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***Abdul-Bari Hejran^{1,2}, Aidyn Kydyrmanov²,
Atiqullah Sarwari^{1,2}, Mohammadullah Mohammadi¹,
Mohammad Yaqoub Sangin¹**

¹Helmand University, Afghanistan, Helmand;

²Al-Farabi Kazakh National University, Republic of Kazakhstan, Almaty

*e-mail: abdulbari.hejran94@gmail.com

THE HEALTH BENEFITS OF NORMAL FLORA IN HUMAN BOD

Normal flora is a natural and permanent place for a number of human microorganisms (bacteria, fungi, viruses, etc.) that exist under normal conditions without harm to a healthy human body. This is useful for the human body. These microorganisms are called normal flora, and in another term, they are referred to as commensal organisms that feed together with the host. Under normal conditions, the internal organs and systems of the body, such as the pancreas, spleen, liver, bladder, gall bladder, nervous system, and circulatory system, are sterile, but they can also become infected. In addition, a child who enters the world in a sterile form will soon acquire a normal flora through milk, food, and the environment. Normal flora is not the same in all humans but varies from person to person based on differences in their physiological, dietary, age, and geological conditions. First off, harmful bacteria cannot compete with the host for nutrients and intake sites in the terminal portion of the intestinal thanks to the existence of benign bacteria in a healthy person's body. Second, it is resistant to the antibacterial chemicals made by the bacteria in the last section of the intestines. Third, babies' immune systems expand and mature as a result of the buildup of microorganisms in their bodies. The fourth is that gut bacteria create certain crucial dietary components, such as vitamin K, which aids in food absorption and digestion. (Although people obtain the required quantity of vitamin K from diet, in the event that there is a shortage of foods high in the vitamin, bacteria generate the vitamin to fulfill the body's requirements.

Keywords: Normal Flora, disease, Immunity, Human body and Pathogen.

Introduction

Normal flora is the actual population of microorganisms, whereas microbiome refers to the aggregate genomes of the microorganisms in a particular environment. The microbiome is today best thought of as a virtual organ of the body because it is estimated that the human gastrointestinal system contains 100 trillion microorganisms (mostly bacteria, but also viruses, fungi, and protozoa). The human genome has roughly 23,000 genes, however the microbiome has over three million genes that produce thousands of metabolites. These metabolites replace many of the activities of the host, affecting its fitness, phenotype, and health in the process [19]. Studies on the human microbiome have received a lot of attention during the past 20 years. Significant areas of the human body, including the skin, mouth cavity, gastrointestinal tract (GIT), respiratory system, and urogenital tract, are colonized by enormous numbers (10–100 trillion) of microbes. Due of the long-lasting impacts on important health concerns, such as metabolism, depression, blood pressure, and brain function, and chronic infectious illnesses, microbiome research has drawn a lot of interest. Numerous bacteria species have effectively adapted to the typical human microbiome through the process of evolution. The majority of these microorganisms could not be grown under in vitro conditions. These microorganisms proliferate inside the human body, take part in vital biological processes, and provide the groundwork for a number of contagious and non-contagious human illnesses. The colonization of germs in bodily compartments that are constantly exposed to external microbes (such as the mouth, respiratory tract, GIT, skin, urethra, and vagina) has also been extensively investigated and is generally acknowledged [7]. Biofilms have been demonstrated to form in healthcare environments on the surfaces of medical devices, dead tissues (such as the sequestra of bones), and inside live tissues. Biomedical equipment including catheters, artificial heart valves, pacemakers, breast implants, contact lenses, and cerebrospinal fluid shunts may all experience the development of these growths on their surface. Gram-positive and Gram-negative bacteria may adhere to and create biofilms on the surfaces of these devices, however *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Pseudomonas aeruginosa* are the most often reported biofilm-forming microorganisms [12]. The body's normal bacterial flora, known as the microbiota, has gained significant attention due to its influence on physiology. Contrary to the commonly reported statistic, recent estimations suggest a closer ratio of human to bacterial cells, though bacteria contribute substantially more genetic material. The microbiota plays a crucial role in immune system and digestive system development, vitamin production, and protection against infections. However, its absence can lead to health issues such as compromised immunity, digestive problems, and neurological underdevelopment. Despite

potential negative consequences, lack of normal flora can prevent tooth cavities and decrease body fat. While all exposed parts of the body harbor normal flora except the lungs, healthy individuals typically have sterile interior organs and bodily fluids, though occasional bacterial presence can occur, such as after dental cleaning [11].

