

Urinary microbiome in liver cirrhosis

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Introduction. The gut microbiota has been shown to be altered in cirrhosis. It should be noted that changes in microbial diversity and landscape occur not only in the feces of patients with cirrhosis, but also in other organs, tissues and biological fluids. It is interesting to find out if there is an association between urobiome and bacterial infections and outcome in cirrhosis.

Materials and methods. 12 adult in-patients with cirrhosis were included in the protocol of collection and low-temperature freezing of urine samples. PCR amplification of the V3–V4 region of the 16S rRNA gene was performed using modified universal bacterial primers (manufactured by Illumina, USA).

Results. Abundance of urinary microbiota by bacteria phylum *Proteobacteria*, *Fusobacteria*, *Coprothermobacterota*, classes *Gammaproteobacteria*, *Fusobacteriia*, *Chloroflexia*, *Vicinamibacteria*, *Acidithiobacillia*, *Coprothermobacteriia*, orders *Enterobacterales*, *Aeromonadales*, *Acidithiobacillales*, *Legionellales*, genus *Klebsiella*, *Morganella*, *Citrobacter*, *Clostridioides* is much higher in patients with urinary tract infection than without it ($p < 0.05$). The urine microbiota in cirrhotic patients who died within 30 days ($n=4$) compared with patients who are alive ($n=8$) has differences and is enriched with *Fusobacteria* taxa (8.57×10^{-4} and 1.85×10^{-5} , $p = 0.016$) and *Tenericutes* (0.12 and 2.11×10^{-4} , $p = 0.048$). The beta diversity of the urinary microbiota has differences in these groups of patients ($p = 0.017$).

Conclusion. Urinary microbiome in cirrhosis depends on the bacterial infections and the prognosis. We have shown that the urobiota differs in cirrhotic patients with and without urinary tract infection and short-term mortality.

Strains of coagulase-negative staphylococci with antimicrobial activity: characteristics of microorganisms colonizing the skin of patients with atopic dermatitis and psoriasis

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Introduction. Skin colonization of *S. aureus* of patients with atopic dermatitis and psoriasis may support inflammatory changes in the skin. The use of commensal coagulase-negative staphylococci with properties antagonistic to *S. aureus* can potentially lead to normalization of the microbiota of the skin and reduction in the severity of the skin disease. The goal of the work was to search for coagulase-negative staphylococci with antagonistic properties towards *S. aureus*, identify genes encoding the formation of bacteriocins, and determine pathogenicity factors.

Materials and methods. The study included patients with atopic dermatitis and psoriasis. The duration of patient recruitment continued for 3 months. The material for the study was obtained from the affected and apparently unchanged skin of the scalp and skin of "dry" areas (skin of the medial surface of the forearm for patients with atopic dermatitis, skin over the extensor surface of the elbow joint for patients with psoriasis). Microorganisms were inoculated on the selective nutrient medium mannitol-salt agar, identification of coagulase-negative staphylococci was carried out using PCR with a search for species-specific housekeeping genes. The selected strains were inoculated using the "double agar" method.

Strains in which antagonistic activity was detected were studied using PCR: we performed a search for bacteriocin genes and pathogenicity factors.

Results. During the study we identified 109 strains of coagulase-negative staphylococci. Under experimental conditions, 11 strains showed antagonistic activity against *S. aureus*. Upon further study, the lanbiotic pep5 was identified. In one strain, the icaAB gene was identified, which is responsible for the ability to form biofilms.

Conclusion. Coagulase-negative staphylococci with antagonistic properties towards *S. aureus* can potentially be used as autoprobiotics or skin probiotics, normalizing the composition of the skin microbiota and preventing the excessive growth of pathogenic microorganisms.

Effect of *Enterococcus faecium* strain-based feed additive on the composition of the lactating cow microbiome

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Introduction: Intensive animal husbandry has a primary impact on animal health as ruminant metabolic pathways are disrupted. In cows, during lactation, there is a sharp stress of metabolism caused by stress, affecting the physiology of cattle and, as a result, leading to disorders in the composition of the scar microbiome.

Materials and methods. The experiment was carried out on the basis of the Uchkhov Pushkinskoye of the FSBEI HE SPbGAU on 40 animals of the 2nd and 3rd stages of lactation. 4 groups were formed: the 1 and 2 groups included animals during the strife period, the 3 and 4 groups included animals during the lactation stabilization period. The probiotic strain *Enterococcus faecium* in the composition of the probiotic Cellobacterin + (BIOTROF Ltd, St. Petersburg) in the amount of 40 g/head per day was introduced into the diet of groups 2 and 4 for 90 days. The purpose of the work is to assess the taxonomic diversity of the rumen fluid of dairy cows depending on the lactation stage and the introduction of a probiotic feed additive.

