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Review Article

OVERVIEW ON GUT MICROBIOME

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ABSTRACT

The assemblage of eukaryotic and prokaryotic kingdom inhabiting the gastrointestinal system is termed as the microbiota and developed alongside human and other eukaryotic systems for millennia, developing a mutually complicated and advantageous connection. The digestive system is home to an estimated number of microorganisms surpassing 10^{14}, which is approximately greater then than the plethora of human cells and more than hundredfold times greater than the amount of genetic information found in the human gene. The microbiome is the native population of microbes (microbiota) in the host and develops along with it. The perception that the microbes predominantly present in human system gives vital environmental functions that act as a welfare for the whole microbial host system, therefore the mass fundamental development. The human gut microbiome is composed of variants of number of bacteria. Particularly, this gut environment depicts tons of bacterial cells which are important factors that manage gut immune system. The metabolic activities such as immunity, nutrition absorption, and digestion are interlinked with this microbial community. Studies developed that abnormalities in the gut microbiome are result of diseases including obesity, inflammatory lung disease, and CVS diseases, carcinoma during advent studies. The assemblage of bacteria, *Archaea*, and eukarya inhabiting the gastrointestinal tract is known as the microbiota and developed alongside the host for millennia, establishing a mutually complex and advantageous relationship. This review focuses on the overall view of the microbe in gut.

Keywords: Gastrointestinal, Gut microbiota, Metabolics, Microbiome, Host.

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INTRODUCTION

The assemblage of prokaryotes and eukaryotes inhabiting the gastrointestinal tract is known as the microbiota and developed alongside the human digestive system for millennia, establishing a mutually perplexing and advantageous relationship. The gastrointestinal track is home to an estimated number of microorganisms surpassing 10^{14}, which is approximately greater to plethora of human cells and more than hundredfold times greater than the amount of genomic content found in the human genome. Nevertheless, the recent reassessment implies that the proportion of human to bacterial cell is very similar to 1:1 due to the significant quality of bacteria within human cells, the microbes which are interacting with host digestive system are frequently described as superorganism. Due to challenges in culturing most intestinal microbial species, advanced sequencing methods such as shotgun metatranscriptomic sequencing, viromic sequencing, 16s rRNA sequencing, 18s rRNA sequencing, and ITS Sequencing are the techniques widely utilized for investigating the gut microbiome, The gastrointestinal system protects a diverse and abundant collection of microbes known as the microbiome. The microbiome has been found to play crucial roles in immunity, nutrition absorption, digestion, and metabolism. Recent studies have revealed a strong association between the onset of various diseases, such as obesity, inflammatory lung diseases, and carcinoma. Further, the detailed microbiota and hierarchy of the microbiome were discussed on upcoming topics [1].

EVOLUTION OF GUT MICROBIOME

The human digestive system stretches 6.5 m long and comprises three build-in organs that are stomach, small intestine, and large intestine. Hence, when researching the human microbiome, we mainly look at the microbiota, the microbiome in the large intestine, as this is obtained using stool samples. This bacterial community contains more microbial biomass than any organ or surface in humans. The number is of 10^{11} microbial cells/mL in the large intestine and only 10^{8} cells in the small intestine. To study the distal colon microbiome, we, and other researchers, have typically used a non-invasive fecal sample as a surrogate. The above-mentioned samples are the mix of microorganisms and human colonocytes taken from different portions of the digestive system and share a similar composition, yet distinct, from intestinal biopsies [2].

Using culture-dependent and -independent methods, the human microbiome can be examined in detail with the gut containing approximately 150–400 species. Mainly, these belong to *Bacteroidetes*, *Firmicutes*, Actinobacteria, and *Proteobacteria* phyla [3].

Phylosymbiosis- 'microbial community relationships that can recapitulate the entire phylogeny of the host'. Such differences are consistent when stratifying by time period, host phylogeny, and diet. The human microbiome also shows signs of phylosymbiosis. Compared with all other primates, the human microbiome composition is most similar to that of old world monkeys and apes, differing substantially from that observed in new world primates and leumurs. It is expected, that the microbial communities of within host species than to those of different host species [4].

MICROBIOTA

There is a growing recognition of the association between gut microbiota and human health. A correct gut flora has long been recognized to be important for the overall health of a person. The average gut microbiota are primarily composed of two major phyla, *Bacteroidetes* and *Firmicutes*, although the gut microbiota in the infants appears random, by age three it begins to approximate that of adults [5].

