Emerging Technologies and Current Advances in Human Bacteriome Research

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Abstract

The human body is recognized as one of the most densely populated microbial ecosystems. The human microbiome, a collection of microbial communities that occur in various anatomical sites, play a profound and indispensable role in promoting overall human health. Among these microorganisms, bacteria, representing the bacteriome, exhibit overwhelming predominance over other microbial groups as these extensively influence the physiological functions of the human body. Microbiome in general and bacteriome in particular, is recognized as a major influencer of health and disease in humans. In recent times, the relationship among human bacteriome, dysbiosis and metabolic disorders or diseases has gained considerable significance. Similarly, health interventions involving the modulation of the human bacteriome such as faecal microbiota transplantation, live biotherapeutics, bioengineered microbes and phage therapy have become attractive area of research with huge futuristic implications. Here, we present the current understanding of the human bacteriome, its compositional modulation for exerting beneficial health effects and the emerging technologies, viz. deep-sequencing, multiomics among others for deeper insights into dynamic interplay among bacterial communities in the human body.

Keywords

Microbiome · Dysbiosis · Bacteriome · Gastrointestinal tract · Next-generation sequencing · Multiomic technologies · Faecal microbiota transplantation · Live biotherapeutics

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7.1 Introduction

The human body is recognized as an ecosystem supporting vast communities of bacteria, archaea, fungi, viruses and protozoa (Locey and Lennon 2016; Singh et al. 2018; Gilbert et al. 2018; Aggarwal et al. 2022). These co-existing commensal and symbiotic microbial communities present on or inside the body represent the human microbiota and the microbiome. Precisely, the microbial cells of the body are referred to as microbiota and the microbiome represents the entire set of genes of these microbes, although these terms are often used interchangeably (Aggarwal et al. 2022; Mousa et al. 2022). Human bacteriome, on the other hand, specifically represents the bacterial inhabitants of the body. Recently, Berg et al. (2020) redefined the term microbiome as "a characteristic microbial community occupying a reasonably well-defined habitat which has distinct physio-chemical properties". The human microbiome is also considered our second genome and the human body inhabiting them is recognized as a superorganism (Gilbert et al. 2018; Aggarwal et al. 2022). The human microbiome has co-evolved for centuries with human beings and is now considered an essential organ for human health (Hooper and Gordon 2001; Gilbert and Neufeld 2014; Michels et al. 2022)

The human microbiota is composed of hundreds of species and strains of bacteria, archaea, fungi, protozoa and viruses. Their genomes containing thousands of genes offer much greater genetic diversity and versatility than our own genome (Locey and Lennon 2016; Perez-Carrasco et al. 2021). The human gut harbours more than 1000 bacterial species belonging to four phyla, namely Firmicutes, Bacteroidetes, Actinobacteria and Proteobacteria (Hooper and Gordon 2001; Fujisaka et al. 2022). In numerical terms, the estimated ratio of bacteria to human cells in the human body is 1.3:1, although at one time it was considered to be 10:1 (Sender et al. 2016; Locey and Lennon 2016). The Human Microbiome Project which was initiated in 2007 revealed interesting facts about the human body ecosystem and marks one of the most significant milestones in the history of biology (Gilbert et al. 2018). The human body carries more microbial cells than its own cells, whereas the number of genes expressed by the human microbiome is 50–100 folds higher than our genome (Hooper and Gordon 2001; Aggarwal et al. 2022). Microbiome-oriented studies have witnessed unprecedented impetus in the last two decades. Abdill et al. (2022) found that publicly available data on human microbiome samples has increased from 3 samples in 2010 to 123,302 in 2020. These microbiome samples are from 115 different countries where the USA represents 40.2% of the total samples. From India, 2997 microbiome samples have been studied and analysed as per available data (Abdill et al. 2022).

7.2 Human Bacteriome Diversity and its Importance

The microorganisms present in a normal human body are collectively known as commensal microbiota which has also been recognized as our forgotten organ. Human microbiota and microbiome have been extensively investigated in a

plentitude of studies for their beneficial roles in several vital functions and overall health. Experimental studies revealed the influence of microbiota in host physiology, digestion, immunity (both innate and adaptive), homeostasis, neurodevelopment and metabolism (Gilbert et al. 2018; Liu et al. 2022a, b; Michels et al. 2022). The majority of human bacteriome is present in the gastrointestinal tract, mainly the large intestine, small intestine and colon (Table 7.1). However, other anatomical sites of the body such as skin, oral cavity, nose, respiratory tract, lungs, eyes, ears and urogenital tract harbour distinct microbial communities (Gilbert et al. 2018; Fujisaka et al. 2022; Aggarwal et al. 2022).

