

# MICROBIOTA AND SCFA PROFILE OF WOMEN WITH FUNCTIONAL CONSTIPATION

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**Background.** Functional constipation is caused by various factors, one of them was luminal factor (dysbiosis of microbiota). The gut microbiota and also short chain fatty acid plays a fundamental role in several aspects of host health and diseases.

**Methods.** A randomized, double-blind, placebo-controlled clinical trial was conducted to evaluate supplementation of fermented milk containing probiotic *Lactobacillus plantarum* IS-10506 ( $1.2 \times 10^{10}$  cfu/day) and placebo on gut microbiota and SCFA profile of 28 women with functional constipation after 21 days supplementation compare to 8 women (non constipation group). Profile of fecal microbiota and fecal SCFA (acetate, propionate, and butyrate) was assessed by *next generation sequencing* (NGS) and GC-MS, respectively.

**Results.** Baseline data showed that there was unbalancing (dysbiosis) of microbiota composition in terms of Firmicutes:Bacteroidetes ratio: a higher ratio was found in constipated subjects. Also, SCFA concentrations were significantly lower in constipated subjects. After 21 days supplementation there was increasing of taxa *Lactobacillus* sp. strongly correlate with the increasing of Lachnospiraceae.other after probiotic intervention. Lachnospiraceae.other seemed to suppress *Roseburia* sp, Ruminococcaceae.g, and *Bilophila* sp. Suppression of *Roseburia* sp, relative abundance strongly correlated with increased SCFA. Based on the Spearman-rho correlation test, *Roseburia* sp has a correlation with all SCFA parameters (acetate rho=0,46, propionate rho=0,49 and butyrate rho=0,43) besides other strong correlations are Christensenellaceae.g\_ and Lachnospiraceae.g\_ with acetate (rho=0,62).

**Conclusion.** Supplementation of fermented milk containing *Lactobacillus plantarum* IS-10506 at a dose of  $1.2 \times 10^{10}$  cfu/day for 21 days improved the balance of microbiota towards eubiosis, increased SCFA (acetate, propionate and butyrate) concentration as an underlying molecular mechanisms of the women with functional constipation.

**Key words:** *Lactobacillus plantarum* IS-10506, functional constipation in women, microbiota profile, SCFA.



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