THE INFLUENCE OF PREOPERATIVE ANTIBIOTIC PROPHYLAXIS OF COLORECTAL CANCER ON THE ABUNDANCE OF SOME TAXONS FROM THE COMPOSITION OF THE INTESTINAL MICROBIOME

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Introduction. The human gastrointestinal tract hosts a complex and dynamic population of microorganisms. The intestinal microbiota plays a fundamental role in human health, preventing the colonization of pathogens, regulating intestinal immunity, and is also involved in homeostasis. The intake of antibiotics has a significant impact on bacterial diversity. Thus, their effects on the host through the gut microbiome are immense and can affect various body functions, including the formation of antibiotic-resistant strains, making hosts more susceptible to infection with pathogens. Uncontrolled administration and broad-spectrum antibiotics reduce the diversity of the intestinal microbiota. In the last decade, studies on the human microbiome have been facilitated by advances in sequencing technologies, and profiling of the genomic composition of microbial communities has allowed the accumulation of new knowledge on the biodiversity, taxonomy, and phylogeny of the gut microbiome.

Aim. It was proposed to identify the composition of the colonic microbiome and the changes induced by antibiotics, using the NGS Ion Torrent technology.

Material and methods. In the study, the aim was to compare the composition of the intestinal microbiome before (M) and after (T) antibiotic prophylaxis in a group of 128 oncological patients. The subjects included in the study represented adult patients with colorectal cancer undergoing surgery involving antibiotic prophylaxis, including patients undergoing neoadjuvant treatment after a break of at least 21 days and who had not undergone mechanical preparation of the colon in the last 30 days before admission and had not administered antibiotics in the last 30 days before admission. Patients' microbiome samples were collected by rectal swab before and after antibiotic prophylaxis, followed by bacterial DNA extraction and subsequent bacterial 16S gene sequencing using Ion Torrent NGS technology. Ten different types of antibiotics were used with an average duration of administration of 5.34 days.

Results. Pooled analysis of cohort M and T samples revealed 26 genera with a mean relative abundance greater than 1%. Out of 167 detected in both research groups, 22 genera have an average relative abundance >1.00% in group M and 18 in group T. The chao1 index varied less among samples in group M compared to samples in group T. In cohort M the highest abundance showed next genera: *Prevotella* (14.73%), Bacteroides (14.24%) and *Faecalibacterium* (7.51%), while in cohort T - *Enterococcus* (38.83%) and *Corynebacterium* (11.32%). In research group M, these two taxa showed an abundance of 0.15% and 2.16%, respectively.

Conclusions. The average relative abundance of *Enterococcus* spp. and *Corynebacterium* spp. taxa from group T indirectly indicates a probable multi-resistance acquired following the large-scale administration of antibiotics in the population of the Republic of Moldova.