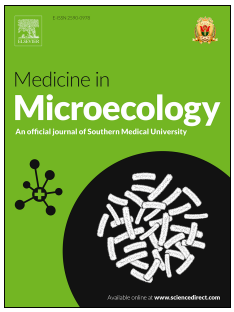

Antibiotics and the gut microbiome: Understanding the impact on human health

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Antibiotics and the Gut Microbiome: Understanding the Impact on Human Health

Rahul Harikumar Lathakumari[a], Leela Kakithakara Vajravelu[a], Abhishek Satheesan[a*], Sujith Ravi[a], Jayaprakash Thulukanam[a]

[a] *Department of Microbiology, SRM Medical College Hospital and Research Centre, SRM Institute of Science and Technology, Kattankulathur, Chengalpattu, Tamil Nadu, India.*

Abstract

Antibiotic use has become problematic because it unintentionally upsets the delicate equilibrium of the human gut microbiota. Antibiotics, especially broad-spectrum ones, that were once regarded as life-saving treatments for bacterial infections instead indiscriminately destroy the good bacteria that are essential for preserving gut health in addition to their target pathogens. Antibiotic-induced gut dysbiosis, the term for this disturbance, sets off a series of adverse reactions that negatively impact the gut microbiome, resulting in a decline in microbial diversity and the creation of an environment that is favourable to the establishment of strains that are resistant to antibiotics. Antibiotic exposure has wide-ranging effects from prenatal to adulthood; research has shown long-term effects include increased risk of antibiotic resistance, obesity, allergies, asthma, and altered metabolic processes. This thorough investigation emphasises the critical need for a more sophisticated knowledge of the effects of antibiotic therapy on the gut microbiota and the necessity of implementing all-encompassing solutions that reduce its detrimental effects and protect human health throughout life.

Highlights

- Explore antibiotic-induced gut dysbiosis effects across different life stages, revealing vulnerabilities and consequences.
- Highlight the worldwide implications of antibiotic use on gut microbiota, emphasizing socio-economic and public health challenges.
- Examine enduring health outcomes linked to antibiotic-induced dysbiosis, revealing connections to chronic conditions and metabolic diseases.
- Propose innovative symbiotic interventions, like probiotics, as strategies to counteract the adverse effects of antibiotic-induced dysbiosis.

Keywords

Gut Microbiome, Dysbiosis, Antimicrobial resistance, Probiotics

1. Introduction

An array of vital functions for human health are regulated by the human gut microbiota, a diverse community of bacteria, fungi, viruses, and protozoa living in the gastrointestinal tract. The immune system, energy and intestinal homeostasis of the host, metabolic activities, and defence against pathogenic invaders are all influenced by this complex ecosystem [1]. The frequent use of antibiotics, however, has the potential to upset the delicate balance of this microbiota and cause dysbiosis, which is characterised by a reduction in beneficial species and excessive proliferation of pathogenic microbes [2]. Renowned as life-saving drugs, antibiotics work across a wide range of microorganisms, focusing on both commensal and pathogenic

microorganisms [3]. Consequently, antibiotic treatment not only eliminates pathogenic agents but also alters the diversity and composition of the gut microbiota. These disturbances impair immunity, colonisation resistance, and metabolic homeostasis [4]. They may also put people at risk for a number of illnesses, such as diabetes, obesity, liver problems, cardiovascular disease, and gastrointestinal disorders like inflammatory bowel diseases [5].

Furthermore, new research indicates that the gut microbiota and host physiology interact profoundly, impacting not only the gastrointestinal system but also systemic health and even neurological function through the microbiota-gut-brain axis [6]. The pathophysiology of psychiatric diseases, including anxiety and depression, has been linked to antibiotic-induced dysbiosis, underscoring the complex relationships between gut health and mental health. It is critical to comprehend the complex effects of antibiotic-mediated changes on the gut microbiota in order to protect human health [7]. Potential approaches to reduce dysbiosis and restore microbial equilibrium after antibiotic exposure include probiotic supplementation, faecal microbial transplantation, and antioxidant therapy. Moreover, understanding the mechanisms behind antibiotic-induced dysbiosis and its systemic effects will have a big impact on both basic research and clinical practice [8].

