Emerging Technologies to Investigate the Potential of Gut Microbiota in Human Health

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Abstract

The human-gut-microbiome is the diverse microbial community consisting predominantly of bacteria although also includes fungus, viruses, protists and other organisms that have tightly coevolved with human genome and diet. Accordingly, these significant communities play a significant role in supporting human robustness as a result of coevolution of microbiome and the host. Understanding the relevance of gut microbiome in modulating host health has grabbed the interest of researchers from multiple fields. Microbiome research, which is inherently interdisciplinary, has benefitted from developments in the systems and the conventional microbiology, biomaterials engineering and synthetic biology. This chapter highlights and provides an update on various technologies in GIM research and their applications in the gastrointestinal microbiota therapy, such as NGS (Next-Generation Sequencing), Omics, Crisper, Microfluidics, Metabolomics, Metatranscriptomics, FMT (Faecal microbiota transplantation) and advanced culturing technology, with the goal of increasing interest in the validation, evaluation and eventual practices of these technologies in the diagnosis as well as therapy incorporation. Here, we will discuss the emerging technologies and their potent effects on gut microbiota analysis.

Keywords

Gut-microbiome · Human-health · Dysbiosis · Emerging technology · High-throughput sequencing · Next-generation technology · Crispr technology · Omics-technology

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10.1 Introduction

The human gastrointestinal tract contains a staggering variety of fungus, viruses, bacteria and protists, as well as trillions of other creatures, making it one of the most complex and diverse ecosystems ever discovered. The phrase 'microbiota' refers to this group of commensals, which is often dominated by bacteria, while the term 'microbiome' refers to their collective genome. The gut microbiome plays a crucial part in the health of host, that includes but it is not restricted to the maturation of immune system and the alteration of intestinal-morphology and angiogenesis, the prevention of pathogenic infection, the fermentation of undigested polysaccharides and the synthesis and conversion of bioactive compounds (Matsuki and Tanaka 2014; Blaut 2018; Valdes et al. 2018; Pires et al. 2019).

Furthermore, the microbiota has found and is considered as a significant modulator of human health, even being proposed as an 'essential organ' of human body (Kashyap et al. 2017; Wang et al. 2017). Whereas significant alterations in microbiome composition have been observed in many disorders, identifying a distinctive makeup of a 'healthy' microbiome has been problematic with respect to inter-individual heterogeneity (Lloyd-Price et al. 2016).

Electrophoresis-based methods, such as denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE) and polymerase chain reaction (PCR)-based methods, such as terminal-restriction fragment length polymorphism (T-RFLP) and random amplified polymorphic DNA (RAPD), have traditionally been used for studying this microbiome independently of culture. The cytogenetic technique of fluorescence in situ hybridisation (FISH) has been used to study certain gut microbiota members, including the pathogens Listeria monocytogenes, Salmonella species, Helicobacter pylori and Yersinia enterocoliticai (Guimarães et al. 2007; Baysal 2014; Becattini et al. 2017; Prudent and Raoult 2019). Russmann et al. (2001) employed fluorescence in situ hybridisation (FISH) for the analysis of Helicobacter pylori strains isolated from patients. There are many issues with these approaches, such as a lack of resolution, specificity and sensitivity, as well as the need for highly targeted probes. Several studies have shown that the gut has a diverse and abundant microbiome, but until recently, interpreting the resulting large data was prohibitively expensive and time-consuming. However, recent improvements in sequencing and culture—or emerging technologies—have changed both that. Such technologies include NGS (Next-Generation Sequencing), Omics, Crisper, Microfluidics, Metabolomics, Metatranscriptomics, FMT (Faecal microbiota transplantation), and advanced culturing technology (Arnold et al. 2016). They have significant advantages over more traditional or older technology. Furthermore, this paper will primarily focus on emerging technology and its advantages over traditional technology and on comprehending the role of emerging technology in host-microbiome interactions (Fig. 10.1).

