

## Microbiome Components, Functions and Uses

Álvaro Zamudio Tiburcio<sup>1\*</sup>, Héctor Bermúdez Ruiz<sup>2</sup> and Silverio Alonso López<sup>3</sup>

<sup>1</sup>Gastroenterologist, Intestinal Microbiota Transplantation, Mexico City, Mexico

<sup>2</sup>Endoscopy Service, Oncology Hospital, National Medical Center, XXI Century, Mexican Social Security Institute, Hospital Trinidad, Mexico City, Mexico

<sup>3</sup>Urologist, Chairman Medical Specialties Naples in Mexico City, Mexico

\*Corresponding Author: Álvaro Zamudio Tiburcio, Gastroenterologist, Intestinal Microbiota Transplantation, Mexico City, Mexico.

Received: June 23, 2022; Published: September 23, 2022

### Abstract

We carried out a comprehensive analysis of the microbiome and its components. This analysis includes all the microorganisms that make it up and the relationships between them and as a whole. Here we also highlighted the importance of viruses, in that they are the largest group, although it's currently the least known. The final piece of our analysis contained the determinants for the different bacterial phylos.

Incorporated in the review are bacteriophages, eukaryotic and giant viruses, as well as archaea, parasites and fungi.

We also concluded on the rational use of the microbiome, as well as its different units. Within these units are probiotics, prebiotics, symbiotics, postbiotics, paraprotiotics, FIF, microbiota transplantation and inactive bacterial cells.

Pointed out is the future that bacteriophages possess as a therapy in different ailments and the substitution that can be made of antibiotics for them, along with giving a turn to the constant resistance that these drugs produce.

**Keywords:** Microbiome (Mic); Intestinal Microbiota (IM); Fecal Microbiota Transplant (FMT); Intestinal Microbiota Transplant (IMT)

### Introduction

#### Microbiome

On April 1, 2001, Joshua Lederberg introduced the world of Microbiome (Mic), defining it as the ecological community of commensal, symbiotic and pathogenic microorganisms that share our body space and have been ignored as determinants of health or disease [1]. Human microbiota presents itself as around 900 or 1000 different species of microorganisms (Extraordinary diversity of genomes) [2]. In the intestinal microbiota (IM), the most important component of the microbiota, located in the colon and rectum, inhabit microorganisms that exceed 10<sup>14</sup> [3]. The Mic has been related to a significant series of functions in a new organ, which affects health and immunological functions [4]. Neurological metabolism [5] connects to the "gut-brain axis" through many different systems.

#### Gut microbiota

Gut microbiota is the most important of all microbiota given its volume in microorganisms. It is defined as the set of microorganisms that live in the intestine, especially the colon and rectum. Among the most significant processes of IM are inflammatory bowel disease

[7], gastric cancer [8], colorectal cancer [9], cardiovascular disorders [10], cutaneous manifestations, such as psoriasis, acne and atopic dermatitis [11]. These conditions can be developed through lifestyle, stress, antibiotics, certain nutrients in diets, and obesity due to its generation of microorganisms (dysbiosis) [12] and viruses.

### Virus

Microorganisms are composed of genetic material protected by packaging protein. This can lead to various diseases by introducing itself as a parasite in the cell or microorganisms, to reproduce in them [13]. The respiratory system is the system most affected by these viruses, although patients generally have minimal symptoms. Microorganisms are mentioned as the second largest group that makes up the Mic [14].

### Virome

(Set of all viruses found in the human body). Like Mic, the virome is influenced by genetics, diet, stress, obesity, and the administration of antibiotics [15]. The virome's interaction with the Mic is so complex because of how harmful and beneficial it can be. The DNA and RNA viruses that collectively form the intestinal virome outnumber bacterial cells by up to 10 to 1 and include eukaryotic viruses (infected eukaryotic cells), endogenous retroviruses, bacteriophages, and archaeal viruses that infect them [16]. Those viruses are equivalent to bacteria [17]. Their various genomes can consist of linear or circular double-stranded or single-stranded DNA or RNA, while RNA genomes can be positive-sense (translated directly into protein, similar to mRNA) or negative-sense [18]. For their classification, the Baltimore scheme is useful, where they are grouped according to the composition of their genomes and their method for genome replication. This scheme is particularly useful, as the viral genome will often be reflected in its method for replication, gene expression, and life cycle [19].

