is not so adequate and therefore, more studies are essential for the progression of a robust biosensing device that can successfully be used for the detection of pollutants directly from the complex environments. Therefore, some of the existing pollutants and their monitoring biosensor are discussed in Table 6.5.

6.4.2 Microbiotechnology for Remediation of Pollutants

Throughout the years, the growth of industrial activity and the spread of urbanization have had a significant impact on the environment. As a result, diverse pollutants from industrial, agricultural, and even domestic spheres have been discharged into the environment. This has led to an acceleration in the overall concentration of pollutants in the environment; consequently, the deterioration of environmental health and its adverse effects on living entities has become a major concern these years. In this context, microbial biotechnology has revolutionized the bioremediation field for environmental pollutants (xenobiotics, petroleum hydrocarbons, "polycyclic aromatic hydrocarbons (PAHs), organic pollutants," heavy metals, toxins, pesticides, etc.). Bioremediation involves removal/detoxification/transformation of the pollutants with the use of biological entity such as microorganisms, mainly the contaminants of soil, water, or sediment which may otherwise threaten public health (Wasi et al. 2013; Abataneh et al. 2017; Dangi et al. 2019).

Furthermore, systemic biology (omics biology) is also gaining attention as an attractive bioremediation method by determining the biological agents with respect to their intricate networks and their inter-relations in various biological processes at the cell/molecular, community, or ecological level, which will provide a clear and true picture of the bioremediation (Dangi et al. 2019). However, there is a need to expand the information of microbial genetics to upsurge the abilities of pollutants degradation at large scale and field experiments for advances in this field. Therefore,

Table 6.5 Microbiotechnology derived biosensing elements for environmental pollutants monitoring

S. no.	Analytes		Biosensing elements	References
1.	Heavy metals	Me, Cd, Ar	Urease enzyme	Pal et al. (2009), Negi and Choephel (2020)
		Me(II), Pb (II) ions	DNA	Knecht and Sethi (2009), Negi and Choephel (2020)
		Cd, Cu, Pb	Sol-gel-immobilized urease	Ilangovan et al. (2006), Negi and Choephel (2020)
		Cd, Pb	*Staphylococcus aureus*	Negi and Choephel (2020)
		Cu, Cr, Pb	*Escherichia coli*	Negi and Choephel (2020)
		Cd, Co, Pb	Monoclonal antibody	Negi and Choephel (2020)
		Ni, Co	*Ralstonia eutropha* with *lux*	Shin (2011)
		As	*E. coli* with *lux*, *lacZ*, *gfp*	Shin (2011)
		Hg, As, Cu, Zn, Pb, Cd	*E. coli* with *luc*, *lux*	Shin (2011)
		Hg	Peroxidase	Negi and Choephel (2020)
2.	Herbicides	"2,4-Dichlorophenoxy acetic acid"	Acetylcholinesterase	Negi and Choephel (2020)
		Diuron, paraquat	Cyanobacteria	Negi and Choephel (2020)
3.	Phenolic compounds	Phenol	Mushroom tissue (tyrosinase)	Silva et al. (2010), Negi and Choephel (2020)
		Phenolics	*E. coli* with *lacZ*	Shin (2011)
		"Phenol, *p*-cresol, *m*-cresol, and catechol"	Polyphenol oxidase	Karim and Fakhruddin (2012), Negi and Choephel (2020)
		m-cresol or catechol	DNA	Claude et al. (2007), Negi and Choephel (2020)
4.	Pesticides	Parathion	Parathion hydrolase (biocatalytic)	Negi and Choephel (2020)
		Carbaryl	Acetylcholinesterase	Negi and Choephel (2020)
		Paraoxon	Alkaline, phosphatase	Negi and Choephel (2020)

(continued)

Table 6.5 (continued)

S. no.	Analytes		Biosensing elements	References
5.	Pathogens	*E. coli*	Electrochemical biosensors; mass-sensitive biosensors; optical biosensor-T4-bioprobe phage	Aliakbar Ahovan et al. (2020), Nnachi et al. (2022)
		P. aeruginosa	Mass-sensitive biosensors	Aliakbar Ahovan et al. (2020), Nnachi et al. (2022)
		Salmonella typhimurium	Immunoassay; aptamer-based assay	Aliakbar Ahovan et al. (2020), Nnachi et al. (2022)
		MRSA	Optical biosensor-BP-14-bioprobe phage	Aliakbar Ahovan et al. (2020)
		Salmonella enteritidis	Bioluminesence-SJ2 bioprobe phage	Aliakbar Ahovan et al. (2020)
		Yersinia pestis	Bioluminescence lux system-Phage A1122 with lux tag	Aliakbar Ahovan et al. (2020)

some of the common microorganisms used for bioremediation of different pollutants are discussed in Table 6.6.

6.5 Microbiotechnology in Livestock Management for Better Human Sustainability

6.5.1 Microbes for Improvement of Aquaculture

The population of human race is increasing in size with every passing year and will likely reach approximately 10^{10} individuals in the next 30 years (Bentzon-Tilia et al. 2016). This growing population needs a steady supply of high-quality protein, which to large extent can be supplied by non-vegetarian food/meat (Bentzon-Tilia et al. 2016). However, the growing demand for seafood may not be met by capture fisheries alone. Hence, production in cultured fisheries should be increased in coming time to fulfill the demand of seafood. Thus, aquaculture production practices have been intensified for fulfilling the global demand (Tuan et al. 2013; Zorriehzahra et al. 2016). Undoubtedly, aquaculture industry has significantly contributed in enhanced production of seafood; however, this industry is facing lots of many problems especially due to environmental and anthropogenic activities (Bentzon-Tilia et al. 2016). In addition, controlling the growth of pathogens using antimicrobials can pose a severe “risk to human health due to the spread of microbial antibiotic resistance (Cabello et al. 2013; Bentzon-Tilia et al. 2016).” These alarming hindrances provoked the aquaculture industry for exploring and developing approaches which may be correspondingly effective as antibiotics, sustainable and