Materials and methods

The research on the health benefits of normal flora in the human body was conducted through consultation of various scientific and academic references, including libraries, other research, and scholarly essays on the subject. A comprehensive analysis was undertaken to ascertain the significance of the microbiota in human health. This analysis aimed to explore the role of normal flora in immune system development, digestive function, vitamin synthesis, and resistance against infections. Various sources were reviewed to understand the impact of normal flora on human physiology and to investigate potential benefits and drawbacks associated with its presence. The information gathered from these sources was synthesized to draw conclusions regarding the importance of maintaining a balanced microbial community in the human body for overall health and well-being.

Results and discussion

Microorganisms Inhabiting the Skin and Techniques for Identifying Them

A healthy skin microbiota is one aspect that impacts how well skin functions. Micro-eukaryotes (mites), viruses, bacteria, fungus, archaea, and phages make up this diverse group of microorganisms. Archaeal 16s rRNA genes make for around 4% of all microbial genes, it was discovered. They demonstrated that Thaumarchaeota species make up around 88 % of all observed operational taxonomic units (OTUs), with Euryarchaeota species making up the remainder. Human skin also contains dust mites, which are mostly found on the face, around the sebaceous glands, and on hair follicles. Dust mites are regarded as commensals since they are present in 23–100 % of healthy individuals. The skin also has Demodex mites (*Demodex folliculorum* and *Demodex brevis*), which are linked to chronic blepharitis and rosacea. Phages play a significant role in the skin microbiota. They have the ability to modify the microbiome's microbial community's physiology and composition. Between 103 and 104 CFU/cm² of microorganisms are typically extracted from the skin surface using conventional culture techniques. However, this ratio reaches 106 CFU/cm² in the areas that are the most humid, such as the groin, armpits, and nostrils. About 106 CFU/cm² of microorganisms live on the scalp, mostly on the forehead and in the area around the ears and head. On the other hand, their density on the upper back, chest, and

arms is between 104 and 105 CFU/cm². The number of microorganisms found in human hair and beards is not insignificant for the skin. The hair shaft is constantly exposed to the environment and can be a potential site for bacteria to accumulate due to its grooved cuticle surface and long, thin structure. The bacterial community of the hair includes of Gram positive and Gram-negative bacteria. In addition, *Staphylococcus aureus* and *Staphylococcus epidermidis* may inhabit the human skin and scalp. However, there are no data on the colonization and adherence of bacteria to hair. Studying the interaction of bacteria with human hair could be of significance in skin infections, wounds, and scalp diseases. Actinobacteria (52 %), Firmicutes (24 %), Proteobacteria (16 %), and Bacteroidetes (6 %), comprise the majority (>90%) of the bacteria found on human skin are classified into four types: The most prevalent species are anaerobic *Cutibacterium acnes* (formerly known as *Propionibacterium acnes*), coagulase-negative staphylococci, *Corynebacterium*, *Micrococcus*, *Streptococcus*, mainly *Staphylococcus epidermidis* (103-104 CFU/cm²) and *Acinetobacter* are the presiding species. It's possible that 45 to 80% of the overall skin microbiome consists of species from the *Cutibacterium*, *Staphylococcus*, and *Corynebacterium* genera, which have been identified from practically all skin regions. It has also been established that human skin contains microorganisms from the Archaea domain, including *Thaumarchaeota*. According to studies using 16S rRNA sequencing, this taxon accounts for around 4% of the microbiome's genes. Additionally, the skin microbiome includes fungus, primarily of the Ascomycota and Basidiomycota kinds. The genus *Malassezia* is the most prevalent. The feet, which are inhabited by *Aspergillus*, *Cryptococcus*, *Rhodotoula*, and *Epicoccum*, demonstrate the greatest diversity of fungus. However, the skin microbiome's most prevalent group is still bacteria.

