

The Composition of the Dominant Fecal Microbiota in COPD Patients Receiving Multispecies Probiotics During and After Antibiotic Intake

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Introduction Healthy individuals have a unique intestinal microbiota (i.e. genetic fingerprint) that is relatively stable in time. Antibiotic intake is known to cause short-term disturbances in the composition of this microbiota and recently medium and long-term disturbances in specific bacterial populations have been described. Probiotics can affect the composition of the intestinal microbiota beneficially and may prevent/restore such disturbances. However, data in chronically ill patients with a potentially disturbed immune system and an altered intestinal microbiota are limited. Aim and Methods The alterations of the dominant fecal microbiota by antibiotics and the possible prevention/restoration by a multispecies probiotic were studied in patients with chronic obstructive pulmonary disease (COPD) treated with antibiotics for a respiratory tract infection. Five gram of a multispecies probiotic (5 lactobacilli, 3 bifidobacteria, 1 Enterococcus) (10^9 cfu/gr) or placebo was given twice daily for two weeks starting simultaneously with standard antibiotic treatment. From each patient fresh fecal samples were collected at day 0, 7, 14 and 63. Changes in the composition of the dominant fecal microbiota were determined by denaturing gradient gel electrophoresis (DGGE) of PCR-amplified V6-V8 regions of bacterial 16S rRNA genes and expressed as "similarity indices" (SI) between two samples and number of bands within each sample. Results Thirty patients completed the study (17 in the probiotic group, mean age 60 yrs (13.3), and 13 in the placebo group, mean age 63 yrs (7.4)). Patients had a history of extensive antibiotic use (1-7 treatments in previous year). SIs were high and remained stable during and after antibiotic treatment. No effect of probiotic intake was observed. Mean band number was also stable over time, ranging from 14.4-15.4 bands. Conclusion In this COPD population no effect of antibiotics and of subsequent probiotic intake could be observed on the dominant faecal microbiota. Low band numbers and high SIs compared to previous findings in healthy volunteers suggest a narrowed diversity of the dominant faecal microbiota due to extensive prior antibiotic use. This observation may have contributed to the lack of effect by probiotic and antibiotic intake in this COPD population.

Table 1: DGGE Similarity indices of the dominant fecal microbiota in % (median (range))

Time interval	0-7	0-14	0-63	7-14	14-63
Probiotic	90 (69-98)	87 (46-96)	88 (65-95)	90 (56-98)	90 (63-98)
Placebo	94 (44-98)	93 (45-98)	84 (39-97)	91 (69-98)	86 (55-98)