The popularity of probiotics is on the rise for preventing and treating various diseases. Despite the increasing number of high-quality clinical trails and ongoing research into the mechanism of probiotics, uncertainties persist regarding their precise effects on the immune system and overall health in different disease states [6].

The host supports the boom of beneficial microbiota by way of liberating unique factors like microRNAs in addition to nonspecific elements

consisting of antimicrobial peptides, mucus, and immunoglobulin A (IgA). Those elements sell the proliferation of certain microorganism by means of inhibiting the boom of others[7].

VARIANTS OF MICROBES IN GUT

As per studies 2,172 species that had been determined in people categorized in 12 distinct phyla, with most people (93.5%) falling under Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes in 12 phyla.Three contained handiest, one species each that had been remote from human beings, one in each of which turned into Akkermansia muciniphila, an intestinal species and the sole representative of the Verrucomicrobia phyla. Out of the recognized species, 386 had been strictly anaerobic in humans, generally inhabiting mucosal vicinity just like the oral cavity and the gastrointestinal system. At the opposite, babies born through C sections showcase a decrease in the range of their microbiota and a put off within the colonization of the *Bacteroides* genus, with a better presence of facultative anaerobes like clostridium species. In evaluation, about 72% of vaginal brought babies have a fecal microbiota composition similar to that of their moms, whereas this in addition drops to 41% in toddlers born through C segment. Infections of enamel and gums will have a major effect on fitness no longer handiest through teeth decay, however, also through their consequences on the cardiac, neural, and immune system. The contradictions are because of disease-producing oral microbes inclusive of *Streptococcus mutans* and the anaerobe *Porphyromonas gingivalis* falls under the *Bacteroidetes* phylum. Protein degrading enzyme gingipain was developed using *P. gingivalis* changed into currently proposed because the thing in the advancement in the treatment Alzheimer's sickness. Speedy passage of intestine contents after swallowing way that the healthful esophagus shows very low range of microorganisms, the incredibly acidic conditioned stomach additionally shows most colonizers. A few novel microbes do however manage to colonize stomach epithelium, especially *Helicobacter pylori* [8].

OVERVIEW OF INTERACTION BETWEEN HOST AND MICROBIOME

There is a sizeable interplay between the host and the microbe which will be seen in this review (Fig. 1). The interplay among the host and the gut microbiome commences at some stage in the delivery method as the newborn's microbiome is installed. Diabetes, weight problems, and the metabolic syndrome are complicated conditions encouraged by way of a ramification of factors including genetic, deit, and environmental factors. Latest studies advise that gut microbiota plays a crucial position in mediating the relationship between the weight loss plan and the onset of weight problems and metabolic issues [9].

The microbiome undergoes a rapid diversification manner for the duration of first 3 years of existence, accompanied by a constant boom in diversity until about the age of 40. After this point, as shown in Fig. 2, the composition of the microbiome tends to remain highly stable. However, it is essential to be aware that brief-term changes within the intestine microbiome can disrupt the normal manufacturing of metabolites. This disruption can then lead to the alteration inside the expression of genes inside the host, probably ensuing in the durable effects [10].

Immunological responses in the intestinal microbiota are mediated by a diffusion of mechanisms that together keep intestinal homeostasis. As proven inside the parent, 1.2 goblet cells produce mucin glycoproteins, while plasma cells generate IgA. Epithelial cells launch antimicrobial proteins in the toll-like receptors or through nucleotide-binding oligomerization domain-containing protein two-structured pathways. Dendritic cells (DCs) capture microorganism and finally take them to Peyer's patches and mesenteric lymph nodes, wherein they facilitate the differentiation of B cells into IgA-secreting plasma cells. Furthermore, the absorbance of polysugar compounds A in *Bacteroides fragilis* through intestinal DCs promotes the development of regulatory T cells (Tregs) that are essential for the secretion of interleukin 10. Moreover, the antimicrobial activity-producing proteins are produced using host cells tend to impact the diversity of the microbiota [11]. On the way to have a look at the microbiome, the researchers utilize a huge range of techniques, lots of which contain next-technology sequencing technology. One normally used method to analyze the taxonomic composition of the intestine microbiome is with the aid of sequencing a phylogenic marker gene. The 16S rRNA gene is regularly selected for this purpose because it is observed in both *Archaea* and bacteria. This gene carries segments that trade between excessive and occasional conservation, making an allowance for polymerase chain reaction priming and taxonomic identity, respectively. This approach is considered to be both clean and efficient in exploring the taxonomic make-up of the intestine microbiome [12].

