



Intestinal microbiota composition in patients with Multiple Sclerosis

Elena Tarasova^{1,2} *, Irina Abdurasulova¹, Anna Matsulevich¹, Dmitriy Skulyabin³, Gennadiy Bisaga³,
Elena Ermolenko¹, Alexander Suvorov¹, Viktor Klimenko¹

¹ Institute of Experimental Medicine of RAMS, St. Petersburg, Russia. ² SRL Explana, St. Petersburg, Russia,
³ S.M.Kirov Military Medical Academy, St. Petersburg, Russia

*tarasovahellen@mail.ru



Objectives

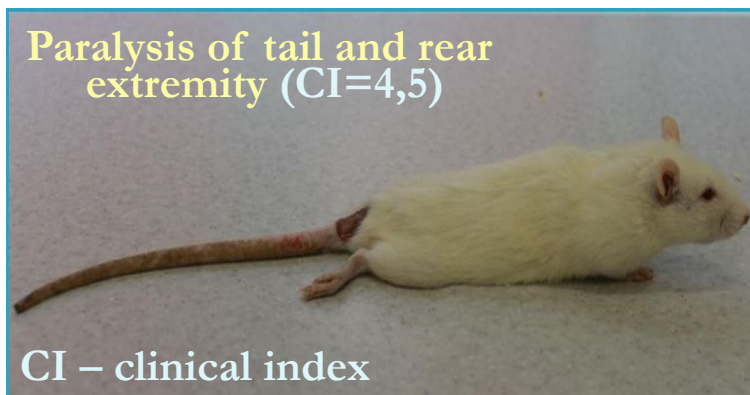
The commensal **gut microbiota** has an immunomodulatory effect, produce antimicrobial factors and inhibits the growth of some pathogenic bacteria. In recent years, there has been an increasing interest in the role of gut microbiota in some autoimmune disorders and especially, in **multiple sclerosis (MS)**, which is an autoimmune chronic demyelinating disease of the central nervous system.

Some intestinal bacteria can stimulate the differentiation of naïve T-cells into Th17 subset. This population of T-cells produce IL-17 and is a major contributor to the development and progression of MS. In the same time, almost 70% of MS patients have different gut dysfunction, which may be the result of dysbiosis of the gut microbiota. There are evidences of 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).

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

Methods

The **EAE** was induced in female of Wistar rats by single inoculation of homologous spinal cord homogenate (HSCH) with complete Freund's adjuvant.

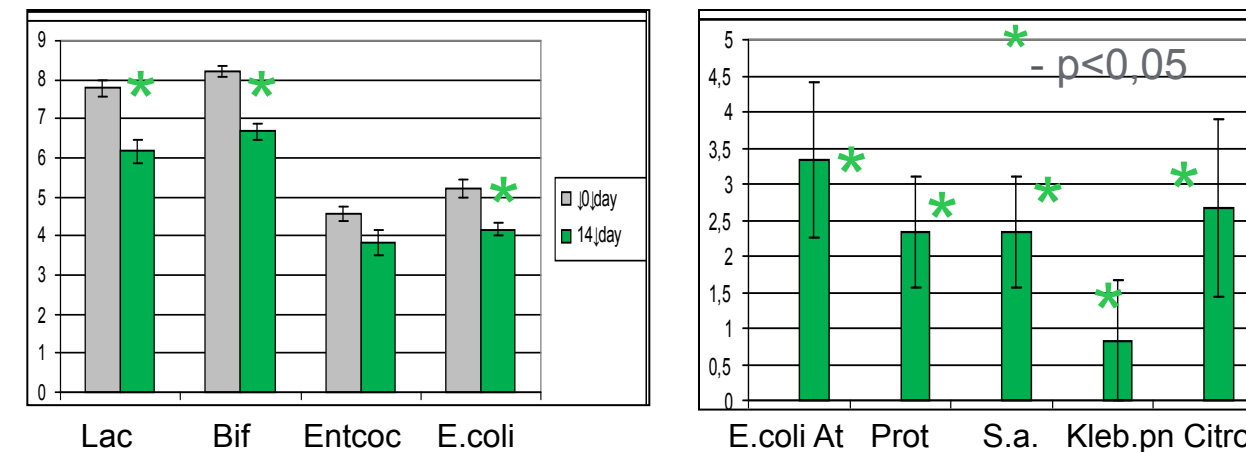


The neurological disorders were evaluated by clinical symptoms: paralysis and paresis.

