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Beneficial Microorganisms in the Human Body: A Review

Farman Rafeq Ahmed[1], Ali M. Saadi[2]*

1Ministry of Agriculture of Iraq, Iraq

2 Department of Animal Production Techniques, Technical Agricultural College, Northern Technical University, Iraq

***Corresponding author**. Email: ali.mohammed@ntu.edu.iq

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Abstract

Microorganisms are tiny living organisms that are widely distributed in nature. Microorganisms are classified into two main categories: beneficial microorganisms and harmful microorganisms. This review focuses on beneficial microorganisms found in the human body that play an important role in health. Microorganisms are mainly found in the small and large intestines and play a vital role in digestion and metabolism. These organisms, which include bacteria and fungi, secrete enzymes that help break down food and absorb nutrients. In addition, these organisms contribute to the production of certain vitamins and regulate immune system function.

Keywords: Human Body, Microorganisms, Algae, Fungi, Protozoa

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1. Introduction

Microorganisms in the human body are present externally on the skin and internally in the respiratory, reproductive, and gastrointestinal tracts (1). These microbes are increasingly recognized not only as opportunistic pathogens but also for their essential roles in long-term health and well-being (2). Research highlights their importance in vitamin synthesis, immune stimulation, metabolism, and various other functions that promote health maintenance and the prevention of chronic illness (3). The human gastrointestinal tract hosts the most diverse and abundant human-associated microbial population identified to date, encompassing thousands of unique microbial species (4).

2. Overview of Microorganisms

Microorganisms are unicellular prokaryotes characterized by a rigid cell wall that protects the cell cytoplasm. These microorganisms are classified as bacteria with diverse cell shapes, including three primary morphological types: spheres (cocci), rods (bacilli), and spirals (spirilla) (5). Among these, cocci and bacilli predominate as the most common forms. Bacterial growth occurs predominantly by binary fission. The morphology of these microorganisms is distinct and varies in planktonic form according to the specific species (6). Measurements indicate bacterial sizes ranging from 1 to 5 µm in length, with typical diameters spanning 0.1 to 1 µm (7).

2.1. Types of Microorganisms

Microorganisms span a broad range of forms that can be subdivided into prokaryotes and eukaryotes. Prokaryotes include archaea and bacteria, and eukaryotes comprise algae, protozoa, and fungi. A clear distinction between these categories is seen in cell organization: prokaryotes are unicellular

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microorganisms that lack a nuclear membrane, organelles, and a defined nucleus, whereas eukaryotes contain a true nucleus and organelles (8). Viruses, subcellular entities composed of DNA or RNA within a protein coat, also infiltrate the human body (9). Consequently, the human microbiota consists of a huge diversity of microorganisms spanning these different kingdoms (5).

2.2. Microbial Diversity

Microorganisms are categorized into three groups based on cell type and genetic material: bacteria and archaea, which are prokaryotes without a nucleus; and eukaryotes, which possess a membrane-bound nucleus. The term "microorganisms" broadly includes viruses (10). Algae, often used to produce alcoholic beverages and various food products, can be pathogenic parasites causing infections such as red tides and certain skin diseases (11).

Fungi—the largest group of microorganisms—have cell walls containing chitin. While most fungal species do not cause human disease, some exhibit parasitic behavior leading to fungal infections. Conversely, others enhance the immune system and serve as important food supplements, with certain species like molds, yeasts, and mushrooms cultivated for commercial purposes (12).

Protozoa, comprising thousands of species, are divided into four classes based on locomotion: Sarcodina, flagellates, ciliates, and sporozoa. They are predominantly parasites found in marine or freshwater environments and are often transmitted to humans through the ingestion of contaminated food or water (13).

3. Human Microbiome

The human digestive tract, oral cavity, skin, airway system, and urogenital tract are colonized by complex microbial communities collectively defined as microbiota, with their collective genomes referred to as the microbiome (14). The microbiome cohabits and co-evolves with the host, constituting an essential component that influences health by promoting immune system development and systemic homeostasis; it even affects host evolution (15). The host-associated microbiome is therefore a key factor in health and disease (16). Efforts to better comprehend its functional features and the interactions occurring within microbial communities are currently underway, yielding new interesting diagnostic, therapeutic, and preventive strategies (6). The composition of the human gut microbiota has been studied extensively, enabling identification of its main components (17). At the phylum level, Bacteroidetes and Firmicutes account for more than 90% of the total gut microorganisms. Actinobacteria, Proteobacteria, and Verrucomicrobia are other minor components. Among these, the genus Bacteroides deserves special attention, since its representatives contribute both to the stability of the microbiota ecosystem and to the general well-being of the host (10). Eukaryotic organisms represent 2 to 5% of the human gut microbiota. In healthy subjects, the Candida genus is largely predominant and is followed by Saccharomyces and Cladosporium. This general pattern changes when the microbiota is altered. In patients affected by colorectal cancer (CRC), for instance, Candida reaches abundances as high as 70% of the total fungal components (11).