The composition of the skin microbiome is significantly influenced by various factors, including the age, sex, and health of the host, as well as hygiene practices, lifestyle, and environment. Changes in host health, aging, or relocation can alter the makeup of the microbiome. Physical and chemical characteristics of the skin, including its dry, slightly acidic surface and the shedding of keratinized skin cells every four weeks, impact microbial colonization. Skin thickness, folds, hair follicle density, and gland activity also play roles in microbial growth. Sebaceous glands provide an optimal environment for certain bacteria, with lipophilic microorganisms primarily present in areas rich in sebaceous glands, such as the head, neck, and upper torso. These lipophilic microorganisms, comprising 46 % *Cutibacterium* species, 16 % staphylococci, and fungi of the genus *Malassezia*, thrive in environments conducive to sebum secretion. Specific compounds released by these glands, like lauric acid and sapienic acid, possess inhibitory activity against Gram-positive pathogens, maintaining skin health. Moreover, regions with folds and gland-rich

areas harbor unique microbial communities, indicating a complex interplay between host characteristics, gland activity, and microbial colonization, all contributing to the diverse composition of the skin microbiome [16]. The biggest organ in the human body, the skin, is home to a variety of microorganisms, most of which are benign or even helpful to their host. The ecology of the skin surface, which varies greatly based on topographical location, endogenous host characteristics, and external environmental factors, is what drives colonization [8]. The composition of microbial communities was discovered to be predominantly reliant on the physiology of the skin site in sequencing surveys of healthy humans, with variations in the relative abundance of bacterial taxa associated with wet, dry, and sebaceous microenvironments. Lipophilic *Propionibacterium* species dominated sebaceous locations, although bacteria that favor moist environments, such *Staphylococcus* and *Corynebacterium* species, were preferentially prevalent there. These moist regions included the bends of the elbows and the soles of the feet [3].

Table 1 – Composition of the human skin microbiota in various locations

Skin Sites				
	Moist	Sebaceous	Dry	Foot
Body Sites Location	groin, axilla, antecubital fossa, toe web	face, chest, back,	arm, leg, volar forearm	Moist-toe interdigital web space dry-plantar heel
Malassezia app	36% CH- 80%AD	65% CH-99%AD	35% CH- 83%AD	53-80%
Fungi	Ascomycota: <i>Aspergillus</i> , <i>Epicoccum</i> , <i>Phoma</i> (levels >5%):			<i>Cryptococcus</i> , <i>Aspergillus</i> , <i>Rhodotorula</i> , <i>Epicoccum</i> , <i>Saccharomyces</i> , <i>Candida</i> , <i>Epidermophyton</i> <i>Microsporum</i> , <i>Trichophyton</i>
Other fungi	9.5%AD-40.2%CH <i>Cladosporium</i> , <i>Cryptococcus</i> CH-Children, AD-Adults.			