### Bacteriophages

Bacteriophages are viruses that most frequently infect prokaryotic organisms (bacteria and archaea) [20]. They are the predominant biological organisms on earth: Prokaryotes, archaea and bacteria, hence their enormous importance [21]. Many of them have an icosahedral head composed of repeating protein subunits known as capsids. These viruses contain this viral genome [22]. Their main difference is the presence or absence of a "tail" structure [23]. Phages, like other eukaryotic viruses, have two distinct life cycles. These are the lytic cycle: a productive process leading to the synthesis of new phage particles, and the lysogenic cycle: a "silent" stage in which the phage genome integrates with the host chromosome [24]. It remains there for many generations and can return to the lytic cycle through the stimulation of gene expression [25]. Currently, around 5,500 different phages that can infect one or several types of bacteria have been discovered [26]. In the lysogenic cycle, they are represented by three families: Caudovirales, Myoviridae and Siphoviridae [27]. There are also intestinal localization phages and pseudolysogenic phages.

### Intestinal phages

Viruses located in the intestine exclusively infect prokaryotic organisms [28]. They are part of the intestinal virome and although they are generally enemies of bacteria, they can also help them seek health, an example of this, is *Clostridium* [29]. Since the discovery of intestinal phages by d'Hérelle in 1917, the understanding of their impact on IM structure remains weak [30]. Viruses, fundamentally bacteriophages, are found as intestinal virome, a component of the intestinal microbiota [31]. There is considerable diversity among phages, but 95% of them are non-enveloped-tailed dsDNA phages, or Caudovirales [32].

### Pseudolysogenic phages

False state in which a phage with DNA genome maintains a latent or persistent, non-lytic relationship with the host bacterium [33]. This makes understanding bacteriophages a little more difficult. Next, we will analyze two of the three domains of living organisms (Archaea and Eukaryotes, attached to viruses), not including bacteria, which are analyzed last.

### Archaeal viruses

Archaeal viruses are unicellular and ribosomal structured organisms. They differentiate from bacteria and eukaryotes due to some of their introns in the genome, as well as the different components of the membrane [34]. Introns along with exons are a series of nucleotides within a gene [35]. The archaeal virus phyllo is constituted by: Crenarchaeota, Euryarchaeota, Korarchaeota, Nanoarchaeota and Thaumarchaeota [36]. The Thaumarchaeota are present in many habitats, where they carry out the aerobic oxidation of ammonia and are a key step in the nitrogen cycle [37]. The record of these microorganisms extends as far back as the geological pattern and the beginning of the organic origins of the Earth [38].

### Eukaryotic viruses

(Bacteriophages or simply phages). They are the genes of viruses and bacteriophages that inhabit an ecosystem, either as microorganisms free or in the form of intracellular inclusions in the cytoplasm or integrated into chromosomes [39]. Within eukaryotic cells, dsRNA is a strong inducer of antiviral defense [40]. Each family of viruses has its own way of entering, replicating, and exiting the host cell [41]. Although many families use similar media at different stages of the replication cycle [42]. Eukaryotic RNA Viruses account for most of the diversity of the virome [43]. Double-stranded RNA viruses are derived from dsRNA bacteriophages or positive-stranded RNA viruses [44].

### Giant viruses

There is still much more to know about viruses. For example, giant viruses are arbitrarily defined as microorganisms that infect eukaryotes with at least 500 protein-coding genes [45]. The first of them, *Acanthamoeba polyphaga* mimivirus, was discovered in 2003 [46]. It is considered that 19 eukaryotic giant viruses are its representatives [47] and that they were authentic living beings [48]. In the interrelation of giant viruses and Mic, it was observed that they encode a wide range of proteins, with putative functions in photosynthesis, as well as diverse processes in the transport of substrates. These viruses are surely associated with most eukaryotic lineages [49].

### Bacteria

The first component of the Mic. is the prokaryotic, unicellular, and micrometric microorganisms with various shapes: rods (bacillus), spheres (coccus), helical rods (spirillum), or curved filaments [50]. Their genomes are double-stranded circular DNA [51]. They reproduce in a process known as binary fission [58]. Allowing them to be Gram-negative or positive [52]. The interrelation of bacteria with Mic is multiple, highlighting the impact that diet has in the first years of life [53], influencing metabolic changes, alterations of the immune system and metabolism [54], through MI metabolites and host receptors by the gut-brain axis [55]. In addition to that, if there is dysbiosis, there could be cognitive disorders [56]. As well as behavioral problems [57]. Molecular techniques have shown that the diversity of IM is much greater than that demonstrated in cultures [58]. The taxa range is between 100 and 300 and pyrosequencing thousands of phylogenotypes [59]. The most detected phyllo are *Bacteroidetes*, *Firmicutes*, *Proteobacteria* and *Actinobacteria*. The lesser extent *Verrucomicrobia*, *Tenericutes*, *Fusobacteria*, *Spirochaetes* and *Cyanobacteria* [60]. These phyllos can produce airborne spores that can infect another person [61].