3.1. Definition and Importance

Beneficial microbes coexist in a symbiotic relationship with the human body (18). The collective microbiome occupies a wide variety of ecological niches throughout the body, including the skin, hair, and mucous membranes (19). The gastrointestinal tract hosts the most diverse and dynamic population of microbes in the body. Nearly 99% of these microbes are bacteria encompassing about 1,000 species (20). They embody several crucial functions related to digestive and immunological health and also play a significant role in metabolism (21).

Microorganisms are ubiquitous, and the sphere of life where they rule comprises environments as diverse as hydrothermal vents and microhabitats on the human body. They can survive even in the most extreme conditions and have evolved complex transduction mechanisms, as well as the ability to swap genetic information across species barriers. Microorganisms contribute significantly to the economy of the planet; they have shaped the evolutionary events on Earth from the beginning and continue to play a role in the ecology of every living system on our planet (22,23).

Microorganisms form the foundation for all ecosystem functions on Earth. Their populations constitute the biggest part of the biomass on the planet. They have contributed enormously to molecular diversity by inventing new mechanisms for transduction and genetic exchange. Considering humans as biological entities that are closely linked to microorganisms, it can be reasoned that homo sapiens and the microbial community that they harbor must be compiled as a superorganism that evolves as one entity over time. Studies have identified the human genome that seems to be altered by the constant presence of microorganisms in or on us (24-26).

Within the human body, three body habitats are generally considered with a predilection for beneficial organisms, including the gut, oral cavity, and skin. These microbiomes may be separated into three categories, including the commensal, symbiotic, and pathogenic (19,27).

3.2. Microbiome Composition

The human microbiome consists of bacterial species that inhabit various body sites, including teeth, skin, nasal cavity, lungs, and the gastrointestinal tract (28). While initial colonization begins at birth through contact with the mother, environmental factors such as diet and lifestyle subsequently influence the abundance and diversity of microbes (10). The oral cavity harbors hundreds of distinct bacterial species, among which Streptococcus species predominate. The nasal passages are home to potentially pathogenic species such as *Staphylococcus aureus* and *Streptococcus pneumoniae* (29). The lungs, once considered sterile, contain microbial communities dominated by Prevotella spp., Veillonella spp., and Streptococcus spp. The gastrointestinal tract boasts the highest density and diversity of resident microbes (30), with distinct microbial communities distributed along its length. Bacteroidetes and Firmicutes constitute more than 90 % of commensal bacteria in the lower gastrointestinal tract. Throughout the rest of the body, the diversity of microbiota among different body sites is relatively low compared to the human gastrointestinal tract, yet it remains substantial (31,32).

4. Roles of Beneficial Microorganisms

A wide range of beneficial functions is maintained by well-characterized microorganisms represented in the human microbiome (25). Numerous commensal microbial-host interactions contribute to the development of specific immunity and the enabling of tissue homeostasis (33). Diverse genera support the digestive system, among which prominent agents include Bifidobacterium, Bacteroidaceae, Clostridium, Eubacterium, Ruminococcus, and Faecalibacterium. Gut Bacteroides species, for instance, metabolize a diverse set of polysaccharides and oligosaccharides, supplying nutrition and vitamins to both their hosts and other intestinal microbial residents (34). Simultaneous addition of species belonging to any one of these genera to a collection of human microbiota strains has been found to enhance the ecological stability and butyrate production of the community (35).

Scavenging of oxygen in the intestinal lumen and other still poorly defined activities support colonization of obligate anaerobes; it is commonly hypothesized that species acting as oxygen

scavengers encourage the growth of anaerobic butyrate-producing bacteria while thriving on substrates other than starch, such as xylan, pectin, and sulfate (10). Daily intake of food ingredients, including dietary fiber and polyphenols, can be metabolized by human gut microbes through complex and cooperative mechanisms (36).

