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### Integration of analysis of the genetics of the vaginal microbiome into the clinical practice of an obstetrician-gynecologist

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**Introduction.** According to world statistics, bacterial vaginosis occupies one of the first places among vaginal diseases. The frequency of its distribution in the population ranges from 12 to 80% and depends on the contingent of women examined. The relevance of the topic is due to the high incidence of BV and the fact that it often causes serious complications in reproductive health. Despite well-known and clear treatment regimens regulated by clinical recommendations and foreign guidelines, relapses of BV occur in 50% of treatment cases, even after therapy in compliance with the principles. The search for new diagnostic and treatment methods in the treatment of BV is very important for maintaining the health of patients.

**Materials and methods.** The study was carried out on the basis of PM Clinic of the Institute of Interdisciplinary Medicine during the period from December 2022 to August 2023.

All patients (15) of the retrospective stage of the study were divided into three groups: with a verified diagnosis of chronic recurrent BV (5); diagnosed with chronic recurrent BV in combination with vulvovaginal candidiasis (5) and a comparison group (5). Patient selection criteria: reproductive age of patients in the examination groups (from 18 to 48 years); a history of at least two episodes of exacerbation of BV over the past 3 years; verification of the diagnosis was carried out based on the Amsel criteria and PCR methods. Research methods: NGS sequencing of the V3-V4 regions of the 16S rRNA gene, RT-PCR © "Femoflor-screen"

**Results.** A comparison of control groups showed that among patients with an isolated recurrent form of bacterial vaginosis or in combination with recurrent vulvovaginal candidiasis, a species predominance of *L.iners* was detected compared to relatively healthy patients, which was revealed using 16S microbiome sequencing. RT-PCR © "Femoflor-screen" does not allow typing of lactobacilli and may demonstrate insufficient information about the patient's health status, such as normal levels of *Lactobacillus spp.* and the absence of the most common pathogens of bacterial vaginosis, while with the help of 16S microbiome sequencing it is possible to identify atypical for a given localization of microorganisms. Criteria for introducing 16S sequencing into work are also proposed.

**Conclusion.** RT-PCR and 16S sequencing methods are complementary, but not mutually exclusive, and therefore should be equally introduced into the work of an obstetrician-gynecologist to simplify diagnosis and reduce the incidence of chronicity of bacterial vaginosis and vulvovaginal candidiasis.

### A probiotic from Malaysia: from lab to market

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Probiotic microorganisms have a long history of safe use and have been documented for their various health benefits. Many strains of lactic acid bacteria (LAB) from the genera of *Lactobacillus* have been identified to possess probiotic properties. They have been much emphasized on their roles to regulate gut well-being, including the alleviation of lactose intolerance, improvement of diarrhoea and inhibition towards pathogenic bacteria in the gut. Recent evidences have illustrated the potential of LAB for brain health, ranging from neurodegenerative diseases to stress, memory and cognition. *Lactobacillus plantarum* DR7, a cow's milk isolate from Penang, Malaysia has shown a reversal of symptoms associated with Alzheimer's Disease in a fruit fly model, accompanied by distinct changes of gut microbiota profiles. In aging and hyperlipidemia rats, DR7 has shown improved stress and anxiety symptoms, accompanied by improved memory. The administration of DR7 for 12-weeks in stressed adults has contributed to improve stress and anxiety scores, in addition to memory and cognitive abilities, primarily via enhancement along the serotonin pathway and maintenance of the dopamine pathway. My talk will highlight the evidence of a probiotic strain, primarily targeting brain and gut health, via models ranging from insects to human, and its journey from laboratory to over 40 countries globally.

### Gut microbiota and urinary tract infections

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**Introduction.** Several studies demonstrate a correlation between gut microbiota composition and urinary tract infections (UTI). The current paradigm of UTI pathogenesis takes into account the contamination of the periurethral space by specific uropathogens residing in the gut, which is followed by urethral colonization and pathogen ascension to the urinary bladder. However, bacterial translocation of pathogens may be a potential mechanism for the penetration of bacteria from the intestine into the urinary tract. Studying the relationship between gut microbiota and UTI represents an important field of research and was the aim of study.

**Materials and methods.** 30 inpatients with liver cirrhosis were enrolled in this study, of which 17 without UTI, 13 with UTI. We perform standard examination of gut microbial profiling using 16S rRNA gene deep sequencing on 30 fecal specimens.

**Results.** In patients with liver cirrhosis, regardless of the UTI, the gut microbiota is represented by the dominant phylum of bacteria *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, *Actinobacteria*. Relative abundance bacteria Phylum *Proteobacteria*, classes *Fimbriimonadia*, *Thermomicrobia*, orders *Enterobacteriales*, *Pseudomonadales*, *Rickettsiales*, *Fimbriimonadales*, *Thermosediminibacteriales*, *Chlamydiales*, family *Enterobacteriaceae*, genus *Escherichia*, *Acinetobacter*, *Enterobacter*, *Serratia* in feces patients with UTI higher than without UTI ( $p < 0.05$ ). It should be noted that some of these bacteria are causative agents of urinary infections.

**Conclusion.** Patients with chronic liver disease and cirrhosis demonstrate a global mucosal immune impairment, which is associated with altered gut microbiota composition and functionality. These changes progress along with the advancing degree of cirrhosis and can be linked with infections, including UTI. Our results support a gut microbiota-UTI axis, suggesting that modulating the gut microbiota may be a potential novel strategy to prevent UTI.