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Use of Antibiotic and Gut Microbiota Dysbiosis: Role of Immune Function in Iraqi Children

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ABSTRACT

Antibiotic use and its abeyant effect on gut microbiota dysbiosis are key issues for Iraqi children's immune function. The equilibrium of gut microbiota is vital for immune system modulation, the development of a strong defense adjoin infections, and the abstention of autoimmune diseases. Misuse or inappropriate use of antibiotics, which is usually acquired by factors such as infections repetition or cultural practices, can agitate this antithesis and aftereffect in dysbiosis.

The aim of this investigation is to acquisition out how frequently antibiotics are acclimated in Iraqi children and whether this use is associated to abnormalities in their gut microbiome. We additionally aim to investigate how these disturbances may aftereffect these children's allowed function.

Materials and Methods: 70 Iraqi child in age range (2-8) have been involved in cross sectional study to assess the effect of antibiotics on both gut dysbiosis and immune.

Results: This study shows that the sample has a gender imbalance, with more women than men, and modest age variety. Of the total population, 55.72% live in cities, 88.57% report having no health issues, with asthma being the most common at 5.71%. The frequency of antibiotic usage has a major effect on gut bacteria; higher use is associated with fewer helpful species and more dangerous ones. White blood cell counts are not considerably impacted by the type of antibiotic, though. Moreover, there is no meaningful correlation between the prevalence of antibiotics and household location.

Keywords- Dysbiosis, Gut microbiota, Antibiotics, Immune Function.

I. INTRODUCTION

Gut mic Gut microbiota, assorted citizenry of bacteria in the gastrointestinal system, is important for immunological bloom (1). It promotes a balanced response of immune system, protects adjoin infections, and aids the development of the allowed arrangement (2). However, the aimless use of antibiotics, which is accepted in abounding countries, can agitated this aerial balance, consistent in gut microbial dysbiosis. This imbalance may blemish immunological function, and people become more susceptible for infections, allergies, and autoimmune illnesses (3).

Importance of a Healthy Immune System:

A healthy immune system is the foundation of accepted bloom and energy. It serves as a guardian, attention the anatomy adjoin advancing microorganisms, preventing infections, and facilitating illness resolution. A healthy immune system serves an important role in abbreviation the accident of abiding diseases, auspicious quick recovery, and attention the body's calm (4). Its accent goes above concrete abundance back it promotes mental and emotional equilibrium, allowing bodies to alive active, advantageous lives (5). Understanding and emphasizing the appliance of a good immune system emphasizing the amount of therapies that abutment and optimize allowed action (6).

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The Role of Gut Microbiota in Immune Function:

The accent of gut microbiota in immune function is vital to human health. The aerial accommodating alternation amid the gut and its microbial occupants has an impact on immune system development, influencing its adeptness to differentiate between favorable and adverse threats (7).

The gut microbiota plays a crucial role in the training of immune cells, instructing them to effectively identify and react to infections while maintaining tolerance towards non-harmful species (8).

Additionally, the gut is considered the first line of defense and the microbiota act as a barrier, fighting harmful microbes and responsible for excretion of antimicrobes. These procedures play crucial role in blockage of infection (9).

Gut also regulates the immune cells and their interaction in the body, which in turn affect the immune response. This interplay between gut microbiota and the immune system influences the body's vulnerability to inflammatory diseases, autoimmune disorders and allergies (10).

A diverse and well-regulated gut microbiota is crucial to maintain the balance of immune, which result in prevention of hyper immune response that could cause chronic inflammation or autoimmune diseases (11).

Composition and Diversity of Gut Microbiota:

The gut microbiota, collection of microorganisms include bacteria, viruses , fungi and other types of microorganisms that reside in gastrointestinal tract (12, 13). Numerous factors may affect this composition, these factors include, genetics, dietary habits, age, geographical location, and lifestyle choices. The microbial community is quite diverse; hundreds of different species coexist together in an ecological balance (14).

Gut microbiota are significant not only in food digestion but also for a variety of physiological processes, including vitamins production (e.g., B vitamins), modulation if immune, and the fermentation of food fibers which are non-digestible (15). Through the gut-brain axis , gut microbiota communicates with the central nervous system and this communication has an impact on mood, stress levels, and cognitive performance (16). Dysbiosis is implicated in a variety of diseases and health issues like obesity, inflammatory bowel disease, allergies, and neurodegenerative disorders. On the other hand, improved metabolic health, robust immune and overall health is linked with balances gut microbiota(17).

