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Gut dysbiosis in cystic fibrosis

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In people with CF, intestinal exocrine malfunction, antibiotic usage [1] and swallowing of infected respiratory mucus [2] likely perturb the normal community of commensal bacteria in the gut. People with CF report various intestinal problems which may be alleviated by probiotic administration [3]. There is also evidence that probiotic bacteria can help people with CF fight respiratory infection [4,5]. However, CF-related gut dysbiosis has only recently been subjected to detailed investigation. Using DGGE and culture-based methods, Duytschaever and colleagues [6] showed that children with CF have a quantitatively and qualitatively different faecal microbiota from their healthy siblings. We conducted a pilot study using culture-independent stool microbiome profiling and found evidence consistent with these results, strengthening the case for more targeted exploration of the gut microbiota in CF.

We obtained stool samples from four people with CF and four unrelated, healthy, age- and sex-matched controls. Total DNA was extracted and the 16S rRNA gene amplified. We analysed bacterial community composition using a high-density phylogenetic microarray (PhyloChip) that has been used extensively in microbial ecology surveys, including analyses of the human gut [7] and CF airways [8]. Full methods are available as Supplementary Content.

In 3 of 4 pairs the CF patient exhibited lower taxonomic richness, evenness and diversity than the healthy control (Fig. 1). Further, non-metric multidimensional scaling [9] revealed greater inter-individual variation in gut microbiota in the CF group than in the healthy controls. Given the range of factors that produce variation in the human gut microbiome it is impossible within this small cohort to speculate whether this is simply a function of disease severity and/or antibiotic use, or of other variables such as host genetics, diet, environment and age.

Finally, consistent with Duyschaever et al.'s data, we found decreased relative abundance of *Bifidobacterium* species in the CF group; these are widely used in probiotic products and one of the species with decreased abundance in our cohort, *Bifidobacterium breve*, may mediate intestinal homeostasis [10]. A full list of taxa with altered relative abundance in the CF group is provided in the Supplementary Content.

While our pilot data set is too small to draw firm conclusions, our data support the hypothesis that people with CF have intestinal microbial dysbiosis. This, together with the prophylactic potential of probiotics for preventing respiratory infections, highlights a need to investigate the intestinal microbiota of CF in a larger cohort. In the future this may inform studies that investigate the prophylactic potential of probiotics for people with CF.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at doi:10.1016/j.jcf.2012.03.007.

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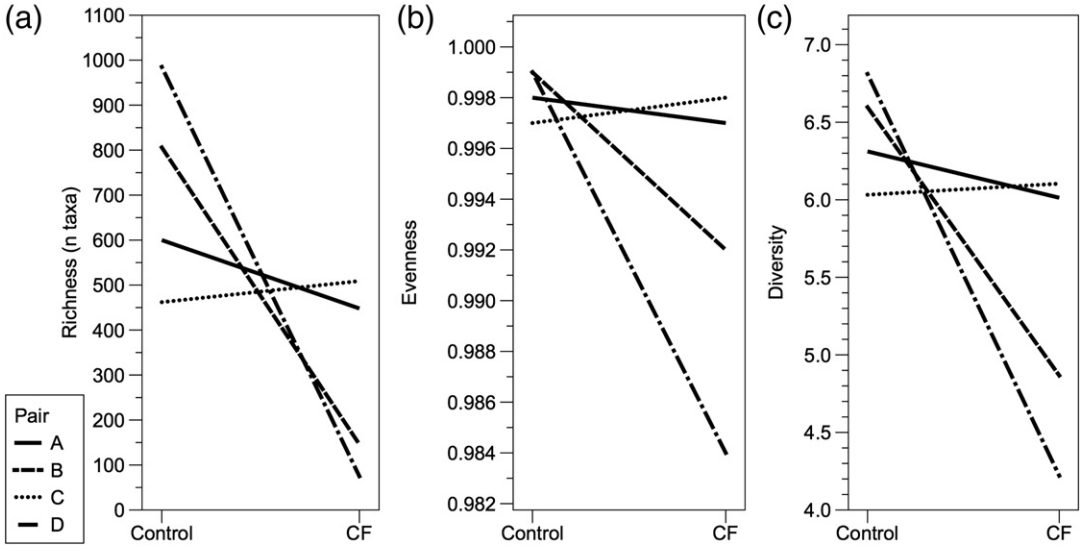

Fig. 1. In three of four participant pairs, the microbial community isolated from the individual with CF showed lower species richness, evenness and diversity than that isolated from the healthy control individual. Evenness measures the relative distribution of community members and diversity is a metric that takes both richness and evenness into account.

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