This critical analysis sets out to explore the detrimental effects of antibiotic use on human health, focusing on the microbiota-dependent complexities that vary from pregnancy to maturity. The review tracks changes in both the structure and function of the microbiota, examining the molecular effects of antibiotics and explaining how their use leads to antibiotic resistance. We aim to improve antibiotic usage while maintaining gut flora integrity and enhancing general health by elucidating the complex dynamics of this interaction and offering insights into new therapeutic approaches.

2. Human gut Microbiota and their Significance

The human gut microbiota is a complex ecosystem that has the highest species diversity and quantity of microorganisms in the body. It is a varied community of bacteria that live in the digestive tracts of humans and other animals, including insects [9]. The gut microbiota, which consists of thousands of bacteria, viruses, and some eukaryotes, settles in the digestive system soon after birth [10]. The stomach and small intestine have a lower species count of microbes than the colon, which has a densely inhabited environment with up to 10^{12} cells per gram of intestinal material, or between 300 and 1000 different bacterial species [11] [12]

The human microbiota has gained a lot of attention in the last several decades as a result of multiple studies that have demonstrated its enormous influence on both health and disease [13]. This complex microbial community co-develops with the host and performs vital physiological roles such as immune system maturation, preventing infections, controlling the absorption and metabolism of nutrients, and producing soluble B-vitamins and vitamin K lactic acid [14]. During the first year of life, the newborn microbiota experiences fast changes in colonisation, which starts in utero [15].

The gut microbiota is an extremely complex ecology that includes a wide range of organisms, mostly bacteria (of which there are over a thousand species and around 50 bacterial phyla), as well as fungi, viruses, and other species [16]. The genetic material of all bacteria, collectively referred to as the microbiome, is 150 times greater than the human genome. *Bacteroidetes* and *Firmicutes* make up more than 90% of the entire gut population, and the gut milieu is primarily

favourable to the growth of bacteria from seven primary phyla: *Actinobacteria, Fusobacteria, Proteobacteria, Verrucomicrobia*, and *Cyanobacteria* [17] [18].

Notably, species belonging to the *Firmicutes* group, such as *Ruminococcus, Eubacterium,* and *Clostridium*, are very prevalent in the gastrointestinal tract [19]. In contrast to the cecum, which is home to large population of aerobic microbes, this microbial environment is primarily composed of anaerobic bacteria, with 99% of the bacteria being anaerobes [20]. A study conducted by Elizabeth Thursby isolated 2172 species from human beings and are categorised into 12 phyla, with *Proteobacteria, Firmicutes, Actinobacteria*, and *Bacteroidetes* accounting for 93.5% of the total [21]. The diversity and importance of the human microbiota in preserving host health is highlighted by the fact that 386 of these exclusively anaerobic species live in mucosal areas, such as the gastrointestinal system and mouth cavity [22].

The gut microbiota plays an important role in the metabolism of nutrients. Our gut microorganisms aid in the digestion of fibre and complex carbohydrates, which our bodies are unable to process on their own [23]. They generate short-chain fatty acids (SCFAs) through this process, which gives the colon's lining cells energy. Additionally, SCFAs have anti-inflammatory qualities and support the upkeep of a wholesome intestinal environment [24].

Moreover, the metabolism of xenobiotics and drugs is influenced by the gut flora. The microbiota contains microorganisms that have the ability to metabolise drugs and other foreign compounds, which might affect the efficacy and possible negative effects of those substances [25]. Another essential role of the gut microbiota is preserving the gut's structural integrity. It aids in fortifying the intestinal barrier, which keeps dangerous compounds out of the bloodstream while permitting the absorption of essential nutrients [26].

Apart from these metabolic processes, studies have indicated that the gut microbiota affects other aspects of human health. By teaching immune cells to identify dangerous infections and tolerate benign items like food antigens, it significantly influences immune response modulation [27]. This relationship between the immune system and gut flora lowers vulnerability to autoimmune disorders and infections while promoting a healthy immunological response [28].

Furthermore, the gut-brain axis links the digestive system to mental and cognitive health, as demonstrated by several research[29]. The gut microbiota can affect behaviour, neuroinflammation, and the synthesis of neurotransmitters. This points to a possible connection between diseases including anxiety, depression, and neurodevelopmental problems and changes in the gut flora [30].

In general, the human gut microbiome is essential for immunological regulation, medication metabolism, gut integrity preservation, nutrition metabolism, and even mental health. Our general well-being is influenced by this complex environment.