4.1. Digestive Health

The largest and most well-studied collective community of bacteria in the human body resides in the digestive tract (37). Dietary and lifestyle factors influence the bacterial composition throughout the entirety of the digestive system (38). In addition to bacteria, viruses, archaea, protozoa, and fungi are present, but bacteria are the predominant microorganisms (39). The transit time through the digestive system regulates the composition of the bacterial population, and different regions of the digestive system maintain distinct microbial communities (10).

The earliest colonization of the digestive tract begins within the first day of birth, and the digestive flora remains relatively stable throughout life after three years of age; however, digestive flora should be classified as “transient permanent” bacteria since continual shedding and replacement eliminates true permanency (40). Fecal analysis may not accurately represent digestive tract composition, but instead highlights predominant microbes. Bacteroidetes and Firmicutes constitute roughly 90% of the gut (41). Functional diversity in the microbiome exceeds the host’s functional capacity; hence, the bacterial genome is significant in evaluating the genetic capability of the entire digestive system (42). Genes involved in polysaccharide and oligosaccharide metabolism are overrepresented in the digestive system to break down essential nutrients (43). Different bacterial species express glycosidases and polysaccharide lyases to break down polysaccharides into absorbable sugars. For example, Bacteroides species metabolize North American dietary polysaccharides and colonic mucins. Early estimates suggested 500–1000 species in the digestive tract; modern sequencing estimates at least 160 species per individual, while up to 1,000 of the 40,000 bacterial species catalogued in public databases have been identified in the digestive system. Larger taxa include Clostridia, Bacteroidia, Bacilli, and Proteobacteria (44,45).

4.2. Immune System Modulation

Human immunity is a powerful and dynamic system that maintains homeostasis, responding rapidly to microbes while avoiding autoimmunity and tolerating beneficial microbes. The microbiota contributes to immune homeostasis, but it remains unclear whether dysbiosis causes immune imbalance or results from it (46,47). Animal models colonized with human microbiota can help distinguish cause from effect and explore the microbiota's role in maintaining immune balance (48). Understanding how dysbiosis influences disease progression is crucial for developing targeted treatments for conditions characterized by chronic gut inflammation (49).

Probiotics, prebiotics and immunomodulation of gut mucosal defences: homeostasis and immunopathology. Probiotics are beneficial microbes that confer health benefits on the host, especially when combined with prebiotics, which are indigestible dietary fibres fermented by microbes (50). There is growing evidence supporting the immune-modulatory ability of probiotic bacteria, suggesting that a combination of prebiotics and probiotics can enhance immune responses. These formulations aim to normalise dysbiotic microbiota associated with immunopathology (51). The review focuses on the immunomodulatory role of probiotics and prebiotics on gut mucosal immunity, including effects on epithelial barriers and adaptive immune responses (52). They play a role in maintaining homeostasis and can influence inflammatory processes related to conditions such as

inflammatory bowel disease, colorectal cancer, and hypersensitivity (53).

The complex of mechanistic effects involved in the modulation of the human immune system by probiotics is only just beginning to become clear. Within gut pathology, the use of prebiotics and probiotics can yield a significant impact on immune responses and immunopathology (54). Areas for future research into immunopathologies and modulation by prebiotics, probiotics, and synbiotics are emphasized. Current studies are investigating the effects of pre-/probiotic modulators on immunosenescence, the modulation of antigen-presenting cell (APC) function, the characterization of probiotic bacterial products, and the application of faecal transplantation (55). Specific probiotic strains are able to enhance the activity of dendritic cells, natural killer cells, and cytotoxic T cells, potentially offering significant benefit to older populations. Within the lamina propria, mucosal macrophages act as a key population in the modulation of local immune responses (56). Probiotics can modulate these cells and may play an important role in the management of gut inflammatory disease and hypersensitivity. To exert this broad range of effects, probiotic bacteria must act through either direct cell–cell interactions or through the production of secretable products (57). Both modes of action include the molecular involvement of pattern recognition receptors (PRRs). Probiotic components engage PRRs through the recognition of conserved microbial molecular patterns, including lipoteichoic acid and other surface molecules, and also specific carbohydrate ligands that are recognised by C-type lectins (58). These interactions instruct tolerogenic or regulatory responses in the mucosa, so establishing beneficial immunomodulatory environments that include the induction of regulatory T cells (59).