Characterization and Role of the Normal Ocular Flora

The enormous and varied commensal bacterial flora that lives in the human cornea and conjunctiva was found thanks to the application of molecular-based methods, such as next-generation sequencing. These microbes work together to form a true microbiota that can prevent potentially harmful microbial species from colonizing the ocular surface. *Pseudomonas*, *Propionibacterium*, *Acinetobacter*, and *Corynebacterium* are the genera that include the most bacteria in the ocular microbiota. Environmental factors, pathological conditions like dry eye syndrome, the use of antibiotics, infections like blepharitis or conjunctivitis, and personal habits like excessive and careless contact lens use, which may also serve as a vehicle for infections by opportunistic pathogenic microorganisms, can all easily alter this homeostatic microbiota. As a result, it is possible for the disturbance of the normal eye microbiota to contribute significantly to the etiology of ocular illnesses [14]. Children with positive conjunctival sac flora in one eye had 32 different bacterial species detected. The most prevalent floras were *S. epidermidis* (54.90 %), *S. aureus* (9.41 %), *S. mitis* (3.14 %), and *S. pneumoniae* (2.75 %). 34 bacterial species were identified in children who had positive conjunctival sac flora in both eyes, including *S. epidermidis* (51.92 %), *S. aureus* (11.19 %), *S. mitis* (6.12%), and *S. pneumoniae* (2.87 %). The number of *S. epidermidis*, *S. aureus*, and *S. pneumoniae* found in the two groups did not differ statistically significantly ($P > 0.05$). However, *Streptococcus* frequency was discovered to be greater in kids with positive conjunctival sac flora in both eyes than in children with positive flora in just one eye [10].

Role of the normal flora of the gastrointestinal tract

A wide variety of microorganisms, including bacteria, fungi, archaea, and viruses, live in the complex, dynamic, and spatially heterogeneous ecosystem known as the human gut microbiota (GM). These microorganisms interact with one another and with the human host. A genetic repertoire that is one order of magnitude greater than the human genome is represented by the collection of genes found in all intestinal microorganisms. It is also sometimes referred to as the "essential organ" of the human body. The GM is the body's greatest micro-ecosystem and works in symbiosis with the host to sustain regular physiological functions in a state of dynamic balance. Firmicutes, Bacteroides, Actinomycetes, and Proteus composition the majority of the Firmicutes, Bacteroides, and Actinomycetes in GM. The Firmicutes/Bacteroidetes ratio is a crucial component for GM disorder reflection. Additionally, GM variety, abundance, and evenness are significant factors that represent the composition of the gut flora [4].

Traditional cancer chemotherapies have issues with poor selectivity and a limited capacity to penetrate tumors. Bacteria, on the other hand, can be precisely

tailored to recognize and react to the tumor microenvironment. To kill cancer cells, one tactic is to use the natural cytotoxicity of bacteria. Salmonella and Clostridium, for instance, have demonstrated an anticancer impact in mouse models. The bacterial buildup in tumor tissues will result in neutrophil infiltration and an anticancer immune response. Such an outcome was also seen in a phase 1 clinical trial that gave patients with metastatic melanoma a modified Salmonella strain. The second method involves using engineered bacteria to deliver eukaryotic expression vectors or directly express anticancer agents in cancer cells. With these techniques, the bacteria can produce cytotoxic agents like Cytolysin A to cause cancer cells to die, deliver cytokines like IL-2 to activate immune cells to destroy cancer cells, and sensitize the immune system against cancer cells by expressing tumor antigen [9]. The biggest point of contact between the sterile human body and pathogens and the environment is the digestive system. It is the most crucial location for the colonization of tens of thousands of microorganisms, including viruses, eukaryotes, and more than a thousand different kinds of bacteria. These microorganisms, referred to as the «gut microbiota» as a whole, are widely known for playing a variety of advantageous functions in preserving human homeostasis, including preserving gut integrity, generating energy, preventing off infections, and controlling host immunity. In actuality, the first time a human comes into contact with an organism is during infancy, especially at birth when a variety of bacteria manage to colonize the baby's body throughout the first few months of life. In more detail, cutaneous, mouth, and nasopharyngeal membranes, as well as other body parts, begin to grow microorganisms. The microbiota in the gastrointestinal system will gradually begin to slowly rise, with a developed oral and salivary microbiome, less bacteria in the stomach, but with an extremely high concentration of bacteria inhabiting the colon [5].