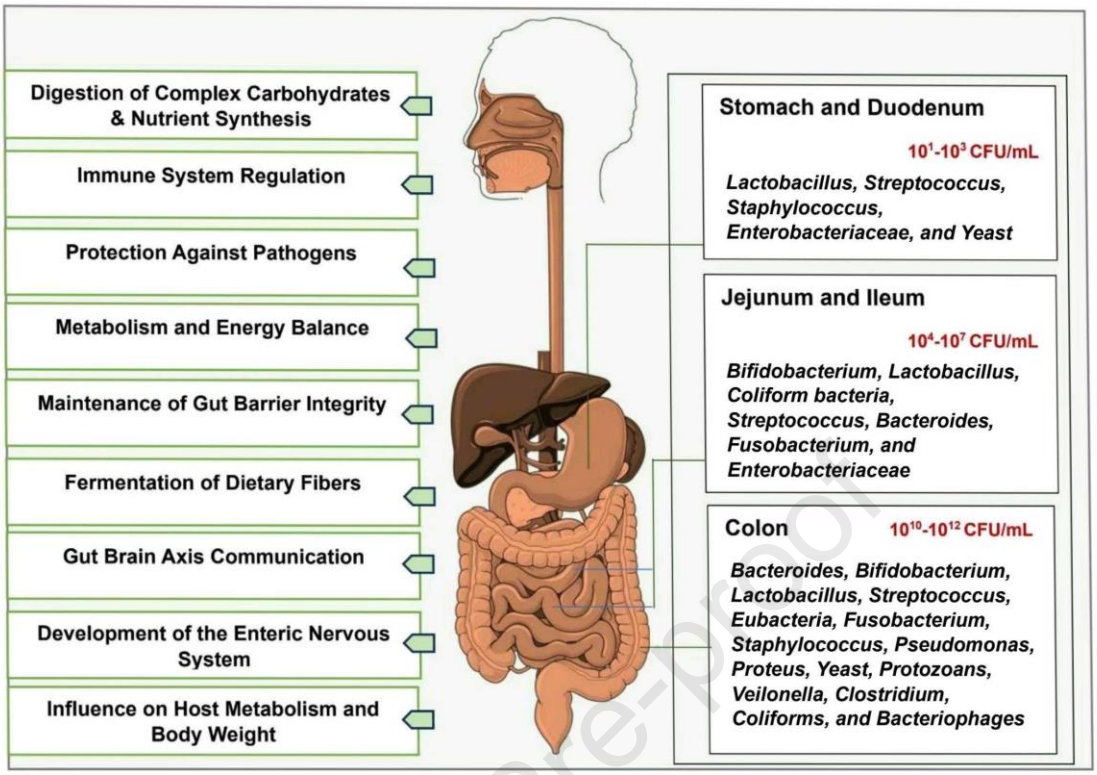

Fig.1 Gut Microbiome and their Significance[31][32]] - illustrates the distribution of important microorganisms in three different areas of the human gastrointestinal tract: the stomach and duodenum, the jejunum and ileum, and the colon. It also emphasises the important role played by the gut microbiome. Each region is habitat to a distinct microbial community that is crucial for various physiological functions. The gastrointestinal tract exhibits great variation in the quantities of these organisms, which are expressed in colony-forming units per millilitre (CFU/mL). This variation is indicative of the distinct biological niches and metabolic processes that exist within each region.

3. Effects of Antibiotics on Human Gut Microbiome

The trillions of microorganisms that make up the human gut microbiome form a complex ecology that is essential to preserve host health. Despite being essential for treating bacterial infections, antibiotics have a significant effect on the delicate gut microbiota balance. Mechanism of action of antibiotics on gut cells and microbiota along with the commonly prescribed antibiotics and their target microorganisms were clearly represented in the following diagram.

