**Introduction**

Intestinal dysbiosis against the ground of type 1 DM they result in development and unfavourable clinical course of chronic diseases.

**Objective:** To study the species content and population level of the microbiota in the large intestine in patients with type 1 DM depending on their age.

**Materials and Methods**

Applying up-to-date bacteriological and mycological methods, the examination of the species content and population level of the microbiota in the large intestine has been conducted in 50 patients with type 1 DM, distributed into three groups depending on their age: from 15 to 20 (n=10); from 21 to 35 (n=14); and from 3 to 60 (n=26).

**Results**

A marked deficiency of autochthonous anaerobic bifidus bacteria and lactic bacteria is formed in the content of the large intestine of patients afflicted with type 1 DM. This deficiency intensifies with age, and a clear manifestation of a decreased role of bifidus bacteria in the large intestine microbiocenosis is prognosticated. A similar situation is formed concerning the bacteria Lactobacillus, Peptostreptococcus and Enterococcus. At the same time, the biological role of bacteroids in microbiocenosis increases, as well as the role of pathogenic (E. coli Hly+) and opportunistic (Proteus, Enterobacter, Citrobacter) enterobacteria, clostridia, staphylococci, and yeast fungi of Candida genus.

**Conclusions**

Negative processes are intensified with age including changes of the species content and population level, constancy index, Berger-Parker domination index, frequency, coefficients of quantitative domination and value. Deficiency of bacteria of Bifidobacterium, Lactobacillus, Peptostreptococcus genera and bacteria of Enterococcus genus is formed, and their role in microbiocenosis decreases. On the contrary, patients with type 1 DM with age demonstrate contamination of the large intestine cavity with pathogenic (E. coli Hly+) and opportunistic (Proteus, Enterobacter, Citrobacter) enterobacteria, clostridia, staphylococci and yeast fungi of Candida genus. These microorganisms become the major ones in microbiocenosis.