



## OPEN ACCESS

*This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.*

Theodore Bilharz Research Institute, Giza, Egypt

Correspondence to:  
Azza Moustafa Fahmy,  
azzafhmy@gmail.com

Additional material is published online only. To view please visit the journal online.

Cite this as: Fahmy AM. Microbiome and Human Health: Recent Insights and Future Directions. Premier Journal of Public Health 2024;1:100002

DOI: <https://doi.org/10.70389/PJPH.100002>

Received: 3 August 2024

Revised: 4 September 2024

Accepted: 13 September 2024

Published: 15 October 2024

Ethical approval: N/a

Consent: N/a

Funding: No industry funding

Conflicts of interest: N/a

Author contribution:  
Azza Moustafa Fahmy –  
Conceptualization, Writing –  
original draft, review and editing

Guarantor: Azza Moustafa Fahmy

Provenance and peer-review:  
Commissioned and externally  
peer-reviewed

Data availability statement:  
N/a

# Microbiome and Human Health: Recent Insights and Future Directions

Azza Moustafa Fahmy

## ABSTRACT

The human microbiome comprises a complicated assembly of microorganisms inhabiting the body and its surfaces. It plays an important role in various physiological functions, such as digestion, immune homeostasis, and disease prevention. The development and improvement of sequencing technologies have advanced our knowledge of these microbial ecosystems and their interactions with host species. Probiotics, prebiotics, and fecal microbiota transplantation are the therapeutic methods in this regard that have been the focus of considerable research regarding their role as a means to alter the microbiome toward better health. Probiotics are preparations of live antibiotic-producing microbes, which favorably affect intestinal barrier integrity, alter the immunologic response of the host, and stimulate the growth of probiotic bacteria. Prebiotics are dietary nondigestible fibers, whose selective fermentation promotes the growth or activity of beneficial bacteria within the gastrointestinal tract, reducing the risk of disease by maintaining gut health. In spite of the fact that it is a very promising technique, with the exception of treatments for *Clostridioides difficile* infections, most require further studies before general use. The gut microbiome is also highly dependent on diet and lifestyle. Diets high in fiber enhance the abundance of symbiotic bacteria, whereas high-fat diets strongly reduce microbial diversity and increase proinflammatory bacterial species. In addition, regular exercise and sleep are critically important for coping with stressful conditions. Poor sleep and chronic stress degrade microbial communities, leading to dysbiosis. Apart from the potential of such research in microbiomes, other challenges include individual variability and ethical concerns; these are very important to note during translation to the clinic. Ongoing microbiome research holds tremendous promise for personalized health and prevention that deserves to be encouraged toward future treatments and human health.

**Keywords:** Microbiome, Microbiota, Probiotics, Human health, Dysbiosis, Immune modulation, Molecular biology

## Introduction

The human microbiome is the collective genome of microorganisms found within and on the human body.<sup>1</sup> This complex ecosystem, which includes bacteria, archaea, viruses, and fungi, colonizes many bodily regions, including the skin, mucosa, gastrointestinal tract, respiratory tract, urogenital tract, and mammary gland.<sup>2</sup> The gut microbiome is the most densely

inhabited of these and has been the primary subject of investigation due to its tremendous impact on host physiology and health.

The human microbiome is important for maintaining health since it influences metabolic and immunological activities.<sup>3</sup> It fluctuates in response to factors such as age, nutrition, lifestyle, hormonal changes, hereditary genes, and underlying disorders. Dysbiosis, or changes in the microbiota, can cause serious illnesses such as cancer, cardiovascular disease, inflammatory bowel disease (IBD), and antibiotic-resistant infections.<sup>4,5</sup> Understanding the host–microbe interactions is critical for detecting and treating these disorders.

Recent developments in sequencing technologies and bioinformatics have transfigured our thought of microbial communities, exposing their complex interactions with the host. These studies have found that nutrition, genetics, age, and environmental exposures all have an impact on the microbiome's composition. Furthermore, dysbiosis has been linked to a variety of diseases, including IBD, obesity, diabetes, and mental health disorders.

Traditional culture-based approaches for researching microorganisms sometimes fail to recreate natural microbial environments, limiting the detection of unidentified microbial species in the human microbiome.<sup>6</sup> Metagenomics, combined with next-generation sequencing (NGS), has substantially increased our understanding by permitting us to examine entire ecosystems in their natural environments.<sup>7</sup> Projects such as the Human Microbiome Project (HMP) and the American Gut Project have greatly expanded our understanding of microbiome composition and function, which is critical for considering host–microbiome interactions and their role in disease development.

The human microbiome is a dynamic and adaptive component of our biology, performing critical roles that the human genome alone cannot achieve.<sup>8</sup> The study of the microbiome improves our understanding of basic human biology and opens up new pathways for therapeutic approaches that target the microbiome to prevent or treat disease.<sup>9</sup> As research advances, the ability to modify the microbiome for health advantages grows more promising, emphasizing the relevance of this topic in future biomedical research and clinical practice.<sup>10</sup>

## Historical View: Early Discoveries and Foundational Studies

From the late nineteenth century to the present, research on the human microbiome has advanced dramatically. Antonie van Leeuwenhoek used a microscope to investigate microbial diversity in the 1680s,

but he made no connection between these bacteria and health.<sup>11</sup> In the early 1900s, Élie Metchnikoff proposed that ingesting lactic acid bacteria could benefit health, laying the framework for future probiotic research.<sup>12</sup> Louis Pasteur and Robert Koch made significant advances in the late nineteenth century by developing methods for examining germs, which led to the identification of bacteria as the cause of diseases such as anthrax, tuberculosis, and cholera. The advent of DNA sequencing technology, particularly 16S rRNA gene sequencing in the 1970s, transformed microbial identification and categorization, allowing scientists to investigate microbial diversity in the human body with higher precision.<sup>13</sup>

The National Institutes of Health initiated the HMP in 2007 to characterize microbial communities across diverse body sites and investigate their roles in health and illness.<sup>14</sup> This investigation demonstrated the variety and complexity of the microbiome, as well as the considerable variation in microbial communities between individuals and body regions due to diet, lifestyle, and genetics.

Research has changed from just cataloging microbial species to comprehending their functional importance. Advances in metagenomics and sequencing technologies have demonstrated that the microbiome has a substantial impact on health, notably in terms of metabolism and obesity risk. The microbiome can influence energy extraction from meals and modulate genes involved in energy storage, indicating its potential as a therapeutic target.<sup>15</sup>

This review will describe current advances in microbiome research and investigate the therapeutic potential of microbiome modification. It solves significant research problems, such as interindividual variability and ethical considerations. The review is important to the scientific and medical communities because it improves understanding of the microbiome's involvement in health and disease, supports the development of customized medicines, and informs public health efforts. It stresses the integration of multi-omics data and identifies future research prospects.

### **The Human Microbiome: Composition and Functions**

The human microbiome is a diverse and dynamic collection of microorganisms, including bacteria, archaea, viruses, and fungi, that live in a variety of anatomical places including the gut, skin, mouth cavity, and respiratory system. These microbial communities play an important role in human health by regulating a variety of physiological systems. The composition and function of the microbiome varied greatly between bodily regions, with each containing distinct microbial communities suited to their specialized environments.

### **Composition of the Human Microbiome**

The human body is colonized by a wide range of microbial populations that differ dramatically across organ systems and across time, impacted by lifestyle and health conditions.<sup>16</sup> The composition and density

of these microbiomes vary according to body site (Figure 1). For example, the upper respiratory tract has a higher population density than the lower parts. The stomach has lower microbial densities than the jejunum, cecum, and colon.<sup>17</sup> Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria are the most common bacterial phyla in the human microbiome, with composition altering according to body habitat.<sup>18,19</sup>

### **Microbial Diversity of Microorganisms in Different Body Sites**

The human body is home to a diverse range of microorganisms that live in a variety of anatomical places, each with its microbial community tailored to its environment. This microbial diversity is essential for sustaining homeostasis and health because different bacterial species contribute distinct tasks based on their location.

- **Gut Microbiome:** The gut microbiome is the most diverse and densely populated microbial community in the human body.<sup>20</sup> It has over 3 million genes, greatly exceeding the 23,000 genes in the human genome.<sup>21</sup> The gut microbiota acts as a “superorganism” alongside the host, playing critical roles in digestion, nutrition absorption, and immune protection. They help metabolize bile acids, lipids, amino acids, vitamins, and short-chain fatty acids (SCFAs) while also preventing pathogenic colonization through gut integrity and competitive exclusion of dangerous microorganisms. Despite changes in microbial composition, the gut microbiota's essential functions remain consistent among individuals.<sup>22</sup>
- **Skin Microbiome:** The density and number of glands and hair follicles on the skin offer unique microenvironments for microbial growth.<sup>23</sup> These changes influence the quantity and composition of microbial communities on the skin.<sup>24</sup> Skin microbiota suppresses pathogens by creating bacteriocins, proteases, phenol-soluble modulins, and fermentation byproducts. They also create anti-virulence chemicals, which limit viruses' capacity to adhere to and enter tissues. Furthermore, skin microorganisms can detect environmental signals and regulate their gene expression in response, impacting pathogen virulence genes. While much study has focused on competitive interactions between skin microorganisms, they also cooperate by exploiting each other's metabolic products.<sup>25</sup>
- **Oral Microbiome:** The mouth cavity contains a diverse microbiome of bacteria, archaea, viruses, and fungi.<sup>26</sup> These microorganisms live in specific areas of the oral cavity, including the tongue, hard palate, tooth surfaces, and gingival fissures. The oral microbiome is important for maintaining oral health because it helps produce biofilms (dental plaque) and prevents pathogen colonization.<sup>27</sup> However, abnormalities in the