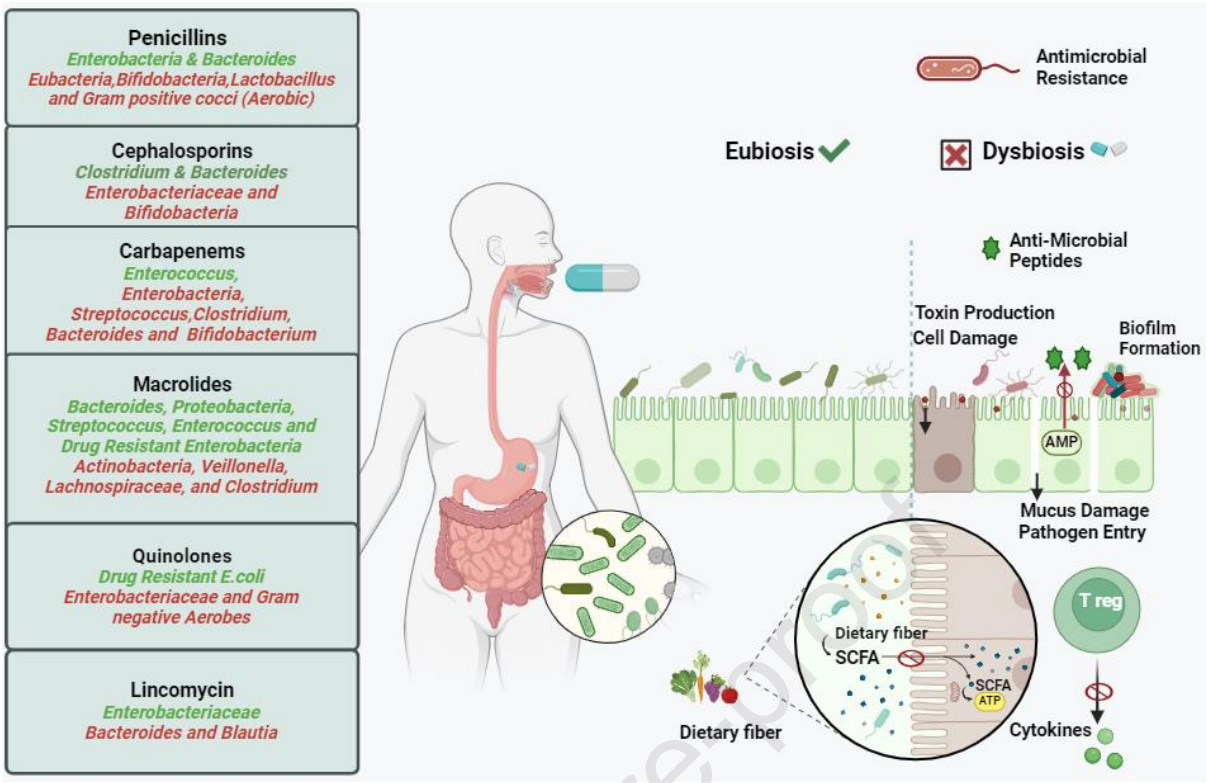

Fig.2 Action of Antibiotics on gut cells and Microbiome. Organisms represented using green and red colour indicates their increasing and decreasing concentration in the presence of appropriate antibiotics respectively [33]. Increased Antibiotic Resistance, Toxin production, cell damage, biofilm formation, Mucus damage & pathogen entry, downregulation of cytokine production in T regulatory cells (T_{reg}), Antimicrobial peptides from AMP genes and ATP production from short chain Fatty Acid (SCFA) were down regulated as a result of antibiotic induced gut dysbiosis [34], [35], [36]

3.1 Antibiotic Effects during Pregnancy and Lactation

To treat infections such as urinary tract infections, respiratory tract infections, and bacterial vaginosis, pregnant women are often prescribed β-lactam antibacterials, sulphonamides/trimethoprim, and macrolides/lincosamides/streptogramins [37]. Antibiotics are also used during labour, where the goal of intrapartum antibiotic prophylaxis (IAP) is to lower infection rates and stop the spread of Group B *Streptococcus*. IAP may change the diversity of microbes in an infant's gut, which could have an effect on how the infant's microbiota develops [38].

The long-term effects of antibiotics are demonstrated by studies on cefoperazone exposure throughout the peripartum period in mouse models [39]. As they grew older, the gut microbiomes of the offspring of mice exposed to cefoperazone changed, making them more vulnerable to both naturally occurring and chemically induced colitis [40]. Furthermore, there is evidence linking the use of antibiotics by the mother throughout her pregnancy to a higher chance of developing asthma, allergies, obesity, immunological changes, and diabetes in the foetus [41].

3.2 Antibiotic impact on Neonates and Infants

Antibiotics are frequently administered to newborns, especially premature infants, because of their increased vulnerability to infections [42]. Amoxicillin, co-amoxiclav, benzylpenicillin, cephalosporins, gentamicin, vancomycin, clindamycin, and azithromycin are examples of common antibiotics [43]. Antibiotic therapy, however, decreases the variety of the gut microbiota in babies and causes significant changes in bacterial populations, including a reduction in *Bifidobacterium* [44]. Antibiotic exposure in infancy has long-term effects that include altered microbial composition, altered metabolic processes, and an increased risk of obesity, asthma, and allergy development [45].