### Parasites

An organism that lives on or in a host and feeds at its expense [62]. There are three major classes: protozoa, helminths, and ectoparasites [63]. Examples of protozoa are the *Amoeba* and *Plasmodium* [64]. Helminths are simple invertebrates, some of them infectious parasites. *Schistosoma* causes severe disease [65]. Although hepatic or splenic involvement is not common, it is a concern [66]. Another example is *Trichinella spiralis*, which can trigger heart failure and respiratory paralysis [67]. The relationship between gastrointestinal parasites and the gut microbiota may have an impact on health [68]. This occurs through changes in the environment, which determines

alterations in the composition of the IM [69]. And it is demonstrated, in gorillas, by significant differences after MI characterization by pyrosequencing [70].

### Ectoparasites

They live on the surface of a host [71]. Examples: flies, ticks, lice, mange mites [72]. Behavioral alterations due to infection by ectoparasites such as louse flies (Diptera: Hoppoboscidae) are known [73]. And migratory taxa can influence the spread of long-term survival as well as reproductive success in birds [74]. The louse fly microbiome is dominated by primary endosymbionts, host species, that can affect both insect vectors and their avian hosts [75]. Due to their enormous resemblance to viruses and bacteria, although with substantial differences, we include Prions (infectious protein particles) [76]. Their misfolded protein is capable of transmitting its morphology to another protein and producing transmissible spongiform encephalopathies [77]. They are considered infectious agents that destroy nucleic acids in contrast to bacteria and viruses [78].

Wild type proteins in abnormal and misfolded  $\beta$ -sheet shapes such as cellular prion protein or amyloid beta are considered to be disease-causing [79]. The seeding of protein aggregates has been adduced as a producer of neurodegenerative disorders, including Parkinson's [80].

### Fungus

Eukaryotic heterophobic organisms with rigid cell walls made of cellulose or chitin. They reproduce by forming spores [81]. Some of them are unicellular, although most are multicellular [82]. Fungi and bacteria decompose the environment [83]. Example diseases of its infection are histoplasmosis, vaginal candidiasis and some thrush [84]. The use of antibiotics causes the yeast to grow uncontrollably [85]. Sequencing has also allowed the study of the Mycobiome, which influences health and susceptibility to diseases and immunity [86]. Well, all the organisms described must be evaluated at the same time, considering their ways of acting, as well as their interactions, in order to reduce the impact that all of them cause; which is not always harmful [87]. The Intestinal Microbiota is very sensitive in the contact and communication between the individual and the external environment. For perfect homeostasis to exist, it must clearly distinguish between pathogens or potential pathogens, on the one hand, and commensal microorganisms in symbiosis with the host, on the other. In the first case, the IM must employ adequate defense elements and in the second case, it has to learn to tolerate, in order to obtain the benefit of the symbiosis [88]. Although some microorganisms stand out in importance in their functions such as the Intestinal Microbiota with its bacteria carrying viruses, they all count.

### Probiotics, prebiotics and synbiotics

They have been tested in many circumstances for their good effects [89]. For example, Bifidobacteria, as beneficial organisms and with a large presence in the gut microbiota, are associated with the non-persistent lactase phenotype, helping to digest lactose, immersed in milk [90]. On the other hand, probiotics have been used in viral diarrhea; specifically, *Lactobacillus rhamnosus* GG, affecting rotavirus attenuation [91]. Psychological stress can be reversed with the use of probiotics [92]. *Saccharomyces boulardii* is one of the most studied probiotics; reduces the risk of diarrhea due to antibiotics, both in children and in adults [93]. It reduces diarrhea due to *Clostridium difficile* and its use is moderately evidenced, trying to be administered together with antibiotics, at doses of 250 to 1000 milligrams in adults and a maximum of 500 milligrams in children [94]. *Lactobacillus*, combined with enterococci or *Saccharomyces boulardii* or alone, reduces antibiotic-induced diarrhea [95]. In relation to the use of probiotics in *C. difficile* disorder, it has been argued that *Saccharomyces boulardii* reduces its incidence [96], although there is no unanimous opinion among the different authors [97]. The European Society for Pediatric Gastroenterology, Hepatology and Nutrition recommends *Lactobacillus rhamnosus* GG and *Saccharomyces boulardii* in children with acute gastroenteritis [98]. The administration of *Lactobacillus acidophilus* or *Lactobacillus casei* improves the eradication of *Helicobacter pylori*, simultaneously using antibiotics [99].

### Bacteriophages treatment

The idea of using bacteriophages to treat Infections has been known since Frederik Twort [100] and Felix d'Hérelle [146] discovered bacterial viruses. Phages infect bacteria and not eukaryotic cells [101]. There are several countries that use bacteriophages as a treatment for bacterial infections, including Georgia, Russia and Poland [102]. Currently, lytic bacteriophages are making a comeback, especially in multiresistant infections [103]. Phages are commonly used in cocktails [104]. Their usage has decreased the presence of *Staphylococcus*, *Pseudomonas*, *Escherichia*, *Klebsiella* and *Proteus* in Eastern countries [105]. The proteins that the phages encode (endolysins, exopolysaccharides and holins) are promising antibacterials [106].