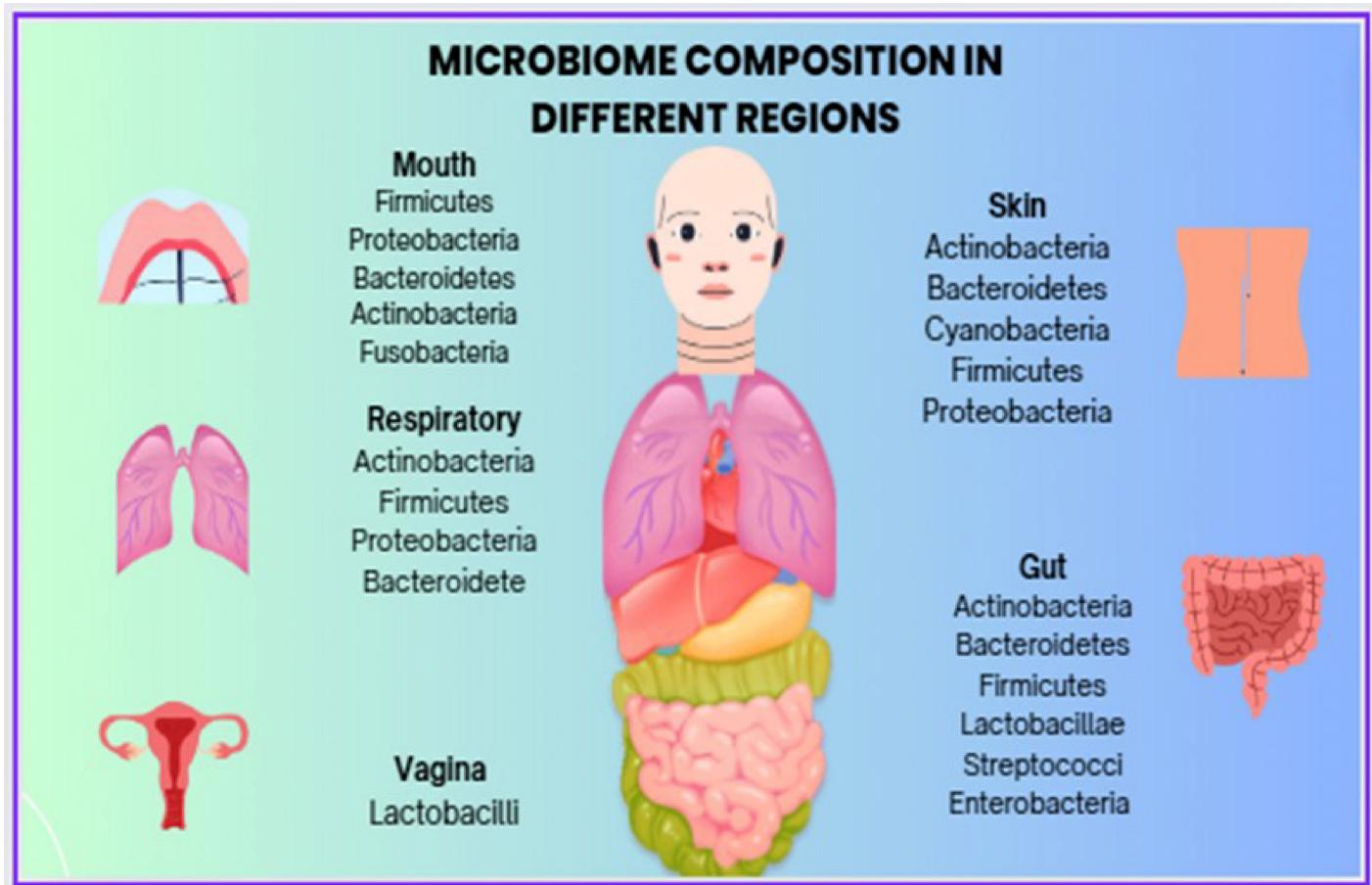


Fig 1 | Microbiome composition in different regions

oral microbiota can cause dental caries, periodontal disease, and other oral infections.<sup>28</sup>

- **Respiratory Tract Microbiome:** The respiratory tract microbiota differs between upper and lower respiratory tracts. The respiratory microbiome contributes to respiratory health by interacting with the host immune system, boosting protective responses, and preventing pathogenic colonization through antimicrobial production. This relationship promotes lung homeostasis by maintaining constant communication among bacteria, epithelial cells, and immune cells. The lung microbiota is regarded as a “mirror of lung health status,” with considerable changes in composition occurring during respiratory illnesses.<sup>29</sup>
- **Urogenital Microbiome:** Men and women have distinct urogenital microbiomes due to differences in anatomy and hormones.<sup>2</sup> *Lactobacillus* species dominate the vaginal microbiome in women, producing lactic acid and contributing to a low pH that protects against infections.<sup>30</sup> The male urogenital tract microbiome is less well understood; however, it contains bacteria such as *Corynebacterium* and *Staphylococcus* species.<sup>31</sup>

#### Factors Prompting Microbial Diversity

Several variables influence microbial diversity in these bodily areas, including diet, age, genetics,

environmental exposures, and lifestyle choices. Antibiotics, for example, can alter microbial populations and cause dysbiosis, which has been linked to a variety of health issues.<sup>32</sup>

#### Role in Health: Functions of the Microbiome in Digestion, Immune Modulation, and Disease Prevention

The human microbiome plays an important role in maintaining health by participating in a variety of physiological processes. This complex population of bacteria makes an important contribution to digestion, immune system regulation, and disease prevention. The relationship between the host and its microbiota is a critical factor in health and disease, impacting both metabolic and immunological functions.

- **Digestion and Metabolism:** The microbiome plays a crucial role in digestion and metabolism, particularly in the gut. It ferments dietary fibers and complex carbohydrates that humans cannot digest, producing beneficial metabolites like SCFAs. These SCFAs are crucial energy sources for the host and promote intestinal health.<sup>33</sup> Butyrate, in particular, is the principal energy source for colonocytes and contains anti-inflammatory qualities, which help the intestinal barrier function and reduce the risk of inflammatory

illnesses.<sup>34,35</sup> Furthermore, the gut microbiota produces important vitamins and cofactors, such as vitamin K and several B vitamins, that are required for host metabolic activities.<sup>36,37</sup> The microbiota also metabolizes bile acids, which influence fat digestion and cholesterol metabolism.<sup>38</sup> Furthermore, gut bacteria play a role in xenobiotic detoxification, helping to biotransform and excrete potentially hazardous substances.<sup>39</sup>

- **Immune Modulation:** The microbiome has a significant impact on immune development and function. It is critical in training the immune system to distinguish between commensal and harmful microorganisms, hence preserving immunological homeostasis. This teaching begins at birth, since maternal microbiome exposure and breastfeeding influence the newborn immune system, supporting the formation of regulatory T cells and other immunological components that limit excessive inflammatory responses.<sup>40</sup> The gut microbiota also affects systemic immunity by affecting the production of cytokines and other immune mediators. For example, certain microbial metabolites, such as SCFAs, can promote the synthesis of anti-inflammatory cytokines like IL-10 while blocking proinflammatory cytokines like IL-17.<sup>41</sup> This regulation promotes a healthy immune response, which protects against autoimmune disorders and allergies. Furthermore, the microbiota helps to maintain mucosal immunity, especially in the gut. It increases the synthesis of secretory immunoglobulin A (IgA), which is essential for neutralizing pathogens and preventing them from adhering to the gut epithelium.<sup>42</sup> The microbiota also supports the maturation of gut-associated lymphoid tissues (GALT), which are critical components of the gut's immune surveillance system.<sup>43</sup>
- **Disease Prevention:** The microbiome promotes disease prevention through colonization resistance, where commensal microbes compete with pathogenic bacteria for resources and habitats. This competitive exclusion is critical in preventing infections by opportunistic pathogens like *Clostridium difficile*, which can thrive when drugs disturb the gut microbiota.<sup>44</sup> The microbiome also produces antimicrobial peptides and bacteriocins, both of which hinder pathogen growth. *Lactobacillus* species in the vaginal microbiome, for example, create lactic acid, which keeps the pH low and hostile to many pathogens, protecting against bacterial vaginosis and sexually transmitted diseases.<sup>45</sup> Furthermore, there is increasing evidence that the microbiome increases the host's susceptibility to chronic diseases, such as obesity and type 2 diabetes. The composition of the gut microbiota can influence human energy metabolism and fat storage, with specific bacterial profiles linked to an increased

risk of metabolic syndrome.<sup>46</sup> The microbiome's role in modulating systemic inflammation has been linked to cardiovascular diseases,<sup>47</sup> autoimmune conditions, and mental health disorders like depression and anxiety,<sup>48,49</sup> indicating its broad impact on overall health.

The microbiome's functions in digestion, immunological regulation, and disease prevention are critical for human health. Its ability to influence a wide range of physiological processes emphasizes the significance of having a healthy and balanced microbiota. Future studies into the complex interactions between the microbiome and the host will uncover new therapeutic targets as well as disease prevention and treatment options.

### Recent Advances and Future Directions in Microbiome Research

#### Technological Advancements

Recent developments in molecular biology and bioinformatics have greatly improved our knowledge of the human microbiome. The key approaches include:

- **NGS:** This innovative technology enables the quick and complete sequencing of large volumes of DNA, yielding extensive information on genome structure, genetic variants, and gene expression. Recent advances have boosted the speed, precision, and affordability of NGS, making it more accessible in a variety of research domains.<sup>50</sup>
- **16S rRNA Sequencing:** This approach identifies and classifies bacteria and archaea by targeting the 16S ribosomal RNA gene. It provides a taxonomic overview but not functional insights.<sup>51</sup>
- **Metagenomics:** Whole-genome shotgun sequencing analyzes the genetic material of microbial communities, including viruses and fungi, providing a comprehensive view. It exposes the genetic basis of metabolic processes and antibiotic resistance.<sup>52</sup>
- **Metabolomics:** Metabolomics is a technology that analyzes metabolites produced by microorganisms to determine their activity. It connects microbial genetic potential to metabolic output, identifying important metabolites such as SCFAs that affect health.<sup>53</sup>
- **Single-Cell Genomics:** Single-Cell Genomics involves isolating and sequencing the genomes of individual microbial cells to research unculturable or rare bacteria and comprehend microbial heterogeneity.<sup>54</sup>
- **CRISPR-Cas Systems:** CRISPR-Cas was originally an adaptive immunological mechanism in bacteria, but it has now been modified for genome editing and regulation in microbiome research. It enables precise modification of microbial genes to investigate their roles.<sup>55</sup>
- **Multi-omics Integration:** By integrating genomes, transcriptomics, proteomics, and

metabolomics, this approach provides a comprehensive understanding of the microbiome's impact on health and disease. It aids in the creation of tailored therapies by correlating microbial composition with functional outcomes.<sup>56</sup>

These tools have accelerated microbiome research, expanding our understanding of microbial diversity, function, and impact on human health. The future of this subject lies in technical advancements, improved bioinformatics tools, and the integration of multiple "omics" data to provide a comprehensive picture of the microbiome's involvement in human health.