4.3. Metabolic Functions

Diverse microorganisms colonize the different body sites, such as skin, respiratory tract, digestive tract, and urogenital tract, for the entire lifespan, performing metabolic functions conducive to the health of their human hosts (60). Some of the direct functions associated with beneficial microorganisms include the synthesis of amines, amino acids, essential vitamins, and SCFA through the fermentation of carbohydrates in the colon (61). Bacterial fermentation in the colon uses non-digestible carbohydrates and results in the production of SCFA, which supplies a considerable fraction of the daily energy requirements of the adult host and participates in the regulation of numerous cellular processes; as a result, SCFA are important for gastrointestinal health (62). Indigestible carbohydrates reaching the distal part of the gut can be a critical determinant of microbiota richness and composition, thereby modulating the diversity and the relative abundance of beneficial and harmful bacteria and their metabolites in colonic contents (63). Beneficial microorganisms in human body sites such as the skin, respiratory tract, digestive tract, and urogenital tract produce a wide range of antimicrobial compounds (4). These compounds can target specific pathogens or instead show a relatively broad-spectrum antimicrobial activity. Additionally, metabolites derived from probiotics or probiotic-modulated microbiota affect the gut-brain axis and brain receptors and reduce neuroinflammation induced by microglia through peripheral pathways (64).

5. Sources of Beneficial Microorganisms

The human body contains about 39 trillion microbial cells, including bacteria, fungi, algae, and other microorganisms. Their composition depends on the species, gender, age, isolation site, and exposure to other microorganisms and antibiotics (65). Microorganisms exhibit several important functions; therefore, the modulation and

maintenance of these microorganisms are essential to maintain good health (66). Beneficial microbes contain mechanisms that maintain the intestinal microbiota well-balanced (67). They also affect the peristalsis; remove ammonia, amines, phenols, and indoles; produce antimicrobial substances; stimulate the immune system; produce substances that inhibit pathogens from colonizing; modulate cholesterol; and intensify the absorption of iron, calcium, and several other minerals (68). These microbes are necessary to balance the microbiota and to maintain human health in the long term; several sources of beneficial microorganisms contain dietary supplements, yoghurt, and probiotic products, amongst others (69).

5.1. Dietary Sources

Probiotics have attracted increasing interest for their unique health benefits. These live microorganisms confirm their beneficial effects on human health when consumed in specific quantities (70). They promote the functionality of the body systems and modify the gut microbiota in achievable and harmless ways. Probiotics are mainly found in fermented foods, such as yogurt, kefir, sauerkraut, kimchi, and miso (71). Other potential resources include the stomach and eyes, which require a micro-ecosystem for their proper functioning. Furthermore, it has been demonstrated that several indigenous and fermented foods, especially fruits and vegetables, contain a variety of beneficial microorganisms that support human health (72).

Probiotics assist in preventing and reducing the adverse effects of antibiotics by replenishing the diversity and functionality of the gut microbiota, as well as restoring the microbiome that is altered due to resistant pathogen infections (73). Several bacterial groups and species, predominantly probiotics, are also associated with the successful and safe operation of the immune system (74). The importance of oxidative stress leads to the consideration of antioxidative bacteria, and several sources have been identified for this purpose (75). Organic acids secreted by beneficial bacteria influence pathogen growth, highlighting the crucial role of beneficial microorganisms in different body systems. A balance is essential, as an overgrowth of either the pathogen or the beneficial bacterial community in the gut environment can lead to metabolic diseases, infections, and inflammation within the body (76).

5.2. Probiotics and Fermented Foods

Fermented foods represent an ancient, commonplace dietary vehicle for introducing beneficial live microorganisms into the gastrointestinal tract. These microbial populations comprise a “transient microbiome” that regularly disperses across the human population (77). Microorganisms indigenous to fermented foods originate from raw materials or the production environment, wherein they must overcome numerous selective pressures—including salt, acids, and low pH—to fulfill a fermentation role (78). Examples are numerous and include fermented cereals, sauerkraut, kimchi, soy products, wines, and fermented sausages. Some fermented food products rely exclusively or partially on well-defined starter cultures (e.g., dairy, cheese, and sausages); such cultures are generally selected for their consistency and performance (79).

Upon delivery to the gut and regardless of which of the aforementioned routes are involved, such microorganisms initially constitute a foreign ecological challenge for the established microbial community. Typically, they possess no competitive advantage or requisite nutrients that might enable them to persist and grow indefinitely within the gastrointestinal tract. At the same time, epidemiological and interventional studies nonetheless consistently link the consumption of fermented foods with improved health, e.g., a reduced risk of condition-specific pathological outcomes (80,81).