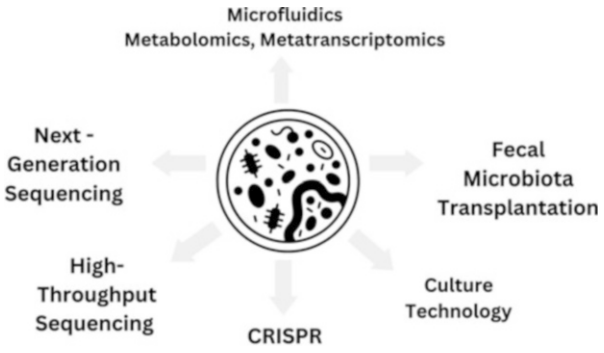

Fig. 10.1 Different Emerging Technologies in Exploring the Potential of Gut Microbiota in Human Health

10.2 The Gut Microbiome and Human Health

Humans are associated in a symbiotic-relationship with up to 10^{14} microorganisms (Savage 1977). Most of these host-specific bacteria are found in the gastrointestinal system, where they have incredible metabolic potential and are important for the maintenance of human health (De Vos and de Vos 2012). The total genetic repertory of all gut microbes represents one order of magnitude more than the genetic repertoire of the human genome (Fan and Pedersen 2020). It is also regarded as the 'essential organ' of the human body to certain extent (Ding et al. 2019). According to Kau et al. (2011), the gut microbiota influences host gene expression as well as immune response, which in turn affects general health. The gut microbiota also improves the host's response to pathogen invasion (Sobhani et al. 2011; Carding et al. 2015; Ramakrishna et al. 2015). Normal gastrointestinal tract residents aid in metabolism of the polysaccharides taken by host (Tremaroli and Bäckhed 2012), as well as interactions between bacteria within the microbiome improve this metabolic capacity, further increasing polysaccharide consumption (Gill et al. 2006).

Furthermore, particularly on association with the host, gut microbiota can produce a variety of metabolic products that can have an impact on human health, either positively or negatively. Indigestible carbohydrates such as hemi-cellulose, cellulose, pectin, resistant starch, lignin and oligosaccharides could be converted into short-chain fatty acids (SCFAs), i.e. propionic, butyric and acetic acids by these bacteria. These fatty acids enter the colon after escaping from the upper gastrointestinal tract during digestion (Lin and Zhang 2017; Thursby and Juge 2017). There are numerous pathogenic effects on the host whenever the production of short-chain fatty acids is disrupted (Perry et al. 2016). The gut microbiota plays a crucial part in manufacture of vitamins including thiamine, biotin, riboflavin, cobalamin, pantothenic acids and nicotine as well as vitamin B & K, thus can also have positive impacts on the host organism (LeBlanc et al. 2013). Additionally, the gut microbiota has peculiar ability to produce certain neurochemicals that can impact the peripheral and central neurological systems (Forsythe et al. 2010). In addition to promoting health, gut microbes can prevent disease by modulating the immune system (Medina

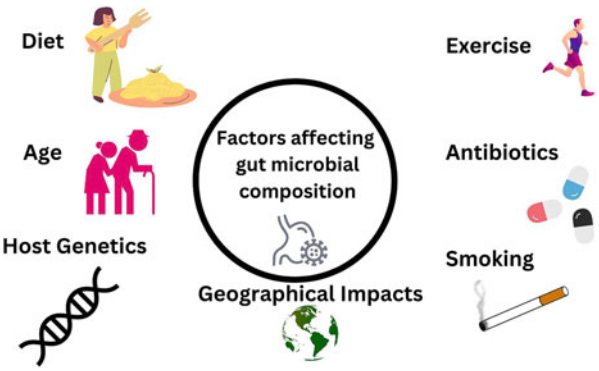

Fig. 10.2 Factors affecting gut microbial composition

et al. 2007). As demonstrated for Bifidobacterium longum, which significantly increases interleukin-10 and proinflammatory cytokines like TNF-production (Medina et al. 2007) that guards against tumour growth in the host (Lee et al. 2008). It is hypothesised that physiological changes in the colon and small intestine, such as nutritional and chemical gradients as well as isolated host immunological activity, impact the make-up of the bacterial communities (Donaldson et al. 2015). Further, a vital role of the interior environment of humans is played by the gut bacteria.