#### Integrative Approaches and Future Directions

The combination of 16S rRNA sequencing, metagenomics, and metabolomics, as well as other "omics" techniques such as proteomics and transcriptomics, provides a full understanding of the microbiome. This multi-omics method contributes to a better understanding of host-microbe interactions by correlating microbial composition with functional consequences.<sup>57</sup> Future research will most likely focus on improving the resolution and accuracy of these methodologies, as well as building better bioinformatics tools for data integration.<sup>50,58</sup>

Future studies will seek to better understand the mechanisms behind host-microbe interactions and their consequences for health. Key areas of focus include investigating how nutrition, antibiotics, and environmental variables affect microbiome composition and function.<sup>59</sup>

#### The Microbiome's Role in Various Diseases

Recent research has emphasized the human microbiome's crucial role in a wide range of diseases, including

metabolic disorders, cancer, IBD, and mental health concerns (Figure 2). These findings highlight the microbiome's impact on host physiology and prospective treatment targets. Here, we look at major research that sheds light on the microbiome's role in certain health issues.

#### Metabolic Disorders

There is emergent evidence that changes in the microbiota composition can cause a variety of disorders, including metabolic diseases like obesity and diabetes.<sup>60</sup> Turnbaugh et al. discovered that obese people have a different gut microbiome composition than lean people, with a larger proportion of Firmicutes relative to Bacteroidetes.<sup>61</sup> This altered microbial composition is expected to improve energy extraction from the food, leading to increased adiposity. Qin et al. discovered that changes in gut microbiota composition and function are linked to insulin resistance and systemic inflammation in type 2 diabetes patients, implying that the microbiome is involved in the disease's pathophysiology.<sup>62</sup>

#### Cancer

The gut microbiota has a substantial impact on host health and has been connected to cancer development.<sup>63</sup> It also affects extra-intestinal malignancies such as hepatocellular carcinoma via organismal dissemination.<sup>2</sup> *Helicobacter pylori* has been linked to stomach cancer, and some bacterial species such as *Fusobacterium* and *Clostridium* are overrepresented in patients.<sup>64</sup> Breast cancer growth has been connected to certain bacterial populations, with pathogenic strains such as *Escherichia coli* and *Staphylococcus epidermidis* causing DNA damage in malignant tissues.<sup>65</sup>

#### Inflammatory Bowel Disease

Dysbiosis, or an imbalance in the gut microbiota, can cause autoimmune disorders including IBD.<sup>66</sup> A disrupted mucus layer can compromise the integrity of the gastrointestinal barrier, which is crucial in avoiding inflammation, resulting in increased proinflammatory and decreased anti-inflammatory cytokines.<sup>67</sup> Researchers discovered alterations in genes involved in microbiome-immune interactions in IBD patients.<sup>68</sup>

#### Cardiovascular Diseases

The gut microbiota produces compounds such as trimethylamine N-oxide, which have been associated with cardiovascular disease by altering lipid metabolism and causing atherosclerosis.<sup>69</sup> Dysbiosis is related to an increased risk of cardiovascular disease, with studies revealing changed gut flora in hypertension individuals.<sup>70</sup>

#### Systemic Infections from Bacterial Translocation

Bacteria can spread from the gut to other body regions, especially in immunocompromised people, resulting in systemic infections.<sup>71</sup> Disturbance of the gut microbiota

Fig 2 | Human microbiome's role in a wide range of diseases

and epithelial injury increases the probability of pathogen translocation such as *E. coli* and *K. pneumoniae*.<sup>72</sup> Uremic toxins produced by dysbiotic flora can cause systemic inflammatory responses, which contribute to disorders such as chronic kidney disease.<sup>73</sup>

### Allergic Diseases

The human microbiome influences allergy illnesses, with dysbiosis impacting lung microbiota and increasing respiratory disease threat.<sup>74</sup> Cesarean delivery, which avoids normal maternal flora transmission, is associated with increased allergy risk in offspring. Lower microbial diversity in early life has been linked to increased allergy sensitivity, such as asthma.<sup>66</sup>

### Health Maintenance

The microbiome is essential for maintaining homeostasis,<sup>75</sup> activating the immune system,<sup>76</sup> and controlling inflammation.<sup>77</sup> It also helps eliminate toxic compounds<sup>78</sup> and plays a role in immunological responses in the female vaginal tract, contributing to infection resistance.<sup>79</sup>

### Mental Health

Dysbiosis, or microbial imbalance, may contribute to the onset and progression of mental diseases.<sup>80,81</sup> The term “psychobiotics” refers to probiotics that improve mental health by modulating the microbiome.<sup>82</sup> This points to possible therapeutic options for treating mental health issues by targeting the gut microbiome. These significant studies emphasize the microbiome’s role in a variety of diseases, emphasizing its potential as a biomarker for disease risk and development, as well as a therapeutic intervention target. Ongoing research into the microbiome’s role in health and disease continues to reveal complex host–microbe interactions, providing new insights into disease causes and opening up new therapy and preventative options.

### Microbiome Modulation: Therapeutic Approaches

#### Probiotics and Prebiotics: Efficacy and Challenges

Extensive research and clinical evidence have shown that probiotics and prebiotics are beneficial in restoring gut microbiota equilibrium and treating a variety of disorders. Probiotics are live bacteria that, when taken in suitable concentrations, provide health advantages. Prebiotics are nondigestible food components that encourage the growth of good microorganisms. Both have the potential to transform illness management.<sup>83,84</sup>

### Probiotics: Efficacy and Mechanisms

Probiotics, which are usually found in the genera *Lactobacillus*, *Bifidobacterium*, and *Saccharomyces*,<sup>85</sup> work in numerous ways to provide health benefits:

- **Enhancement of Gut Barrier Function:** Probiotics enhance gut barrier function, preventing infections and poisons from entering the bloodstream.<sup>86</sup>

- **Immunomodulation:** Mazzotta et al. found that they influence the immune response by boosting anti-inflammatory cytokines, increasing regulatory T-cell activity, and producing bacteriocins to suppress harmful bacteria.<sup>87</sup>
- **Competition with Pathogens:** Probiotics compete with harmful bacteria for nutrients and adhesion sites, reducing infections.<sup>88</sup>
- Recent studies have shown that probiotics can reduce the duration and severity of acute infectious diarrhea in children,<sup>89</sup> improve symptoms of irritable bowel syndrome (IBS),<sup>90</sup> and boost the immune response to vaccinations.<sup>91</sup>

### Prebiotics: Efficacy and Mechanisms

Prebiotics preferentially enhance the development and activity of beneficial gut bacteria, resulting in the synthesis of SCFAs such as acetate, propionate, and butyrate, which have health-promoting properties:<sup>92</sup>

- **Promotion of Beneficial Microbiota:** Prebiotics promote the growth of beneficial bacteria like *Bifidobacterium* and *Lactobacillus*, leading to a balanced and healthy microbiota composition.<sup>93</sup>
- **Production of SCFAs:** SCFA production is important for gut health, as butyrate provides energy to colonocytes, promotes gut barrier integrity, and has anti-inflammatory properties.<sup>94</sup>
- **Modulation of Lipid Metabolism:** Prebiotics reduce blood cholesterol levels and change bile acid metabolism, which is partially mediated by SCFA.<sup>95</sup>

Prebiotics have been found to promote gut health, increase mineral absorption, lower the risk of colorectal cancer,<sup>96</sup> and help control metabolic disorders like obesity and type 2 diabetes by improving metabolic profiles.<sup>97</sup>

### Fecal Microbiota Transplantation: Current Status, Applications, and Controversies

Fecal microbiota transplantation (FMT) (Figure 3) is the process of transferring stool from a healthy donor into a recipient’s gastrointestinal tract to reestablish a balanced and diversified gut microbiota in patients suffering from dysbiosis.<sup>98</sup>

#### Applications of FMT

- FMT is a conventional treatment for recurrent *Clostridium difficile* infection (CDI) when traditional antibiotics fail. It restores gut microbiota and suppresses *C. difficile* growth through food competition and immune system stimulation.<sup>99</sup>
- **IBD:** FMT is an investigational treatment for IBD, including Crohn’s disease and ulcerative colitis. Some studies suggest beneficial outcomes, such as remission or symptom reduction, but the results are variable, and FMT is not yet considered a standard treatment for IBD.<sup>100</sup>
- **IBS:** FMT may help with IBS, although results depend on donor selection and patient variables.<sup>101</sup>