Microbial diversity, abundance and predominance in different sites of the human body are impacted either by environmental factors such as pH, temperature, osmolarity, salts, oxygen levels, sebum and nutrient concentration or by intrinsic factors such as ethnicity, genetics, age and gender (Aggarwal et al. 2022). Similarly, the human bacteriome is diverse and dynamic in nature and is influenced by diet, food types, age, habits, gender, body-mass-index, demographics, genetics, probiotics, prebiotics, antibiotics usage and other environmental factors (Girija and Ganesh 2022; Villemin et al. 2022). The human microbiome of different sites can be used as a reliable biomarker or microbial signature to assess the risk of occurrence of several metabolic conditions and disorders. Therefore, deeper insights into the microbiota of the human body under different physiological conditions are needed. These data may assist the scientific community and health professionals in designing and developing newer diagnostic tools and therapeutic interventions. Among different microbes present in the human body, the most prominent role is exhibited by gut microbiota or gut microbiome. It is essential for food digestion, vitamin production, protection against pathogens and immune system development (Arnold et al. 2016; Mirzaei and Maurice 2017; Fujisaka et al. 2022; Mousa et al. 2022). Gut microbiota is known to influence almost all physiological functions of the body including that of the brain, pancreas, heart, kidney, skin and eyes (Yan et al. 2017; Wang et al. 2021; Sani et al. 2021; Matsukawa et al. 2021; Sorboni et al. 2022; Wehedy et al. 2022; Zhou et al. 2022; Liu et al. 2022a, b). The gut bacteriome is represented by numerous bacterial species from mainly four phyla as shown in Table 7.1. In the Indian population, the gut microbiome exhibited the predominance of *Prevotella copri* and *Faecalibacterium prausnitzii* which can be attributed to the high content of resistant starch in Indian diets (Dubey et al. 2018).

Human bacteriome has been recognized as a vital player in systemic health. Dysbiosis refers to the lack of balance among microbial communities within certain areas of the body that may lead to the onset or progression of certain chronic diseases or disorders (Byrd et al. 2018; Gurung et al. 2020; Aggarwal et al. 2022; Carmona-Cruz et al. 2022). Bacteriome perturbations or dysbiosis is detrimental to the host health and can lead to chronic metabolic diseases such as obesity, type II diabetes mellitus, insulin resistance syndrome, cancers, allergies, gingivitis, periodontitis, endocarditis, asthma, osteoporosis, inflammatory bowel disease, ulcerative colitis, Crohn disease, rheumatoid arthritis, neurological disorders, Parkinson's disease, Alzheimer's disease or atopic eczema among others (Lamont et al. 2018; Perez-Carrasco et al. 2021; Aggarwal et al. 2022; Kenneally et al. 2022; Sorboni et al.

Table 7.1 Prominent bacterial phyla and/or genera present in different sites of the human body and dysbiosis-associated diseases

Organ/site	Predominant bacterial phyla[a]	Predominant bacterial genera/ species	Disease/ disorder due to dysbiosis	Reference
Gastrointestinal tract or gut	*Firmicutes*, *Bacteroidetes*, *Proteobacteria*, *Actinobacteria*, *Fusobacteria*, *Verrucomicrobia*	*Bacillus*, *Clostridium*, *Clostridioides difficile*, *E. coli*, *Collinsella*, *Eubacterium*, *Enterococcus*, *Enterobacter*, *Lactobacillus*, *Ruminococcus*, *Staphylococcus*, *Bacteroides*, *Prevotella*, *Bifidobacterium*, *Akkermansia muciniphila,*, *Faecalibacterium prausnitzii*, *Roseburia*, *Veillonella*	Inflammatory bowel disease, obesity, type II diabetes, ulcerative colitis, Crohn's disease, celiac disease	Fujisaka et al. (2022), Sorboni et al. (2022), Michels et al. (2022), Liu et al. (2022a, b), Mousa et al. (2022)
Skin	*Actinobacteria*, *Firmicutes*, *Proteobacteria*, *Bacteroidetes*	*Cutibacterium acnes*, *Staphylococcus epidermidis*, *Staphylococcus aureus*, *Corynebacterium*	Atopic dermatitis, psoriasis vulgaris, acne vulgaris	Byrd et al. (2018), Aggarwal et al. (2022), Carmona-Cruz et al. (2022)
Jejunum	*Actinobacteria*, *Firmicutes*, *Proteobacteria*, *Bacteroidetes*	*Streptococcus salivarius*, *S. mitis*, *Rothia mucilaginosa*, *Actinomyces odontolyticus*, *Granulicatella adiacens*, *Corynebacterium kroppenstedtii*, *Prevotella*, *Veillonella*, *Fusobacterium*	–	Villmones et al. (2022)
Oral cavity	*Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Fusobacteria*, *Proteobacteria*, *Spirochaetes*	*Actinomyces*, *Corynebacterium*, *Capnocytophaga*, *Eubacterium*, *Eikenella*, *Fusobacterium*, *Granulicatella*,	Dental caries, gingivitis and periodontitis	Kilian et al. (2016), Lamont et al. (2018), Aggarwal et al. (2022)