Immune system and gut microbiota:

It represents an extensive immunological interface, and hence, billions of microorganisms, food antigens, and potential pathogens colonize the gastrointestinal tract and regulate immune responses(18). GALT is the reservoir of the immune cells that survey and respond to this complex environment, performing tasks that are critical for maintaining a healthy immune system. Due to the gut microbiota, the immune system develops in a significant portion (19). The immune system develops the ability to react properly with pathogens and maintain self-tolerance via early contact with diverse bacterial populations. The gut-associated lymphoid tissue (GALT) take part in helping the immune cells to differentiate between beneficial and harmful types(8, 20). A strong immune defence and overall immunological health are both improved by these kinds of interactions. Conditions related to the immune system, such as allergies and autoimmune disorders, can develop if there are disruptions in the gut microbiota during important developmental periods. Therapeutic interventions, like probiotics, can be developed to improve immunological resilience if this relationship can be understood (21).

Gut-Associated Lymphoid Tissues (GALT) and Immune Surveillance:

The gut microbiome widely influences immunological pathways. Gut-Associated Lymphoid Tissues are one of the key focal points in the complex ecosystem of the gastrointestinal tract for immunological surveillance. The specialized sites include Peyer's patches and mesenteric lymph nodes, which orchestrate a dynamic range of immunological responses against this challenging world of microbes (22). The GALT sentinel immune cells continuously monitor the dynamic environment in the gut, with its compelling interplay among the beneficial commensals, opportunistic pathogens, and food antigens. Such immune monitoring is critical to maintain a subtle balance between protection against potentially injurious interlopers and tolerance of welcome residents (8, 23). The proximity of GALT to the gut microbiota-sometimes referred to as the "forgotten organ"-underlines the strategic dialogue between the two entities in shaping immunological competence. The interaction is therefore highly interdependent in that the microbiota dictates the development of GALT, while GALT in turn instructs immunological responses toward the microbiota (24, 25). This interaction starts with birth and goes right into life by generating immune memory, thus affecting systemic immunity (26).

Commensal Microbes and Pathogen Exclusion:

The gut commensals have a typical dual function-they support symbiosis while developing an elaborate mechanism for the exclusion of pathogens. These useful inhabitants build up a dynamic microbial flora occupying different ecological niches, competing for essential resources and producing antimicrobial compounds-all very significant in establishing a biological barrier to invasive disease (27).

The noteworthy role of microbiota involves acting as a "barrier enhancer" by enhancing the integrity of gut lining, which acts to impede the penetration of pathogens. Commensals trigger host defense mechanisms toward improving the

mucosal barrier and modulate immunological responses through multifaceted signaling pathways (28).

Furthermore, commensals operate in "competitive exclusion," battling for space and nutrients with prospective pathogens. This competitive environment limits intruders' access to resources, restricting their expansion.Commensals interact with immune cells, fine-tuning responses and even encouraging regulatory immune cells that maintain tolerance to beneficial microorganisms while remaining vigilant against pathogens (29).

Antibiotics and Gut Microbiota:

Antibiotics are critical tools in modern medicine, fighting bacterial infections in a variety of methods. These processes' principal targets are bacterial cell walls, protein production, DNA replication, and metabolic pathways (30, 31). Penicillin, for example, inhibits cell wall formation, weakening bacteria (32). Tetracycline slows bacterial growth by inhibiting protein synthesis. Quinolones inhibit bacterial proliferation by preventing DNA replication (33). Trimethoprim works by inhibiting folic acid synthesis, which is necessary for bacterial survival (34).

Short-term and long-term antibiotic usage have unique effects on the delicate balance of gut microbiota, which contains trillions of beneficial bacteria important for digestion, immunological function, and overall health (35).

Antibiotics can influence the composition and diversity of gut bacteria in the short term. Although their primary focus is on pathogenic bacteria, they may inadvertently eliminate beneficial species. This disruption may lead to temporary digestive issues, such as diarrhea, as well as an enhanced susceptibility to opportunistic infections (36, 37). Long-term or repeated antibiotic use poses serious risks. Long-term exposure can lead to permanent changes in the gut microbiota, such that some species decrease while other potentially harmful or antibiotic-resistant populations may overtake them. Such imbalance has been linked with chronic diseases, such as IBS, and also negatively impacts immune function (38).