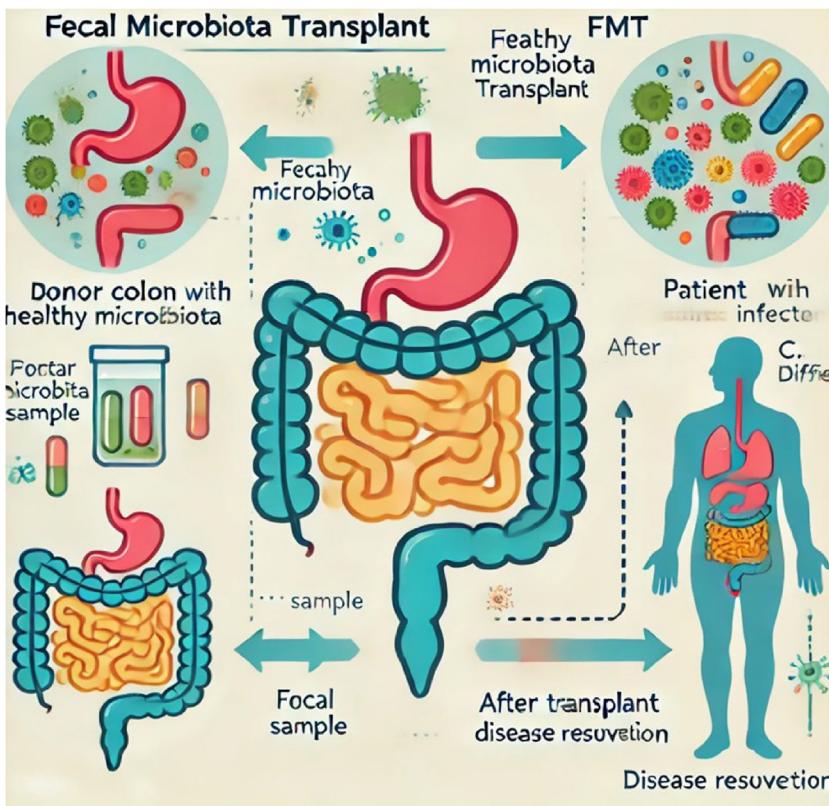


Fig 3 | Fecal microbiota transplantation

- **Metabolic Syndrome and Obesity:** Early studies indicate that FMT from lean donors can temporarily increase insulin sensitivity in obese recipients, suggesting potential metabolic benefits. However, long-term efficacy and safety remain unknown.<sup>102</sup>
- **Neuropsychiatric Disorders:** Preliminary studies and case reports on FMT for neuropsychiatric disorders, such as autism and depression, have yielded inconsistent results. More study is required to better understand the mechanisms and treatment benefits.<sup>103</sup>

#### Diet and Lifestyle Interventions: Modulating the Microbiome and Implications for Health

The human microbiome, particularly the gut microbiota, is a dynamic ecosystem impacted by diet and lifestyle, which can alter its composition and function, affecting general health and disease risk. Recent research emphasizes the ability of dietary and lifestyle interventions to regulate the microbiome, hence enhancing health and avoiding or alleviating illnesses.

#### Dietary Influences on the Microbiome

Diet is a primary modulator of gut flora.

- **High-Fiber and Complex Carbohydrate Diets:** Encourage beneficial bacteria such as *Bifidobacterium* and *Lactobacillus* to create SCFAs for health benefits.<sup>104</sup>

- **High-Fat Diets:** High-fat diets can reduce microbial diversity and boost proinflammatory microorganisms.<sup>105</sup>
- **Polyunsaturated Fats and Plant-Based Proteins:** Polyunsaturated fats and plant-based proteins promote beneficial microorganisms.<sup>106</sup>
- **Polyphenols:** Polyphenols, found in fruits, vegetables, tea, and wine, improve gut health by boosting beneficial bacteria and SCFA production.<sup>107</sup>

#### Lifestyle Factors Affecting the Microbiome

Several lifestyle factors have a substantial influence on the gut microbiome:

- **Physical Activity:** Regular exercise enhances microbial diversity, and SCFA-producing bacteria, improves gut barrier function, and reduces inflammation.<sup>108</sup>
- **Sleep and Circadian Rhythms:** Poor sleep and altered circadian rhythms can promote dysbiosis, resulting in inflammation and metabolic disorders.<sup>109</sup>
- **Stress and Psychological Factors:** Chronic stress can negatively impact the gut-brain axis, leading to increased gut permeability and inflammation, which can worsen gastrointestinal and mood disorders.<sup>110</sup>
- **Medication Use:** Antibiotics and other drugs can change the microbiome, leading to reduced diversity and pathogen overgrowth, affecting gut health.<sup>111</sup>

#### Challenges and Debates in Microbiome Research

Microbiome research has advanced rapidly, revealing the vital role that microbial communities play in human health and disease. The heterogeneity of study outcomes presents a significant problem in this subject, making replication and interpretation challenging. This variation is mostly due to individual variances in microbiome composition and function, which are influenced by genetics, diet, lifestyle, environment, and host physiology. Addressing these discrepancies is critical to improving the dependability of research findings and their use in therapeutic settings.

#### Factors Contributing to Interindividual Variability

Several variables affect interindividual variability in microbiome studies:

- **Genetic Influences:** Host genetics influence immunological responses, metabolism, microbial colonization, and community organization. Genetic differences, particularly in immunological function genes, might influence host-microbe interactions, with research indicating heritability in gut microbiota composition across related individuals.<sup>112</sup>
- **Diet and Lifestyle:** Dietary choices and lifestyle factors including physical activity, stress, and sleep patterns have a substantial impact on the microbiota. High-fat diets, for example,

may reduce beneficial bacteria while increasing proinflammatory bacteria.<sup>110</sup>

- **Environmental Factors:** Geographical location, sanitation, pollution, and antibiotic use can impact microbiome composition. Environmental variables, such as cleanliness levels and urban/rural living situations, contribute to variability.<sup>113</sup>
- **Age and Developmental Stage:** The microbiome evolves from infancy to maturity, impacted by nutrition, medication usage, and immune system alterations in the elderly.<sup>114</sup>

**Ethical and Privacy Concerns: Issues Related to Microbiome Data Privacy and Ethical Considerations**

Microbiome research, despite its potential, raises serious ethical and privacy problems. The unique and individualized character of microbiome data raises concerns about consent, data ownership, confidentiality, and potential misuse.

- **Privacy and Data Security:** Microbiome data might expose sensitive information about a person's health, lifestyle, and genetics. Even anonymized data is at risk of being re-identified, particularly with big data analytics. Protecting privacy requires robust data security and transparent data exchange policies.<sup>115</sup>
- **Informed Consent and Data Ownership:** It can be tough to ensure participants understand the breadth of data collection and future usage. Clear consent forms and open communication regarding data usage and ownership are critical. Participants should also understand their rights, which include the ability to withdraw from studies.<sup>116</sup>
- **Ethical Use of Microbiome Data:** The potential applications of microbiome data in healthcare and elsewhere create ethical concerns concerning access and use. Concerns include discrimination in insurance or employment based on microbiome characteristics, as well as the marketing of microbiome products that may make deceptive promises.<sup>117</sup>
- **Equity and Access:** Microbiome research should benefit all populations to prevent health inequities. Researchers and policymakers must devise measures to promote equal access to microbiome-based treatments and diagnostics.<sup>118</sup>
- **Environmental and Public Health Considerations:** Research on environmental samples might yield significant insights, but it must adhere to privacy and environmental ethics. Monitoring microbial populations in public and private settings necessitates careful consideration of these variables.<sup>119</sup>

**Future Directions and Research Gaps in Microbiome Research**

**Challenges and Research Gaps**

Microbiome research has shown complicated relationships between microbial ecosystems and human

health, with implications for therapeutic interventions and customized medicine. However, significant problems and research gaps must be addressed, with an emphasis on three key areas:

- **Personalized Microbiome-Based Therapies:** Developing tailored microbiome-based therapies is problematic due to considerable heterogeneity in microbial populations among individuals.<sup>120</sup>
- **Longitudinal Studies:** Longitudinal studies are needed to understand the evolution of the microbiome and its impact on health and disease progression, which is currently under-researched.<sup>121</sup>
- **Integration with Other “omics” Technologies:** Integrating microbiome data with other “omics” technologies (genomics, proteomics, and metabolomics) is crucial for a comprehensive understanding of the microbiome's role in health and disease. However, this requires advanced analytical methods and interdisciplinary collaboration.<sup>122</sup>

Addressing these issues will be critical for furthering microbiome research and converting results into therapeutic applications.

**Implications for Future Research and Public Health**

The impact of microbiome research on healthcare practices and policies is significant. As we get a better understanding of the microbiome's involvement in health and disease, we should expect more tailored and preventive healthcare methods. For example, microbiome analysis could become a common diagnostic technique, leading to tailored therapies such as food changes, probiotics, or microbiome transplants.<sup>33</sup>

Furthermore, incorporating microbiome data into electronic health records and public health surveillance systems may improve the ability to monitor and manage infectious disease outbreaks, track antibiotic resistance, and understand population health trends. This research has the potential to inform public health policies and programs aimed at promoting healthy microbiome compositions in various groups.<sup>123</sup>

However, these improvements highlight the need for strong regulatory frameworks to assure the safety and efficacy of microbiome-based goods and services. Policymakers will need to address ethical concerns about data privacy and equal access to microbiome-based healthcare breakthroughs.

**Microbiome-Based Pharmaceuticals**

Microbiome-based pharmaceuticals, sometimes known as “pharmabiotics,” include live bacterial therapies, bacteriophages, and microbial metabolites intended to treat certain disorders (Figure 4).

- **Live Bacterial Therapeutics:** These use genetically created or naturally existing microorganisms to provide therapeutic effects. For example, *E. coli* Nissle 1917 is utilized to treat gastrointestinal diseases.<sup>124</sup>