Several additional factors, such as nutrition, host genetics, age, exercise, use of antibiotics, smoking and geographic influences, all alter the composition of the gut microbes (Bäckhed et al. 2015; Schanche et al. 2015; Chen et al. 2018; Clarke et al. 2014; Biedermann et al. 2013; Ramnani et al. 2012). Additionally, similar compositional alterations in the microbiota (dysbiosis) have been linked to a number of illnesses, including obesity (Shen et al. 2013), diabetes (Naseer et al. 2014), colorectal cancer (Azcárate-Peril et al. 2011) and the allergies (Panzer and Lynch 2015) (Fig. 10.2).

10.3 NGS (Next-Generation Sequencing) Technology

Analysing the gut microbiota in the past relied on isolation and culture, but the accuracy of the research was severely hampered by the challenge of growing anaerobic bacteria, that are prevalent in the intestine. Research on the intestinal microbiome has recently been drawn to the development of next-generation sequencing (NGS), that could precisely assess microbial components without culture (Tang et al. 2020).

10.4 Fundamental Considerations in the Use of NGS

When examining the gut microbiota, one of the first questions to ask is which microorganisms are present in a particular sample. Finding the plethora and the functional profiles of the microorganisms present, as well as comprehending intra-species and population heterogeneity, are further questions that can be answered by NGS analysis (Durazzi et al. 2021). In order to answer these queries, NGS techniques directly sequence microbial DNA or RNA, for instance, from faecal, blood and/or tissue samples. Amplicon sequencing and shotgun metagenomic sequencing are the two main NGS methodologies currently in use, because of NGS's decreasing cost. However, because it enables the determination of the transcriptome, which is an additional step for characterising the function of the microbiota, RNA sequencing is also a valid and, in some respects, superior method for classifying microbes (Cottier et al. 2018; Clooney et al. 2016). NGS platforms are often used and come in a number of configurations. Among these are the Roche 454 GS FLX, Oxford Nanopore, Illumina (MiSeq and HiSeq), Ion Torrent/Ion Proton/Ion Proton and SOLiD 5500 series (Malla et al. 2019).

10.5 16S rRNA Gene Amplicon Sequencing

Through use of the metagenomic techniques and high-throughput sequencing technologies, the gut microbiome has been thoroughly studied. In order to analyse the diversity, community structure and functionality of microbial species, metagenomics involves the sequencing of the entire community's DNA (Albenberg and Kelsen 2016). To determine the microbial make-up of a community in an environment like the gut, bioinformatics and the hypervariable region of 16S rRNA gene sequencing have been extensively used. The gut microbiome of persons living in Amazon was characterised by 16S rDNA Illumina sequencing (Pires et al. 2019), which revealed a significant variance in composition when compared to individuals living in industrialised environments. Similar to this, Barone et al. (2019) used data from the 16S rRNA gene sequencing to understand gut microbiota response to a contemporary Palaeolithic diet in a setting of a Western lifestyle. The 16S rRNA gene is a perfect target because it is widely distributed and highly conserved among bacteria (without that, bacteria would not be able to translate mRNA in to the proteins and would therefore be non-functional), as well as because it has nine hypervariable regions (V1–V9) that vary within different bacterial species as well as genera. As a result, it is possible to construct PCR primers so that the forward and reverse primers bind to conserved areas but amplify an intervening variable region (Wensel et al. 2022). With the help of this technique, it is no longer necessary to cultivate individual bacteria, clone certain genes, or blot for a particular RNA in order to identify community members (Arnold et al. 2016). The biased nature of the databases used for comparisons is a significant flaw in this approach (Ajayi et al. 2020).