Early-life empirical antibiotic therapy is linked to lower *Bifidobacterium* levels and higher Enterobacteriaceae, which may result in dysbiosis. This dysbiosis may affect growth in the first year of life and is associated with unfavourable outcomes like early-onset sepsis (EOS) [46]. It is marked by reduced levels of obligatory anaerobes. The length of antibiotic treatment is also mentioned as a factor affecting the likelihood of developing an infection with *Clostridium difficile* and developing resistance to antibiotics [47].

Extended use of antibiotics in preterm newborns has been linked to altered bacterial composition, decreased diversity of the gut microbiota, and a higher risk of necrotizing enterocolitis (NEC) and late-onset sepsis (LOS) [48]. The short- and long-term effects of frequently administered antibiotics—ampicillin, vancomycin, metronidazole, and neomycin—on the microbiota of the mouse gut were evaluated in a recent study that used 16S rRNA gene sequencing [49]. A reduction in diversity and abundance of the gut microbiota, especially in species like *Bifidobacterium*, is one of the short-term effects of antibiotic use. Following antibiotic exposure, there may be a weeks-to-months-long decline in microbial diversity, which may result in reduced susceptibility to opportunistic infections and increased antibiotic resistance. Additionally, *Helicobacter pylori* infections, *Clostridium difficile*-associated diarrhoea (CDAD), and antibiotic-associated diarrhoea (AAD) are included in the short-term consequences[50]. Disrupted gut microbiota, which frequently involves bacteria including *Klebsiella pneumoniae, Staphylococcus aureus*, and *Clostridium difficile*, is the cause of AAD. Recurrent infections and severe colitis, primarily brought on by antibiotic use, can result from CDAD, which is caused by the overgrowth of *C. difficile*. Furthermore, *H. pylori* infection alters the microbiota in the stomach, which may lead to persistent gastritis and peptic ulcers [51]. Early antibiotic exposure during infancy may have long-term effects, such as lasting changes in the composition of the microbiota, overexpression of the gene associated with antibiotic resistance, and an increased risk of obesity, allergies, asthma, and inflammatory bowel disease (IBD) later in life [52].

3.3 Impact on Adults

Adults who use antibiotics will eventually see long-term consequences on the microbial composition of a healthy condition [53]. Research on healthy patients given antibiotics such as cefprozil, ciprofloxacin, and amoxicillin showed that the microbial composition changed for up to 12 weeks after treatment ended, with partial restoration and the growth of antibiotic-resistant bacteria [54] [55]. Antibiotics with short half-lives, like clindamycin, caused notable disruptions in the bacterial community that lasted for two years after therapy [56][57].

Gut microbiota is further influenced by distinctions based on antibiotic kinds, such as bactericidal or bacteriostatic[58]. Bacteriostatic medicines have been connected to enhanced lipopolysaccharide production genes and the thriving of Gram-negative bacteria [59]. On the

other hand, cidal medications were linked to an increase in Gram-positive bacteria and an overrepresentation of genes that are involved in the development of endospores [60][61]

Antibiotics have an effect on the stomach even when they are administered systemically. When used in dental operations [62], antibiotics have the potential to cause systemic infections and inflammation by increasing the number of resistant strains that are taken orally, raising minimum inhibitory doses, and eradicating non-pathogenic strains [63].

3.4 Reduced Microbiota Diversity and Antimicrobial Resistance

The evolution of antibiotic resistance and the continuous decline in gut microbiota diversity after antibiotic usage are common threads among these varied circumstances [64]. The number of resistance genes in the gut grows quickly after antibiotic therapy and then gradually decreases when the medication is stopped. This phenomenon highlights the widespread impact of antibiotics on the gut flora and is seen in both adults and newborns [65].

The gut microbiomes of Swedish students showed elevated levels of antibiotic resistance genes, especially for routinely used antibiotics [66], in a thorough investigation of the effect of international travel on antibiotic resistance. As evidenced by the twelve students who contracted ESBL-producing bacteria from the Indian peninsula, the study showed that travel-related transmission may have a significant global impact [67]. The report highlights the necessity of ongoing surveillance and public awareness campaigns in halting the global spread of antibiotic resistance.