(continued)

Table 7.1 (continued)

Organ/site	Predominant bacterial phyla[a]	Predominant bacterial genera/ species	Disease/ disorder due to dysbiosis	Reference
		Gemella, *Neisseria*, *Rothia*, *Prevotella*, *Porphyromonas*, *Treponema*, *Peptostreptococcus*, *Propionibacterium*, *Haemophilus*, *Leptotrichia*, *Lactobacillus*, *Staphylococcus*, *Streptococcus*, *Veillonella*		
Stomach (gastric mucosa)	*Proteobacteria*, *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, *Fusobacteria*	*Clostridium*, *Dialister*, *Helicobacter*, *Fusobacterium*, *Peptostreptococcus*, *Parvimonas*, *Streptococcus*, *Slackia*, *Veillonella*	Gastric cancer	Aggarwal et al. (2022), Mousa et al. (2022), Liu et al. (2022a, b)
Nose/nostrils	*Actinobacteria*, *Firmicutes*, *Proteobacteria*	*Staphylococcus aureus*, *Staphylococcus epidermidis*, *Cutibacterium acnes*, *Corynebacterium*, *Moraxella*	Chronic rhinosinusitis	Gilbert et al. (2018), Aggarwal et al. (2022)
Respiratory tract and lungs	Firmicutes, Proteobacteria, Bacteroidetes	*Prevotella*, *Corynebacterium*, *Haemophilus*, *Neisseria*, *Veillonella*, *Streptococcus*	Asthma, chronic obstructive pulmonary disease, pulmonary fibrosis, cystic fibrosis	Aggarwal et al. (2022), Mousa et al. (2022)
Esophagus	*Firmicutes*, *Bacteroides*, *Actinobacteria*, *Proteobacteria* *Fusobacteria*	*Streptococcus*, *Veillonella*, *Prevotella*, *Fusobacterium*, *Tannerella*, *Aggregatibacter*, *Porphyromonas*	Oesophageal cancer	Lv et al. (2019), Laserna-Mendieta et al. (2021), Muszyński et al. (2022)
Urogenital tract (bladder and vagina)	*Firmicutes*, *Bacteroidetes*, *Proteobacteria*, *Actinobacteria*	*Lactobacillus*, *Streptococcus*, *Corynebacterium*, *Prevotella*,	Urgency urinary incontinence, bladder	Perez-Carrasco et al. (2021),

(continued)

Table 7.1 (continued)

Organ/site	Predominant bacterial phyla[a]	Predominant bacterial genera/ species	Disease/ disorder due to dysbiosis	Reference
		Staphylococcus, *Escherichia*, *Enterococcus*, *Corynebacterium*, *Citrobacter*, *Gardnerella vaginalis*	cancer, bacterial vaginosis	Kenneally et al. (2022)

[a]Nomenclature of bacterial phyla has been changed recently (Oren and Garrity 2021). However, for the sake of clarity, old bacterial phyla names have been used here

2022; Michels et al. 2022; Table 7.2). It is now widely accepted that gut microbiota communicates with distant organs, viz. brain, lungs, kidney, liver and heart through an array of signalling molecules. Dysbiosis of gut microbiota composition has been implicated in the development and progression of several neurological disorders including anxiety, stress, depression, epilepsy, stroke, Parkinson's disease, multiple sclerosis, Alzheimer's disease and schizophrenia (Cekanaviciute et al. 2017; Sani et al. 2021; Sorboni et al. 2022). These pathophysiological outcomes of microbiome perturbations emphasized the significance of the microbiota–gut–organ axis (Liu et al. 2022a, b; Radjabzadeh et al. 2022).