Results. As a result of data processing, significant differences ($p \leq 0.05$) were found in taxa SR1, *Fibrobacteraceae*, F082 and *Acetobacteraceae* between control and experimental groups within the divided animals at the filum level. In animals of lactation stabilization, differences were noted in the families *Prevotellaceae*, SR1, *Fibrobacteraceae*, *Bacteroidales* RF16 and RF39. The content of *Bacteroidales* RF16, which has increased significantly in experimental group No. 4 (relative to control group No. 3), demonstrates a positive effect of the probiotic additive on the microbiome, since there is evidence of a negative correlation between the presence of *Bacteroidales* RF16 bacteria and the concentration of isobutyrate and isovalerate in the rumen of an animal. Concentrations of isobutyrate and isovalerate in the rumen of cows are associated with plant food metabolism and the rumen fermentation process.

Conclusion. The obtained data indicate an improvement in the processes of microbial digestion when a probiotic feed supplement is introduced into the diet. The work was supported by the RCSI No. 20-016-00168.

Identifying beneficial microorganisms with multiple health-promoting functions

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Studies on isolation of bacteriocinogenic microorganisms have become routine for the research teams and we are building extensive data base for several new antimicrobial producing cultures. The role

of bacteriocins was clearly acknowledged as one of the beneficial sides of the probiotics. Antimicrobial peptides produced by different microorganisms, including lactic acid bacteria (LAB), are considered to be important potential alternatives in the development of new approaches for the improvement of food safety and in the combating of microbial infections both in humans and in veterinary practice. The concept of multiple beneficial properties for the same bacterial culture is a scientific fact, but still not as deeply investigated. Are this can be the next scientific challenge? Characterization of the new beneficial cultures, including bacteriocinogenic with aim to be applied as viable microbes in *in situ* biopreservation process include some well-established steps: correct identification, safety evaluation (of producer and antimicrobial agent), characterization of the bacteriocin and suggested application. In this regards, research and screening for new strains with more than one beneficial property were accelerated with aim to implement in the food fermentation processes microbial starter that can be considered as multifunctional and if possible, to be with probiotic or bioprotective properties in addition to their starter cultures performance. Safety has always been and will be driving priority in selection of new functional microbial cultures. However, in addition, combination between production of antimicrobial proteins (bacteriocins) and antioxidants can be considered as interesting application scenario in the selection of new starter cultures. Beneficial properties that such as cultures can bring to the fermented food products will be resulting in reduction of chemical additives and cover exigences of the consumers for more natural and freer of the artificial preservatives food commodities. Appropriate selection of safe microbial cultures with appropriate antimicrobial and antioxidant properties is the first step of the large research projects, where technological properties and *in situ* suggested beneficial properties need to be validated in further research.

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Different subtypes of post-stroke pain syndrome: features of the gut microbiota

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The aim. To study the composition of the gut microbiota in patients with different type of post-stroke pain syndrome.

Materials and methods. 42 patients (60.5±8.9 years old) were examined, which were divided into two groups: the main group with the presence of post-stroke pain syndrome (26 patients, 62.2±9.03 years old) and the comparison group without post-stroke pain syndrome (18 patients, 58.0±8.44 years). The main group was divided into subtypes of post-stroke pain: musculoskeletal pain (n=3), shoulder pain (n=5), central pain (n=11) and headache (n=5). To study the characteristics of the gut microbiota and assess its significance in the development of associated diseases, high-throughput sequencing was performed according to the 16S protocol using the Illumina MiSeq platform. Data analysis was performed using the BaseSpace Sequence Hub software (Illumina, USA), the 16S Metagenomics application, and the DRAGEN Metagenomics application.

Results and discussions. No significant difference between groups patients with and without post-stroke pain was found. When comparing subgroups of central and headache, a significant decrease in the *Bacteroidaceae* family (p=0.0244) and *Bacteroides* genus (p=0.0088) was found in individuals with post-stroke headache. There was a decrease in the representation of the *Oscillospiraceae* family in the headache group compared to patients with shoulder pain (p=0.0061).

Conclusions. A study was conducted to study the characteristics of the gut microbiota in patients with different subtypes post-stroke pain syndrome. The features of the species composition of the intestinal microbial representation have been established, which may indicate possible new mechanisms of the pathogenesis of the occurrence of this type of pain.