Table 6.6 Microorganisms and different pollutants bioremediation

S. no.	Microorganisms	Degradable compound	References
1.	*“Penicillium chrysogenum”*	“Monocyclic aromatic hydrocarbons, benzene, toluene, ethyl benzene and xylene, phenol compounds”	Abataneh et al. (2017)
2.	*“P. alcaligenes, P. mendocina, P. putida, P. veronii, Achromobacter, Flavobacterium, Acinetobacter”*	“Petrol and diesel polycyclic aromatic hydrocarbons toluene”	Abataneh et al. (2017)
3.	*“Pseudomonas putida”*	“Monocyclic aromatic hydrocarbons, e.g. benzene and xylene”	Abataneh et al. (2017)
4.	*“Phanerochaete chrysosporium”*	“Biphenyl and triphenyl methane”	Abataneh et al. (2017)
5.	*“A. niger, A. fumigatus, F. solani, P. funiculosum”*	“Hydrocarbon”	Abataneh et al. (2017)
6.	*“Alcaligenes odorans, Bacillus subtilis, Corynebacterium propinquum, Pseudomonas aeruginosa”*	“Phenol”	Abataneh et al. (2017)
7.	*“Tyromyces palustris, Gloeophyllum trabeum, Trametes versicolor”*	Hydrocarbons	Abataneh et al. (2017)
8.	*“Candida viswanathii”*	“Phenanthrene, benzopyrene”	Abataneh et al. (2017)
9.	“Green algae and diatoms, *Cyanobacteria, Bacillus licheniformis”*	Naphthalene	Abataneh et al. (2017)
10.	*“Acinetobacter* sp., *Pseudomonas* sp., *Ralstonia* sp., *Microbacterium* sp.*”*	Aromatic hydrocarbons	Abataneh et al. (2017)
11.	Gloeophyllum Striatum	“Pyrene, anthracene, dibenzothiophene, lignin peroxidase”	Abataneh et al. (2017)
12.	*“Naegleria, Vorticella, Arabidopsis, Asarum, and Populus* (metagenomics)”	Hydrocarbons	Dangi et al. (2019)
13.	*Bacillus subtilis* HUK15 (genomics)	Hexachlorocyclohexane (HCH)	Dangi et al. (2019)
14.	*Aspergillus nigera semo A, Talaromyces purpurogenus semo F, and Aspergillus flavus semo M* (transcriptomics)	Degradation of hydrocarbons	Dangi et al. (2019)

(continued)

Table 6.6 (continued)

S. no.	Microorganisms	Degradable compound	References
15.	*Rhizobiales, Burkholderiales, and Actinomycetales* (metaproteomics)	Polycyclic aromatic hydrocarbon	Dangi et al. (2019)
16.	*"Pseudomonas putida* KT2440 (fluxomics)"	Hydrocarbons	Dangi et al. (2019)
17.	*"Bacillus, Staphylococcus"*	Endosulfan	Abataneh et al. (2017)
18.	*"Enterobacter"*	Chlorpyrifos	Abataneh et al. (2017)
19.	*"Pseudomonas putida, Acinetobacter* sp., *Arthrobacter* sp.*"*	FitorazWP76, Decis2.5EC, malathion	Abataneh et al. (2017)
20.	*Acinetobacter* sp., *Pseudomonas* sp., *Enterobacter* sp., *and Photobacterium* sp.	"Chlorpyrifos and methyl parathion"	Abataneh et al. (2017)
21.	*Koribacter, Acidimicrobium, Bradyrhizobium, Burkholderia, Solibacter, Singulisphaera, Desulfomonile* (metagenomics)	Organophosphorus-containing pesticides	Dangi et al. (2019)
22.	*Sphingomonas* sp. *GY2B* (proteomics)	Phenanthrene	Dangi et al. (2019)
23.	*Fusarium* sp.	Oil	Abataneh et al. (2017)
24.	*Pseudomonas aeruginosa, Corynebacterium propinquum, Bacillus subtilis, Alcaligenes odorans*	Oil	Abataneh et al. (2017)
25.	*Bacillus cereus* A	Diesel oil	Abataneh et al. (2017)
26.	"*Pseudomonas aeruginosa, P. putida, Arthobacter* sp., *and Bacillus* sp.*"*	Diesel oil	Abataneh et al. (2017)
27.	*"Pseudomonas cepacia, Bacillus cereus, Bacillus coagulans, Serratia ficaria, Citrobacter koseri"*	Diesel oil, crude oil	Abataneh et al. (2017)
28.	*Saccharomyces cerevisiae*	Pb, Me, Ni	Abataneh et al. (2017)
29.	*"Cunninghamella Elegans"*	Heavy metals	Abataneh et al. (2017)

(continued)

Table 6.6 (continued)

S. no.	Microorganisms	Degradable compound	References
30.	“*Pseudomonas fluorescens* and *Pseudomonas aeruginosa*”	Fe, Zn, Pb, Mn, Cu	Abataneh et al. (2017)
31.	*Lysinibacillus sphaericusCBAM5*	Co, Cu, Cr, Pb	Abataneh et al. (2017)
32.	*Mycobacterium profundi strain S49T*	Fe	Abataneh et al. (2017)
33.	“*Aspergillus versicolor, A. fumigatus, Paecilomyces* sp., *Trichoderma* sp., *Microsporum* sp., *Cladosporium* sp.”	Cd	Abataneh et al. (2017)
34.	*Geobacter* sp.	Fe(III), U(VI)	Abataneh et al. (2017)
35.	“*Bacillus safensis (JX126862) strain (PB-5 and RSA-4)*”	Cd	Abataneh et al. (2017)
36.	“*Pseudomonas aeruginosa, Aeromonas* sp.”	U, Cu, Ni, Cr	Abataneh et al. (2017)
37.	“*Aerococcus* sp., *Rhodopseudomonas palustris*”	Pb, Cr, Cd	Abataneh et al. (2017)
38.	“*Brevibacterium epidermidis* EZ-K02 (metagenomics)”	As, Co, Cd	Dangi et al. (2019)
39.	*Pseudomonas aeruginosa* sanai (proteomics)	Cd	Dangi et al. (2019)

eco-consumer-friendly (Standen et al. 2013; Lazado et al. 2015; Zorriehzahra et al. 2016).