7.3 Modulation of Human Bacteriome

The accumulated and ever-increasing microbiome knowledge, understandings and datasets as well as the outcomes of several clinical trials indicated that human microbiota is amenable to dynamic shifts in abundance and diversity by dietary modifications, fermented foods, probiotics, prebiotic polysaccharides, postbiotics, microbial infections and pre-existing metabolic conditions (Marco et al. 2017; Leeuwendaal et al. 2022; Fujisaka et al. 2022). The modulation of the human microbiome, particularly the gut microbiota, is thus considered an attractive strategy for creating better therapeutics, diagnostic tools and disease markers for health diseases (Arnold et al. 2016; Chua et al. 2017; O'Toole et al. 2017; Aggarwal et al. 2022; Callens et al. 2022; Villemin et al. 2022; Fig. 7.1). Faecal microbiota transplantation (FMT) was first performed in human subjects by van Nood et al. (2013) in which the duodenal infusion of donor faeces was carried out in recurrent *Clostridioides difficile* patients. This strategy witnessed a high success rate and paved the way for microbiome-mediated health interventions. Gut bacteriomes could potentially be modulated or reprogrammed by specific medicines or antibiotics, engineered microbes, live bacterial therapeutics, phage therapy and microbiome mimetics to alleviate the symptoms of several metabolic diseases or to minimize their occurrence (Mirzaei and Maurice 2017; El Haddad et al. 2022; Mousa et al. 2022; Milligan-McClellan et al. 2022; Aggarwal et al. 2022).

Table 7.2 Relationship between bacteriome dysbiosis and metabolic diseases in the human body

Disease/disorder	Key bacterial taxa/species/phyla/families[a]	Reference
Atherosclerosis	*Firmicutes*, *Proteobacteria*, *Lachnospiraceae*, *Erysipelotrichaceae*, *Pseudomonas luteola*	Koren et al. (2011)
Oral squamous cell carcinoma	*Porphyromonas gingivalis* *Fusobacterium nucleatum*	Irfan et al. (2020)
Esophageal cancer	*Tannerella forsythia*, *Streptococcus anginosus*, *Aggregatibacter actinomycetemcomitans*, *Porphyromonas gingivalis*, *Fusobacterium nucleatum*	Lv et al. (2019), Laserna-Mendieta et al. (2021), Muszyński et al. (2022)
Pancreatic ductal adeno carcinoma	*Clostridium bolteae*, *Acinetobacter*, *Klebsiella pneumoniae*, *Streptococcus mutans*, *Parabacteroides*, *Pseudomonas*	Matsukawa et al. (2021), Mousa et al. (2022)
Obesity	*Fusobacterium*, *Lactobacillus reuteri*, *Akkermansia muciniphila*, *Bifidobacterium animalis*, *Bacteroides fragilis*, *Lactobacillus plantarum*, *Staphylococcus aureus*, *Ruminococcus gnavus*	Michels et al. (2022), Mousa et al. (2022)
Type 2 diabetes	*Akkermansia muciniphila*, *Blautia*, *Bacteroides vulgatus*, *Clostridium hathewayi*, *C. symbiosum*, *C. coccoides and C. leptum*, *Escherichia coli*, *Lactobacillus*, *Veillonella denticariosi*, *Fusobacterium*, *Bifidobacterium*, *Faecalibacterium*, *Roseburia*, *Ruminococcus*, *Fusobacterium*	Zhou et al. (2022), Barlow and Mathur (2023)
Inflammatory bowel disease, Crohn's disease and ulcerative colitis	*Clostridium*, *Faecalibacterium prausnitzii*, *Escherichia coli*, *Ruminococcus*, *Actinomyces*, *Veillonella*	Caruso et al. (2020), Qiu et al. (2022)
Gingivitis and periodontitis	*Aggregatibacter actinomycetemcomitans*, *Porphyromonas gingivalis*, *Bacteroides*, *Catonella*, *Desulfobulbus*, *Eikenella*, *Peptostreptococcus*	Kilian et al. (2016), Lamont et al. (2018)
Coronary artery disease and hypertension	*Clostridium*, *Klebsiella*, *Faecalibacterium*, *Streptococcus*, *Parabacteroides*, *Roseburia*, *Lactobacillus*	Yan et al. (2017), Mousa et al. (2022)
Pulmonary disorders	*Alloprevotella*, *Dubosiella*, *Clostridium*, *Helicobacter*, *Lactobacillus*, *OIsenella*, *Parasutterella*, *Rikenella*	Mousa et al. (2022)