### Post-biotics

Bioactive compounds can be used to promote health and are generated in a matrix during fermentation [107]. Either probiotic metabolites or components resulting from the fermentation of probiotics in the intestine [108]. Some foods that can help increase the concentration of post-biotics in the gut: Sauerkraut, kefir, sourdough bread, pickles, soft cheeses, millet soup, buttermilk, tempeh and yogurt [109].

### Pili

Pili are mainly composed of oligomeric pilin proteins, they are arranged helically to form a cylinder [110]. There is a conviction of the beneficial effect of postbiotics, even in healthy people [111]. They relieve infant colic, different types of diarrhea and atopic dermatitis.

### Para-probiotics

Inactivated (non-viable) microbial cells that confer health benefits to consumers. They regulate adaptive and innate systems, being anti-oxidant, anti-proliferative, and anti-inflammatory. They are safe and can be used on the disabled or elderly. They are included in the group of nutraceuticals [112].

### FIF or fortified food formula

It has been suggested that they can be very suitable for children around 5 years, however, we must not forget the dietary diversity, based around vegetables [113].

### Dormant bacterial cells

Bacteria can exist in states metabolically inactive, allowing them to survive conditions that are not conducive to growth. Such dormant bacterial cells can feel when conditions have improved and restart growth, otherwise, they would be affected by their neighbors. We will soon see a new therapy, that of inactive bacterial cells, as has already been tested in some types of cancer [114].

### Fecal microbiota transplant (FMT)

Its effectiveness in infection have been proven in recurrence due to *Clostridium difficile*, with successes of up to more than 90% [115]. In inflammatory bowel disease, especially chronic ulcerative colitis nonspecific improvement has also been noted with the IMT, as in the irritable bowel syndrome and neurodevelopmental disorders [116]. For perform the TMI, we must not forget the recommendations of the FDA, in relation to with the great COVID-19 pandemic [117].

### Conclusion:

- Further investigation of the interconnectivity of the virome with other elements of the microbiome is essential to fully define the role of the gut virome in human health.

- The current therapeutic arsenal to modulate the microbiome is broader every day since we have: probiotics, prebiotics, symbiotics, bacteriophages (phages), postbiotics, paraprobiotics, FIFs, intestinal microbiota transplant, and inactive bacterial cells.
- If someone manages to get different experts from the Microbiome to work together, such as virologists, microbiologists, parasitologists, geneticists, immunologists, gastroenterologists, neurologists, etc. We will not only be able to achieve substantive progress, but we will also achieve new knowledge in favor of not only human health.
- It is useful to reduce the intake of carbohydrates and fats; and, if possible, swallow precursors of intestinal postbiotics.
- Administer antibiotics only rationally.
- Learn to manage your stress, either with physical exercise, according to your circumstances, or with specific mental activities.
- Help decrease the number of cesarean sections.

### Conflicts of Interest

The authors declare that do not have affiliation or participation in organizations with financial interests.

### Ethical Approval

This report does not contain any study with human or animal subjects carried out by the authors.

### Informed Consent

The authors obtained informed written consent from the patients, in order to develop this article.

### Bibliography

1. Lederberg J and McCray A. "Ome sweet 'omics: -- A genealogical treasury of words". *The Scientist* 15.7 (2001): 8.
2. Thursby E and Juge N. "Introduction to the human gut microbiota". *Biochemical Journal* 474.11 (2017): 1823-1836.
3. Hillman ET, *et al.* "Microbial Ecology along the Gastrointestinal Tract". *Microorganisms in Environmental* 32.4 (2017): 300-313.
4. Belkaid Y and Hand T. "Role of the Microbiota in Immunity and inflammation". *Cell* 157.1 (2014): 121-141.
5. Visconti A., *et al.* "Interplay between the human gut microbiome and host metabolism". *Nature Communicatos* 10.4505 (2019).
6. Anadure RK., *et al.* "The Gut-brain Axis". February 2019/02/16. In book: API Textbook of Medicine (2019): 1-5.
7. Jandhyala SM., *et al.* "Role of the normal gut microbiota". *World Journal of Gastroenterology* 21.29 (2015): 8787-8803.
8. Brawner KM., *et al.* "Gastric Microbiome and Gastric Cancer". *The Cancer Journal* 20.3 (2014): 211-216.
9. Wong SH and Yu J. "Gut microbiota in colorectal cancer: mechanisms of action And clinical applications nature reviews". *Gastroenterology and Hepatology* 16 (2019): 690-704.
10. Kazemian N., *et al.* "Gut microbiota And cardiovascular disease: opportunities and challenges". *Microbiome* 8.36 (2020).
11. Salem I., *et al.* "The Gut Microbiome as a Major Regulator of the Gut-Skin Axis". *Frontiers in Microbiology* 9 (2018): 1459.