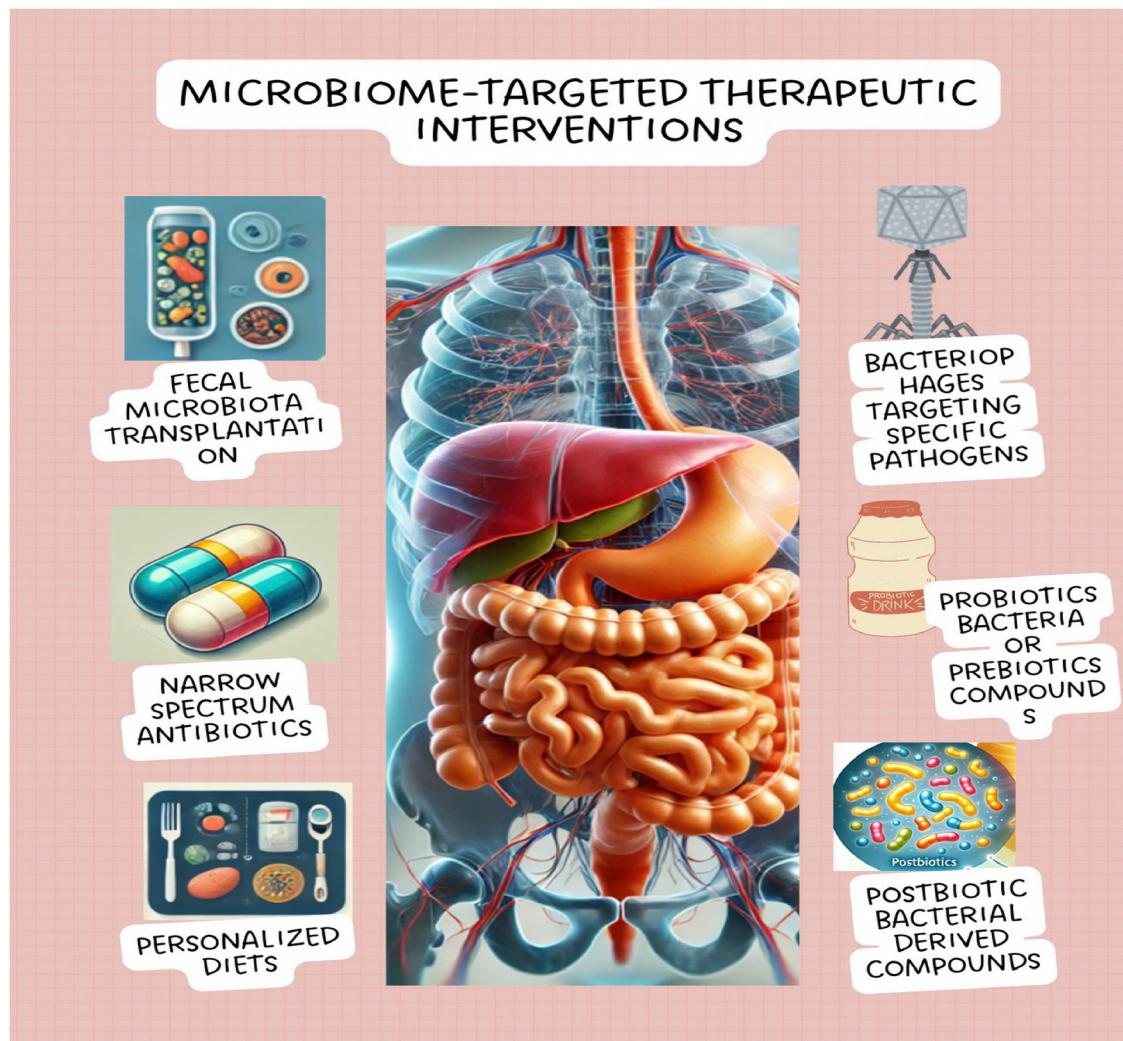


Fig 4 | Microbiome-targeted therapeutic interventions

- **Bacteriophages:** Bacteriophages are viruses that selectively infect and kill bacteria. They provide a tailored method for eradicating harmful germs while preserving healthy microorganisms. Phage treatment is being investigated for antibiotic-resistant infections and other bacterial disorders.<sup>125</sup>
- **Microbial Metabolites:** SCFAs and other microbial metabolites have therapeutic potential.<sup>126</sup> Butyrate, an SCFA generated by gut bacteria, has anti-inflammatory characteristics and is being studied as a treatment for IBD and metabolic diseases.<sup>127</sup>

#### Challenges and Future Directions

While microbiome-based therapeutics show significant promise, numerous issues must be addressed:

- **Individual Variability:** The human microbiome is extremely personalized, impacted by genetics, food, environmental factors, and lifestyle. Personalized techniques are required to ensure the effectiveness of microbiome-based therapeutics.

- **Safety and Regulation:** Ensure the safety and efficacy of microbiome-based medicines through thorough clinical testing and regulatory control. Standardizing practices and creating clear regulatory frameworks are critical.
- **Mechanistic Understanding:** More research is needed to determine how the microbiota affects health and disease. This understanding will help to design tailored medicines and enhance clinical outcomes.

#### Conclusion

The human microbiome has a significant impact on digestion, immunological function, and disease prevention. Advances in molecular biology have helped us better comprehend these microbial ecosystems. Probiotics, prebiotics, and FMT are therapeutic approaches that show promise in treating a variety of disorders by restoring microbial balance. Diet, exercise, and stress management have a substantial impact on the microbiota.

Despite its potential, microbiome research confronts numerous hurdles, including individual diversity

and ethical considerations. Personalized medicines necessitate a thorough understanding of individual microbiomes, requiring additional study and ethical considerations. Integrating microbiome data into healthcare could transform illness management and lead to more effective, individualized therapies, underscoring microbiome research's bright potential in improving human health.

## References

- Shreiner AB, Kao JY, Young VB. The gut microbiome in health and in disease. *Curr Opin Gastroenterol* [Internet]. 2015;31(1):69–75. Available from: <http://journals.lww.com/00001574-201501000-00012>
- Whiteside SA, Razvi H, Dave S, Reid G, Burton JP. The microbiome of the urinary tract—a role beyond infection. *Nat Rev Urol* [Internet]. 2015;12(2):81–90. Available from: <https://www.nature.com/articles/nrurol.2014.361>
- Ogunrinola GA, Oyewale JO, Oshamika OO, Olasehinde GI. The human microbiome and its impacts on health. *Int J Microbiol* [Internet]. 2020;2020:1–7. Available from: <https://www.hindawi.com/journals/ijmico/2020/8045646/>
- Morgan XC, Huttenhower C. Chapter 12: Human Microbiome Analysis. Lewitter F, Kann M, editors. *PLoS Comput Biol* [Internet]. 2012;8(12):e1002808. Available from: <https://dx.plos.org/10.1371/journal.pcbi.1002808>
- Pascal M, Perez-Gordo M, Caballero T, Escrivese MM, Lopez Longo MN, Luengo O, et al. Microbiome and allergic diseases. *Front Immunol* [Internet]. 2018;9. Available from: <https://www.frontiersin.org/article/10.3389/fimmu.2018.01584/full>
- Dekaborah E, Suryavanshi MV, Chettri D, Verma AK. Human microbiome: an academic update on human body site specific surveillance and its possible role. *Arch Microbiol* [Internet]. 2020;202(8):2147–67. Available from: <https://link.springer.com/10.1007/s00203-020-01931-x>
- Berg G, Rybakova D, Fischer D, Cernava T, Vergès M-CC, Charles T, et al. Microbiome definition re-visited: old concepts and new challenges. *Microbiome* [Internet]. 2020;8(1):103. Available from: <https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-020-00875-0>
- Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI. The human microbiome project. *Nature* [Internet]. 2007;449(7164):804–10. Available from: <https://www.nature.com/articles/nature06244>
- Vieira AT, Fukumori C, Ferreira CM. New insights into therapeutic strategies for gut microbiota modulation in inflammatory diseases. *Clin Transl Immunol* [Internet]. 2016;5(6). Available from: <https://onlinelibrary.wiley.com/doi/10.1038/cti.2016.38>
- Hou K, Wu Z-X, Chen X-Y, Wang J-Q, Zhang D, Xiao C, et al. Microbiota in health and diseases. *Signal Transduct Target Ther* [Internet]. 2022;7(1):135. Available from: <https://www.nature.com/articles/s41392-022-00974-4>
- Leewenhoek A. An abstract of a letter from Mr. Anthony Leevvenhoek at Delft, dated Sep. 17. 1683. Containing some microscopical observations, about animals in the scurf of the teeth, the substance call'd worms in the nose, the cuticula consisting of scales. *Philos Trans R Soc London* [Internet]. 1684;14(159):568–74. Available from: <https://royalsocietypublishing.org/doi/10.1098/rstl.1684.0030>
- Mackowiak PA. Recycling Metchnikoff: probiotics, the intestinal microbiome and the quest for long life. *Front Public Heal* [Internet]. 2013;1. Available from: <http://journal.frontiersin.org/article/10.3389/fpubh.2013.00052/abstract>
- Nair P, Woese and Fox: Life, rearranged. *Proc Natl Acad Sci* [Internet]. 2012;109(4):1019–21. Available from: <https://pnas.org/doi/full/10.1073/pnas.1120749109>
- Eloe-Fadrosh EA, Rasko DA. The human microbiome: from symbiosis to pathogenesis. *Annu Rev Med* [Internet]. 2013;64(1):145–63. Available from: <https://www.annualreviews.org/doi/10.1146/annurev-med-010312-133513>
- Davis CD. The gut microbiome and its role in obesity. *Nutr Today* [Internet]. 2016;51(4):167–74. Available from: <https://journals.lww.com/00017285-201607000-00003>
- Johnson CL, Versalovic J. The human microbiome and its potential importance to pediatrics. *Pediatrics* [Internet]. 2012;129(5):950–60. Available from: <https://publications.aap.org/pediatrics/article/129/5/950/73825/The-Human-Microbiome-and-Its-Potential-Importance>
- Belizário JE, Napolitano M. Human microbiomes and their roles in dysbiosis, common diseases, and novel therapeutic approaches. *Front Microbiol* [Internet]. 2015;6. Available from: <http://journal.frontiersin.org/Article/10.3389/fmcb.2015.01050/abstract>
- Wang B, Yao M, Lv L, Ling Z, Li L. The human microbiota in health and disease. *Engineering* [Internet]. 2017;3(1):71–82. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2095809917301492>
- Palmer C, Bik EM, DiGiulio DB, Relman DA, Brown PO. Development of the Human Infant Intestinal Microbiota. Ruan Y, editor. *PLoS Biol* [Internet]. 2007;5(7):e177. Available from: <https://dx.plos.org/10.1371/journal.pbio.0050177>
- Thursby E, Juge N. Introduction to the human gut microbiota. *Biochem J* [Internet]. 2017;474(11):1823–36. Available from: <https://portlandpress.com/biochemj/article/474/11/1823/49429/Introduction-to-the-human-gut-microbiota>
- Valdes AM, Walter J, Segal E, Spector TD. Role of the gut microbiota in nutrition and health. *BMJ* [Internet]. 2018;k2179. Available from: <https://www.bmjjournals.org/lookup/doi/10.1136/bmj.k2179>
- Brestoff JR, Artis D. Commensal bacteria at the interface of host metabolism and the immune system. *Nat Immunol* [Internet]. 2013;14(7):676–84. Available from: <https://www.nature.com/articles/ni.2640>
- Chen YE, Fischbach MA, Belkaid Y. Skin microbiota–host interactions. *Nature* [Internet]. 2018;553(7689):427–36. Available from: <https://www.nature.com/articles/nature25177>
- Byrd AL, Belkaid Y, Segre JA. The human skin microbiome. *Nat Rev Microbiol* [Internet]. 2018;16(3):143–55. Available from: <https://www.nature.com/articles/nrmicro.2017.157>
- Glathardt T, Lima RD, de Mattos RM, Ferreira RBR. Microbe interactions within the skin microbiome. *Antibiotics* [Internet]. 2024;13(1):49. Available from: <https://www.mdpi.com/2079-6382/13/1/49>
- Wade WG. The oral microbiome in health and disease. *Pharmacol Res* [Internet]. 2013;69(1):137–43. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S1043661812002277>
- Lamont RJ, Koo H, Hajishengallis G. The oral microbiota: dynamic communities and host interactions. *Nat Rev Microbiol* [Internet]. 2018;16(12):745–59. Available from: <https://www.nature.com/articles/s41579-018-0089-x>
- Upadhyay M, Swaroop A, Sinhal VK, Srivastava A, Garg SK, Singh VP, et al. Role of Human Oral Microbiome in Diseases. *J Pure Appl Microbiol* [Internet]. 2024;18(1):168–76. Available from: <https://microbiologyjournal.org/role-of-human-oral-microbiome-in-diseases/>
- Natalini JG, Singh S, Segal LN. The dynamic lung microbiome in health and disease. *Nat Rev Microbiol* [Internet]. 2023;21(4):222–35. Available from: <https://www.nature.com/articles/s41579-022-00821-x>
- Chen X, Lu Y, Chen T, Li R. The female vaginal microbiome in health and bacterial vaginosis. *Front Cell Infect Microbiol* [Internet]. 2021;11. Available from: <https://www.frontiersin.org/articles/10.3389/fcimb.2021.631972/full>
- Bajic P, Van Kuiken ME, Burge BK, Kirshenbaum Ej, Joyce CJ, Wolfe AJ, et al. Male bladder microbiome relates to lower urinary tract symptoms. *Eur Urol Focus* [Internet]. 2020;6(2):376–82. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2405456918302207>
- Alagiakrishnan K, Morgadinho J, Halverson T. Approach to the diagnosis and management of dysbiosis. *Front Nutr* [Internet]. 2024;11. Available from: <https://www.frontiersin.org/articles/10.3389/fnut.2024.1330903/full>
- Song E-J, Shin J-H. Personalized diets based on the gut as a target for health maintenance: from current evidence to future possibilities. *J Microbiol Biotechnol* [Internet]. 2022;32(12):1497–505. Available from: <http://www.jmb.or.kr/journal/view.html?doi=10.4014/jmb.2209.09050>
- Facchini S, Bertin L, Bonazzi E, Lorenzon G, De Barba C, Barberio B, et al. Short-chain fatty acids and human health: from metabolic pathways to current therapeutic implications. *Life* [Internet].