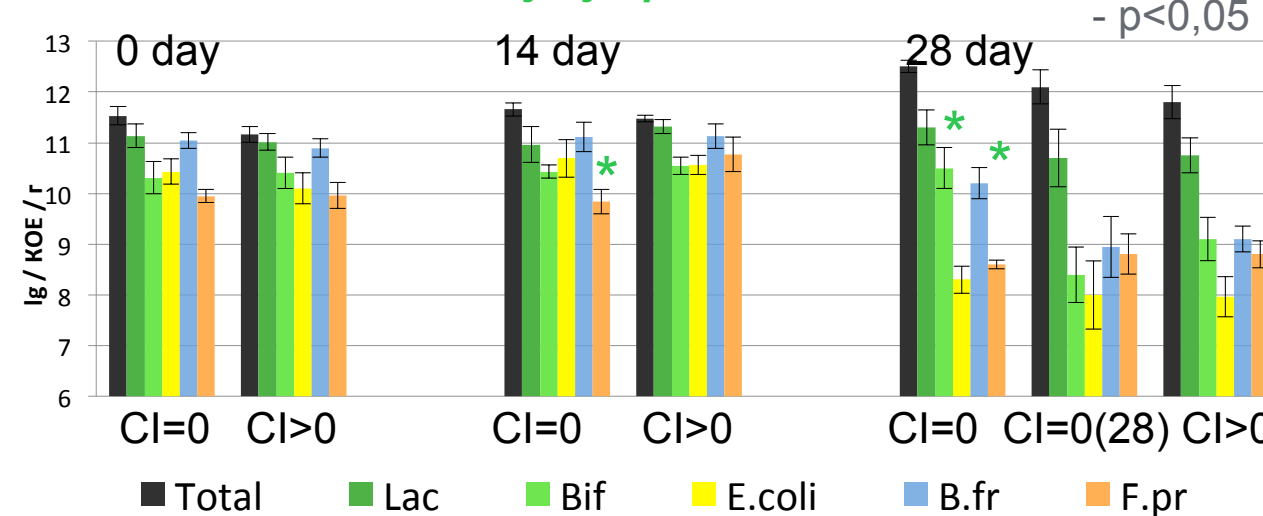
The group of patients included 24 patients (16 females and 8 males) diagnosed with MS. Changes in the gut microbiota were analyzed by real time PCR (RT-PCR) and bacteriological method. For identification of bacteria we use kit “**Colonoflor-16**” (Alpha Lab, Russia)

Results

Microbiota composition before the EAE induction (0 day) and on the peak of clinical manifestations in EAE (14th day) (bacteriological analysis).



The analysis of microbiota composition by real time PCR method in fecal samples of rats with neurological disorders and without any symptoms of the EAE



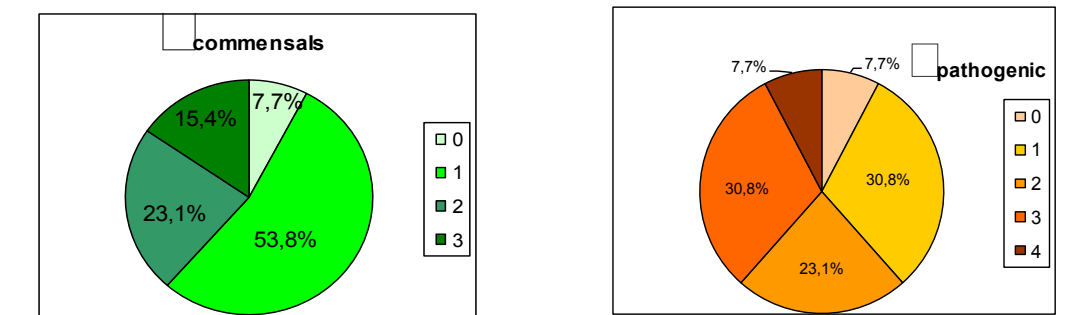
Total – total bacterial count, Lac - *Lactobacillus spp.*, Bif - *Bifidobacterium spp.*, E. coli - *Escherichia coli*, E. coli At – atypical *Escherichia coli*, B. fr. – *Bacteroides fragilis*, B. theta. – *Bacteroides thetaiotaomicron*, Prot - *Proteus spp.*, F. pr. – *Faecalibacterium prausnitzii*, S.a. - *Staphylococcus aureus*, Entcoc - *Enterococcus spp.*, Kleb.pn.- *Klebsiella pneumoniae*, Clo. perf. – *Clostridium perfringens*, Citro – *Citrobacter spp.*, Entero – *Enterobacter spp.*, Candida – *Candida spp.*