10.6 Whole-Genome Shotgun (WGS)

By enhancing the knowledge acquired by 16S/18S rDNA amplicon sequencing, whole-genome shotgun (WGS) sequencing can identify DNA viruses and reveal details about the composition of genes and metabolic pathways (Palmero et al. 2010). Bacteriophages, which are primarily bacterial DNA viruses, predominate in the gut virome, which also contains a varied population of eukaryotic viruses with both DNA and RNA encoding (Reyes et al. 2015, 2010). By influencing the bacterial ecology and interacting directly with host cells, the virome has a significant impact on host health (Reyes et al. 2015; Focà et al. 2015). However, as the majority of current findings which are based on the 16S/18S rRNA amplicon sequencing data, virome data are frequently left out of microbiome compositional investigations. By destroying their bacterial hosts while lytic growth or by changing gene expression while the lysogenic conversion (Mills et al. 2013), bacteriophages can modify the composition of the microbiome. The genes engaged in DNA replication, amino acid, carbohydrate, lipid metabolism, signal transduction as well as transcription control have also been found to be encoded by the eukaryotic viruses as bacteriophages in the gut (Reyes et al. 2015; Focà et al. 2015).

To obtain the right gut microbiome samples for NGS, though, is essential. The intestinal microbiome cannot be accurately represented by the sampling techniques currently used to gather samples from intestinal aspiration, faeces and mucosal biopsy, all of that which may have certain flaws (Tang et al. 2020).

10.7 Omics Technology in Gut Microbiota

'Meta-omics' approaches offer a way to investigate and comprehend the systems biology of the gut microbiome at many stages of expression (Lamendella et al. 2012). Here, we will talk about several cutting-edge meta-omics techniques used in the human digestive system. The study of complex human diseases has been revolutionised by the development of modern 'omics' methodologies and techniques that offer an unprecedented genome-wide perspective of genetic diversity, gene expression, interactions with microbes and environmentally responsive epigenetic alterations (Donlin et al. 2019; Nemtsova et al. 2019; Kishikawa et al. 2019).

10.8 Metagenomics

It refers to the environment's whole-community DNA being sequenced without being targeted (Escobar-Zepeda et al. 2015). Shotgun sequencing is frequently used to profile the taxonomic composition of a sample, such as faeces, with a diverse microbial community (down to the strain level) and to evaluate the functional potential of the sample. Large-scale studies of complex microbiomes have been made possible by metagenomics, which has also helped to clarify functional variations between the states of health and sickness. In addition to characterising

non-bacterial microbial communities including fungi and viruses that have recently been revealed to possibly play a significant influence in host health, it enables strain-level resolution of gut bacteria (Gilbert and Dupont 2011; Oulas et al. 2015). By concurrently examining two facets of a microbial community—who is present and what they might be able to do—metagenomics offers the chance to learn more about both. Though effective, this method has a lot of drawbacks: In comparison, it is substantially more expensive than 16S rRNA gene sequencing. Additionally, there are numerous bacterial genomes that have not yet been fully annotated, and there are concerns about the correctness and even coverage of databases (Segal et al. 2019).

10.9 Metatranscriptomics

In metatranscriptomics, RNA sequencing is used to examine the transcriptional activity of microbiota (Aggarwal et al. 2022). While metagenomics outlines the community's microbiota's genetic potential, metatranscriptomics provides information about the actual genetic endeavour within a community phenotype and the genomic potential of a community's microbiota (Segal et al. 2019). Metatranscriptomics, as opposed to metagenomics, enables the detection of active microorganisms, genes and the associated pathways in microbial communities (Aggarwal et al. 2022). In the human microbiota, metatranscriptomics techniques have facilitated a deeper comprehension of host–microbiota interactions, active microbiota and their pathways and expression alterations in disease progression (Nowicki et al. 2018; Schirmer et al. 2018). As a result, the metatranscriptome provides dynamic, contextualises microbial functional activity to the human phenotype and, when combined with metagenomics, offers a profound understanding of the molecular pathways by which gut bacteria contribute to both health and illness (Bashiardes et al. 2016; Lavelle and Sokol 2018). It has tremendous utility in reorienting our knowledge of the descriptive gut microbiome towards a deeper comprehension of host-microbial causative pathways in causing disease and homeostasis (Segal et al. 2019). The field of metatranscriptomics has a number of significant limitations. Host contamination can be found in substantial amounts in tissues like colonic biopsies, when the biomass is composed almost entirely of host cells. Deep sequencing of the full mRNA is required in such scenarios to establish a representative insight into the mucosally adherent microbial pattern of gene expression. The translated protein or microbial transcriptome databases are incomplete and contain many genes that have not yet been assigned a recognised function. The microbial functional profile is frequently interpreted insufficiently and somewhat biasedly as a result of this information gap, although this is likely to alter as this field develops over time (Segal et al. 2019).