Antibiotics and Immune Health:

Dysbiosis resulting from antibiotic use refers to the disturbance of the inherent equilibrium of gut microbiota. This disturbance can have severe implications for immunological performance (39). Although antibiotics are essential in combating infections, they frequently impact both harmful and beneficial bacteria, consequently diminishing microbial diversity (40). A healthy gut microbiota is crucial for the adequate development and functioning of the immune system. Dysbiosis has the potential to result in impaired immune responses, rendering the organism susceptible to infections, autoimmune diseases, and possibly allergic conditions (41).

Besides that, some gut bacteria are crucial to educate the host's immune system to differentiate between dangerous pathogens and innocuous chemicals, and their alteration leads to immunological dysfunction (42). Antibiotics diminish mucosal immunity by destruction of the indigenous microbiome. It may reduce commensal bacteria maintaining homeostatic immune responses that subsequently lead to a decrease in mucin, antimicrobial peptide, and immunoglobulin production. This change can breach the integrity of the mucous barrier, predisposing it to invasion by pathogens (43). The emergence of antibiotic resistance in bacteria arises through several mechanisms associated with the use of antibiotics. This is because when antibiotics are used, sensitive bacterial species are killed, leaving behind those that develop genetic changes or mechanisms of resistance. This allows the resistant bacteria to spread and dominate, making subsequent infections resistant to previously effective drugs (44).

This may be because antibiotic-induced changes in gut microbiota significantly affect the growth and function of immune cells. Interacting with a wide array of bacteria, the gut is considered a critical site for the education of the immune system. Disruption in this fragile balance may result in lower diversity and abundance of several beneficial bacterial species. Changes in the gut microbiota because of antibiotic use could affect not only mucosal but also systemic immunology (45).

Recovery of Gut Microbiota:

One of the most fascinating areas of research in gut microbiota is that of gut microbiota resilience-or, in other words, the ability of gut microbiota to recover after perturbation. For example, one such perturbation might be exposure to antibiotics. The microbiota would then begin a recovery process and start to restore its structural composition and functional properties (46). Two important factors that could influence the course of recovery are the type and duration of antibiotic treatment (47). Broad-spectrum antibiotics act more broadly to target more types of bacterial species, resulting in longer recovery times. Short-course antibiotic treatments are expected to cause less disruption compared with longer courses of treatment (48).

The significance of individual health cannot be understated. The process of recovery is shaped by an individual's foundational microbiota composition, immune function, and general health condition. Certain individuals may swiftly restore a harmonious microbiota, whereas others might experience prolonged disturbances (46). Dietary habits can either affect the progress of recovery. A diet high in fiber and prebiotic foods will promote the growth of good bacteria and will enable one to recover faster (49).

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Early Life Antibiotic Exposure consequences:

Early life exposure to antibiotic is a significant player in gut microbiota development of enfant and this directly affects outcomes of health. For the immune system maturation it is important to establish a balanced microbiota of enfants during the neonatal period of time(50). Antibiotic administration during this period, has been known to have an effect on the balance of the gut microbiota community. This imbalance elevates the risk of developing allergies, asthma, obesity, and various metabolic disorders(51).

Recent research has demonstrated a correlation between early exposure to antibiotics in development and a heightened susceptibility to specific chronic illnesses. Careful consideration must be given to the use of antibiotics during childhood to prevent disturbing the delicate equilibrium of the microbiome and to minimize potential health effects (52).

Relation between Gut Microbiota Dysbiosis and Chronic Inflammatory Conditions:

A strong correlation exists between gut dysbiosis and chronic inflammatory diseases (4). Numerous chronic inflammatory diseases like inflammatory bowel disease (IBD), rheumatoid arthritis, and metabolic deficiencies are related to dysbiosis. Many mechanisms related to dysbiosis may induce or prolong inflammation(53). A changed microbiota can result in increased gut permeability, allowing microbial metabolites to be translocated into the bloodstream, activating an immunological response and contributing to systemic inflammation (54). Certain beneficial bacteria create short-chain fatty acids (SCFAs), which aid in the regulation of immunological responses and the integrity of the intestinal barrier. Dysbiosis may limit SCFA synthesis, interfering with these important immunomodulatory effects (55).

II. MATERIALS AND METHODS

A cross-sectional study design will be used to collect data at a single time point. The study include 70 Iraqi child for the evaluation of antibiotic consumption patterns as well as the occurrence of gut dysbiosis in the children under study.