Conclusions

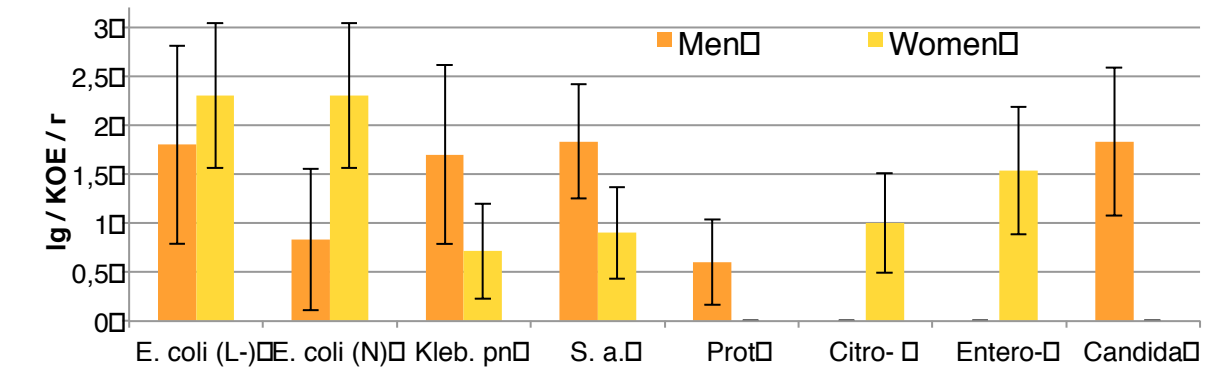
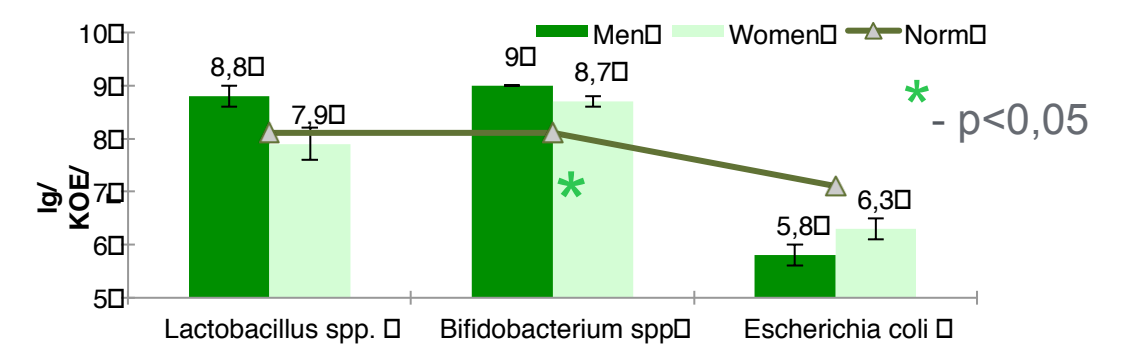
MS patients as well as rats with EAE show the presence of intestinal microbiota dysbiosis, resulting from the decline in the number of symbiotic bacteria and increase in contingent-pathogenic microorganisms. Dysbiosis may have implications for the pathogenesis of MS. It open possibility to treat disturbances in inteastinal bacterial content with antibacterial therapy, pro- and prebiotics or faecalotherapy taking into account the personal and gender characteristics.

Results

% of MS patients with different microbiota changing



Composition of microbiota in samples of patients with MS (bacteriological analysis)



Composition of microbiota in samples of patients with MS by real time PCR method