6. Impact of Antibiotics on Microbiome

Antibiotic treatment has prompted the emergence of resistant bacterial strains and disrupted the microbial equilibrium crucial for human well-being (82). Antibiotics hinder the diversity of microbiota, diminishing beneficial species while encouraging potential pathogens. The intestinal tract serves as a gene pool, where antibiotics further the selection of resistant bacteria capable of environmental and host dissemination. While therapeutic dosages reduce species diversity and promote resistance, parenteral administration partially mitigates these effects. Sub-therapeutic doses influence microbial taxa associated with sugar metabolism, linking to weight gain, yet still facilitate the selection of resistant strains (83,84). The widespread use of antibiotics in animal farming as growth promoters underscores the need for understanding pharmacodynamics to optimize therapy and minimize adverse consequences. Standardized protocols coupled with comprehensive genomic methodologies, such as shotgun metagenomics, are imperative for elucidating microbiota composition, function, and resistance gene dynamics, ultimately enhancing strategies to conserve and restore microbial communities post-perturbation (85).

6.1. Antibiotic Resistance

The use of antibiotics disrupts microbiome homeostasis, which promotes overgrowth of harmful microbes and renders antibiotics less effective (86). Maintaining a healthy microbiome reduces the expansion of pathogenic microbes and limits the transfer of antibiotic resistance genes. Probiotics support microbiome restoration and reduce the gut resistome, the collection of all the antibiotic resistance genes in the microbiome (87).

6.2. Restoration of Microbiome

The phenomenon of antibiotic resistance is not a problem confined to pathogenic bacteria but is also increasingly reported among the beneficial members of the gut microbiota. The occurrence of antibiotic resistance genes in the gut of human infants correlates with the presence of these genes in the mother's gut and breast milk (4). The loss of crucial species of beneficial and commensal gut microorganisms that harbour antibiotic resistance, ally with other resident microbes, and cooperate with the host to provide beneficial functions may adversely affect the host metabolism and epithelial barrier function (88). The recovery of beneficial species is therefore an important issue when immediate reestablishment of the gut microbiome is necessary following the antibiotic treatment (89).

The associated complexity through the presence of several hundred commensal and beneficial species with nested physiologies in the gut makes the recovery a challenging task. However, the importance of a balanced microbiota for gut homeostasis and functionality is well documented (30). Dysbiotic microbiota is characterized by altered composition, reduced diversity and stability, and increased levels of pro-inflammatory bacteria. In individuals with a healthy microbiome, this is observed as a rapid recovery phase during the antibiotic treatment, in which the disappearance and sequential reappearance of bacterial 16S rRNA gene sequences follow a clearly observable pattern (90). A variety of specific commensal species have the capacity to restore intestinal health in patients by reducing inflammation and strengthening the epithelial barrier (91).

Several of these species, including Bifidobacterium, *Faecalibacterium prausnizii*, *Roseburia intestinalis*, *Eubacterium hallii*, and *Akkermansia muciniphila*, metabolize dietary fibres into short-chain fatty acids, which in turn provide enterocytes with an energy source and exert anti-inflammatory effects. The intestinal microbiota, composed of pro- and anti-inflammatory microbes, has an essential role in maintaining gut homeostasis and functionality. The human gut contains over 3000 bacterial species, with approximately 200 species present in an individual microbiome, predominantly sourced from the Firmicutes and

Bacteroidetes phyla. Impaired barrier function is linked to a variety of diseases, highlighting the significance of a balanced microbiota for gut health (92,93).

7. Microbial Imbalance and Health

The microbiota has a fundamental role in the maintenance of the host's health; the prevailing relationship between microorganisms and the host is a very complex cooperation between the immune system and the microbiota itself (94).

Diverse beneficial functions provided by the normal intestinal microbiota include enhancement of the intestinal barrier; protection against colonization by pathogens; regulation of the development of the gut epithelium and its physiology; digestion of dietary carbohydrates; synthesis of vitamins; and local and systemic immune stimulation (95). Therefore, changes in the composition or function of the microbiota may contribute to disease; the various microbiota-mediated mechanisms through which colonic microbial communities can influence host health are beginning to emerge (96).

