Intestinal microbiota composition in patients with Multiple Sclerosis

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Background: It is now established that healthy intestinal gut microbiota has immunomodulatory effects, produces antimicrobial factors and inhibiting the growth of some pathogenic bacteria. In the last years, there has been an increasing interest in the role of the gut microbiota in some autoimmune disorders and especially, in the pathogenesis of multiple sclerosis (MS). MS is a chronic inflammatory demyelinating autoimmune disease of the central nervous system. Some intestinal bacteria can stimulate Th17 cells. This T cells population have most encephalitogenic ability in multiple sclerosis . At the same time almost 70% of MS patients have different gastrointestinal problems, which may be the result of intestinal microbiota dysbiosis. There are evidences of the involvement of intestinal microbiota in experimental autoimmune encephalomyelitis (EAE) – an animal model of multiple sclerosis (Berer et al., 2011; Ochoa-Reparaz et al., 2009, 2010). Previously we have shown changes in microbiota composition in EAE model in rats (Abdurasulova et al., 2015).

The aim of this study was to analyze the composition of intestinal microbiota in patients with MS

Material/methods: Feces from the 24 patients diagnosed with MS (16 females and 8 males) were colected. *Lactobacillus spp., Bifidobacterium spp., Enterococcus spp., Escherichia coli, Faecalibacterium prausnitzii, Bacteroides fragilis/thetaiotamicron, Clostridium difficile/perfringes, Fusobacterium spp., Staphylococcus aureus, Proteus mirabilis/vulgaris, Klebsiella pneumoniae/oxytoca, Citrobacter diversus, Shigella spp., Salmonella spp*. were studied using real-time polymerase chain reaction (RT PCR) method and some of them by bacteriological technique.

Results: Changes in the composition of microorganisms were detected in all fecal samples. It is reduced the level of commensal bacteria and the appearance or excessive growth of opportunistic bacteria. Reduction of non-pathogenic *E. coli* was detected in 90% of samples and growth of enteropathogenic *E. coli* was noted in 68% cases. Using RT PCR method in 30% of patients dysbiosis was characterized by a higher ratio of *Bacteroides fragilis* to *Faecalibacterium prausnitzii*. A similar pattern was observed in EAE model (Abdurasulova et al., 2015). Using bacteriology method in women group detected decrease proportions of lactobacilli and the excessive proliferation of atypical *E. coli, Citrobacter spp*. and *Acinetobacter spp*., whereas men mostly showed high rates of detection of *S. aureus , Klebsiella spp., Proteus spp*. and *Candida spp*.

Conclusions: Patients with MS has been found dysbiosis the intestinal microbiota, which can not only promote the development of disorders of the gastrointestinal tract, but also provoke the exacerbation of the disease. It is necessary to restore the homeostasis of the intestinal microbiota in patients with MS using antibacterial therapy, including probiotics.