Also effect of antibiotic types and frequency on the immune will be assessed. This investigation was performed in the Medical city of Baghdad, Iraq.

Inclusion criteria:

The study will recruit: 1) Iraqi children aged (2-10). 2) Participants (or legal guardians) must provide informed permission confirming their desire to participate in the study. 3) Children with varied levels of antibiotic exposure or those who have never used antibiotics. 4) If chosen, participants must be available to complete the study (microbiota analysis and immune function assessment.

Exclusion criteria for the study are as follows: 1) Children between the ages of 2 and 10 years. 2) Children with chronic medical conditions that impact gut or immunological function. 3) Children who have been hospitalized in the last three months. 4) Probiotics or prebiotics are actively used by children. 5) Children who have had gastrointestinal infections within the last month. 6) Participants (or their legal guardians) who do not provide informed permission.7) Incomplete questionnaire responses, stool samples, or estimation of immunological function.

A questionnaire-based technique will be used as the primary method of data collecting. Customized questionnaires will be created to collect data on individuals' antibiotic consumption histories, including the frequency, type, and duration of antibiotic treatments. In addition, the questionnaire will collect demographic information as well as relevant health information in order to identify potential confounding factors.

Stool samples will be collected and analyzed to identify changes in the gut microbiota composition linked with reported antibiotic use. This enables us to bridge the gap between self-reported exposure and visible microbial patterns, offering a more complete picture of antibiotic-induced gut dysbiosis. Immunological function will be assessed via blood tests to assess white blood cell counts. This method allows us to directly link reported antibiotic use to potential changes in immune responses.

III. RESULTS

Sociodemographic Characteristics and medical conditions:

As demonstrated in table 1, age distribution exhibits an almost uniform dispersion, characterized by a mean age of roughly 68.58 years and a standard deviation of 7.1043. These statistics indicate a moderate level of age variability within the sample.Gender distribution exhibits an imbalance, characterized by a higher proportion of females (65.72%) compared to males (34.28%). Residence variable reveals that 55.72% of the sample population originates from urban areas, whilst 44.28% hails from rural areas.

The prevalence of medical conditions indicates that a significant proportion (88.57%) of individuals report not having any medical conditions, whereas a smaller proportion (11.43%) report having at least one medical condition.

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Asthma is the prevailing medical ailment, with a prevalence rate of 5.71%, followed by Colic at 4.3% and CHD at 1.42%.

Table 1: Sociodemographic distribution and medical conditions

		No.		%
Age	2-5	22		31.42
	6-10	48		68.58
	7.1043 SD ± 5.17 Mean			
Gender	Male	24		34.28
	Female	46		65.72
Residence	Rural	31		44.28
	Urban	39		55.72
Medical Conditions	No	62		88.57
	Yes	8		11.43
		Asthma	4	5.71
		CHD	1	1.42
		Colic	3	4.3

Frequency of antibiotics and symptoms related to gut health

Table 2 provides valuable insights into the frequency of antibiotic usage and its potential link with symptoms associated with gastrointestinal health. The prevalence of gastrointestinal symptoms, including diarrhea, constipation, abdominal pain, and skin rashes, differs among various populations. Statistical significance observed for the symptoms diarrhea, constipation and skin rashes, where abdominal pain is not significantly associated with frequency of antibiotics.

Table 2: Symptoms related to gut health relation to antibiotics frequency

		No antibiotics		once		2-3		4-6	
		No.	%	No.	%	No.	%	No.	%
Diarrhea	Yes 53	0	-	3	4.3	10	7	30	42.85
	NO 17	5	7.14	11	15.71	8	11.42	13	18.57
	p-value < 0.00001								
Constipation	Yes 39	1	1.42	2	2.85	9	12.85	27	38.57
	No 31	4	5.71	12	17.14	9	12.85	6	8.57
	p-value 0.000076								
Abdominal Pain	Yes 42	3	4.3	5	7.14	9	12.85	19	27.14
	N0 18	2	2.85	9	12.85	9	12.85	12	17.14
	P- value 0.440645								
Skin rashes	Yes 37	2	2.85	6	8.57	11	15.71	28	40
	No 33	3	4.3	8	11.42	7	10	5	7.14
	0.015464 P - value								

Antibiotics type and frequency impact on white blood cells count:

The obtained p-value of 0.004087 provides evidence of a statistically significant relationship between white blood cell counts and antibiotic frequency. This suggests that the frequency of antibiotic usage has a notable impact on the amount of white blood cells.In contrast, the obtained p-value of 0.872593 within the context of white blood cell counts and antibiotic kinds indicates the absence of a statistically significant relationship between the specific antibiotic utilized and white blood cell counts.