(continued)

Table 7.2 (continued)

Disease/disorder	Key bacterial taxa/species/phyla/families[a]	Reference
Parkinson's disease	*Prevotellaceae*, *Enterobacteriaceae*	Liu et al. (2022a, b)
Neurodegenerative diseases (Alzheimer's disease and dementia)	*Bacteroides*, *Bifidobacterium*, *Clostridium*, *Lactobacillus*, *Aggregatibacter actinomycetemcomitans*, *Porphyromonas gingivalis*	Mousa et al. (2022)
Multiple sclerosis	*Akkermansia muciniphila*, *Acinetobacter calcoaceticus*, *Fusobacterium*	Cekanaviciute et al. (2017)
Prostate cancer and bladder diseases	*Actinobaculum urinale*, *Anaerococcus*, *Propionimicrobium lymphophilum*, *Cutibacterium acnes*, *Streptococcus anginosus*, *Varibaculum cambriense*	Kenneally et al. (2022)
Urothelial carcinoma or transitional cell carcinoma	*Acinetobacter*, *Actinomyces*, *Anaerococcus*, *Fusobacterium*, *Sphingobacterium*, *Herbaspirillum*, *Porphyrobacter*, *Bacteroides*	Perez-Carrasco et al. (2021)
Bacterial vaginosis	*Lactobacillus*, *Gardnerella vaginalis*	
Depression, anxiety and other psychiatric disorders	*Bacteroides*, *Coprococcus,* *Eggerthella*, *Eubacterium*, *Hungatella*, *Subdoligranulum*, *Ruminococcus*, *Lachnoclostridium*, *Sellimonas*	Radjabzadeh et al. (2022), Mousa et al. (2022)
Skin-related diseases (atopic dermatitis, psoriasis vulgaris, acne vulgaris	*Corynebacterium mastitidis*, *C. bovis*, *Cutibacterium acnes*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus*, *Gemella*, *Dermacoccus*, *Coprobacillus*, *Ruminococcus*, *Streptococcus*	Byrd et al. (2018), Aggarwal et al. (2022), Carmona-Cruz et al. (2022)
Chronic kidney disease (CKD)	*Alistipes*, *Bifidobacterium*, *Collinsella*, *Eggerthella*, *Fusobacterium*, *Lactobacillus*, *Paraprevotella*, *Pseudobutyrivibrio*	Krukowski et al. (2022), Wehedy et al. (2022)

[a]Nomenclature of bacterial phyla has changed recently (Oren and Garrity 2021). However, for the sake of clarity, old bacterial phyla names have been used

Another microbiome-based approach for extracting health benefits is live bacterial therapeutics or biotherapeutics. In this microbiome-modulation strategy, well-defined single species-based or rationally selected consortium-based live bacterial therapeutics are derived from healthy subjects after extensive screening, optimization and safety assessment (Gulliver et al. 2022). Live biotherapeutics are non-vaccine biological products that contain live organisms for the prevention and treatment of a disease or condition in humans (Gulliver et al. 2022). Towards