The majority of bacteria recovered from the conjunctival and lid border regions are staphylococci that are coagulase-negative. Greater bacterial isolation is obtained from the lid edge than from the conjunctival region [15]. A substantial source of bacterial contamination in the hospital setting is textiles, which have a microbiological load and composition very distinct from that of hard surfaces [13]. The gut microbiota offers a variety of advantageous features to the host because of its substantial genetic content and metabolic complement. These microorganisms have some of the most crucial functions in maintaining the mucosal barrier's integrity, supplying nutrients including vitamins, and defending against infections. Additionally, a healthy immune system depends on the interaction of the mucosal immune system with commensal microbiota. For instance, competing for attachment sites or food sources or by creating antimicrobial compounds, the microbiota's physical presence in the GI tract also affects pathogen colonization

[18]. The composition or change in the gut microbiota of people with depression and anxiety can have a big impact on their psychological symptoms. The presence or change of depressive and anxious symptoms was significantly correlated with the composition and modification of the gut microbiota. Treatment for several mental health problems with probiotics or prebiotics reduced their symptoms [2].

Table 2 – Effects of penicillins, alone or in combination with other drugs, on intestinal microflora

Compound	Bacteria suppressed	Bacteria proliferated	Overgrowth	Reference
Ampicillin	Enterobacteria, enterococci, and anaerobic bacteria		Candida in some	Leigh (1979)
Ampicillin and sulbactam	Enterobacteria, enterococci, and anaerobic bacteria		Candida or C. difficile in some	Kager and colleagues (1982)
Piperacillin	Enterobacteria, enterococci, and anaerobic bacteria		Candida or C. difficile in some	Kager and colleagues (1983)
Amoxicillin	Enterobacteria	Resistant entero-bacteria	Candida or C. difficile in some	Gipponi and colleagues (1985)
Ticarcillin and clavulanic acid	Enterococci		Candida or C. difficile in some	Nord and colleagues (1989)
Skin Sites				
	Moist	Sebaceous	Dry	Foot
Body Sites Location	groin, axilla, antecubital fossa, toe web	face, chest, back,	arm, leg, volar forearm	Moist-toe interdigital web space dry-plantar heel
Malassezia spp	36% CH-80%AD	65% CH-99%AD	35% CH-83%AD	53-80%

Fungi	Ascomycota: Aspergillus, Epicoccum, Phoma (levels >5%):	Cryptococcus, Aspergillus, Rhodotorula, Epicoccum, Saccharomyces, Candida, Epidermophyton Microsporum, Trichophyton
Other fungi	9.5%AD-40.2%CH Cladosporium, Cryptococcus	

The role of the normal micro biome in immune system development

The development of the hosts immune system is significantly influenced by early colonization of the mucosal surfaces of the mammalian host. During the initial years of life, when microbiota composition displays the maximum intra- and inter-individual variability before stabilizing at around three years of age, the most crucial events in the teaching of host immunity may occur. The 'window of opportunity' that has been opened up, meanwhile, may also make newborns more vulnerable to external influences on their microbiota, which might have detrimental long-term effects on their immunity. Since infectious illnesses are the main cause of child mortality, the immaturity of the immune system in newborns and babies is underlined by a heightened sensitivity to many infectious infections. On the other hand, prematurely born newborns also typically have an increased predisposition for excessive inflammation, as seen by the potentially fatal condition necrotizing enterocolitis. It is generally accepted that the majority of microbial colonization happens after delivery, primarily emanating from the maternal microbiota, and that most investigations to far have not observed a repeatable microbial colonization already present in gestation. This initial colonization is modulated by a number of factors, including the distribution method and its effects on the diversity of the early microbiota throughout the body. It is generally known that maternal antibodies given to newborns through breastmilk provide essential passive defense against infections. The commensal microbiota of pregnant mice drives antibody-mediated protective immunity through nursing, according to an intriguing new study [20]. Although it is conventional to think of human blood as being sterile, current research suggests that healthy individuals may have a blood microbiome [17].

