

METABOLIC PROFILING OF THE IMPACT OF SYNBIOTIC INTERVENTION ON FAECAL METABOLITES IN HEALTHY SUBJECTS

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Introduction and objectives: Dietary intervention with pre- or probiotics has been associated with various health benefits. Targeted, hypothesis-driven approaches have mainly focussed on the quantification of SCFAs in faecal samples as mediators of beneficial effects of pre- and probiotic administration. However, the emergence of metabolomics allows to evaluate the colonic metabolism from a top-down approach bypassing the need for an a priori hypothesis. In the present study, we evaluated the impact of synbiotic administration on faecal metabolite profiles and microbiota composition in healthy subjects.

Materials and methods: The synbiotic combination (6.5×10^9 *L. casei* Shirota cells + 10g OF-IN (b.i.d.)) was evaluated in 9 healthy volunteers (4m/5f). Immediately before the start of the study, during the treatment (direct effect) and at the end of a 4-wk treatment (indirect effect), faecal samples were obtained. A purge-and-trap system, coupled on line to a GC-MS (type time-of-flight) was applied to analyse the metabolites and DGGE was used to monitor the microbiota composition.

Results and discussion: A total of 139 different VOCs were identified in the faecal samples, with an average of 58 ± 4 VOCs per subject, and 17 VOC were found in all samples. Cluster analysis based on the relative indices of all VOC demonstrated that the VOC fingerprints clearly clustered in 3 groups, discriminating between baseline, during and after synbiotic treatment. Application of a Type 3 test revealed that the metabolites profiles from the 3 conditions were significantly different ($p=0.0001$). Subsequently, we identified 3 VOCs, acetate, dimethyl trisulfide and ethyl benzene, that were, after correction for multiple testing, significantly affected. The acetate levels increased, whereas the dimethyl trisulfide levels decreased during and after the intervention. This indicates that not only the actual presence of the synbiotic but also changes in the colonic microbiota contributed to the effect. For ethyl benzene only an effect, due to the actual presence of the synbiotic in the colon, was observed. Statistical comparison of the intensities of all band-classes from DGGE revealed no differences

We report a detailed analysis of the influence of synbiotic intake on the pattern of fermentation metabolites in the colon. The significant increase in acetate and reduction of dimethyl trisulfide and ethylbenzene may rise potential for pre- and/or probiotics in health maintenance and prevention of disease.