Studies have shown that managing microbial communities associated with fish and their habitat can provide an efficient solution to various issues. This management not only improves nutrient levels in water but also reduces fish pathogenic bacteria, enhances larval survival, eliminates the need for antimicrobials, and boosts nutrient utilization and immunity (Bentzon-Tilia et al. 2016; Zorriehzahra et al. 2016). Probiotics are among the strategies that can reduce the aquaculture industry’s reliance on antibiotics and serve various functions, including nutrient recycling, organic matter degradation, and disease protection. They play a crucial role in not only reducing antibiotic use but also contributing to nutrient management and disease prevention (Bentzon-Tilia et al. 2016; Zorriehzahra et al. 2016). These beneficial activities of microbes on aquatic species have contributed immensely to the growth, development, and sustainability of aquaculture. Hence, the microbial communities in fish/aquaculture industry have immense potential for improving the aquaculture and most of these microbes with their beneficial effect on aquatic host are discussed in Table 6.7.

6.5.2 Probiotics for Livestock Animals: An Industry Level Exploration

With the fast-rising worldwide demand for animal food products, it has become crucial for livestock farmers to increase livestock productivity to fulfill the rising demands (Lambo et al. 2021). In this context, feed additives such as antibiotic growth promoters, enzymes, mineral supplements, probiotics, etc. provide a safe and healthy way to enhance the animal health, productivity, and their general well-being. However, due to the rise of antimicrobials resistance and their cost concerns, probiotics **gained popularity** in the livestock industry in both animals and consumers of animal products. Consequently, livestock industry has recognized them as non-toxic, non-pathogenic supplements/additives that could enhance disease resistance against the pathogens, improves the intestinal microbial balance, digestion, immunity, and performance in administered animals as discussed in the following table (Jiménez 2010; Lambo et al. 2021).

Therefore, probiotics stand a good chance of substituting the use of antibiotics in livestock industry and are believed to “have a significant impact on the animal nutrition, health, and productivity.” However, the effect of probiotics as well as their responses of host animals varies among the published literature and this variation may be attributable to the kind/strains of microbes used single/multi H strain, their viability in gut; dosage; the physiological health of the host animal, the environment, diet, and the route of administration. In addition, cross-contamination of the human food chain by probiotics used in animal feed cannot be minimized, therefore for the food safety and security to be successful, the established safety measures in probiotic development must be adhered (Alayande et al. 2020). Also, additional research is required to comprehend the interaction processes between the single/combined bacteria and the host’s gut microbiota, as well as their direct comparisons should be examined for optimal advantages (Table 6.8).

6.6 Microbiotechnology in Food Security

6.6.1 Production of Microbial Oils Rich in Omega-3

Lipids are natural molecules that can be grouped based on their ability to dissolve in certain solvents. They include substances like triacylglycerols (found in fats), phospholipids (containing phosphoric acid), glycolipids (with glucose), and sphingolipids. Lipids serve as a rich source of metabolic energy, providing 9 calories per gram. Lipids also are identified to be important additives of several herbal processes, which consist of power storage, cascade molecular signaling, plasma

Table 6.7 List of beneficial microorganisms and their beneficial effect on aquatic host (adapted from Zorriehzahra et al. 2016)

S. no.	Microorganism		For aquatic species	Beneficial impact	References
	Genus	Species			
1.	Aeromonas	*A. Hydrophila; A. sobria* GC2	*Oncorhynchus mykiss*	Reduce infections and protects against *Aeromonas salmonicida*; "*Lactococcus garvieae*; *Streptococcus iniae*; *Aeromonas bestiarum;* and *Ichthyophthirius multifiliis"*	Irianto and Austin (2002a, b), Pieters et al. (2008), Brunt and Austin (2005)
2.	"Agarivorans"	"*A. albus* F1-UMA"	*"Haliotis rufescens"*	Increases survivability	Silva-Aciares et al. (2011)
3.	Alteromonas	*A. Macleodii* 0444	*Perna canaliculus; Pecten maximus*	Protects against *Vibrio splendidus*, *V. coralliilyticus,* and *V. splendidus*	Kesarcodi-Watson et al. (2010, 2012)
4.	Burkholderia	*B. cepacia* Y021	*Crassostrea corteziensis; Nodipecten subnodosus*	Increases survivability	Granados-Amores et al. (2012)
5.	"Enterobacter"	*"E. amnigenus"*	*Oncorhynchus mykiss*	"Increases protection toward *Flavobacterium psychrophilum"*	Burbank et al. (2011)
6.	"Neptunomonas"	*Neptunomonas* 0536	*"Perna canaliculus"*	Protect against *V. splendidus*	Kesarcodi-Watson et al. (2010, 2012)
7.	Shewanella	*S. putrefaciens*	*Sparus aurata* L.	Improves growth	García de la Banda et al. (2012)
8.	Bacillus	*B. circulans PB7; B. subtilis; B. licheniformis; B. subtilis UTM 126; B. subtilis E20;* *B. megaterium*; *B. pumilus*; *Bacillus* P64; *Bacillus* 48	*Labeo rohita;* Trout; *Litopenaeus vannamei*; *Ictalurus punctatus; Pangasianodon hypophthalmus; P. japonicus; O. niloticus; Centropomus undecimalis*	Improves feed conversion ratio; growth; immunity status and protects against *A. hydrophila; Yersinia ruckeri; V. harveyi*; *Edwardsiella ictaluri*	Zorriehzahra et al. (2016)
9.	Brochothrix	*Thermosphacta* ba211	*Oncorhynchus mykiss*	Protects against *A. bestiarum*	Pieters et al. (2008)