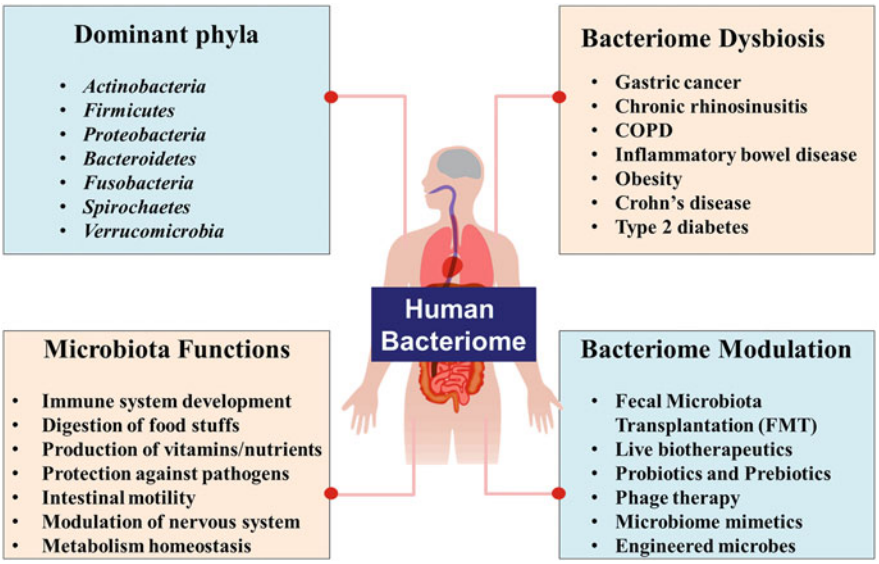

Fig. 7.1 Human bacteriome in human health, consequences of its dysbiosis and modulation interventions for preventive and therapeutic effects

microbiome-based biotherapeutics, several bacterial species have shown promising outcomes. As reviewed by Yadav and Chauhan (2022), *Christensenella* sp., *Akkermansia muciniphila*, *Lactobacillus johnsonii*, *Bifidobacterium longum*, *Oxalibacterium formigenes* and *Bacteroides* spp. are known to protect against depression, atherosclerosis, cancer, Crohn's disease, kidney stones adiposity, respectively. Microbiome modulation is also explored for the development of personalized therapeutics against hypotension by using gut bacteria and their metabolites (Sun et al. 2022). Phage-mediated bacteriome manipulations for managing gastrointestinal diseases are considered a better alternative than antibiotic therapy. By using exogenous phages, engineered phages or phage-containing faecal transplantation, the gut bacteriome balance can be restored with consequent control over gastrointestinal disease progression (El Haddad et al. 2022). Microbiome-based therapeutics are now considered a reliable option for the management of gut inflammatory conditions such as inflammatory bowel disease, Crohn's disease and ulcerative colitis. The administration of probiotic strains of *Lactobacillus* and *Bifidobacterium* has offered encouraging outcomes in people with gut-related disorders (Caruso et al. 2020; Qiu et al. 2022)

7.4 Technologies for Bacteriome Research

Culture-dependent approaches have been used traditionally for studying the microbiota of the human body and many other biological systems (Sirohi et al. 2012; Arnold et al. 2016; Aggarwal et al. 2022). However, as many microbial species are not cultivable, the culture-independent approaches based on amplicon sequencing, deep-sequencing technologies and multi-omics have gained considerable favour. These technologies afforded a deeper understanding of the microbiome and provided enormous sets of data for a detailed analysis and interpretation. The microbiome-based databases, projects and latest microbiome-oriented technologies are summarized in Tables 7.3 and 7.4, respectively. Next-generation sequencing (NGS), functional omics technologies and advanced bioinformatics tools allow high-throughput community-level analyses of bacteriome of healthy and diseased human subjects in an efficient, cost-effective and reliable manner (Zhang et al. 2019; Aggarwal et al. 2022; Yu et al. 2022). Human Microbiome Project (HMP1), Integrative Human Microbiome Project (iHMP), Metagenome of Human Intestinal Tract (MetaHIT) and several other public-funded and private-funded microbiome projects relied on an array of advanced next-generation sequencing, deep sequencing, "omics" technologies and sophisticated bioinformatics databases for microbiota identification, data generation, interpretation and analysis. To gain a better understanding of intricate interactions between diverse bacterial species in healthy persons and alteration in bacterial diversity and abundance under a dysbiosis state, high-throughput sequence-based studies are being performed for elucidating their genomic configurations and functional contributions using culture-independent next-generation sequencing technologies mainly 16S rRNA amplicon sequencing and shotgun metagenomic sequencing (Dubey et al. 2018; Zhang et al. 2019; Aggarwal et al. 2022; Yu et al. 2022; Table 7.4). Next-generation sequencing allows for high-volume studies of microbiome samples of different anatomical sites of the human body in a rapid, efficient and reliable manner. With the spectacular expansion of genomic information owing to technological advancements in the field of metagenomics, about 130,000 bacterial genomes have been sequenced and more than 20,000 metagenomic projects are accessible in the public domain (Aggarwal et al. 2022). Metagenomics, metatranscriptomics, metaproteomics and metabolomics further enhance our understanding of microbiota diversity, functional associations and kinetics of their abundance or decline (Mousa et al. 2022; Milligan-McClellan et al. 2022). Despite technical challenges and high-cost deterrents, high-throughput sequencing technologies are poised to further our knowledge of the microbiome and allow us for implementing microbiome–intervention based preventive and therapeutic strategies in the near future.