12. Harakeh SM., *et al.* "Gut Microbiota: A Contributing Factor to Obesity". *Frontiers in Cellular and Infection Microbiology* 6 (2016): 95.
13. Vidyasagar A. "What Are Viruses?" *Lives Science* (2016).
14. Robinson CM and Pfeiffer JK. "Viruses and the Microbiota". *Annual Review of Virology* 1 (2014): 55-69.
15. Langdon A., *et al.* "The effects of antibiotics on the Microbiome". *Genome Medicine* 8 (2016): 39.
16. Clemente JC., *et al.* "The Impact of the Gut Microbiota on Human Health: An Integrative View". *Cell* 148.6 (2012): 1258-1270.
17. Sender R., *et al.* "Revised Estimates for the Number of Human And Bacteria Cells in the Body". *Plos Biology* (2016).
18. Aseervatham J. "How to calculate the Multiplicity of infection (MOI)?" *Research Gate* (2016).
19. Lefkowitz EJ., *et al.* "Virus taxonomy: the database of the International Committee on Taxonomy of Viruses (ICTV)". *Nucleic Acids Research* 46.D1 (2018): D708-D717.
20. Kaman LM and Porter LD. "Bacteriophages". *Stat Pearls* (2020).
21. Grose JH and Casjens SR. "Understanding the enormous diversity of Bacteriophage: the tailed phages that infect the bacterial family Enterobacteriaceae". *Virology* (2014): 421-443.
22. Drulis-Kawa Z., *et al.* "Learning from Bacteriophages - Advantages and Limitations of Phage and Phage-Encoded Protein Applications". *Current Protein and Peptide Science* 13.8 (2012): 699-722.
23. Prasad BV and Schmid MF. "Principles of Virus Structural Organization". *Viral Molecular Machines* 726 (2012): 17-47.
24. Veesler D and Cambillau C. "A Common Evolutionary Origin for Tailed- Bacteriophage". *Microbiology and Molecular Biology Reviews* 75.3 (2011): 423-433.
25. Clokie RJ., *et al.* "Phages in nature". *Bacteriophage* 1.11 (2011): 31-45.
26. Jorquera D., *et al.* "The challenge of controlling Foodborne Diseases: bacteriophages as a new biotechnological tool". *Revista Chilena de Infectologia* 32.6 (2015): 678-688.
27. Hsiao WL., *et al.* "The Microbes of the Intestine: An Introduction to Their Metabolic and Signaling Capabilities". *Endocrinology and Metabolism Clinics of North America* 37.4 (2008): 857-871.
28. Sartor RB and Wu GD. "Roles for Intestinal Bacteria, Viruses, and Fungi in Pathogenesis of Inflammatory Bowel Diseases and Therapeutic Approaches". *Gastroenterology* 152.2 (2017): 327-339.
29. Andrews KJ. "Understanding Emerging and Re-emerging Infectious Diseases". *NIH Curriculum Supplement Series* (1999).
30. Fruciano E. "Phage as an antimicrobial agent: d'Herelle's heretical theories And their role in the decline of phage prophylaxis in the West". *Canadian Journal of Infectious Diseases and Medical Microbiology* 18.1 (2007): 19-26.
31. Garmaeva S., *et al.* "Studying the gut virome in the metagenomic era: challenges and Perspectives". *BMC Biology* 17 (2019): 84.
32. Hatfull GF. "Dark Matter of the Biosphere: the Amazing World of Bacteriophage Diversity". *Journal of Virology* 89.16 (2015): 8107-8110.