(continued)

Table 6.7 (continued)

S. no.	Microorganism		For aquatic species	Beneficial impact	References
	Genus	Species			
10.	"Clostridium"	*Butyricum*	*Oncorhynchus mykiss; Miichthys miiuy*	Increases immunity and protects against vibriosis; *A. hydrophila;* and *V. anguillarum*	Pan et al. (2008)
11.	Enterococcus	*E. faecium* SF 68 *E. faecium* MC13	*"Anguilla anguilla Penaeus monodon"*	Protects against *Edwardsiellosis*; *V. harveyi;* and *V. parahaemolyticus*	Chang and Liu (2002), Swain et al. (2009)
12.	Kocuria	*Kocuria SM1*	*O. mykiss*	"Protects against *V. anguillarum and V. ordalii"*	Sharifuzzaman and Austin (2010)
13.	Lactobacillus	*L. acidophilus;* *L. rhamnosus;* *L. rhamnosus;* *L. fructivorans;* *L. plantarum; L. plantarum*	*Nile tilapia; Clarias gariepinus; O. mykiss; O. niloticus; S. aurata*	Increases growth performance, immunity, heat tolerance and protects against *P. fluorescens; S. iniae; A. salmonicida; E. tarda*; *L. garvieae*	Zorriehzahra et al. (2016)
14.	"Lactococcus"	*"lactis AR21"*	*Rotifers*	Improves growth, levels of biochemical constituents and protects against *V. anguillarum*	Seenivasan et al. (2012)
15.	"Leuconostoc"	*L. mesenteroides CLFP 196*	*O. mykiss*	Reduces mortality due to *L. garvieae*	Vendrell et al. (2008)
16.	Micrococcus	*M. luteus; Micrococcus MCCB 104*	*O. mykiss; M. rosenbergii*	Protects against *A. salmonicida*	Irianto and Austin (2002a), Jayaprakash et al. (2005)
17.	Pediococcus	*Pediococcus acidilactici*	*O. mykiss*	Reduces vertebral column compression syndrome	Aubin et al. (2005)
18.	Rhodococcus	*Rhodococcus SM2*	*O. mykiss*	Improves immunity and protects against *V. anguillarum*	

19.	“Streptococcus”	*“S. phocae P180; S. faecium”*	*P. monodon; Oreochromis niloticus (Nile tilapia)*	Increases growth and protects against *V. harveyi* infection; as growth promoters	Swain et al. (2009), Lara-Flores et al. (2003)
20.	Streptomyces	–	*“P. monodon”*	“Growth improved and water quality was also increased”	Das et al. (2006), Newaj-Fyzul et al. (2014)
21.	Vagococcus	*V. fluvialis*	*Sea bass*	“Protects against *V. anguillarum* infection”	Sorroza et al. (2012)
22.	“Dunaliella”	*Tertiolecta*	*Artemia*	Protects against *Vibrio campbellii* and *V. proteolyticus*	Marques et al. (2006)
23.	Yarrowia lipolytica	*Y. lipolytica*	*“Pinctada mazatlanica”*	Improves growth	Aguilar-Macías et al. (2010)

Table 6.8 Various probiotics and their beneficial effect on livestock animals (ruminants, poultry, and swine) (adapted from Mahesh et al. 2021; Lambo et al. 2021)

S. no.	Probiotics	Beneficial effect	References
A. Ruminants			
1.	*Bacillus foraminis*, *B. firmus, B. licheniformis*, *Staphylococcus saprophyticus bovis*	Reduces feed intake and acetate to propionate ratio	Yang et al. (2012)
2.	*"Lactobacillus plantarum, L. acidophilus, L. casei, L. salivarius, L. gallinarum, L. reuteri, Streptococcus bovis"*	Stimulates lactate utilizers, stabilizes rumen pH, reduces fecal shedding of *E. coli* O157, and improves the immune function	Mahesh et al. (2021)
3.	*"E. faecalis; L. rhamnosus"*	Improves weight gain, lowered gut pH and maintains the ecology ruminal microbiota	Lan et al. (2016)
4.	*"L. acidophilus; L. casei; B. thermophilum; E. faecium"*	Increases milk fat and organic acids viz. butyric, caproic acid	Hu et al. (2021)
5.	*"L. acidophilus, L. plantarum, B. bifidum, B. subtilis, A. oryzae"*	Increases dry matter intake, milk yield and composition, serum albumin, and reduced globulin during postpartum	Ishaq et al. (2015)
6.	*"L. farraginis, L. reuteri, L. rhamnosus"*	"Increases feed: milk ratio, dry matter intake, milk yield, % milk fat, and protein"	Salvedia et al. (2015)
7.	*"L. casei Zhang, L. plantarum P-8"*	"Improves milk production and milk IgG content, lactoferrin, lysozyme, and lactoperoxidase as well as the rumen fermentative and beneficial bacteria population"	Maake et al. (2021)
8.	*"L. acidophilus, S. cerevisiae, E. faecium, A. oryzae, B. subtilis"*	"Increases percentage of lymphocyte and genes associated with immunity and homeostasis"	Aalaei et al. (2018)
9.	*"L. fermentum, L. plantarum, M. elsdenii, S. cerevisiae"*	Improves "nutrient digestibility, rumen fermentation characteristics, and nitrogen retention"	Shreedhar et al. (2016)
10.	*Megasphaera elsdenii*	Enhances lactate utilization in rumen and synthesis of propionate from lactate	Mahesh et al. (2021)
11.	*Propionibacterium freudenreichii, P. jensenii, and P. acidipropionici*	Enhances lactate utilization in rumen, synthesis of propionate from lactate and regulates ruminal pH	Mahesh et al. (2021)
12.	*Prevotella bryantii*	Moderates' rumen fermentation	Mahesh et al. (2021)
13.	*Bacillus subtilis, B. licheniformis,* and *B. coagulans*	Supporting rumen microbes, moderates rumen fermentation, and improves feed degradation	Mahesh et al. (2021)