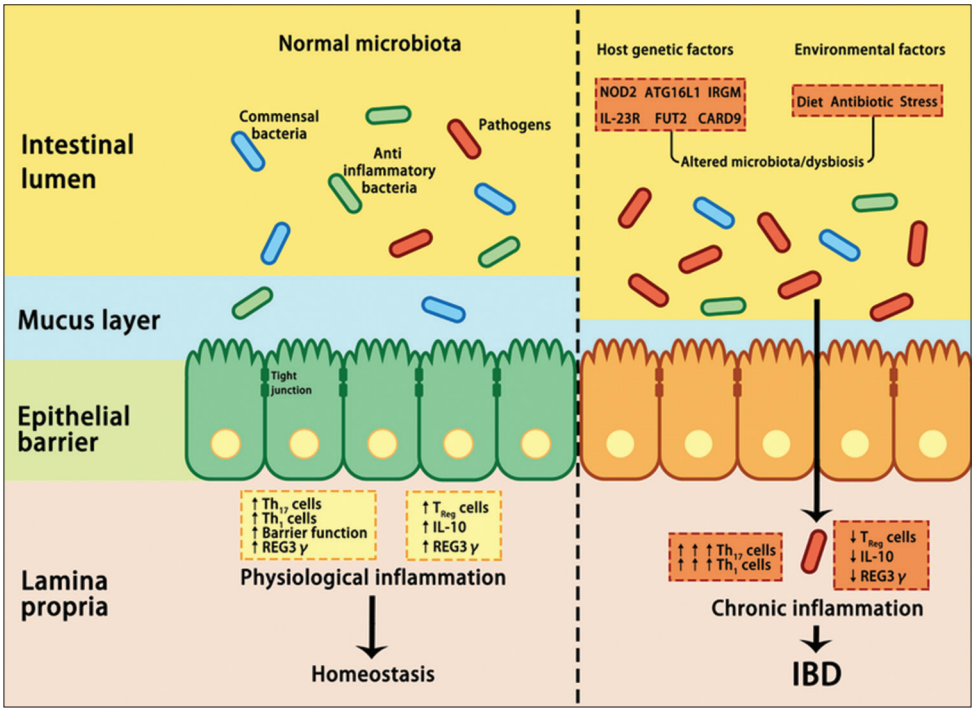

Fig. 1: Interaction between the gut microbiome and the host [13]

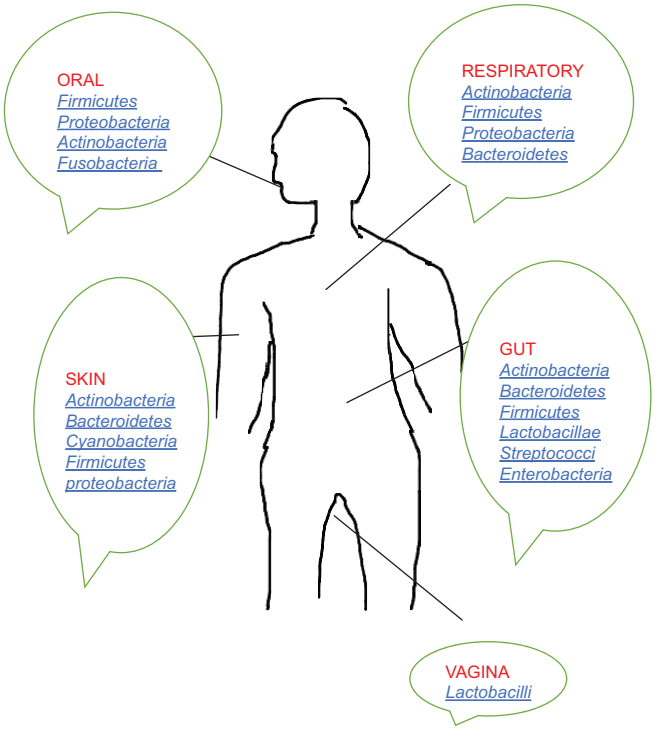

Fig. 2: Diversity and species of microbes on human body

WONDERS BY GUT MICROBES

There are tremendous beneficial works done by gut microbes rather focusing on only hazards of their action. In this para, we can have some of their wonders as followed by the heading [12]. Safeguard us against infections, enhance all cognitive functions that the gut bacteria have been associated with (synthesis of serotonin which serves as the body's innate mood enhancer), maintain blood sugar levels, influence body structure, enhance cardiovascular health by lowering cholesterol, and also fortify our immune system. When it comes to the research on gut diseases, these organisms play crucial roles as mentioned in interactions between host and microbiota further helps in clinical trials with species such as zebra fish gut and human gut microbe studies and in some rodent species [13].