33. Sausset R., *et al.* "New insights into Intestinal phages". *Mucosal Immunology* 13 (2020): 205-215.
34. Cenens W., *et al.* "Phage–host Interactions during pseudolysogeny". *Bacteriophage* 3.1 (2013): e25029.
35. Krupovic M., *et al.* "Viruses of archaea: Structural, functional, environmental and evolutionary Genomics". *Virus Research* 244 (2018): 181-193.
36. Paggi JM., *et al.* "Numerous recursive sites Contribute to accuracy of splicing in long introns in flies". *PLOS Genetics* 14.8 (2018): e1007588.
37. Pester M., *et al.* "The Thaumarchaeota: an emerging view of their phylogeny and ecophysiology". *Current Opinion in Microbiology* 14.3 (2011): 300-306.
38. Cavalier-Smith T. "The phagotrophic origin of eukaryotes and phylogenetic Classification of Protozoa". *International Journal of Systematic and Evolutionary Microbiology* 52.2 (2): 297-354.
39. Keen EC and Dantas G. "Close Encounters of Three Kinds: Bacteriophages, Commensal Bacteria, and Host Immunity". *Trends in Microbiology* 26.11 (2018): 943-954.
40. Kreuze JF., *et al.* "Viral Class 1 RNase III Involved in Suppression of RNA Silencing". *Journal of Virology* 79.11 (2005): 7227-7238.
41. Hulo C., *et al.* "The Ins and outs of eukaryotic viruses: Knowledge base and ontology of a viral Infection". *PLoS One* 12.2 (2017): e0171746.
42. Chinchar VG. "Replication Of Viruses". *Encyclopedia of Virology* (1999): 1471-1478.
43. Koonin EV., *et al.* "Origins and evolution of viruses of eukaryotes: The ultimate modularity". *Virology* 479-480 (2015): 2-25.
44. Ahlquist P. "Parallels among positive-strand RNA viruses, reverse-Transcribing viruses and double-stranded RNA viruses". *Nature Reviews Microbiology* 4.5 (2006): 371-382.
45. Brandes N and Linial M. "Giant Viruses-Big Surprises". *Viruses* 11.5 (2019): 404.
46. Wessner DR. "Discovery of the Giant Mimivirus". *Nature* 3.9 (2010): 61.
47. Schulz F., *et al.* "Hidden diversity of soil giant viruses". *Nature Communications* 9.4881 (2018).
48. Carrie A. "Could Giant Viruses Be the Origin of Life on Earth?" National Geographic (2014).
49. Schultz F., *et al.* "Giant virus diversity and host interactions through global metagenomics". *Nature* 578.7795 (2020): 432-436.
50. Sapkota A. "Bacterial Sizes, Shapes and Arrangement with Examples". *Microbes Notes* (2020).
51. Krupovic M., *et al.* "Genomics of Bacterial and Archaeal Viruses: Dynamics within the Prokaryotic Virosphere". *Microbiology and Molecular Biology Reviews* 75.4 (2011): 610-635.
52. Binary Fission. *Biology dictionary*. BD Editors (2019).
53. Sizar O and Unakal CG. "Gram Positive Bacteria". *Stat Pearls* (2020).
54. Cerdó T., *et al.* "Early nutrition and gut microbiome: Interrelationship between bacterial metabolism, immune system, brain Structure, and neurodevelopment". *The American Journal of Physiology - Endocrinology and Metabolism* 317.4 (2019): E617-E630.



55. Bretin A., *et al.* "Microbiota and metabolism: what's New in 2018?" *The American Journal of Physiology - Endocrinology and Metabolism* 315.1 (2018): E1-E6.
56. Martin AM., *et al.* "The Influence of the Gut Microbiome on Host Metabolism Through the Regulation of Gut Hormone Release". *Frontiers in Physiology* 10 (2019): 428.
57. Novotný M., *et al.* "Microbiome and Cognitive Impairment: Can Any Diets Influence Learning Processes in a Positive Way?" *Frontiers in Aging Neuroscience* 11 (2019): 170.
58. Luca M., *et al.* "Cognitive-Behavioural Correlates of Dysbiosis: A Review". *International Journal of Molecular Sciences* 21.14 (2020): 4834.
59. National Institutes of Health (US); Biological Sciences Curriculum Study. NIH Curriculum Supplement Series. Bethesda (MD): National Institutes of Health (US); 2007". *Understanding Human Genetic Variation* (2017).
60. Linder P., *et al.* "Taxon sampling effects in molecular Clock dating: An example from the African Restionaceae". *Molecular Phylogenetics and Evolution* 35 (2005): 569-582.
61. Parulekar NN., *et al.* "Characterization of bacterial community associated with phytoplankton Bloom in a eutrophic lake in South Norway using 16S rRNA gene Amplicon sequence analysis". *PLoS One* 12.3 (2017): e0173408.
62. Swick M., *et al.* "Surviving Between Hosts: Sporulation and Transmission". *Microbiology Spectrum* 4.4 (2016).
63. Vlčkova K., *et al.* "Relationships Between Gastrointestinal Parasite Infections and the Fecal Microbiome in Free-Ranging Western Lowland Gorillas". *Frontiers in Microbiology* 9 (2018): 1202.
64. Cao B and Guiton PS. "Important Human Parasites of the Tropics". *Frontiers for Young Md* 6 (2018).
65. Yaeger RG. "Protozoa: Structure, Classification, Growth, and Development". In: Baron S, editor. *Medical Microbiology*. 4th edition. Galveston (TX): University of Texas Medical Branch at Galveston (1996): 77.
66. King CH. "Schistosomiasis: Challenges And Opportunities". In: Institute of Medicine (US) Forum on Microbial Threats. *The Causes And Impacts of Neglected Tropical and Zoonotic Diseases: Opportunities For Integrated Intervention Strategies*". Washington (DC): National Academies Press (US) (2011): A12.
67. WHO. *Schistosomiasis* (2020).
68. Rawla P and Sharma S. "Trichinella Spiralis (Trichinellosis)" (2020).
69. Mejia R., *et al.* "Impact Of intestinal parasites on microbiota and cobalamin gene sequences: a Pilot study". *Parasites and Vectors* 13.200 (2020).
70. Hasan N and Yang H. "Factors affecting the composition of the gut microbiota, And its modulation". *Peer Journal* 7 (2019): e7502.
71. Cummings PJ., *et al.* "Pyrosequencing for Microbial Identification and Characterization". *The Journal of Visualized Experiments* 78 (2013): 50405.
72. McCabe RA., *et al.* "Characterizing the microbiome of ectoparasitic louse flie Feeding On migratory raptors". *PLOS ONE* (2020).