(continued)

Table 6.8 (continued)

S. no.	Probiotics	Beneficial effect	References
14.	*Ruminococcus flavefaciens*	Moderates' rumen fermentation	Mahesh et al. (2021)
15.	*Pediococcus acidilactici*	Faster development of rumen function	Mahesh et al. (2021)
B. Poultry			
1.	*"L. acidophilus, L. casei, E. faecium, B. thermophilum"*	Decreases "gizzard weight, abdominal fat, and increased antibody production"	Abou-Kassem et al. (2021)
2.	*"L. acidophilus, L. casei, E. faecium, B. bifidum"*	Improves body weight, and protection against "new castle disease and infectious bursal disease"	Goto et al. (2016)
3.	*"L. salivarius, L. reuteri. L. crispatus, L. johnsonii"*	Downregulates "the expression of cecal tonsils cytokine gene and enhanced antibody-mediated immune responses against a highly immunogenic T cell-dependent antigen"	Mostafa et al. (2014)
4..	*"L. acidophilus, B. subtilis DSM 17299, C. butyricum"*	Increases body weight, digestibility of ileal amino acid, and humoral immune response	Xu et al. (2017)
5.	*"L. acidophilus, L. casei, B. thermophilum, E. faecium"*	Reduces ileal *E. coli*	Adjei-Fremah et al. (2018)
6.	*"A. oryzae, B. subtilis, S. cerevisiae, L. plantarum, Rhodopseudomonas capsulate"*	Improves egg protein quality	Direkvandi et al. (2020)
7.	*"L. casei, L. acidophilus, Bifidobacterium"*	Improves "growth performance, carcass trait, antioxidant capacity gut microbiota, and immunity"	Talebi et al. (2008)
8.	*"L. casei, L. lactis, L. plantarum, Carnobacterium divergens, S. cerevisiae"*	Increases femur elongation and area, elastic strength of tibia and reduced bone strength	Tomaszewska et al. (2018)
C. Swine			
1.	*"L. acidophilus, B. subtilis, S. cerevisiae"*	Improves growth performance and gut microbiota	Liu et al. (2018)
2.	*"L. plantarum* L21, *L. plantarum* L80, *L. paraplantarum* L103, *B. subtilis, L. acidophilus, S. cerevisiae"*	Increases "growth performance, fecal lactobacillus population, and reduced fecal *E. coli*"	Ray et al. (2020)
3.	*"B. coagulans, B. licheniformis, B. subtilis, C. butyricum"*	Improves body weight, growth performance, nutrient digestibility, fecal lactobacilli, and meat quality	Ramlucken et al. (2020)
4.	*"L. amylovorus, L. reuteri LAB 26, L. reuteri LAB 49, L. johnsonii, L. salivarius, L. mucosae"*	Increases bacteria population in the jejunum and influenced the expression of specific intestinal mucosa cytokines	Biswas et al. (2022)

(continued)

Table 6.8 (continued)

S. no.	Probiotics	Beneficial effect	References
5.	*B. subtilis, B. licheniformis*	Increases weight gain, “improved nutrient digestibility in sows and reduced” *E. coli* population in sows	Chung et al. (2015)

membrane structure, and lots of others (Kannan et al. 2021). Glycerol, esters, and fatty acids are the primary constructing blocks of fat and oils.

Fatty acids can be categorized into saturated, monounsaturated, and polyunsaturated types. Saturated fatty acids have no double bonds and are in foods like meat and butter. Monounsaturated fatty acids have one double bond and are also produced by the body. On the other hand, polyunsaturated fatty acids (PUFAs), which have multiple double bonds, are considered essential and must be obtained from the diet. PUFAs are crucial for maintaining human health and play a significant role in preventing and treating various diseases (Masurkar et al. 2015).

Polyunsaturated fatty acids (PUFAs) are defined by their long carbon chains with a carboxyl group at one end and a methyl group at the other. They have multiple double bonds in their structure. Eating too many saturated fatty acids (SFAs) has been linked to health issues like arteriosclerosis, which involves the thickening of artery walls, chest pain called angina pectoris due to blocked heart arteries, and other circulation problems. This happens because SFAs are solid at room temperature and can become hard even when heated or pressurized. In contrast, unsaturated fatty acids remain liquid at room temperature and are less stable (Lee 2013).

Even there are various PUFAs in nature; just a few are critical from a physiological standpoint. Most of the pertinent ones fall beneath the omega series, such as omega-3, 6, 9 fatty acids. Linoleic acid (LA) is that this kind of essential PUFAs that would only be furnished through manner of diet, as modified into previously mentioned (Spector and Kim 2015). Another double bond will have to be added to the fatty acid chain for arachidonic acid (AA) (20:4), an EFA that is a member of the *n*-6 FAs, to be converted from LA (18:3, *n*-6) (Spector and Kim 2015). An analogue of LA, -linoleic acid (ALA) (18:3, *n*-3) is produced through manner of de novo synthesis and is a member of the omega-3 (*n*-3) family. Because of their exquisite useful functionality and numerous health advantages, “eicosapentaenoic acid (EPA) (20:5, *n*-3) and docosahexaenoic acid (DHA) (22:6, *n*-3) have turn out to be critical nutrients. Figure 6.3 illustrates many PUFA varieties.”

6.6.1.1 Safety Profile of Omega-3 Fatty Acids

Eating more *n*-3 fatty acids may raise low-density lipids, which can lead to serious illness over time. So, despite their many benefits, it is important to know how much to eat. According to the National Institutes of Health, it is recommended to consume at least 650 mg of *n*-3 fatty acids per day (Oh 2005; Weylandt et al. 2015).