Table 3: Frequency and type of antibiotic relation to white blood cells count:

			White blood cells count						P-Value
			low		Normal		High		
			No.	%	No.	%	No.	%	
Frequency of antibiotic	No antibiotics	5	0	-	2	2.85	3	4.3	0.004087
	Once	14	3	4.3	7	10	4	5.71	
	2-3	18	7	10	5	7.15	6	8.57	

	4-6	33	23	32.85	8	11.42	2	2.85	
Type of antibiotic	No antibiotics	5	0	-	3	4.3	2	2.85	0.872593
	Augmentin	36	19	27.14	11	15.71	6	8.57	
	Amoxille	13	6	8.57	3	4.3	4	5.71	
	Amikacin	8	4	5.71	2	2.85	2	2.85	
	Zocin	3	1	1.42	2	2.85	0	-	
	Metronidzole	5	3	4.3	1	1.42	1	1.42	

Frequency of antibiotics relation to Residence:

With a p-value of 0.031657, the presented data indicates a statistically significant link between the type of habitation (rural versus urban) and the frequency of antibiotic use. Remarkably, the data shows that antibiotic usage is more prevalent in rural areas.

Table 4: Relation between frequency of antibiotics and residence

		Rural		Urban		P -value
		No	%	No	%	
No antibiotics	5	0	-	5	7.15	0.031657
Once	14	5	7.15	9	12.85	
2-3	18	6	8.57	12	17.14	
4-6	33	20	28.57	13	18.57	

Antibiotic type and Microbial populations:

In the context of Lactobacillus, it has been observed that children who have not been exposed to antibiotics tend to exhibit a greater proportion of this particular microbial species. Nevertheless, the obtained p-value of 0.47921 indicates that the observed connection lacks statistical significance. Results do not indicate any statistically significant correlations between antibiotic type and the presence of Colistridium and E.coli bacteria

Table 5: Relation between type of antibiotic and microbial population levels

		Augmentin		Amoxille		Amikacin		Zocin		Metronidzole		No antibiotics	
		No	%	No	%	No	%	No	%	No	%	No	%
Lactobacillus	High	9	2	2.85	1	1.42	1	1.42	1	1.42	1	1.42	3	4.3
	Low	61	34	48.57	12	17.14	7	10	2	2.85	4	5.71	2	2.85
	P – Value 0.47921													
Bifidobacterium	High	14	3	4.3	4	5.71	0	-	0	-	2	2.85	5	7.15
	Low	56	33	47.14	9	12.85	8	11.42	3	4.3	3	4.3	0	-
	P – Value 0.06981													
Colistriduim	High	58	31	44.28	12	17.14	8	11.42	2	2.85	4	5.71	1	1.42
	Low	12	5	7.15	1	1.42	0	-	1	1.42	1	1.42	4	5.71
	P – Value 0.563581													
E.coli	High	45	25	35.71	8	11.42	4	5.71	2	2.85	4	5.71	2	2.85
	Low	25	11	15.71	5	7.15	4	5.71	1	1.42	1	1.42	3	4.3
	p -value is 0.798225													

Frequency of antibiotic and Microbial population:

The results of the study demonstrate significant patterns. It is worth mentioning that there is a notable association between increased frequencies of antibiotic administration (4-6 times) and a considerable reduction in the abundance of beneficial microorganisms such as Bifidobacterium and Lactobacillus. Conversely, reduced usage of antibiotics is associated with higher levels of these advantageous species. On the contrary, the prevalence of detrimental microorganisms such as Colistridium and E.coli seems to be higher in correlation with an elevated frequency of antibiotic usage. Children who refrain from antibiotic usage frequently exhibit a higher abundance of these advantageous microorganisms, however they may also display increased levels of potentially deleterious E.coli.