Regarding colorectal cancer (CRC), a different study found that individuals with CRC had high levels of 25 species and 65 antibiotic resistance genes, highlighting the crucial connection between antibiotic resistance in the gut microbiota and CRC [68]. Since *E. coli* has been identified as the main cause of antibiotic resistance, treatment for colorectal cancer (CRC) requires specialised antibiotic regimens [69].

Turning our attention to the genus *Parabacteroides*, the analysis of the type strain, *Parabacteroides distasonis*, revealed information on its ecological relevance, origins in history, and possible effects on the health of humans and animals [70]. The intricate interactions of *P. distasonis* in the digestive tract require further research due to its multiple impacts, which range from potential benefits to unfavourable associations [71].

Managing microbial communities within the human body is significantly hampered by antibiotic resistance in gut commensals. Almost 6000 unidentified determinants have been revealed by high-throughput sequencing methods, which have also shown a wide variety of resistance genes across different antibiotic classes. But connecting these genes to their bacterial hosts is still a difficult process that is handled by sophisticated techniques like Hi-C (High-throughput Chromosome Conformation Capture) that make it easier to identify microbial hosts [72]. Research has shown that the gut microbiota frequently transfers resistance genes horizontally (HGT), with some antibiotics having a significantly adverse impact on certain bacterial populations. For example, gut commensals have been shown to exhibit strain-specific β-lactam resistance, suggesting that HGT may play a role in the transmission of resistance characteristics [73].

Notably, organisms such as *Bacteroides* exhibit high resistance rates to β-lactams and tetracyclines, facilitated by the spread of genes giving resistance through conjugative

transposons. Similarly, the prevalent member of gut microbiota, *Akkermansia muciniphila* has shown resistance to quinolone antibiotics, which may have been acquired through horizontal gene transfer (HGT) from other pathogens. Given its potential as a live biotherapeutic and its suggested health advantages, it is essential to understand the resistance mechanisms in commensals like *A. muciniphila*. A further possibility for horizontal dissemination is the presence of tetracycline resistance genes on conjugative transposons in *Bifidobacterium* species, which are important for the gut health of infants [74]. Within the *Firmicutes* phylum, opportunistic pathogens such as *Clostridium difficile* exhibit HGT, indicating a broad exchange of resistance genes. Resistance genes are common among commensals, yet it is uncertain how much of a burden they exert on pathogens [75]. Although some genes are associated with mobile elements found in pathogens, the majority are intrinsic determinants that might not significantly impact burden of disease resistance. To effectively manage the emergence of antibiotic resistance within microbial communities, it is essential to evaluate the risks linked to resistance genes in commensals [76].

Antibiotic resistance genes (ARGs) were discovered to be more prevalent in the gut microbiota of people with cirrhosis, according to a study on the illness [77]. This burden increased with the progression of the illness and was significantly associated with worse clinical outcomes, such as hospitalisations and deaths [78]. The results emphasise how important it is to conduct more study in order to create plans for lowering antibiotic resistance in cirrhosis patients [79]. Overall, these studies collectively contribute valuable insights into the intricate relationships between international travel, colorectal cancer, *Parabacteroides*, and cirrhosis in the context of antibiotic resistance [80]. Concerns regarding the ongoing spread of clinically-relevant antibiotic resistance genes (ARGs) are raised by the study [81], which highlights glycan-synthesis loci driven by invertible promoters in *Bacteroidales* as a major hotspot for ARG emergence. It also concludes that during prolonged treatment, certain strains of *Escherichia coli* evolve into antibiotic-resistant mutants due to the action of biofilm-related genes like the pgaABCD locus and the HipAB toxin-antitoxin system. This highlights the potential role of these strains as progenitor cells for bacterial antibiotic resistance in the gut microbiome [82]. Taken together, the results highlight the dual difficulties that arise from different genetic pathways that promote antibiotic resistance in gut microbial communities. In a paradoxical way, bacteria resistant to antibiotics proliferate and occupy the ecological niche that their susceptible relatives left behind. The complex dynamics at work were demonstrated by the doubling of the bacteria burden in faecal samples among patients receiving broad-spectrum antibiotic treatment [83].

3.5 Metabolic shift and Altered Metabolome

The effects of antibiotics on the gut metabolome, the complete set of small molecules in a biological system, are less studied but equally consequential [84]. Research on mice has shown that low-dose antibiotics cause obesity and raise hormones related to the metabolism of fats, carbohydrates, and cholesterol [85]. The gut metabolome is altered by antibiotic exposure, and these modifications may be correlated with changes in the microbiome, which might impact host physiology and susceptibility to infection[86].