- 2024;14(5):559. Available from: <https://www.mdpi.com/2075-1729/14/5/559>
- 35 Canani RB. Potential beneficial effects of butyrate in intestinal and extraintestinal diseases. *World J Gastroenterol* [Internet]. 2011;17(12):1519. Available from: <http://www.wjgnet.com/1007-9327/full/v17/i12/1519.htm>
- 36 LeBlanc JG, Milani C, de Gori GS, Sesma F, van Sinderen D, Ventura M. Bacteria as vitamin suppliers to their host: a gut microbiota perspective. *Curr Opin Biotechnol* [Internet]. 2013;24(2):160–8. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S095816691200119X>
- 37 Hill MJ. Intestinal flora and endogenous vitamin synthesis. *Eur J Cancer Prev* [Internet]. 1997;6:S43–5. Available from: <http://journals.lww.com/00008469-199703001-00009>
- 38 Kriaa A, Bourgin M, Potiron A, Mkaouar H, Jablaoui A, Gérard P, et al. Microbial impact on cholesterol and bile acid metabolism: current status and future prospects. *J Lipid Res* [Internet]. 2019;60(2):323–32. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S0022227520326444>
- 39 Koppell N, Maini Rekdal V, Balskus EP. Chemical transformation of xenobiotics by the human gut microbiota. *Science* [Internet]. 2017;356(6344). Available from: <https://www.science.org/doi/10.1126/science.aag2770>
- 40 Belkaid Y, Hand TW. Role of the microbiota in immunity and inflammation. *Cell* [Internet]. 2014;157(1):121–41. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S0092867414003456>
- 41 Lavelle A, Sokol H. Gut microbiota-derived metabolites as key actors in inflammatory bowel disease. *Nat Rev Gastroenterol Hepatol* [Internet]. 2020;17(4):223–37. Available from: <https://www.nature.com/articles/s41575-019-0258-z>
- 42 Sterlini D, Fadlallah J, Slack E, Gorochov G. The antibody/microbiota interface in health and disease. *Mucosal Immunol* [Internet]. 2020;13(1):3–11. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S1933021922002367>
- 43 Brandtzaeg P, Farstad IN, Johansen F, Morton HC, Norderhaug IN, Yamanaka T, et al. The B-cell system of human mucosae and exocrine glands. *Immunol Rev* [Internet]. 1999;171(1):45–87. Available from: <https://onlinelibrary.wiley.com/doi/10.1111/j.1600-065X.1999.tb01342.x>
- 44 Pérez-Cobas A, Moya A, Gosalbes M, Latorre A. Colonization resistance of the gut microbiota against *Clostridium difficile*. *Antibiotics* [Internet]. 2015;4(3):337–357. Available from: <https://www.mdpi.com/2079-6382/4/3/337>
- 45 Amabebe E, Anumba DOC. The vaginal microenvironment: the physiologic role of lactobacilli. *Front Med* [Internet]. 2018;5. Available from: <https://www.frontiersin.org/article/10.3389/fmed.2018.00181/full>
- 46 Hartstra AV, Bouter KEC, Bäckhed F, Nieuwdorp M. Insights into the role of the microbiome in obesity and type 2 diabetes. *Diabetes Care* [Internet]. 2015;38(1):159–65. Available from: <https://diabetesjournals.org/care/article/38/1/159/37808/Insights-Into-the-Role-of-the-Microbiome-in>
- 47 Sanchez-Rodríguez E, Egea-Zorrilla A, Plaza-Díaz J, Aragón-Vela J, Muñoz-Quezada S, Tercedor-Sánchez L, et al. The gut microbiota and its implication in the development of atherosclerosis and related cardiovascular diseases. *Nutrients* [Internet]. 2020;12(3):605. Available from: <https://www.mdpi.com/2072-6643/12/3/605>
- 48 Peirce JM, Alviña K. The role of inflammation and the gut microbiome in depression and anxiety. *J Neurosci Res* [Internet]. 2019;97(10):1223–41. Available from: <https://onlinelibrary.wiley.com/doi/10.1002/jnr.24476>
- 49 Walker ER, McGee RE, Druss BG. Mortality in mental disorders and global disease burden implications. *JAMA Psychiatry* [Internet]. 2015;72(4):334. Available from: <http://archpsyc.jamanetwork.com/article.aspx?doi=10.1001/jamapsychiatry.2014.2502>
- 50 Satam H, Joshi K, Mangrolia U, Waghoor S, Zaidi G, Rawool S, et al. Next-generation sequencing technology: current trends and advancements. *Biology (Basel)* [Internet]. 2023;12(7):997. Available from: <https://www.mdpi.com/2079-7737/12/7/997>
- 51 Clarridge JE. Impact of 16S rRNA gene sequence analysis for identification of bacteria on clinical microbiology and infectious diseases. *Clin Microbiol Rev* [Internet]. 2004;17(4):840–62. Available from: <https://journals.asm.org/doi/10.1128/CMR.17.4.840-862.2004>
- 52 Pérez-Cobas AE, Gomez-Valero L, Buchrieser C. Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. *Microb Genomics* [Internet]. 2020;6(8). Available from: <https://www.microbiologyresearch.org/content/journal/mgen/10.1099/mgen.0.000409>
- 53 Zhang Y, Chen R, Zhang D, Qi S, Liu Y. Metabolite interactions between host and microbiota during health and disease: Which feeds the other? *Biomed Pharmacother* [Internet]. 2023;160:114295. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S0753332223000835>
- 54 Hosokawa M, Nishikawa Y. Tools for microbial single-cell genomics for obtaining uncultured microbial genomes. *Biophys Rev* [Internet]. 2024;16(1):69–77. Available from: <https://link.springer.com/10.1007/s12551-023-01124-y>
- 55 Shabbir MAB, Shabbir MZ, Wu Q, Mahmood S, Sajid A, Maan MK, et al. CRISPR-cas system: biological function in microbes and its use to treat antimicrobial resistant pathogens. *Ann Clin Microbiol Antimicrob* [Internet]. 2019;18(1):21. Available from: <https://ann-clinmicrob.biomedcentral.com/articles/10.1186/s12941-019-0317-x>
- 56 Chen C, Wang J, Pan D, Wang X, Xu Y, Yan J, et al. Applications of multi-omics analysis in human diseases. *MedComm* [Internet]. 2023;4(4). Available from: <https://onlinelibrary.wiley.com/doi/10.1002/mco.2.315>
- 57 Peng W, Huang J, Yang J, Zhang Z, Yu R, Fayyaz S, et al. Integrated 16S rRNA sequencing, metagenomics, and metabolomics to characterize gut microbial composition, function, and fecal metabolic phenotype in non-obese type 2 diabetic Goto-Kakizaki Rats. *Front Microbiol* [Internet]. 2020;10. Available from: <https://www.frontiersin.org/article/10.3389/fmicb.2019.03141/full>
- 58 van den Bogert B, Boekhorst J, Pirovano W, May A. On the role of bioinformatics and data science in industrial microbiome applications. *Front Genet* [Internet]. 2019;10. Available from: <https://www.frontiersin.org/article/10.3389/fgene.2019.00721/full>
- 59 Afzaal M, Saeed F, Shah YA, Hussain M, Rabail R, Socol CT, et al. Human gut microbiota in health and disease: Unveiling the relationship. *Front Microbiol* [Internet]. 2022;13. Available from: <https://www.frontiersin.org/articles/10.3389/fmicb.2022.999001/full>
- 60 Vrieze A, Van Nood E, Holleman F, Salojärvi J, Koote RS, Bartelsman JFWM, et al. Transfer of intestinal microbiota from lean donors increases insulin sensitivity in individuals with metabolic syndrome. *Gastroenterology* [Internet]. 2012;143(4):913–916.e7. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S001650851200892X>
- 61 Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* [Internet]. 2006;444(7122):1027–31. Available from: <https://www.nature.com/articles/nature05414>
- 62 Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, et al. A metagenome-wide association study of gut microbiota in type 2 diabetes. *Nature* [Internet]. 2012;490(7418):55–60. Available from: <https://www.nature.com/articles/nature11450>
- 63 Manrique P, Bolduc B, Walk ST, van der Oost J, de Vos WM, Young MJ. Healthy human gut phageome. *Proc Natl Acad Sci* [Internet]. 2016;113(37):10400–5. Available from: <https://pnas.org/doi/full/10.1073/pnas.1601060113>
- 64 Round JL, Mazmanian SK. The gut microbiota shapes intestinal immune responses during health and disease. *Nat Rev Immunol* [Internet]. 2009;9(5):313–23. Available from: <https://www.nature.com/articles/nri2515>
- 65 Urbaniak C, Gloor GB, Brackstone M, Scott L, Tangney M, Reid G. The microbiota of breast tissue and its association with breast cancer. Goodrich-Blair H, editor. *Appl Environ Microbiol* [Internet]. 2016;82(16):5039–48. Available from: <https://journals.asm.org/doi/10.1128/AEM.01235-16>
- 66 Ipci K, Altintoprak N, Muluk NB, Senturk M, Cingi C. The possible mechanisms of the human microbiome in allergic diseases. *Eur Arch Oto-Rhino-Laryngology* [Internet]. 2017;274(2):617–26. Available from: <https://link.springer.com/10.1007/s00405-016-4058-6>
- 67 Caballero-franco C. Studies on the interaction between gastrointestinal bacteria and epithelial cells. *In Vivo*. 2009.
- 68 Glassner KL, Abraham BP, Quigley EMM. The microbiome and inflammatory bowel disease. *J Allergy Clin Immunol* [Internet]. 2020;145(1):16–27. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S001674919314861>