Normal flora of the nasal cavity and month

Actinobacteria, Firmicutes, and occasionally Proteobacteria dominated the communities of bacteria in the nasal cavities. The most common Actinobacteria families found in the nasal cavity were Corynebacteriaceae and Propionibacteriaceae. Corynebacteriaceae levels varied amongst patients from

1.5% to 62.8%, and Propionibacteriaceae levels ranged from 0.4 % to 42.4 %. Actinobacteria from the families Micrococcaceae and Actinomycetaceae were found in lower concentrations in the communities at both oral cavity locations. Only one oral cavity sample had more than 1 % of the community made up of Corynebacteriaceae. Most oral cavity samples lacked Propionibacteriaceae, and when it was found, it never topped 1 % of the community. The oral cavity and nasal cavities of healthy adult adults, respectively. Up until recently, culture-independent techniques have not been used to define the bacterial population of the healthy human nasal cavity. The microbiota of the healthy human nares, which are anterior to and adjacent to the nasal cavity, has been studied by several investigations. Increased risk of Staphylococcus aureus infection in other body regions is associated with S. aureus carriage in the nares. Additionally, rivalry and competitiveness with other nares microbiota individuals appear to affect S. aureus nares carriage. The nasal cavity is different from the nares despite being close by. It has a distinctive form of epithelium, including ciliated pseudostratified columnar epithelial cells and goblet cells that produce mucus as well as a non-keratinized stratified squamous epithelium that changes into a normal respiratory epithelium. The nares, in contrast, contain a stratified squamous epithelium that is keratinized and has sebaceous glands and hairs. The bacterial community makeup of the human nasal cavity has been the subject of very few investigations [1].

Role of normal flora of the urinary reproductive system

The colonization of a pathogen in any area of the urinary tract, including the kidney, ureter, bladder, and urethra, is known as a urinary tract infection (UTI). One of the most widespread infectious illnesses, infection of the urinary tract affects individuals of all ages, results in over 150 million cases worldwide each year, costs the global economy more than \$6 billion in treatment expenditures, and affects people of all ages. Pyelonephritis (kidney), cystitis (bladder), and urethritis (urethra) are the three types of UTIs, and they might differ in severity (complicated versus uncomplicated). People who are otherwise healthy and do not have any structural or neurological issues with their urinary system are susceptible to uncomplicated UTIs. Lower UTIs (cystitis), greater UTIs (urethritis), or pyelonephritis are the different classifications for these diseases. Numerous factors, including present UTI symptoms, a history of UTI and catheterization, sexual activity, vaginal infection, diabetes, obesity, and genetic susceptibility, can lead to cystitis. UTIs that are complicated are ones that are associated with elements that affect the hosts immune system or the urinary tract. Potential UTI consequences include urinary obstruction, urinary retention brought on by neurological disorders, immunosuppression, renal failure, renal transplantation, pregnancy, and the presence of foreign objects such calculi, indwelling catheters,

or other drainage devices. The low pH of the vaginal cavity is maintained by the addition of *Lactobacillus* species, which are an essential part of the normal flora of the vagina. When the number of these bacteria decreases, the pH rises and pathogenic organisms grow. For example, when antibiotics are prescribed, the normal flora is destroyed and a number of other organisms grow. Other examples of this are pathogens such as yeast-like fungus and *Candida albicans*, which have normal flora in the form of minor normal flora, vagina, small intestine and mouth. Urine is sterile in the bladder and kidneys, so it becomes infected in the last part of the urethra. Organisms present in the outer layer of the skin and in the perineum, eventually lead to infection [6].