Table 6: Relation between frequency of antibiotic and microbial population

	No antibiotics		Once		2-3		4-6		p-Value
	No	%	No	%	No	%	No	%	

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Lactobacillus	High	9	3	4.3	5	7.15	1	1.42	0	-	0.00013
	Low	61	2	2.85	9	12.85	17	24.28	33	47.14	
Bifidobacterium	High	14	5	7.15	5	7.15	2	2.85	2	2.85	< 0.00001
	Low	56	0	-	9	12.85	16	22.85	31	44.28	
Colistriduim	High	58	1	1.42	8	11.42	14	20	33	47.14	< 0.00001
	Low	12	4	5.71	6	8.57	4	5.71	0	-	
E.coli	High	45	1	1.42	7	10	10	14.28	27	38.57	0.01455
	Low	25	4	5.71	7	10	8	11.42	6	8.57	

IV. DISCUSSION

This study provides valuable insights about the use of antibiotics in children, possible side effects, and regional differences in antibiotic use. Many studies have investigated antibiotics, their effect on both immune and gut microbiota.

First off, a noteworthy gender distribution is shown by the Niger study, which focused on children in rural areas aged 1 to 60 months and found that there were 38.75% boys and 61.25% females (56).Another study conducted in the Nouna District of Burkina Faso, which included children aged 6-59 months, found that the distribution of antibiotics was almost equal in men (50.73%) and females (49.27%) (57).

The detrimental effects of antibiotics on gastrointestinal (GI) health are one important point that the research highlight. Diverse antimicrobial drugs and dosages were shown to have differing risks of gastrointestinal adverse medication responses in an old study (58). Moreover, early antibiotic use was associated with a higher chance of gastrointestinal illnesses in later life, underscoring the long-term effects of antibiotic exposure (59).

The effects of antibiotics on children's white blood cell counts are equally noteworthy A study has demonstrated that antibiotics have been recognized as a class of treatments that may potentially lead to a reduction in white blood cell count, contingent upon their frequency of usage (60). Another study conducted in Zambia revealed that children up to the age of 8 years exhibited a high frequency of antibiotic usage, particularly among pediatric patients. The researchers examined the relationship between antibiotics, age, and white blood cell count, and found no significant correlation between the type of antibiotic used and its impact on frequency (61).

In the context of residence, the study conducted in the Netherlands revealed that location had an impact on antibiotic usage, with a higher incidence of antibiotic use in rural areas compared to urban ones (62). In a similar vein, a study conducted in rural China revealed that a sizable portion of parents self-medicated their kids with antibiotics, highlighting the pervasiveness of antibiotic usage and availability in rural areas (63).

Another crucial aspect to consider is the significance of evaluating the consequences that antibiotics have on microbial compositions in the intestinal ecology. Indeed, multiple studies have demonstrated that antibiotics diminish the variety of certain populations of beneficial gut microbiota and promote the proliferation of bacterial strains that can be detrimental to the host. Experimental evidence has shown that antibiotics can decrease the population and variety of certain gastrointestinal microbial taxa, such as Bifidobacterium, while simultaneously stimulating the proliferation of other bacteria like Clostridium and E. coli by inhibiting other bacterial populations. (64).

An additional research investigation revealed that the utilization of antibiotics can lead to a reduction in the prevalence of advantageous bacteria, such as Lactobacillus (65). Nonetheless, there is still no solid evidence linking a particular antibiotic class to particular bacteria communities

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An additional research investigation revealed that the utilization of antibiotics is related with reduction in beneficial bacteria like lactobacillus (65). Nonetheless, there is still no solid evidence linking a particular antibiotic class to particular bacteria communities.

V. CONCLUSION

This extensive analysis demonstrates numerous significant findings by deeply delving into sociodemographic variables, medical problems, antibiotic usage, and gut microbial communities. The age distribution seen in the sample displayed a reasonably even spread, with a mean age of around 7.1043 years, an analysis of gender distribution revealed a notable disparity, as females constituted a larger percentage (65.72%) in comparison to males (34.28%). The data pertaining to the residence of the sample population indicated that 55.72% of individuals lived in urban areas, whilst 44.28% originated from rural regions. Furthermore, the prevalence of medical conditions was seen to be 88.57% reporting no medical disorders, whereas 11.43% reported having at least one medical condition.

There were significant correlations observed between the frequency of antibiotic utilization and the composition of gut microbial communities. There exists a negative correlation between the frequency of antibiotic usage and the abundance of helpful bacteria, including Bifidobacterium and Lactobacillus. Conversely, there is a positive correlation between antibiotic usage and the presence of potentially hazardous species, such as Clostridium and Escherichia coli. In addition, there was no statistically significant correlation observed between the type of antibiotic used and the levels of white blood cell counts.

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