GUT MICROBIOME DIVERSITY

The composition of the intestine microbiome performs an important function in figuring out human fitness. Diverse environmental factors and doubtlessly host genetic variation were validated to have an impact on its makeup [14]. The gut microbiome plays a giant function in influencing mind functions inclusive of stress, tension, depressive symptoms, and social conduct. This connection between the microbiome, intestine, and mind is known as the microbiome-intestine-brain axis, which operates through neural, immune, and endocrine signaling pathways [15].

Whilst most studies were performed on animal models, restrained studies on human beings have often centered on psychiatric problems. On this study, the connection between the configuration and variability of the intestine microorganism and human character trends is explored. Regression fashions are utilized to account for ability confounding variables, revealing that positive bacterial genera abundances are related to character traits. Moreover, variety analyses imply that people living under range of social atmosphere tend to have vast fluctuations in intestine microbiome, recommending that social interconnections may also impact the microbial constituents of the human gut [16].

While reading microbiome facts, our recognition is frequently on species-stage analyses, or even with the capacity to clear up traces, we thrive for abundant meaningful databases and expertise in the significance of strain-stage variant outdoor of one restricted variety of experimental organisms. The gene of bacteria is fantastically plastic, with advantages in gene and loss occurring at nucleotide are comparable or better to *de novo* aberrations in DNA. Consequently, the protected segment of genetic sequence is mostly a part of the pangenome, mainly to substant variation in physical expression, adjoints the trends and is important in host-microbial interlinkages [17].

On this overview, we explore the mechanisms that provide upward push to pressure variant and methods that can be used to study it. We recognize that while stress diversity can pose a main barrier in decoding and generalizing microbiome facts, it is able to additionally be a powerful device for mechanistic studies. We then spotlight current examples demonstrating the significance of strain version in colonization, virulence, and xenobiotic metabolism. Moving past taxonomy and the species idea can be vital for destiny mechanistic studies to recognize microbiome shape and function [18].

DETECTION OF GUT MICROBES

Sequencing partial 16S rRNA genes is a fee-powerful method for assessing the microbial composition of surroundings, together with the human gut [19]. However, the downstream evaluation entails categorizing reads into microbial agencies using treating every unique collection as a wonderful microbe, acquiring taxonomic labels from sequences through database queries, or clustering similar sequences [20].

Despite the fact that those methods do now not fully capture the evolutionary relationships among microbes, which limits the potential to perceive differently plentiful microbial agencies between diseased and manage cohorts, still we have been able to visualize the diversity. In this have a look at, we introduce series, primarily based biomarkers, a method that aggregates and corporations microbes the usage of unmarried variants and combinations of versions within their 16S sequences [21]. Further, a few byproducts produced by way of intestine microbes metabolisms have been spotted, for instance; the gut microbiota has an enormous impact on chronic kidney disorder (CKD) and high blood pressure. Metabolites derived from intestine microbiota, which include trimethylamine-N-oxide (TMAO) and trimethylamine, are taken into consideration uremic toxins and are related to CKD, atherosclerosis, colorectal cancer, and cardiovascular hazard. Therefore, the identification and measurement of TMAO, a metabolite produced through gut microbes, is essential for diagnosing conditions such as atherosclerosis, thrombosis, and colorectal most cancers (CRC). Maximum of the studies on microbiomes involves creating ecological maps of the community and the usage of superior sequencing strategies to apprehend how microorganisms make contributions to health and sickness [22].

This era, which does not rely upon culturing microorganisms, usually involves important sequencing techniques: amplicon sequencing, which targets particular areas of bacterial DNA to pick out exclusive species, and shotgun sequencing, which captures all of the genetic material in a pattern after which portions it back collectively the use of bioinformatic equipment. A particular organization of *Ruminococcus gnavus* lines has been determined to incorporate 199 microbial genes which can be associated with oxidative stress responses, adhesion, iron acquisition, and mucous utilization, which can be unique to inflammatory bowel sickness (IBD). Those genes are particular to this clade of *R. gnavus* traces, indicating a potential function in the pathogenesis of IBD [23].