Conclusion

The human body's natural environments for normal flora include the skin, eyes, mouth, and some portions of the gastrointestinal tract, the respiratory tract, and the urinary reproductive system. These areas are in close contact with the environment or the body's environment. The advantages for skin health will be mentioned first, then the others. The bacteria that are present in the environment are all absorbed by human skin, but these transient floras are either quick to move and are rapidly eliminated by washing or perish on their own. Because the skin's surface is often dry, it is not a favorable environment for germs to flourish. The salivary glands release a kind of liquid that contains sodium chloride, which causes a hyperosmotic environment to develop on the surface of the skin and generates an unfriendly environment for microbes. The surface of the skin is somewhat acidic. A well-established normal flora guards us against illness, especially (but not exclusively) from pathogens that affect the gastrointestinal system. For the immune system to develop and operate properly, normal flora is essential. The regular flora assists in fostering a strong immune system, which shields us from many kinds of diseases. We might also be more immediately protected by the normal flora. First, infections cannot establish themselves because of the normal flora's physical and nutritional conditions. This is comparable to how weeds are prevented from growing in an established grass. Just simply not enough room. However, if the lawn is harmed, weeds will grow fast and strongly. This is best shown by *Clostridium botulinum*. Infant botulism can occur in children under the age of one because their normal flora has not yet developed enough to protect them against *C. botulinum* infection. Honey is one frequent cause of these infections, while *C. botulinum* endospores may be found elsewhere. Adults and older children who have established flora are immune to *C. botulinum* intestinal infections. Anyone whose normal flora has been disturbed may get seriously infected by *C. difficile*, a different type of *Clostridium*. This nosocomial infection is typically brought on by prolonged use of broad-spectrum antibiotics. Since *C. difficile* is

more resistant to antibiotics than the majority of gut bacteria, it can thrive after the other bacteria are gone. It's frequently referred to as a superinfection when an infection develops on top of one that already exists. Exotoxins produced by *C. difficile* destroy the intestinal lining, which then sheds off in sheets in the feces. This sometimes-deadly illness can result in severe diarrhea, dehydration, and ultimately intestinal rupture. Fecal transplants have recently become a fairly typical therapy for the most severe *C. difficile* infections since the illness was brought on by a deficiency in normal flora. Second, normal flora bacteria may generate certain chemicals that specifically target prospective diseases. These substances may be antibiotics, although other substances can potentially prevent the growth of potential infections. For instance, *Candida* and *Streptococcus mutans* both often live in the mouth. *Candida* can overgrow in the mouth and produce thrush in its severe form. *Candida* is held in check by the *S. mutans* autoinducer competence stimulating factor, which stops it from evolving into its virulent state. *Streptococci* and *Candida* engage in a similar relationship in the vagina. A yeast infection-causing *Candida* can overgrow when the population of *Streptococcus* is reduced by antibiotic treatment.

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**Абдул-Бари Хеджран^{1,2}, Айдын Қыдырманов², Атикулла Сарвари^{1,2}, Мохаммадулла Мохаммади¹, Мохаммад Якуб Сангин¹*

¹Гильменд университеті, Ауғанстан, Гильменд;

²Әл-Фараби атындағы Қазақ ұлттық университеті,

Қазақстан Республикасы, Алматы қ.

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АДАМ АҒЗАСЫНДАҒЫ ҚАЛЫПТЫ ФЛОРАНЫҢ ДЕНСАУЛЫҚҚА ПАЙДАСЫ

Қалыпты флора – бұл қалыпты жағдайда дені сау адам ағзасына зиян келтірмейтін адам микроорганизмдерінің (бактериялар, саңырауқұлақтар, вирустар және т.б.) санының табиғи және тұрақты орны. Бұл адам ағзасына пайдалы. Бұл микроорганизмдер