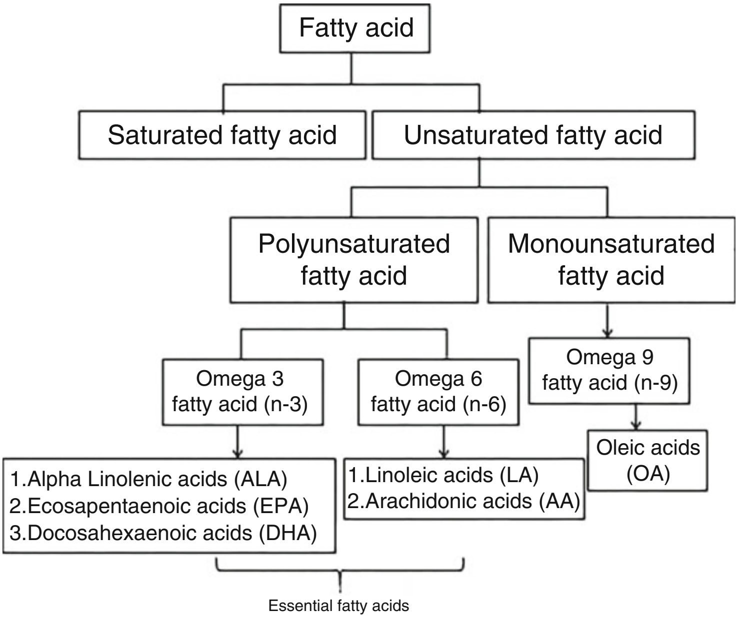

Fig. 6.3 Classification of fatty acids

6.6.2 Development of Microbial Protein for Future Sustainability

Microbes can help create clean energy and convert renewable resources into fuels. They also assist plants in absorbing more nutrients, which is known as "nutrient recycling." Microbes provide essential energy sources to plants, and in return, plants offer them their waste products as nourishment. Microbial proteins contain vitamins, carotene, and carbs in good amounts. These proteins can be produced under regular conditions, which means they aren't affected by land or environmental restrictions like drought or flood.

6.6.2.1 MP as Food

In the context of livestock and aquaculture nutrition, microbial protein offers a high-quality alternative to animal-based protein sources such as fish meal. When we consider human nutrition, microbial protein meets the essential amino acid requirements set by the FAO/WHO, making it a valuable direct dietary option for people as well. Historically, coastal populations have relied on algae as a consistent source of protein and nutrients for many centuries. Nowadays, algae and microalgae are also used in the food industry as ingredients in various foods and dietary supplements (Ravindra 2000; Becker 2007). Yeast has a long history of use in food production, dating back to the earliest bread baking and grape fermentation. It has been employed as a direct food source, such as during World War II when it was distributed to the military and the public. Today, yeast plays a significant role in the production of various microbial-based products for the food industry and beyond. Its primary applications include baking and alcohol fermentation, with an estimated global market value of up to 9.2 billion Euros in 2019 and an expected annual growth rate of 7.9%. Another notable food source is fungi, which have also been consumed by humans. One well-known type of fungal-based protein, known as mycoprotein, is marketed under the name Quorn$^{\mathrm{TM}}$ and is available in approximately 15 different countries worldwide (Wiebe 2004). Mycoproteins excel in replicating the taste and texture of meat, making them a popular alternative to traditional animal-based products. Currently, the production of mycoprotein for Quorn$^{\mathrm{TM}}$ products amounts to 25,000 tonnes per year, with a market value of approximately 214 million euros and an expected annual growth rate of 20% in the years ahead.

6.6.2.2 Added Value Applications

Microorganisms are having the potential to provide an extensive variety of added-cost merchandise which might be appropriate for each animal and human vitamin, similar to being an excellent supply of nutritious protein (Vandamme and Revuelta 2016). The average protein yield achievable from algae, fungi, and microorganisms, along with other potential value-added products, has been extensively researched and developed.

6.6.2.3 Production of Microbial Protein from Waste Streams

The call for animal-sourced food is expected to boom substantially over the following couple of decades, particularly in rising economies, because of populace increase and developing earnings levels (FAO 2018). In numerous low-income countries, animal-derived foods will continue to play a crucial role in addressing the micronutrient deficiency in the diets of young and vulnerable populations (Nelson et al. 2018). However, it is increasingly important to explore new, previously uncharted nonagricultural protein production methods to meet the rising demand for protein, both for direct human consumption and as inputs for animal production, while minimizing environmental impact. In this context, there is growing interest in the potential of microbial protein as an alternative protein production method (Jones et al. 2020; Matassa et al. 2020; Pikaar et al. 2018a). Microbial proteins encompass algae, yeast, bacteria, and fungi (Matassa et al. 2016). Organic waste streams, along with gaseous substrates such as methane, carbon dioxide, and hydrogen, can be harnessed to produce microbial proteins for use in human food, animal feed, and as slow-release natural fertilizers (Matassa et al. 2020; Pikaar et al. 2018a, b). Although, it is not however economically feasible to replace traditional soybeans with microbial proteins, mycoprotein is now a doable opportunity for fish meal in aquaculture and meat in human. Moreover, as energy charges fall, conventional feed charges rise, or environmental pollution is charged, extraordinary microbial protein production strategies also can fast start to look increasingly more appealing. Circular feeds are much more likely to be ordinary via way of means of the overall populace than different plant-primarily based totally proteins, which can be gaining a quick increasing marketplace among high-earnings consumers (Pikaar et al. 2018a, b). Several SDGs may be substantially impacted via way means of round feed technology, each favorably and unfavorably. For instance, microbial protein may also lower the call for soybean meal, that is presently basically used for animal feed, in addition to the profitability of the soybean industry, the growth of soybean cultivating regions (the latest motive force of land-use change), and greenhouse fuel line emissions. It can also have a fantastic effect on the SDG intention of biodiversity and the soybean sector's profitability (SDG). But soybeans do not simply yield protein. Soybeans do not just provide protein. Hence, a decrease in soybean oil supply might lead to increased palm oil production and consumption, which could have a ripple effect on deforestation (SDG) and potentially raise the prevalence of non-communicable diseases (NCDs; SDG) (Chen et al. 2011; Kadandale et al. 2019). Additionally, microbial protein may decrease the call for fish used as animal feed, which may gain fish populations (SDG). If broadly used, round feed ought to partly uncouple the manufacturing of protein-wealthy animal feed from land use, presenting a second course for decreasing greenhouse fuel line emissions, even as the results for the marketplace energy and pricing of feed deliver consolidation in the meals' gadget are unknown. Conversely, an ample and cheaper deliver of feed may decrease the value of elevating animals and lift the call for cattle products. This impact ought to result in better greenhouse fuel line emissions and probably greater obesity (You and Henneberg 2016; Wang and Beydoun 2009) and NCDs in regions in which meat consumption is already high (SDG). The dietary reputation and fitness of undernourished subpopulations, in particular youngsters and pregnant or lactating women, may be advanced via way of means of extra intake of livestock products (Shapiro et al. 2019). Small-scale cattle farmers' livelihoods can be impacted via way means of decrease feed (SDG). Furthermore, recycling food waste could also enhance the economic value of waste (SDG). Apart from potential trade-offs with existing livelihood options and their environmental impacts, such as the reduced availability of animal manure as a source of organic soil nutrients in mixed crop-livestock systems, this effect could create new sources of income from waste collection, distribution, and processing.