The human body is colonized by a large number of microorganisms, which live in a peaceful symbiosis with the host. The most heavily colonized site of the human body is the gastrointestinal tract (GIT), in which more than 10^14 bacteria reside 96. This micro-organism population is 10 times larger than the total number of human somatic and germ cells (97). Phylotypes belonging to the Firmicutes and Bacteroidetes dominate a healthy adult's intestine, representing more than 90% of the bacterial population (98). Despite this shared phylogenetic structure, the composition of the microbiota demonstrates a distinct variation between individuals. For this reason, the microbiota can be compared to a fingerprint specific to an individual (99). The human gut microbiota acts as a barrier to invading pathogens, exerts metabolic functions, and regulates innate and adaptive immune responses. The link between gut microbial imbalance and disease has been well illustrated for inflammatory bowel disease (IBD) (100). There is growing evidence supporting the hypothesis that alteration in the microbiota composition precedes the development of colitis, demonstrating that the recruitment of pro-inflammatory T-cells might be secondary to the dysbiosis; nevertheless, it is also likely that chronic inflammation induced by the dysbiotic microbiota sustains its development by influencing host–microbial mutualistic interactions (101).

7.1. Dysbiosis

Dysbiosis denotes the impairment of homeostasis within the intestinal microbiota, characterized by altered composition, diversity loss, and increased proinflammatory bacteria, potentially inducing epithelial barrier disruption 30. Age-related changes in the intestinal microbiota have been noted (96). The colonic microbiota constitutes a densely populated ecosystem that maintains both gut homeostasis and functionality. Accordingly, the gut microbiota appears to be involved in the etiopathogenesis of numerous gastrointestinal inflammatory conditions and other diseases, not only localized in the gut (46).

Under certain conditions, dysbiosis contributes to an array of disorders affecting both the gastrointestinal tract and distant organs (102). The most beneficial commensal strains can counteract and correct dysbiotic alterations by reducing inflammation and reinforcing epithelial barrier function; these species can be classified as next-generation probiotics (103). Among these, bifidobacteria represent the most beneficial gut microbes. *Faecalibacterium prausnitzii*, *Roseburia intestinali*s, and *Eubacterium hallii* generate short-chain fatty acids that nourish enterocytes and other colonocytes and exert anti-inflammatory effects. *Akkermansia muciniphila* influences intestinal metabolic and barrier functions (104).

7.2. Associated Health Conditions

The human body in a healthy state harbors an enormous number of microorganisms, with the majority composed of beneficial animal-associated microorganisms (105). Following breakdowns in the balance of these beneficial microbes, the subsequent transition to opportunistic and/or pathogenic is well-established, and various diseases and/or disorders have been defined following such transitions (106). Several conditions have been shown to associate directly with deficiencies in beneficial microbes such as certain Bifidobacterium spp. and Lactobacillus spp., for example. Deficiencies of these microorganisms have been linked explicitly to a variety of infectious conditions at several sites in the human body at various ages and physiological/drug states (15). Commonly associated health conditions following breakdowns in beneficial microorganisms include nutritional deficiencies, immune disorders, obesity, colitis, irritable bowel syndrome, asthma, and many others (107). Previous research has defined key components as consisting of several microorganisms that associate with healthy individuals. These microorganisms belong mainly to the Enterobacteriaceae, Bifidobacteriaceae, and Lactobacillaceae families (4).

8. Conclusion

The number of microorganisms in the human body is estimated at approximately 3.8 × 10^13, slightly exceeding the number of human cells. This complex microbial ecosystem is denoted by the human microbiome: a dynamic community of microorganisms that interacts with the host through their genetic complement, the metagenome. Although influenced by environmental and genetic variables, three main gut microbiome profiles—enterotypes—are identified by the dominant genera Bacteroides, Prevotella, and Ruminococcus.

The human microbiome plays a pivotal role in orchestrating fundamental physiological processes such as nutrient absorption, immune modulation, adiposity, energy balance, and brain development. A generally accepted distinction exists between the microbiome, encompassing all microbiota, whereas the microbiota pertains only to the assemblage of living microorganisms. Beneficial or friendly microorganisms exert multiple effects of broad relevance to the host, including immune stimulation, exclusion of pathogens, anti-inflammatory action, antimutagenic and anticancer activities, wound healing, cholesterol reduction, and vitamin production.

Vegetables, fruits, and fermented foods are naturally rich sources of beneficial microorganisms. Probiotics, defined by the World Health Organization as live microorganisms that, when administered in adequate amounts, confer a health benefit on the host, represent an additional source. Despite continuous antibiotic discovery, increasingly resistant pathogenic bacteria have created renewed interest in beneficial microorganisms that can influence resistance trends. Historical reliance on antibiotics saw the premature end of many health-promoting associated microorganisms due to resistance acquisition and harmful side effects, underscoring the need to revisit beneficial microbial mediation.

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