10.10 Metaproteomics

Alternately, metaproteomics can be used as substitutive method of observing gene activity in the microbiome. In a 2009 study, metaproteomics was first used to assess microbial function in ambient and gut microbiota samples from twins (Wilmes and Bond 2006; Verberkmoes et al. 2008). Numerous research have so far shown how human microbiome samples can be used for metaproteomics analysis (Issa Isaac et al. 2019; Long et al. 2020; Tanca et al. 2017). Since it has lower throughput than metatranscriptomics deep sequencer-based analysis, metaproteomics is not as popular. Metaproteomics can also provide information on post-translational modifications in proteins and the expression of proteins released from the host cell, even though metatranscriptomics is unable to explain these circumstances (Zhang et al. 2017). The inadequacy and a typical study's millions of tandem mass spectra (MS/MS) were produced with inadequate validation of the anticipated protein databases utilised for peptide matching (Lamendella et al. 2012).The ability of post-translational changes to affect microbiome function without changing their composition underlies the significance of metaproteomics in gaining mechanistic insights into the phenotypes connected to the microbiome. Multimeta-omics approaches have been used to thoroughly recognise the gene activity of the microbiota as well as interconnections between the microbiota and the host, taking into account the benefits and drawbacks of meta-omics approaches (Aggarwal et al. 2022).

10.11 CRISPR

According to Hille and Charpentier (2016), CRISPR-Cas is currently the sole adaptive immune system in prokaryotes. Although now it is generally acknowledged as a genetics tool, CRISPR was first identified in archaea as an immune system. Through the introduction of DNA breaks and homologous recombination that use donor DNAs, CRISPR is primarily used for gene editing (Aggarwal et al. 2022). Numerous organisms, even those whose genomes were before thought to be difficult to edit, have experienced an acceleration in genome engineering due to CRISPR-directed homologous recombination (Reardon 2019). In order to characterise the gene function of phenotypes connected to the microbiome, CRISPR has been further utilised to create the microbiome as well as commensal bacteria. Despite the widespread availability of CRISPR-driven gene editing for many organisms, most commensal bacteria with low homologous recombination activity experience cell death as a result of DNA breakage brought on by CRISPR/Cas9 rather than gene editing. Therefore, CRISPR/Cas9 cannot be applied to bulk of the commensal bacteria that are non-models. CRISPRi, CRISPRa, or base editors may be less harmful options for these microorganisms. CRISPRi and CRISPRa can be applied as customised transcription factors for building genomic circuits because of their great degree of programmability. Because of its lesser toxicity when compared to utilising bacteria, microbiome editing with base editors is likely to soon be used in therapies, unlike CRISPR/Cas9 gene editing, which introduces changes through

DNA strand breaks as well as subsequent homologous recombination. A variety of genomic DNA can be modified with CRISPR (Aggarwal et al. 2022). Despite the fact that a significant portion of commensal microorganisms are not cultivable, DNA delivery is nevertheless the very first step in experimental modification for downstream processes.