- 69 Zhu Y, Li Q, Jiang H. Gut microbiota in atherosclerosis: focus on trimethylamine N-oxide. *APMIS* [Internet]. 2020 May 30;128(5):353–66. Available from: <https://onlinelibrary.wiley.com/doi/10.1111/apm.13038>
- 70 Nesci A, Carnuccio C, Ruggieri V, D'Alessandro A, Di Giorgio A, Santoro L, et al. Gut microbiota and cardiovascular disease: evidence on the metabolic and inflammatory background of a complex relationship. *Int J Mol Sci* [Internet]. 2023;24(10):9087. Available from: <https://www.mdpi.com/1422-0067/24/10/9087>
- 71 Doudakmanis C, Bouliaris K, Kolla C, Efthimiou M, Koukoulis GD. Bacterial translocation in patients undergoing major gastrointestinal surgery and its role in postoperative sepsis. *World J Gastrointest Pathophysiol* [Internet]. 2021;12(6):106–14. Available from: <https://www.wjgnet.com/2150-5330/full/v12/i6/106.htm>
- 72 Parfrey LW, Walters WA, Lauber CL, Clemente JC, Berg-Lyons D, Teiling C, et al. Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. *Front Microbiol* [Internet]. 2014;5. Available from: <http://journal.frontiersin.org/article/10.3389/fmicb.2014.00298/abstract>
- 73 Tang Z, Yu S, Pan Y. The gut microbiome tango in the progression of chronic kidney disease and potential therapeutic strategies. *J Transl Med* [Internet]. 2023;21(1):689. Available from: <https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-023-04455-2>
- 74 Yuksel N, Gelmez B, Yildiz-Pekoz A. Lung microbiota: its relationship to respiratory system diseases and approaches for lung-targeted probiotic bacteria delivery. *Mol Pharm* [Internet]. 2023;20(7):3320–37. Available from: <https://pubs.acs.org/doi/10.1021/acs.molpharmaceut.3c00323>
- 75 Thomas S, Izard J, Walsh E, Batich K, Chongsathidkiet P, Clarke G, et al. The host microbiome regulates and maintains human health: a primer and perspective for non-microbiologists. *Cancer Res* [Internet]. 2017;77(8):1783–812. Available from: <https://aacrjournals.org/cancerres/article/77/8/1783/625126/The-Host-Microbiome-Regulates-and-Maintains-Human>
- 76 Rojo D, Méndez-García C, Raczkowska BA, Bargiela R, Moya A, Ferrer M, et al. Exploring the human microbiome from multiple perspectives: factors altering its composition and function. *FEMS Microbiol Rev* [Internet]. 2017;41(4):453–78. Available from: <https://academic.oup.com/femsre/article/41/4/453/3052758>
- 77 Hakansson A, Molin G. Gut microbiota and inflammation. *Nutrients* [Internet]. 2011;3(6):637–82. Available from: <https://www.mdpi.com/2072-6643/3/6/637>
- 78 Claus SP, Guillou H, Ellero-Simatos S. The gut microbiota: a major player in the toxicity of environmental pollutants? *NPJ Biofilms Microbiomes* [Internet]. 2016;2(1):16003. Available from: <https://www.nature.com/articles/npjbiofilms20163>
- 79 Adapen C, Réot L, Menu E. Role of the human vaginal microbiota in the regulation of inflammation and sexually transmitted infection acquisition: Contribution of the non-human primate model to a better understanding? *Front Reprod Heal* [Internet]. 2022;4. Available from: <https://www.frontiersin.org/articles/10.3389/frph.2022.992176/full>
- 80 Bhatia NY, Jalgaonkar MP, Hargude AB, Sherje AP, Oza MJ, Doshi GM. Gut-brain axis and neurological disorders-how microbiomes affect our mental health. *CNS Neurol Disord - Drug Targets* [Internet]. 2023;22(7):1008–30. Available from: <https://www.eurekaselect.com/207885/article>
- 81 Liu L, Wang H, Chen X, Zhang Y, Zhang H, Xie P. Gut microbiota and its metabolites in depression: from pathogenesis to treatment. *eBioMedicine* [Internet]. 2023;90:104527. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2352396423000920>
- 82 Dziedzic A, Maciąk K, Bliżniewska-Kowalska K, Gałecka M, Kobierecka W, Saluk J. The power of psychobiotics in depression: a modern approach through the microbiota–gut–brain axis: a literature review. *Nutrients* [Internet]. 2024;16(7):1054. Available from: <https://www.mdpi.com/2072-6643/16/7/1054>
- 83 Ji J, Jin W, Liu S, Jiao Z, Li X. Probiotics, prebiotics, and postbiotics in health and disease. *MedComm* [Internet]. 2023;4(6). Available from: <https://onlinelibrary.wiley.com/doi/10.1002/mco.2.420>
- 84 Chaudhari A, Dwivedi MK. The concept of probiotics, prebiotics, postbiotics, synbiotics, nutribiotics, and pharmabiotics. In: *Probiotics in the Prevention and Management of Human Diseases* [Internet]. Elsevier; 2022. p. 1–11. Available from: <https://linkinghub.elsevier.com/retrieve/pii/B9780128237335000131>
- 85 Fijan S. Microorganisms with claimed probiotic properties: an overview of recent literature. *Int J Environ Res Public Health* [Internet]. 2014;11(5):4745–67. Available from: <https://www.mdpi.com/1660-4601/11/5/4745>
- 86 Zheng Y, Zhang Z, Tang P, Wu Y, Zhang A, Li D, et al. Probiotics fortify intestinal barrier function: a systematic review and meta-analysis of randomized trials. *Front Immunol* [Internet]. 2023;14. Available from: <https://www.frontiersin.org/articles/10.3389/fimmu.2023.114354/full>
- 87 Mazzotta C, Tognon M, Martini F, Torreggiani E, Rotondo JC. Probiotics mechanism of action on immune cells and beneficial effects on human health. *Cells* [Internet]. 2023;12(1):184. Available from: <https://www.mdpi.com/2073-4409/12/1/184>
- 88 Plaza-Díaz J, Ruiz-Ojeda FJ, Gil-Campos M, Gil A. Mechanisms of action of probiotics. *Adv Nutr* [Internet]. 2019;10:S49–66. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2161831322001995>
- 89 García-Santos JA, Nieto-Ruiz A, García-Ricobaraza M, Cerdó T, Campoy C. Impact of probiotics on the prevention and treatment of gastrointestinal diseases in the pediatric population. *Int J Mol Sci* [Internet]. 2023;24(11):9427. Available from: <https://www.mdpi.com/1422-0067/24/11/9427>
- 90 Sharma S, Kumar S, Sajjad S, Sharma S. Probiotics in irritable bowel syndrome: a review article. *Cureus* [Internet]. 2023. Available from: <https://www.cureus.com/articles/125889-probiotics-in-irritable-bowel-syndrome-a-review-article>
- 91 Abavisan M, Ebadpour N, Khoshrou A, Sahebkar A. Boosting vaccine effectiveness: the groundbreaking role of probiotics. *J Agric Food Res* [Internet]. 2024;16:101189. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2666154324002266>
- 92 Davani-Davari D, Negahdaripour M, Karimzadeh I, Seifan M, Mohkam M, Masoumi S, et al. Prebiotics: definition, types, sources, mechanisms, and clinical applications. *Foods* [Internet]. 2019;8(3):92. Available from: <https://www.mdpi.com/2304-8158/8/3/92>
- 93 Gibson GR, Probert HM, Loo J Van, Rastall RA, Roberfroid MB. Dietary modulation of the human colonic microbiota: updating the concept of prebiotics. *Nutr Res Rev* [Internet]. 2004;17(2):259–75. Available from:
- 94 Roy S, Dhaneshwar S. Role of prebiotics, probiotics, and synbiotics in management of inflammatory bowel disease: Current perspectives. *World J Gastroenterol* [Internet]. 2023;29(14):2078–100. Available from: <https://www.wjgnet.com/1007-9327/full/v29/i14/2078.htm>
- 95 Adebola OO, Corcoran O, Morgan WA. Prebiotics may alter bile salt hydrolase activity: Possible implications for cholesterol metabolism. *PharmaNutrition* [Internet]. 2020;12:100182. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2213434420300074>
- 96 Mishra P, Badiyanvi VM, Jain S, Subramanian S, Maharaj SV, Kumar A, et al. Prebiotics: Ignored player in the fight against cancer. *Cancer Rep* [Internet]. 2023;6(11). Available from: <https://onlinelibrary.wiley.com/doi/10.1002/cnr.21870>
- 97 Lockyer S, Stanner S. Prebiotics – an added benefit of some fibre types. *Nutr Bull*. 2019;44(1):74–91.
- 98 Gupta S, Allen-Vercoe E, Petrof EO. Fecal microbiota transplantation: in perspective. *Therap Adv Gastroenterol* [Internet]. 2016;9(2):229–39. Available from: <http://journals.sagepub.com/doi/10.1177/1756283X15607414>
- 99 Soveral LF, Korczagin GG, Schmidt PS, Nunes IS, Fernandes C, Zárate-Bladés CR. Immunological mechanisms of fecal microbiota transplantation in recurrent Clostridioides difficile infection. *World J Gastroenterol* [Internet]. 2022;28(3):4762–72. Available from: <https://www.wjgnet.com/1007-9327/full/v28/i3/4762.htm>
- 100 Boicean A, Birlutiu V, Ichim C, Anderco P, Birsan S. Fecal microbiota transplantation in inflammatory bowel disease. *Biomedicines* [Internet]. 2023;11(4):1016. Available from: <https://www.mdpi.com/2227-9059/11/4/1016>
- 101 Abdelghafar YA, AbdelQadir YH, Motawea KR, Nasr SA, Omran HAM, Belal MM, et al. Efficacy and safety of fecal microbiota transplant in irritable bowel syndrome: An update based on meta-analysis of randomized control trials. *Heal Sci Reports* [Internet]. 2022;5(5). Available from: <https://onlinelibrary.wiley.com/doi/10.1002/hsr2.814>
- 102 Zhang Z, Mocanu V, Cai C, Dang J, Slater L, Deehan EC, et al. Impact of fecal microbiota transplantation on obesity and metabolic syndrome—a systematic review. *Nutrients* [Internet].