6.6.3 Microbial Fuel Cells for Generation of Electricity

Bioelectricity production is the process by which organisms generate energy through the production of electrons during their metabolic processes. These generated electrons can be collected to maintain a steady or continuous source of power generation. When provided with the right substances, bacterial cells can metabolize them and produce electrons that can be retrieved and used by connecting them through a circuit. These components can be combined to create an assembly called a 'microbial fuel cell' (MFC), which serves as an energy source. The microorganisms' anaerobic digestion of the substrate is crucial for the creation of the electrons resulting from their metabolism. The mentioned reactions illustrate the metabolic processes that were initially carried out by microorganisms without oxygen and later with oxygen (Moqsud et al. 2013).

6.6.3.1 Microbial Fuel Cell

Most MFCs consist of two separate chambers: the anodic chamber, housing the anode, and the cathodic chamber, housing the cathode. These chambers are separated by a proton exchange membrane (PEM). A suitable substrate is provided to the microbes in the anodic chamber, where it is aerobically broken down to release electrons. These electrons are then transported from the anode to the cathode through an external circuit. Meanwhile, the protons generated in this process selectively pass through the exchange membrane. Both of these byproducts created by the microorganisms in the anodic compartment migrate to the cathode and combine with oxygen to form water (Sharma and Li 2010).

MFCs, utilizing electrochemically active bacteria (EAB) to oxidize various carbon sources, including organic waste, are devices capable of converting chemical energy into electrical energy (Angenent et al. 2004, 2004; Lovley 2008; Logan 2009). The MFC chambers may be fabricated from Plexiglas, polycarbonate, or glass (Rhoads et al. 2005). Anode electrodes may be crafted from substances such as "carbon paper, carbon cloth, graphite, and graphite felt (Zhang et al. 2011; Zhuo et al. 2011; Wei et al. 2011; Sangeetha and Muthukumar 2013)." To keep the electrode's cardio nature, an air cathode is needed, and this may be built of platinum (Pt) or Pt-black catalyst substances. The natural substrates within side the anode chamber might be utilized by the microorganisms to supply electrons, in order to then tour thru the outside circuit to the cathode and be absorbed with the aid of using the answer within side the cathode chamber. The ion trade membrane lets in the produced "protons to head from the anode to the cathode (Wang et al. 2013)." Permanganate (MnO_4) and ferricyanide $[(Fe(CN_6))^3]$ answers can characteristic as green catholytes however aren't long-lasting (Jang et al. 2004; Wei et al. 2012).

6.6.3.1.1 Design

Depending on elements just like the quantity of chambers, the way of operation, etc., there are numerous designs for the constructing of an MFC. These classes specifically consist of:

6.6.3.1.1.1 Two-Chamber MFC

This format is an everyday MFC with chambers which might be separated through manner of approach of an ion extrude membrane. These are currently best applied in laboratories and normally characteristic in batch mode, though they can also "characteristic" in non-forestall mode (Du et al. 2007).

6.6.3.1.1.2 Single-Chamber MFC

An anodic chamber and an air cathode are the best additives of a single-chamber MFC, that is, wherein protons and electrons are exchanged. "For the constructing of a single-chamber MFC, diverse designs, including Table 6.9, were suggested."

6.6.3.1.1.3 Stacked MFC

A stack of MFCs related in collection or parallel collectively is known as a microbial fuel (Aelterman et al. 2006). By acquiring numerous configurations of the hydraulic waft and electrode, MFC may be layered. These are available in four special varieties; along with (i) “parallel electrode connections in parallel waft mode (ii), collection electrode connections in collection waft mode (iii), and (iv) collection electrode connections in parallel waft mode (Choi and Ahn 2013).” While treating wastewater (Choi and Ahn 2013), discovered that the use of parallel electrode connections (collection waft mode) elevated the general balance of the oxidation-discount potentials and led to more COD removal, Colombia efficiencies, and maximal strength densities.