73. Mathinson BA and Pritt BS. "Laboratory Identification of Arthropod Ectoparasites". *Clinical Microbiology Reviews* 27.1 (2014): 48-67.
74. Eeva T., et al. "Species and abundance of ectoparasitic flies (Diptera) in pied Flycatcher nests in Fennoscandia". *Parasites and Vectors* 8.648 (2015).
75. Sturrock AM., et al. "Reconstructing the Migratory Behavior and Long-Term Survivorship of Juvenile Chinook Salmon under Contrasting Hydrologic Regimes". *PLOS ONE* (2015).
76. Gurung K., et al. "The microbiome of pest insects: it is not just bacteria". *Entomologia Experimentalis et Applicata* (2019).
77. D'Argenio V and Sarnataro D. "Microbiome Influence in the Pathogenesis of Prion and Alzheimer's Diseases". *International Journal of Molecular Sciences* (2019): 4704.
78. Poggiolini I., et al. "Prion Protein Misfolding, Strains, and Neurotoxicity: An Update from Studies on Mammalian Prions". *International Journal of Cell Biology* (2013): 910314.
79. Vargas-Parada L and Reynaud E. "Protein Misfolding and Degenerative Diseases". *Nature Education* 3.9 (2010): 28.
80. Kupfer L., et al. "Prion Protein Misfolding". *Current Molecular Medicine* 9.7 (2009): 826-835.
81. Zhou J and Liu B. "Alzheimer's Disease and Prion Protein". *Intractable and Rare Diseases Research* 2.2 (2013): 35-44.
82. González A. "Fungi". In: Gargaud M., et al. (Editions) *Encyclopedia of Astrobiology*. Springer, Berlin, Heidelberg (2011).
83. Biologydictionary.net Editors. "Fungi". *Biology Dictionary, Biology dictionary* (2017).
84. Sam QH., et al. "The Fungal Mycobiome and Its Interaction With Gut Bacteria in the Host". *International Journal of Molecular Sciences* (2017).
85. Frey-Klett P., et al. "Bacterial-Fungal Interactions: Hyphens between Agricultural, Clinical, Environmental, and Food Microbiologists". *Microbiology and Molecular Biology Reviews* 75.4 (2011): 583-609.
86. Vaginal yeast infection (thrush): Overview. *InformedHealth.org*. Created (2022).
87. Tiew PY., et al. "The Mycobiome in Health and Disease: Emerging Concepts, Methodologies and Challenges". *Mycopathologia* 185.2 (2020): 207-231.
88. National Academies of Sciences, Engineering, and Medicine; Division on Earth and Life Studies; Board on Life Sciences; Board on Environmental Studies and Toxicology; Committee on Advancing Understanding of the Implications of Environmental-Chemical Interactions with the Human Microbiome. *Environmental Chemicals, the Human Microbiome, and Health Risk: A Research Strategy*. Washington (DC): National Academies Press (US); 2017 Dec 29. 4, *Current Methods for Studying the Human Microbiome* (2017).
89. Eloje-Fadros EA and Rasko DA. "The Human Microbiome: From Symbiosis to Pathogenesis". *Annual Review of Medicine* 64 (2013): 145-163.
90. Markowiak P Śliżewska. "Effects of Probiotics, Prebiotics, and Synbiotics On Human Health". *Nutrients* 9.9 (2017): 1021.
91. Gerbault P., et al. "Evolution Of lactase persistence: an example of human niche construction". *Philosophical Transactions of the Royal Society B – Journals* 366.1566 (2011): 863-877.