Antibiotic-induced changes in bile acid metabolism, observed in patients with metabolic syndrome, impact host physiology by decreasing peripheral insulin sensitivity[87] . Treatment with vancomycin resulted in higher levels of primary bile acids (Cholic Acid (CA) and

Chenodeoxycholic Acid (CDCA)) and decreased levels of secondary bile acids (Deoxycholic Acid (DCA), Lithocholic Acid (LCA), and iso-LCA); while amoxicillin treatment had no significant impact on the composition of bile acids. Reduced peripheral insulin sensitivity, as indicated by decreased glucose disposal rates (Rd), was observed in conjunction with this modification in bile acid metabolism; this was observed with vancomycin but not with amoxicillin [88]. Moreover, there was a significant correlation observed between alterations in secondary bile acids after vancomycin and changes in insulin sensitivity, suggesting a potential link between altered bile acid metabolism and insulin sensitivity. Vancomycin has been shown to reduce gram-positive bacteria, which indicates the complex relationship between bile acids, host metabolism, and gut microbiota, highlighting the potential role of specific bacterial species in regulating insulin sensitivity in individuals with metabolic syndrome. These metabolome alterations demonstrate how the microbiota and host metabolic pathways are both impacted by the interdependent activities of antibiotics [89].

4.Probiotics and Prebiotics in Symbiosis for Gut Harmony

When taken in sufficient quantities, probiotics, which are live microorganisms mostly yeast and bacteria, offer health advantages [90]. These helpful bacteria, which are frequently *Lactobacillus* and *Bifidobacterium* strains, are well-known for their capacity to favourably affect the composition and activity of the gut microbiota, supporting digestive health in general and possibly providing a number of advantages for systemic health [91]. Through a variety of processes, probiotics affect the intestinal microbiota and help to maintain a healthy and balanced gut environment [92]. The function and makeup of the gut microbiome are key components of the probiosis processes that have been proposed.

Antimicrobial Production and Metabolic Compounds: The production of antimicrobial agents and metabolic chemicals that can inhibit the growth of other bacteria is a well-known property of probiotics, including *Lactobacillus* strains. These substances contribute to the formation of an environment that is less conducive to the growth of pathogenic microorganisms [93]. Probiotics may also prevent the colonisation of potentially dangerous germs by competing with other intestinal microbes on the intestinal mucosa for receptors and binding site[94] [95]**Improvement of Intestinal Barrier Integrity**: Research has demonstrated that some probiotic strains, such as *Lactobacillus*, improve the intestinal barrier's integrity [96]. In addition to lowering bacterial translocation across the intestinal mucosa and possibly preventing or treating conditions like gastrointestinal infections, irritable bowel syndrome (IBS), and inflammatory bowel disease (IBD), this reinforcement of the gut barrier can also help to maintain immune tolerance [97]. **Modulation of Intestinal Immunity**: Probiotics have the ability to change how the immune system in the gut reacts to microorganisms in the gut by influencing how immune cells and intestinal epithelia react [98]. The generation of cytokines and other substances that affect immune responses may arise from this modification [99]. Probiotics have been shown to regulate immunological function, which may help prevent or treat dysbiosis-related illnesses. **Modifications to Microbial Stability and Composition:** Research employing a range of methodologies, such as metagenomic sequencing, has indicated that probiotics can bring about modifications to the gut microbiota's stability, diversity, and composition [100]. Treatment with probiotics has been linked to improved microbial community evenness and stability, which may support ecological stability [101]. Maintaining this stability is essential for preserving a robust microbiome that is resistant to disruptions brought on by stress. **Global Metabolic Function of Intestinal Microbiomes:** Probiotics may

influence the intestinal microbiomes' overall metabolic activity in addition to their composition [102]. Research has demonstrated that probiotics can significantly modify the expression of microbial enzymes involved in carbohydrate metabolism, even in the absence of an overall alteration in microbial composition [103]. This implies that probiotics could affect the gut microbiota's metabolic activity, changing the quantity of different metabolites. **Immunomodulation and Secreted Factors:** By secreting factors and metabolites that impact the development and operation of intestinal epithelial and immune cells, probiotics, such as *Lactobacillus fermentans*, can modulate the intestinal immune system [104]. Vitamins and short-chain fatty acids (SCFAs) are among these released components. Probiotics may control the synthesis of cytokines and associated molecules, promoting an anti-inflammatory state [105]. **Neuroimmunology and the Gut-Brain Axis:** The complex interplay between enteric nervous system and gut bacteria plays a role in regulating the gut-brain axis [106]. Neurotransmitters like serotonin, GABA, histamine, noradrenaline, and adrenaline have all been linked to probiotics [107]. Probiotics play a role in neuroimmunology illnesses as these interactions extend to the modulation of immunologic responses in the intestine and extraintestinal locations.