Table 7.3 Human microbiome projects, microbiome-related databases and microbiome-data analysis software/packages

Project/database	Description	Weblink
Human microbiome project (HMP)	First phase of NIH human microbiome project, established in 2007	https://hmpdacc.org/
The HMP data portal	Repository of human microbiome datasets from both HMP1 and iHMP	https://portal.hmpdacc.org/
The integrative human microbiome project (iHMP)	Second phase of NIH human microbiome project, established in 2014	https://hmpdacc.org/ihmp/overview/
Metagenome of human intestinal tract (MetaHIT)	Collaborative project funded by the European Commission for analysis of gut microbiota (2008–2012)	https://cordis.europa.eu/project/id/201052
Microbiome centers consortium (MCC)	Collaborative network of microbiome centers for sharing and developing resources and data	http://microbiomecenters.org/
GMrepo	Database of human gut metagenomes	https://gmrepo.humangut.info/
gutMDisorder	A comprehensive database for gut microbiota dysbiosis	http://bio-annotation.cn/gutMDisorder
GIMICA	Database for host genetic and immune factors shaping human microbiota	https://idrblab.org/gimica/
DISBIOME	Database for linking the microbiome to diseases	https://disbiome.ugent.be/
Amadis	Database for microbiota and disease association	http://gift2disease.net/GIFTED
MEtaGenome atlas (gutMEGA)	Database for published quantitative human gut microbiota datasets	http://gutmega.omicsbio.info
MicrobiomeDB	A data discovery and analysis platform for microbiome datasets	https://microbiomedb.org/mbio/app/
Forensics microbiome database (FMD)	Database of human microbiome obtained from multiple body sites for predicting the geographical location of subjects	http://fmd.jcvi.org/
Expanded human Oral microbiome database (eHOMD)	Database of bacteria in the human mouth and aerodigestive tract	https://www.homd.org/
Microbiome drug database	Global database of microbiome companies developing pharmaceuticals	https://www.microbiometimes.com/drug-database-2/
PharmacoMicrobiomics database	Database for microbiome-drug interactions	http://www.pharmacomicrobiomics.org
Microbiome search engine 2 (MSE 2)	Platform for the taxonomic and functional search of microbiomes	http://mse.ac.cn/

Table 7.4 Conventional and advanced technologies for human bacteriome analysis

S. No.	Current technologies for bacteriome analysis
1.	Culture-dependent approaches (a) in vitro microbiome culturing models (HuMiX, SHIME) (b) High-throughput platforms for drug–microbiome interactions (c) High throughput ex vivo microbiome RapidAIM assay
2.	Culture-independent approaches (a) Low-throughput sequencing (16S rRNA-based amplicon sequencing) (b) Next-generation sequencing (high-throughput genome-wide sequencing) • Shotgun metagenomics • Metatranscriptomics • Metaproteomics • Metabolomics (c) Whole-community functional assays (d) Whole-metagenome shotgun (WMS) sequencing (e) Integrative multi-omics for functional data analyses (f) HPLC-MS

Adapted from Arnold et al. (2016), Zhang et al. (2019), Yu et al. (2022) and Milligan-McClellan et al. (2022)

7.5 Conclusion and Future Directions

A plethora of evidences suggest the direct involvement of microbiota dysbiosis in the development and manifestation of chronic metabolic diseases. Our understanding of human microbiota and bacteriome has been revolutionized in the last decades by high-throughput next-generation sequencing technologies. These developments afforded compositional, abundance and functional analyses of the microbiome under varying conditions of host health. Microbiome-oriented research has emerged as a multidisciplinary field encompassing microbiology, biochemistry, molecular biology, neurology, clinical practice, biomaterials engineering, systems biology and synthetic biology. The significance of the microbiome in human health has received considerable impetus due to technological advancements, viz. deep-sequencing, microfluidics assays and high-throughput culturing and enhanced focus on microbiome-interventional strategies and personalized medicines. The rejuvenated emphasis on the microbiome is going to witness further attention from interdisciplinary scientific community in the near future. Unravelling the mechanistic details of microbiota-host cross-talk is desired in order to devise preventive and therapeutic strategies against various human chronic diseases.

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