қалыпты флора деп аталады, ал басқаша айтқанда, олар иесімен бірге қоректенетін комменсальды организмдер деп аталады. Қалыпты жағдайда ұйқы безі, көкбауыр, бауыр, қуық, өт қабы, жүйке жүйесі, қан айналымы жүйесі сияқты ағзаның ішкі мүшелері мен жүйелері стерильді, бірақ олар да жұқтыруы мүмкін. Сонымен қатар, стерильді түрде дүниеге келген бала сүт, тамақ және қоршаған орта арқылы көп ұзамай қалыпты флораға ие болады. Қалыпты флора барлық адамдарда бірдей емес, бірақ физиологиялық, тамақтану, жас және географиялық жағдайлардағы айырмашылықтарға байланысты адамнан адамға өзгереді. Біріншіден, зиянды бактериялар сау адамның денесінде жақсы бактериялардың болуына байланысты қоректік заттар мен ішектің терминалдық бөлігіндегі қабылдау орындары үшін иесімен бәсекелесе алмайды. Екіншіден, ол ішектің соңғы бөлігіндегі бактериялар жасаған бактерияға қарсы химиялық заттарға төзімді. Үшіншіден, нәрестелердің иммундық жүйесі олардың ағзаларында микроорганизмдердің жиналуы нәтижесінде кеңейіп, жетіледі. Төртіншіден, ішек бактериялары тағамның сіңуіне және ас қорытуына көмектесетін К дәрумені сияқты маңызды диеталық компоненттерді жасайды. (Адамдар К дәруменінің қажетті мөлшерін тамақтан алғанымен, дәруменг тағамдардың жетіспеушілігі болған жағдайда, бактериялар бай ағзаның қажеттіліктерін қанағатандыру үшін дәрумен шығарады.

Кілтті сөздер: Қалыпты флора, ауру, иммунитет, адам ағзасы және қоздырғыш.

Абдул-Бари Хеджран^{1,2} Айдын Кыдырманов², Атикулла Сарвари^{1,2}
Мохаммадулла Мохаммади¹, Мохаммад Якуб Сангин¹

¹Университет Гильменда, Афганистан, Гильменд;

²Казахский национальный университет имени аль-Фараби,
Республика Казахстан, г. Алматы,

³Казахский национальный университет имени аль-Фараби, пр. Аль-
Республика Казахстан, г. Алматы.

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ПОЛЬЗА НОРМАЛЬНОЙ МИКРОФЛОРЫ В ОРГАНИЗМЕ ЧЕЛОВЕКА

Нормальная микрофлора – это естественное и постоянное место обитания для ряда микроорганизмов человека (бактерии, грибы,

вирусы и др.), которые существуют в нормальных условиях без вреда для здорового организма. Это полезно для человеческого организма. Эти микроорганизмы называются нормальной микрофлорой, а в другом термине они называются комменсальными организмами, которые питаются вместе с хозяином. В нормальных условиях внутренние органы и системы организма, такие как поджелудочная железа, селезенка, печень, мочевого пузырь, желчный пузырь, нервная система и кровообращение, являются стерильными, но также могут заражаться. Кроме того, ребенок, который появляется на свет в стерильной форме, вскоре приобретет нормальную микрофлору через молоко, пищу и окружающую среду. Нормальная микрофлора не одинакова у всех людей, но изменяется от человека к человеку в зависимости от различий в их физиологических, пищевых, возрастных и географических условиях. Прежде всего, вредные бактерии не могут конкурировать с хозяином за питательные вещества и места всасывания в терминальном отделе кишечника благодаря наличию благоприятных бактерий в организме здорового человека. Во-вторых, оно устойчиво к антимикробным химическим веществам, вырабатываемым бактериями в последнем отделе кишечника. В-третьих, иммунная система младенцев расширяется и созревает в результате накопления микроорганизмов в их организмах. Четвертое - кишечные бактерии создают определенные важные компоненты питания, такие как витамин К, который способствует усвоению и перевариванию пищи. (Хотя люди получают необходимое количество витамина К из пищи, в случае нехватки продуктов, богатых витамином, бактерии производят витамин, чтобы удовлетворить потребности организма).

Ключевые слова: Нормальная микрофлора, болезнь, иммунитет, человеческое тело и патоген.

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Торайғыров университеті

140008, Павлодар қ., Ломов к., 64, 137 каб.

«Toraighyrov University» баспасы

Торайғыров университеті

140008, Павлодар қ., Ломов к., 64, 137 каб.

8 (7182) 67-36-69

e-mail: kereku@tou.edu.kz

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