- 2019;11(10):2291. Available from: <https://www.mdpi.com/2072-6643/11/10/2291>
- 103 van Heijst BF, Deserno MK, Rhebergen D, Geurts HM. Autism and depression are connected: A report of two complimentary network studies. *Autism* [Internet]. 2020;24(3):680–92. Available from: <http://journals.sagepub.com/doi/10.1177/1362361319872373>
- 104 Fu J, Zheng Y, Gao Y, Xu W. Dietary fiber intake and gut microbiota in human health. *Microorganisms* [Internet]. 2022;10(12):2507. Available from: <https://www.mdpi.com/2076-2607/10/12/2507>
- 105 Zhang P. Influence of foods and nutrition on the gut microbiome and implications for intestinal health. *Int J Mol Sci* [Internet]. 2022;23(17):9588. Available from: <https://www.mdpi.com/1422-0067/23/17/9588>
- 106 Di Rosa C, Di Francesco L, Spiezia C, Khazrai YM. Effects of animal and vegetable proteins on gut microbiota in subjects with overweight or obesity. *Nutrients* [Internet]. 2023;15(12):2675. Available from: <https://www.mdpi.com/2072-6643/15/12/2675>
- 107 Wang X, Qi Y, Zheng H. Dietary polyphenol, gut microbiota, and health benefits. *Antioxidants* [Internet]. 2022;11(6):1212. Available from: <https://www.mdpi.com/2076-3921/11/6/1212>
- 108 Sohal MJ, Yassine HM, Sohal A, Thani AAA. Impact of physical exercise on gut microbiome, inflammation, and the pathobiology of metabolic disorders. *Rev Diabet Stud* [Internet]. 2019;15(1):35–48. Available from: <https://www.ingentaconnect.com/content/10.1900/RDS.2019.15.35>
- 109 Withrow D, Bowers SJ, Depner CM, González A, Reynolds AC, Wright KP. Sleep and circadian disruption and the gut microbiome-possible links to dysregulated metabolism. *Curr Opin Endocr Metab Res* [Internet]. 2021;17:26–37. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2451965020301320>
- 110 Madison A, Kiecolt-Glaser JK. Stress, depression, diet, and the gut microbiota: human–bacteria interactions at the core of psychoneuroimmunology and nutrition. *Curr Opin Behav Sci* [Internet]. 2019;28:105–10. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S2352154618301608>
- 111 Patangay DV, Anthony Ryan C, Dempsey E, Paul Ross R, Stanton C. Impact of antibiotics on the human microbiome and consequences for host health. *Microbiologyopen* [Internet]. 2022;11(1). Available from: <https://onlinelibrary.wiley.com/doi/10.1002/mbo3.1260>
- 112 Tabrett A, Horton MW. The influence of host genetics on the microbiome. *F1000Research* [Internet]. 2020;9:84. Available from: <https://f1000research.com/articles/9-84/v1>
- 113 Ahn J, Hayes RB. Environmental influences on the human microbiome and implications for noncommunicable disease. *Annu Rev Public Health* [Internet]. 2021;42(1):277–92. Available from: <https://www.annualreviews.org/doi/10.1146/annurev-pubhealth-012420-105020>
- 114 Nagpal R, Mainali R, Ahmadi S, Wang S, Singh R, Kavanagh K, et al. Gut microbiome and aging: Physiological and mechanistic insights. *Nutr Heal Aging* [Internet]. 2018;4(4):267–85. Available from: <https://www.medra.org/servlet/aliasResolver?alias=iospress&doi=10.3233/NHA-170030>
- 115 Cho J-C. Human microbiome privacy risks associated with summary statistics. Oliveira PH, editor. *PLoS One* [Internet]. 2021;16(4):e0249528. Available from: <https://dx.plos.org/10.1371/journal.pone.0249528>
- 116 Kadam R. Informed consent process: a step further towards making it meaningful! *Perspect Clin Res* [Internet]. 2017;8(3):107. Available from: [https://journals.lww.com/10.4103/picr.PICR\\_147\\_16](https://journals.lww.com/10.4103/picr.PICR_147_16)
- 117 Ma Y, Chen H, Lan C, Ren J. Help, hope and hype: ethical considerations of human microbiome research and applications. *Protein Cell* [Internet]. 2018;9(5):404–415. Available from: <https://academic.oup.com/proteincell/article/9/5/404/6760111>
- 118 Foxx AJ, Franco Meléndez KP, Harirharan J, Kozik AJ, Wattenburger CJ, Godoy-Vitorino F, et al. Advancing equity and inclusion in microbiome research and training. Wolfe BE, editor. *mSystems* [Internet]. 2021;6(5). Available from: <https://journals.asm.org/doi/10.1128/mSystems.01151-21>
- 119 Manalisidis I, Stavropoulou E, Stavropoulos A, Bezirtzoglou E. Environmental and health impacts of air pollution: a review. *Front Public Heal* [Internet]. 2020;8. Available from: <https://www.frontiersin.org/article/10.3389/fpubh.2020.00014/full>
- 120 Kashyap PC, Chia N, Nelson H, Segal E, Elinav E. Microbiome at the frontier of personalized medicine. *Mayo Clin Proc* [Internet]. 2017;92(12):1855–64. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S0025619617307322>
- 121 Zhou X, Shen X, Johnson JS, Spakowicz DJ, Agnello M, Zhou W, et al. Longitudinal profiling of the microbiome at four body sites reveals core stability and individualized dynamics during health and disease. *Cell Host Microbe* [Internet]. 2024;32(4):506–526. e9. Available from: <https://linkinghub.elsevier.com/retrieve/pii/S1931312824000568>
- 122 Dey D, Mekala LP, Mohammed M. Integrating omics technologies to understand microbial systems. In: *Omics Technologies for Sustainable Agriculture and Global Food Security Volume 1* [Internet]. Singapore: Springer Singapore; 2021:191–212. Available from: [https://link.springer.com/10.1007/978-981-16-0831-5\\_9](https://link.springer.com/10.1007/978-981-16-0831-5_9)
- 123 Stockdale JE, Liu P, Colijn C. The potential of genomics for infectious disease forecasting. *Nat Microbiol* [Internet]. 2022;7(11):1736–43. Available from: <https://www.nature.com/articles/s41564-022-01233-6>
- 124 Charbonneau MR, Isabella VM, Li N, Kurtz CB. Developing a new class of engineered live bacterial therapeutics to treat human diseases. *Nat Commun* [Internet]. 2020;11(1):1738. Available from: <https://www.nature.com/articles/s41467-020-15508-1>
- 125 Lin DM, Koskella B, Lin HC. Phage therapy: an alternative to antibiotics in the age of multi-drug resistance. *World J Gastrointest Pharmacol Ther* [Internet]. 2017;8(3):162. Available from: <http://www.wjgnet.com/2150-5349/full/v8/13/162.htm>
- 126 Yang HJ, Kim JH. Role of microbiome and its metabolite, short chain fatty acid in prostate cancer. *Investig Clin Urol* [Internet]. 2023;64(1):3. Available from: <https://icurology.org/DOIx.php?id=10.4111/icu.20220370>
- 127 Shin Y, Han S, Kwon J, Ju S, Choi T, Kang I, et al. Roles of short-chain fatty acids in inflammatory bowel disease. *Nutrients* [Internet]. 2023;15(20):4466. Available from: <https://www.mdpi.com/2072-6643/15/20/4466>