10.12 Faecal Microbiota Transplantation (FMT)

FMT is the most avant-garde therapy strategy (Quaranta et al. 2019). FMT involves injecting a healthy donor's faeces suspension into the patient's intestinal tract to cure a specific disorder linked to altered gut microbiota (Cammarota et al. 2017; Filip et al. 2018). Regardless of how FMT is administered, there is sufficient evidence to conclude that it is a highly effective treatment option for a number of intestinal illnesses, with the capacity to restore gut microbiota compositions and functions that are identical to those of recipients (Li et al. 2016). FMT can also be utilised to treat other extra-intestinal disorders caused by altered microbiota. Colorectal cancer, Parkinson's disease, atherosclerosis, coronary artery disease (CAD), rheumatoid arthritis, multiple sclerosis, irritable bowel syndrome, insulin resistance, obesity, autism, diarrhoea, allergic disorders, metabolic syndrome, colon cancer, anti-tumour immunity and neuropsychiatric disorders are a few clinical conditions for which FMT may be a potent therapeutic strategy (Holvoet et al. 2017; Johnsen et al. 2018; Aroniadis et al. 2018; Quaranta et al. 2019). In contrast to probiotics and prebiotics, whose colonisation appears to be temporary, it can be formed in a single-dose regimen, providing therapeutic potential, and it promotes microbial diversity without upsetting microbial gut ecology, which is employed in antibiotic treatment (Weingarden and Vaughn 2017). It is unclear exactly how FMT works to cure certain disorders. It may be caused by changes in the bacterial compositions, altered metabolic profiles of the hosts, the presence of donor-derived peptides that alter host immune responses and the participation of novel species of gut microbiota found in the healthy donor faeces (Gianotti and Moss 2017). Despite all of these benefits, there are still a lot of unfavourable side effects and challenges that this trend must overcome. It has been demonstrated that after therapy, the microbiota of the treated individuals resembles that of the donor. FMT's safety issue originates from the intricacy of the faeces microbial community, which is another drawback (Hansen and Sartor 2015). Numerous studies have demonstrated the potential for the transmission of microorganism-based infections or detrimental disease phenotypes such as metabolic syndromes, diabetes, obesity, and chronic cardiovascular diseases (Harsch and Konturek 2019).

10.13 Microfluidic

The gastrointestinal microbiota may be traced, examined and controlled at the single-cell level due to microfluidics technology (Ajayi et al. 2020). Organ Chips are basically microfluidic cell culture tools that were initially created utilising

techniques modified from the production of computer microchips (e.g. soft lithography), they imitate tissue- and organ-level physiology by having constantly perfused chambers filled with living cells (Bhatia and Ingber 2014). Liu and Walther_Antonio discovered two potent microfluidic tool that could be harnessed in sorting of cells, cell screening, cell culture, metabolic screening/analysis, gene expression and genome applications. This approach made it possible to thoroughly examine particular bacterial species and determine how they assist keeping the integrity of the gastrointestinal tract (Ajayi et al. 2020). The establishment of organs on chip is yet another intriguing advancement in microfluidics for microbiome research. Additionally, the intestine is the location where majority of the commensal microbes in the gut microbiome reside and communicate with the host immune machinery and gut lymphoid tissues, which greatly aids in maintaining intestinal homeostasis (Garrett et al. 2010; Round and Mazmanian 2009).

10.14 Microfluidic Intestine Chip Models

The support for laminar fluid flow is provided by microfluidic devices with hollow micro-channels below 1 mm in width and fluid volume management from nanolitre to microlitre scales, thus making them feasible for use in living cell culture. The fluidic control also allows for a strictly regulated spatiotemporal allocation of nutrients, growth factors, drugs, or even sometime toxins to the intestinal epithelium developed over the microfluidic channels (Bein et al. 2018). A common porous polycarbonate or polyester membrane with ECM coating that has one of its surfaces cultivated with immortalised human intestinal epithelial cells separates two hollow channels that make up Intestine Chips (Gao et al. 2013). The solid polymer substance that obstructed the epithelium's abluminal surface prevented this design from allowing investigation of intestinal barrier function. Additionally, the HuMiX multichannel intestinal chip has been explained which uses nanoporous membranes to divide layers of intestinal Caco-2 epithelium from a luminal microbial compartment (Shah et al. 2016).

