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**Changes in the composition of intestinal microbiota,
level of endotoxin markers and bacterial metabolites
in mice cancer models**

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Summary

Monitoring of changes in the composition and metabolic activity of the intestinal microbiome during tumor development was carried out on a prostate cancer model and on the MC38 colorectal cancer model in mice. In addition, feed with a high content of potato starch or α -cellulose was introduced as a factor promoting the maintenance or restoration of intestinal microbiome homeostasis. The microbiome was studied by NGS sequencing, by assessment of the short-chain fatty acids (SCFA) and their receptors GPR41, GPR109A and HADC, and by measuring the concentration of 3-hydroxy fatty acids (3-OH FAs), chemical markers of lipopolysaccharide (endotoxin) of Gram-negative bacteria.

In the course of prostate cancer in mice, based on the analysis of the level of bacterial metabolites and LPS markers, significant variability of the intestinal microbiome was shown during the disease process. The concentration of short-chain fatty acids determined in the feces was significantly higher in individuals with cancer compared to the control group, and the dynamics of microbiome changes was the highest in the phase of intensive tumor growth.

In the MC38 mouse colorectal cancer model, disturbances in the homeostasis of the intestinal microbiome associated with disease progression were found, it was also shown that the factor generating the greatest variability of the intestinal microbiome was the introduction of a high-fiber diet (α -cellulose or potato starch). Increased content of fiber (α cellulose) in feed correlated with reduced concentration of short-chain fatty acids and LPS markers; this suggests moderation of the inflammatory process and slowing down the translocation of LPS from the intestine into the bloodstream. There was an increase in *Bacteroidetes* and *Verrucomicrobia* and a decrease in *Actinobacteria* and *Firmicutes* observed. The presence of α -cellulose in the feed promoted the growth of *Akkermansia muciniphila* and inhibited *Lactobacillus reuterii*.

The increased content of fiber (potato starch) in the feed correlated with an increase in the concentration of short-chain fatty acids in healthy mice and mice with tumor MC38, it was also associated with an increase in the level of *Bifidobacterium*, *Parvibacter*, representatives of the *Coriobacteriaceae* and *Ruminococcaceae*, *Faecalibaculum* and the family *Clostridiales* vadin BB60 group, and the order of *Rhodospirillales*.

The obtained correlations of the taxonomic composition, the concentration of bacterial metabolites and LPS markers confirmed the value of these features in the microbiome studies as complementary to NGS sequencing in the search for interactions occurring in the gut microbiome during the development of cancer.