6.6.3.1.2 Applications

6.6.3.1.2.1 Production of Bioelectricity

The use of herbal carbohydrate substrates that is derived from municipal, “industrial and agricultural wastes for the generation of bioelectricity are the precept feature of an MFC.” Another advantage of MFCs is the direct conversion of fueling molecules into power without the arrival of heat. By averting the Carnot cycle, which lowers the overall performance of thermal energy conversion, a higher conversion overall performance (gt; 70%) is possible (Du et al. 2007). MFCs have made advances in power generation all through the previous couple of years; however, the reality is that they will be now not currently a cost-effective technology for producing power. Substrates which consist of domestic wastewater and glucose, respectively, had been used to create power outputs of 10–50 and 250–500 mW/m^2, respectively (Logan 2004). “A mixed consortium of microbial community” and a sincere substrate like glucose were utilized (Rabaey et al. 2003) to offer a power density of 3.6 W/m^2 (Rabaey et al. 2003). The use of the particular microorganism Rhodoferax ferrireducens, that could oxidize glucose to CO_2 without the requirement for electron mediators to move the electrons to the anode, end up suggested with the useful resource of the use of Chaudhuri and Lovely in 2003 (Rabaey et al. 2003). As a result, the need for a virtual mediator is removed, setting up the door for future changes to the MFC format that might boom its overall performance. Another approach that might be used to enhance power generation and examine simultaneously through several unique applications is stacking MFCs. Six separate MFC gadgets were joined in a stacked configuration with the useful resource of the use of Aelterman et al. (2006), yielding a maximum power output of 258 W/m^3 on an hourly average. Although the power output of MFC is not as right as that of various fueling cells, such as methanol-driven FCs, the fluctuation in substrate consumption gives the device some brought appeal (Rabaey and Verstraete 2005). Additionally, a self-retaining phototrophic MFC has been advanced that produces non-forestall power output beneath illumination without the need for substrate, such as organics or nutrients, and if improved, have to feature as a reliable possibility deliver of sustainable energy (He et al. 2008). The metabolic interest of *Rhodobacter sphaeroides* ended up being used to assemble an MFC for the in situ oxidation of photo-natural hydrogen for the producing of power. “Therefore, this MFC technology” has the functionality to be used as a sustainable energy deliver. The concept of a bio-battery that could recharge domestic system and exceptional devices requiring

Table 6.9 Reports on designs proposed for the construction of a single-chamber MFC

Design	Anode	Cathode
"Rectangular"	"Mn^{4+} graphite anode"	"Fe^{3+} graphite cathode"
"Cylindrical"	"Carbon paper without wet proofing"	"Carbon electrode/PEM assembly or rigid carbon paper without PEM"
"Tubular"	"Granular graphite matrix"	"Ferricyanide solution"
"Flat plate"	"Carbon paper"	"Carbon cloth"
"Concentric design"	"Graphite"	"Air porous made up of carbon/Pt catalyst"

low voltage, additionally may be used with MFC technology. The primary and crucial format of an MFC has long past through several revisions, developing a foundation for the development of new thoughts and applications.

6.6.3.1.2.2 Bio-hydrogen Production

Typically, in MFCs, microorganism performs as catalysts, oxidizing the substrates with inside the anodic chamber to provide protons and electrons which might be then added to the cathode through the wire (externally) and the PEM, respectively. They each integrate to make water, casting off the opportunity of hydrogen synthesis. The electrode that generates power or the microorganism that make decreased metabolites like methane or hydrogen fueling can function the remaining electron acceptor for the microorganism with inside the anodic compartment at some stage in substrate oxidation (Rabaey et al. 2004). In an MFC, outside capability software enabled the formation of hydrogen on the cathode with the aid of using overcoming the thermodynamic barrier via the interplay of electrons and protons. This gives a capability manner to alternate the MFCs operation in order that its miles centered on generating bio-hydrogen. In an MFC, superior microorganisms have been taken from the anodic chamber and blanketed microbial consortia that, upon identification, have been recognized to additionally consist of a few species able to developing hydrogen. In this investigation, while the electron switch fee increased, the hydrogen manufacturing rates, which have been to start with as much as 43 5%, reduced underneath the detection limit. As a result, this examines indicates that power manufacturing and hydrogen introduction are neither affected nor because of each other in MFCs and are extraordinarily implausible to take place on the identical time.

6.6.3.1.2.3 Wastewater Management

Industrial, municipal, and different wastewater effluent function a key useful resource for strength harvesting and on the equal time show to be a great substrate for bioremediation. The chronic trouble of wastewater control has been solved flawlessly via way of means of microbial gasoline era. Maximum strength density, Colombia efficiencies, and COD are the primary three elements that decide how green MFC era is. When the usage of natural substrates like acetate, glucose, and sucrose, MFC era continually achieves better most strength densities (494 mW/m^2) than while the usage of a complicated "substrate like wastewater (146 mW/m^2)

(Feng et al. 2008). Domestic wastewater (Liu et al. 2004), swine wastewater (Min et al. 2005), meat packing wastewater (Heilmann and Logan 2006)," meals processing wastewater, "hydrogen fermentation reactor effluent (Oh and Logan 2005)," and brewery wastewater have all been examined the usage of MFCs for strength generation (Kim et al. 2004). Complex natural substrates, inclusive of wastewater remnants from numerous sources, can also additionally pose capacity troubles that might intrude with the manufacturing of electricity, inclusive of toxicity because of an excessive ammonia attention or because of the manufacturing of risky acids at some stage in "hydrolysis and substrate fermentation (Min et al. 2005)".

6.6.3.1.2.4 Biosensors

In the sector of biosensors, MFCs are regularly used to evaluate the pollutant content material of numerous wastewater effluents. The organic oxygen calls for numerous remedy plant effluents may be calculated in the usage of MFC technology. Due to the proportionate dating among the Colombia yield and the organic electricity of wastewater, MFCs have this capability (Kim et al. 2003).

6.7 Conclusion

Human sustainability depends on a higher agricultural yield so that the population may be fed. A lot of hindrances exist in our nature due to anthropogenic activity. Some factors exist naturally; however, these factors are getting increased day by day due to the greedy nature of the human race. The entire web of the ecosystem on our planet is getting damaged due to the overexploitation of nature. Microbiotechnology, a flourishing arena, may help to create a better environment for higher plant production, reduce pollution, and develop new sustainable energy sources. Advanced technologies should be implicated at the field level and should be transferred at the farmer level so that all corners of our society may get benefitted and human civilization may sustain well for longer time period in sustainable manner.

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