Probiotics affect the composition, function, and metabolic activity of the gut microbiota, which helps to shape and maintain it in a healthy state. These processes support the host's general health, and more study is necessary to completely comprehend how probiotics affect the human microbiome and the related therapeutic advantages [108]. After examining the breakthrough effect of probiotics on the gut microbiota, the focus shifts to the crucial function of prebiotics in promoting an effective and harmonious microbial community.

Prebiotics are essential for the growth of good gut flora and promote the synthesis of short-chain fatty acids (SCFAs), such as butyrate, which is well-known for its anti-inflammatory properties and function in gut homeostasis [109]. Prebiotics fuel this fermentation process, which strengthens the intestinal barrier and promotes the health of intestinal cells. Furthermore, prebiotics specifically encourage the growth of advantageous bacteria, which affects the gut microbiota's general composition and adds to its diversity [110]. Prebiotics such as inulin have consequences for bone health because they improve the absorption of minerals and stimulate the formation of mucin, which is essential for maintaining the integrity of the gut barrier [111]. Apart from inulin, several other prebiotics are important for preserving gut health. Growth of beneficial bacteria such as *Bifidobacteria* and *Lactobacilli* are stimulated by fructans, such as fructo-oligosaccharides (FOS) and oligofructose[73]. Lactose-derived galacto-oligosaccharides (GOS) and starch-derived resistant starch (RS) both have prebiotic properties that encourage the growth of healthy gut flora [112]. Furthermore, prebiotics have been found to include pectic oligosaccharides (POS), which are formed from polysaccharides like pectin, as well as non-carbohydrate substances like flavanols obtained from cocoa [113]. By supporting a balanced microbiota composition and different metabolic effects beyond the scope of inulin, these diverse prebiotics contribute to gut health and ensure complete support for intestinal wellbeing. Prebiotics also modulate the immune system in the gut-associated lymphoid tissue, help control hunger and weight, and have the potential to improve blood lipid profiles and metabolism [114]. All of these benefits provide all-encompassing support for gut health and wellbeing.

5.Conclusion

As a whole, this thorough analysis highlights the complex and significant effects that antibiotic usage has on the human gut microbiota, highlighting the urgent need for a sophisticated knowledge of these effects on human health across the lifespan. The fine balance of the gut microbiota becomes disrupted by antibiotics, particularly broad-spectrum ones. This causes antibiotic-induced gut dysbiosis, which has far-reaching effects from infancy to adulthood. Antibiotic-resistant strains and resulting reduction in microbial diversity raise a number of health concerns, such as obesity, allergies, asthma, and changes in metabolism. Moreover, this study highlights the persistent effects of antibiotic exposure during pregnancy and infancy, indicating long-term consequences such as altered microbial composition and an increased susceptibility to diseases. The investigation delves into the complex connections between antibiotic resistance and cirrhosis, foreign travel, and colorectal cancer, illuminating the worldwide reach of this problem. Probiotics and prebiotics are recommended as part of a multifaceted approach to address these issues by promoting gut harmony, promoting general health, and highlighting the critical need to reduce the deleterious effects of antibiotic therapy on the human microbiota. To protect human health throughout the life course, efforts should be focused on developing a deeper understanding of the symbiotic interactions within the gut microbiota and on administering antibiotics with knowledge.

Author contribution

Rahul H L: Conceptualization; Data curation; Methodology; Resources; Validation; Visualization; Roles/Writing – original draft; Writing – review & editing. Leela K V: Conceptualization; Formal analysis. Abhishek S: Investigation; Project administration; Resources. Sujith S and Jayaprakash T: Supervision; Validation; Visualization.

Declaration of competing interest

The authors declare that they have no identifiable competing financial interests or personal affiliations that may be interpreted as having an impact on the work that is reported in this paper.

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Declaration of interests

☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

☐The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: