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**Microbiome research**

**Increased microbial diversity in paediatric patients with *Dientamoeba fragilis* infection**

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**Background:** *Dientamoeba fragilis*, an anaerobic intestinal protozoan parasite, localizes in the colon. In most cases, children are asymptomatic carriers, but it has also been associated with symptomatic disease. Common complaints include abdominal pain, flatulence and diarrhoea. Diagnosis of *D. fragilis* infection (dientamoebiasis) is most common under 20 years of age, with a peak incidence at 7 years of age. Since *D. fragilis* is a known predator of bacteria, we hypothesized that *D. fragilis* might exert its pathogenic effect indirectly by altering the intestinal microbiota. To unravel the possible relation to the intestinal microbiota, we compared the intestinal microbiota in children with dientamoebiasis and healthy controls.

**Material/methods:** Children with proven, symptomatic, *D. fragilis* infection were included. All patients were recruited from 2 Dutch hospitals, in Amsterdam and Hilversum, the Netherlands. Faecal samples were collected before initiation of therapy and stored within 1h at -20°C. All patients were treated with jodiumchloroxyquinoline according to current care guidelines. Samples of healthy controls were tested for *D. fragilis* by PCR as well. Faecal samples of both groups were analysed by IS-pro, a clinically applicable PCR-based microbiome profiling technique.

**Results:** Faecal samples of 7 patients with dientamoebiasis (median 7 years) and 21 age-matched healthy controls (median 7 years) were collected so far. All patients were tested positive and all healthy controls negative for *D. fragilis*. Preliminary results showed distinct differences in microbiota between the two groups. Correlation dendrogram showed clustering of healthy controls, while patients with dientamoebiasis were all separated and their microbiota profiles were much more diverse (see figure 1). Diversity of *Bacteroidetes*, *Firmicutes/ Actinobacteria/ Fusobacteria/ Verrucomicrobia* (FAFV), *Proteobacteria* and all phyla together were significantly higher (p1.9e-16; p9e-08; p0.00016; p1.9e-16 respectively).

**Conclusions:** Children with dientamoebiasis showed a statistically significant higher diversity of intestinal microbiota compared to healthy controls, per phylum and within all phyla together. This is in

line with our hypothesis, that *D. fragilis* effects the composition of the intestinal microbiota. In a broader sense, the finding that the predatory *D. fragilis* causes an increase in the diversity of the gut microbial ecosystem is in line with general ecological theory. Whether the observed dysbiosis is the cause of the symptoms present in children with dientamoebiasis has to be elucidated in future studies.