92. Ansari F, *et al.* "The Effects of Probiotics And Prebiotics on Mental Disorders: A Review on Depression, Anxiety, Alzheimer, and Autism Spectrum Disorders". *Current Pharmaceutical Biotechnology* 21.7 (2020).
93. Kelesidis T. "Efficacy and safety of the probiotic *Saccharomyces boulardii* for the prevention and therapy of gastrointestinal disorders". *Therapeutic Advances in Gastroenterology - SAGE Journals* 5.2 (2012): 111-125.
94. Goldenberg JZ, *et al.* "Probiotics for the prevention of *Clostridium difficile*-associated diarrhea in Adults and children". *Cochrane Database of Systematic Reviews* 12 (2017): CD006095.
95. D'Souza AL, *et al.* "Probiotics in prevention of Antibiotic associated diarrhoea: meta-analysis". *British Medical Journal* 324.7350 (2002): 1361.
96. Hickson M. "Probiotics in the prevention of antibiotic-associated diarrhoea And *Clostridium difficile* infection". *Therapeutic Advances in Gastroenterology - SAGE Journals* 4.3 (2011): 185-197.
97. Mills JP, *et al.* "Probiotics for Prevention of *Clostridium Difficile* Infection". *Current Opinion in Gastroenterology* 34.1 (2018): 3-10.
98. Szajewska H, *et al.* "Use of probiotics for management of acute gastroenteritis: a position Paper by the ESPGHAN Working Group for Probiotics and Prebiotics". *Journal of Pediatric Gastroenterology and Nutrition* 58.4 (2014): 531-539.
99. Hernández Hernández A, *et al.* "Novedades en probióticos: evidencias, indicaciones y seguridad". *Pediatría Integral* (2020).
100. Wegh C, *et al.* "Postbiotics And Their Potential Applications in Early Life Nutrition and Beyond". *International Journal of Molecular Sciences* 20.19 (2019): 4673.
101. Lehti TA. "Phagus crossing the border to eukaryotes". *Microbiology* (2017).
102. Sybesma Wilbert, *et al.* "Bacteriophages as Potential Treatment for Urinary Tract Infections". *Frontiers in Microbiology* 7.465 (2016): 11.
103. Tkachev PV, *et al.* "Two Novel Lytic Bacteriophages Infecting *Enterococcus* spp. Are Promising Candidates for Targeted Antibacterial Therapy". *Viruses* 14.4 (2022): 831.
104. Abedon ST, *et al.* "Phage Cocktail Development for Bacteriophage Therapy: Toward Improving Spectrum of Activity Breadth and Depth". *Pharmaceuticals* 14.10 (2021): 1019.
105. Kifelew LG, *et al.* "Efficacy of Lytic Phage Cocktails on *Staphylococcus aureus* And *Pseudomonas aeruginosa* in Mixed-Species Planktonic Cultures And Biofilms". *Viruses* 12.5 (2020): 559.
106. Abdelrahman F, *et al.* "Phage-Encoded Endolysins". *Antibiotics* 10.2 (2021): 124.
107. Frutos MJ. "Non-Dairy Fermented Beverages as Potential Carriers to Ensure Probiotics, Prebiotics, and Bioactive Compounds Arrival to the Gut and Their Health Benefits". *Nutrient* 12.6 (2020): 1666.
108. Hemarajata P and Versalovic J. "Effects of probiotics on gut microbiota: Mechanisms of intestinal immunomodulation and neuro-modulation". *Therapeutic Advances in Gastroenterology - SAGE Journals* 6 (2013): 39-51.
109. Nataraj BH, *et al.* "Postbiotics-parabiotics: the new Horizons in microbial biotherapy and functional foods". *Microbial Cell Factories* 19.168 (2020).

110. Piepenbrink KH and Sundberg EJ. "Motility and adhesion through type IV pili In Gram-positive bacteria". *Biochemical Society Transactions* 44.6 (2016): 1659-1666.
111. Tsilingiri K and Rescigno M. "Postbiotics: What else?" *Beneficial Microbes* 4.1 (2012): 69-75.
112. Siciliano RA, *et al.* "Paraprobiotics: A New Perspective for Functional Foods and Nutraceuticals". *Nutrients* 13.4 (2021): 1225.
113. Happe RP and Gambelli L. "Infant formula". *Specialty Oils and Fats in Food And Nutrition* (2015).
114. Pace JL, *et al.* "Inactivated whole-cell bacterial vaccines: current status and novel Strategies". *Vaccine* 16.16 (1998): 1563-1574.
115. Liubakka A and Vaughn BP. "Clostridium difficile Infection and Fecal Microbiota Transplant". *AACN Advanced Critical Care* 27.3 (2016): 324-337.
116. Wang JW, *et al.* "Fecal Microbiota transplantation: Review and update". *Journal of the Formosan Medical Association* 118.1 (2019): S23-S31.
117. U.S. Food and Drug Administration. Fecal Microbiota for Transplantation: New Safety Information - Regarding Additional Protections for Screening Donors for COVID-19 and Exposure to SARS-CoV-2 and Testing for SARS-CoV-2 (2020).

**Volume 18 Issue 10 October 2022**

**All rights reserved by Álvaro Zamudio Tiburcio, *et al.***