APPLICATIONS OF GUT MICROBIOME

While focusing on the applications of intestine microbiome, first, insects constitute the most successful category of animals, excelling in each range and adaptableness throughout a wide variety of ecological environments. Research suggests that the gut of an insect harbors about ten instances greater microbial entities than the total quantity

of insect cells, and it possesses a microbial gene pool that may be a hundred instances greater than the genetic cloth determined within the insect itself. A huge portion of the research has concentrated on elucidating the dynamics among the host organism and its symbiotic microbiota [24]. Second, bugs rely on a symbiotic dating with intestine-associated micro-organism to assimilate atmospheric nitrogen because the capability for nitrogen fixation is predominantly found in microorganism and is outwardly missing in all eukaryotic organisms. Extensively, nitrogen-fixing *Enterobacter* species had been diagnosed within the southern pine beetle, which, at the side of sure fungal companions, may additionally enhance nitrogen availability for the developing larvae [25]. In addition, the human gastrointestinal tract harbors a sizable populace of fungi, constituting approximately 0.1% of the overall gut microbiota. Those fungi are critical for preserving intestinal homeostasis and are implicated within the improvement of numerous illnesses. Fecal microbiota transplantation (FMT) entails the introduction of fecal material from wholesome donors inside the gastric tract of sufferers, with the objective of restoring the intestinal composition of microorganisms. To begin with, this method became clinically recognized for its awesome effectiveness in treating refractory *Clostridioides difficile* infections [26]. Considering that point, a growing body of clinical trials has explored the utility of FMT for a spread of different scientific situations. However, the clinical effectiveness of FMT has proven to variability among distinct individuals and illnesses, indicating that bacterial engraftment on my own does not fully account for the differences in remedy results. Latest research has highlighted the importance of gut fungi in the therapeutic outcomes of FMT. A examine that specialized in patients with recurrent *C. difficile* infections located that fungal engraftment from healthful donors to recipients changed into observed, with FMT responders showing a better rate of fungal colonization. This location indicates that the transplantation of the intestine mycobiome may additionally play a beneficial position inside the usual efficacy of FMT [27].

MICROBIAL INVOLVEMENT IN CARCINOGENIC ACTIVITIES ON HUMANS

The Gutflora metabolizes undigested nutritional substrates and endogenous residues. Sure metabolic byproducts were connected to carcinogenic processes, inclusive of tumor promoting (which include ammonia and secondary bile acids), mutagenesis (fecapenaenes), and carcinogenesis (N-nitroso compounds) [28]. The protective advantages of intestinal bacterial metabolism encompass the binding of carcinogens, cleansing of methylmercury, and the synthesis of lignans and isoflavones. It is properly established that weight-reduction plan affects gut microflora metabolism and the progression of cancer. Studies indicate that nutritional consumption influences gut bacterial enzymes, main to the manufacturing of dangerous byproducts which include ammonia, phenols, and cresols for the duration of the metabolism of nutritional protein. The problematic connections among diet, gut microflora metabolism, and their consequences on the host are complex, yet they may preserve important in elucidating the epidemiological hyperlinks between outside factors and the threat of colorectal cancer [29].

In this analysis, we have tested the emerging proof regarding the position of the microbial network in the development of CRCs. The presence of healthful gut microbiota is critical for preserving intestinal homeostasis and might actually have anti-cancer residences. However, it is important to notice that this microbial community also develops diverse metabolic products that can be hazardess to gene, further feature a negative impact on the behavior of epithelial cells. Dysbiosis, which refers to disturbances inside the regular microbial balance, is frequently observed in patients with CRCs. Several microbial species, along with specific strains of *B. fragilis*, *Escherichia coli*, *Streptococcus gallolyticus*, *Enterococcus faecalis*, and *Fusobacterium nucleatum*, have been related to CRC. These findings shed light on the complicated dating among the intestine microbiota and colorectal carcinogenesis [30]. Although microbiota allows in as anti-oncogenic activities in people, there are a few microbial activity that causes genetic versions (translational and transcriptional aberrations) in human intestine causing tumors through dysbiosis (imbalance in microbial community in gut); those tumors were diagnosed as CRC which turned into the major trouble in worlds developed united states like U.S. [31]. Human beings are constantly uncovered to probably harmful chemical compounds that input the intestinal tract through ingested. The gut microbiome is the incredible microbial populace and the environment of the host it resides, and its miles revolutionizing how doctors reflect the consideration on germs in human immunity and illness. The grasping of the almost all the microbes in human bodies carry out fundamental atmosphere features that serve as the advantage for the whole microbe and owners body, the maximum basic improvement in host ecosystem. Normally, this atmosphere accommodates tons of microbes that occupy a essential function in human fitness control. Immunity, nutrients absorption, digestion, and metabolism have all been connected to the microbiome. Scientist found that modifications in the microorganism in gut are interlinked to the advancements in treatments on sicknesses consisting of weight problems, inflammatory pulmonary disorder, and carcinoma these days [32].

