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Microbial Composition of Human Gastroduodenal Zone

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Abstract*—Human microbiota has a significant impact on the condition and development of the macroorganism, its longevity, ability to withstand infectious and noninfectious diseases. In many cases, representatives of microbiota can become etiological agents of chronic degenerative processes in the organism; In turn, the macroorganism and the environment affect its composition. In this brief review is discussed the composition and variation of the microbiota of the gastroduodenal zone*.

***Keywords*—** *Microbiota, gastroduodenal diseases, gastric acid, stomach, duodenum*.

The microbiota of the human digestive tract is a complex ecosystem. It is characterized by heterogeneity, relative constancy in different parts, and the presence of maximally colonized areas.

Microbes may be located superficially. At this time, they are closely associated with the mucous membrane of the organ (mucosal, parietal microflora) or the organ lumen. In the process of evolution, the microbiota differentiated into two large groups - local, resident (indigenous, autochthonous) and transient (passage, allochthonous) microbiota. The latter is not uncommon in different areas of the macroorganism as well as in the external environment [1].

The parietal microbiota is localized on the mucus of epithelial cells or in close association with mucosal cells. It is mainly formed at the expense of the maternal microflora. The content microflora is formed from the wall microflora as well as from microorganisms from the environment and other organs.

The human gastroduodenal area differs greatly from other parts of the digestive system in its relatively sparse microbial composition. The acidity of gastric juice, peristalsis, and the composition of secretory immunoglobulins and duodenal mucus are important in the maintenance of local antibacterial resistance of this zone. Along with this pancreatic juice has some antibacterial properties. Its bactericidal activity against *E. coli, Shigella spp., Salmonella spp., Klebsiella pneumoniae* and bacteriostatic activity against Staphylococcus, P. aeruginosa was established [2].

It used to be thought that the stomach of a healthy person was a sterile organ. The development of modern research methods has changed this view [3]. This organ was found to contain a significant amount of microbiome. In 1982 the discovery of *Campylobacter pyloridis* (later - *Helicobacter pylori*) dispelled the dogma about the sterility of the stomach. Five major phyla have been identified in the stomach: *Firmicutes, Bacteroidites, Actinobacteria, Fusobacteria,* and *Proteobacteria.* In general, *Prevotella, Streptococcus, Veillonella, Rothia* and *Haemophilus* predominate in the stomach of a healthy person [4]. Colonization of the upper intestine by coliform organisms is abnormal and characteristic of some infectious pathogens, such as *Vibrio cholerae* and enterotoxigenic *Escherichia coli*.

The composition of the gastric microbiota at the species level is dynamic and depends on factors such as dietary habits, medications, inflammation of the gastric mucosa, and *H. pylori* colonization. Protozoa also is found in gastric juice, and cytomegalovirus and Herpes simplex virus are found in mucosal biopsies [5]. *Candida* appears in 15% of patients, H. pylori appear in gastric ulcer disease and gastritis [6].

The stomach is a relatively inhospitable environment for bacterial reproduction. It is home to bacteria from the mouth as well as bacteria present in food. Acidification reduces the number of bacteria, which increases significantly after a meal (about 10^3-10^6 organisms per gram of food). Minimize the number of microorganisms after food processing.

In patients with antral gastritis, in contrast to *H. pylori*-negative patients, the number of proteobacteria decreases and the number of Firmicutes increases, among which *Streptococcus* predominates. Such a significant difference between the antral region and the stomach body in patients with atypical gastritis as compared to *H. pylori*-negative patients is not observed. Dysbiosis of gastric microbiota is linked with the development of cancer if here represent H. pylori-infection [10]. In carcinogenesis are involved different events: generation of tumor-promoting metabolites, DNA damage, suppression of antitumor immunity, and etc. Different bacteria can produce short-chain fatty acids and due to this, inhibit inflammation and carcinogenesis [11].

When studying the normal gastric microbiota, it is seen that both aerobes and facultative anaerobes, as well as obligate anaerobes (bacteria and fungi) are common here. Duodenal microflora includes lactobacilli, bifidobacteria, bacteroides, enterococci, yeasts, sarcinia and sometimes saprophytic bacteria [7].

The poverty of microbes in the stomach is due to the selective properties of gastric juice, which is due to the presence of hydrochloric acid and lysozyme in it [8]. The gastric acid inhibits grouth of indigenous microorganisms [9]. The colonization of gastric contents depends on the pH of the gastric juice. At pH less than 3.0, the number of microorganisms is 10^2-10^3 per 1 ml, and at a pH greater than 3.0 it is 10^5-10^7 per 1 ml. Gastric juice is considered to have bactericidal properties at pH 4.0. Only those microbes that have the ability to exist in an acidic environment can survive

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in gastric juice. The number of microbes in the duodenum increases slightly after a meal and then returns to baseline levels during digestion [8].

The bactericidal feature of gastric secretions is affected by alterations in pH. In hypochlorhydria the number of bacteria found in the stomach increases and may include faecal type bacteria as well as oral flora. Such conditions occur in pernicious anaemia and after partial gastrectomy and vagotomy and pyloroplasty. Patients with hypochlorhydria are more susceptible to enteric infections such as cholera and salmonellosis since a lower infective dose will breach the weakened gastric bactericidal barrier [5].

Antibiotics, long-term use of proton pump inhibitors and H_2-antagonists, and atrophic gastritis affect the composition of the gastric microbiota. This composition depends on gastric acid secretion. Abundant bacterial growth occurs when pH> 3.8. There is a negative influence of the environment on the microflora of the gastrointestinal tract. Aspirate from the duodenum and small intestine contains about 10^3 microorganisms per 1 ml of contents. Transient bacteria (streptococci, lactobacilli, bacteroides) are cultured from this portion. Detection of 10^5-10^7 bacteria in the 1 ml aspirate indicates a disorder of the digestive system (e.g., achlorhydria, malabsorption syndrome). Stomach acidity, rapid peristalsis, and the presence of bile partially explain the low number of microorganisms in the upper digestive system. The low number of microorganisms in the duodenum is explained by peristalsis of the intestine and the presence of natural barriers, such as the pylorus sphincter, Baugin's valve, etc., although among these factors, the leading role belongs to the small intestine itself - the morphofunctional condition of its mucosa, the physical and chemical composition of gastric juice [4].

In conclusion, the microbiota of gastroduodenal zone is a complex host ecosystem with a diverse and highly developed microbial community consisting of different species. The interactions that occur between this complex microbial ecosystem and the human host are the focus of medical study today, as the number of diseases associated with dysbiotic changes is increasing.

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