10.15 Mechanically Active Gut Chip Model

A more refined two-channel microfluidic Gut Chip prototype has been designed that permits human intestinal-epithelium to flourish and coexist along with immune cells, capillary endothelium and even the commensal microbial cells to develop, cohabit and communicate while in vitro undergoing peristalsis-like mechanical deformations and physiologically relevant fluid flow (Kim et al. 2015). Polydimethylsiloxane (PDMS), a gas-permeable, flexible, silicone polymer is used to design the Gut Chip which is crystal clear, so that it enables imaging at high-resolution using differential interference contrast, phase contrast or immunofluorescence-confocal-microscopy. It is bordered on either side by hollow, full-height side on chambers and has two parallel microchannels (<1 mm-wide) that are separated from one another

by thin (w20 mm), flexible, porous, ECM-coated PDMS membrane (Kim et al. 2012, 2015; Kim and Ingber 2013; Huh et al. 2013). It is significant to note that coculture of living commensal microbes is also possible since the Gut Chip maintains continuous fluid flow, villi creation and mucus production (e.g. Lactobacillus rhamnosus GG) (Kim et al. 2012).

The fundamental application of microfluidics is to research bacterial cells' real-time susceptibility to antibiotics (Cama et al. 2020). Additionally, it has clinical applications for diagnosis, drug delivery, studying the pathophysiology of gastrointestinal illnesses and personalised or individualised medicine (Ajayi et al. 2020).

10.16 Advanced Culturing Techniques

With the development of various bacterial culture techniques over time, it is now feasible to cultivate a sizable number of hitherto uncultivated gut bacteria (Ajayi et al. 2020). Culturomics is one such cultural method. According to Lagier et al. (2016), culturomics is a method of culturing that uses various culture conditions along with 16S rRNA gene amplification/sequencing and matrix-assisted laser desorption/ionisation time of flight (MALDI-TOF) for identification. High-throughput culture techniques offer the clear advantage of improving the culturability of bacterial populations that would otherwise be 'non-culturable', allowing for a more thorough investigation of identified species. This method requires specialised laboratories, takes a lot of time and is highly complex. Additionally, this method can be helpful in the preparation and administration of probiotics. Only a small portion of the microorganisms that live in the gut can be cultured. Despite the fact that recent studies using gnotobiotic mice and anaerobic culturing methods were able to successfully culture 50% of the species of bacteria identified by 16S rDNA amplicon sequencing, covering nearly 70% known genera and >90% families (Goodman et al. 2011; Faith et al. 2010), the majority of the diversity present inside the gut microbiota is at the strain level, making identification and cultivation a challenging task. Additionally, individual microorganisms' morphology, physiology and biochemistry may be researched, and it is simple to assess how they react to or interact with medications. This makes it possible to treat gut disorders effectively. Traditional microbiology approaches have been advanced by advances in culturing technology, including the use of anaerobic environments and gnotobiotic animals. Since so many initially uncultivable bacteria may now be grown in environments created to mimic their natural growth circumstances, it is possible to isolate hitherto undescribed species (Connon and Giovannoni 2002). Additionally, improvements in culture control technology have made it possible to trigger gastrointestinal (GIT) parameters such as acidity and bile content (Adamberg et al. 2014). High-throughput culturing is now achievable due to new culturing technology and the knowledge offered by NGS (Connon and Giovannoni 2002).

10.17 Future and Conclusion

Our inability to culture majority of gut microorganisms, the fact that most of these bacteria are novel and lack any closely related previously cultivated strains and the lack of practical biomarkers of the microbiome functioning in body have all severely limited traditional studies on the exploration potential of the human gut microbiota. An emerging perspective is being created on the role that our gut microbiome plays in human systems biology thanks to recent developments in tools like NGS (next-generation sequencing), Omics, Crispr, Microfluidics, Metabolomics, Metatranscriptomics as well as FMT (faecal microbiota transplantation) and advanced culturing technology. To better understand these host-microbe interactions and to promote human health, these techniques give us better knowledge and information.

New gut microbiome research endeavours are made possible by these technical developments taken together. The gut microbiome is a key regulator of human health and will continue to draw researchers among a variety of scientific disciplines. At the same time, technological advances across many scientific disciplines will abide to give us tools we need to further unveil the potential of the gut microbiome as a target for personalised medicine. Additionally, this new technology will undoubtedly help us gain a clearer knowledge of gut microbial dysbiosis, which will help to lessen the burden this condition puts on human health.

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