E. coli

E. coli is a bacteria species, own family of *Enterobacteriaceae* and gram poor stress. This microorganism is most abundant species inside the intestine among other species. *E. coli* lives within the gastrointestinal tract and lower gut and facilitates in the ruin down meals and produce vitamins in human. It maintains intestinal pH wherein *E. coli* also enables to hold balance of other bacterial within the intestine. The increase in number of *E. coli* within the gut can lead to infections in the bladder, urinary tract, and diarrhea [33].

H. pylori

H. pylori is a Gram-negative bacteria, family of *Helicobacteraceae*, this bacteria colonize in human gut pylori produces an enzyme called urease which neutralizes stomach acid in its immediate environment, allowing it to survive and burrow into the stomach lining, causing irritation peptic ulcers and, in some cases, stomach cancer inflammation further known to affect gastric homeostasis that contribute to changes in the microbiota [31].

Lactobacillus acidophilus

L. acidophilus is a bacteria species, Gram-positive homofermentative anerobic microbe which lives in the human gut, mainly in the small intestine helps in probiotics function by promoting a balanced gut microbiome, primarily through the suppression of pathogenic bacteria. This is achieved through several mechanisms, including the production of lactic acid, competition for adhesion sites on the intestinal lining, and enhancement of the immune response. Consequently, these actions contribute to improved digestion and nutrient absorption, being a novel gut microbe [32].

Candida albicans

C. albicans is a classification of yeast found in the human intestine plant life; this species is located in mouth, skin, and intestines. In addition this is commensal organism however pathogenic occasionally. *C. albicans* typically colonizes mucosal surfaces without inflicting symptoms, if you want to result in candidiasis. While the stability of healthy eukarya and yeast inside the intestine is disturbed, *Candida* can overgrow, on the grounds that ensuing as pathogenic flora by way of disrupting the gut microbiome [34].

Bifidobacterium bifidum

B. bifidum is a bacteria species, Gram-positive bacteria, falls under *Bifidobacteriaceae* family found in gastrointestinal tract, oral cavity, human blood, helps to develop healthy microflora in new born infants and used to treat diarrhea. Some strains of *B. bifidum* can produce vitamins like vitamin K, which is important for blood clotting [35].

Corynebacterium matruchotii

C. matruchotii is a species of bacteria in the *Corynebacteriaceae* family, Gram-positive bacteria. *C. matruchotii* is predominantly linked to the oral microbiome, especially within dental plaque. At present, the majority of research is directed toward understanding its potential role in oral health complications, such as dental caries, attributed to its capacity to facilitate biofilm development and mineralization [36].

Clostridium perfringens

C. perfringens is a Gram-nice, anerobic, spore-forming bacillus belonging to the *Clostridiaceae* circle of relatives. This bacterium may be an element of the regular intestine microbiota; but, while it proliferates excessively, it can exhibit pathogenic characteristics. It produces various toxins that could result in gastrointestinal issues, which include diarrhea and, in greater excessive times, necrotizing enterocolitis. This is especially regarding for at-threat companies consisting of toddlers and people with weakened immune structures. Therefore, at the same time as *C. perfringens* usually exists harmlessly in the intestine, it has the ability to disrupt intestinal fitness through toxin production under conducive conditions for its growth [37].

CONCLUSION

The intestinal microbiota is accountable for a multitude of significant functions that shape the host's physiology, as follows the maturation of the immune system, the response of the intestines to epithelial cell injury, and the metabolism of xenobiotics and energy. These tasks are predominantly carried out by four bacterial phyla in the gut microbiome of the majority of mammals. The primary objective of most of this research has been to establish a "Core microbiome" [38]. This is a significant goal, as it suggests that there is a common set of crucial species or strains shared by all individuals that play a role in defining human health and can potentially be utilized for identifying drug targets. However, the data from these studies have presented conflicting findings on this matter [39].

AUTHOR CONTRIBUTIONS

The first two authors have done extensive literature search and the corresponding author sketched the sequence of the entire article and added points.

CONFLICT OF INTEREST

The authors express that there is no conflict of interest.

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