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Celiac disease (CD) is an immune-mediated enteropathy triggered by the ingestion of gluten in genetically susceptible individuals. Environmental and genetic factors contribute to the pathogenesis of CD. Gluten exposure provides the disease as the high protein content of gluten is relatively resistant to proteolytic digestion in the intestinal tract with consequent altered immune response in susceptible individuals. The most consistent genetic component depends on the presence of HLA-DQ2 and HLA-DQ8, which are necessary but not sufficient to develop CD. Fewer than 10% of those individuals with an increased genetic susceptibility develop clinical disease and most of them only many years after the first gluten exposure.

The involvement of intestinal colonization in the malabsorption of immune responses in the animal models, showing that both the intestinal associated immune system and systemic immune mature on, activation of the intestinal microbiota. Little is known about the potential role of the microbiota in CD. Compared to healthy individuals, CD patients seem to be characterized by a different composition of the gut microbiota. However, pathogens colonizing the intestine are responsible for the development of the disease.

STUDY DESIGN

AIM
Describe the colonization pattern of HLA DQ2/DQ8 positive infants at risk of CD and identify microbicota alterations as predictive marks of gluten tolerance loss.

METHODS

Whole stools were collected at 7, 35 days and 6, 10, 12, 18 and 24 months of age (Table 1).

DNA extraction

454 amplicon sequencing and 454 pyrosequencing of barcoded 16s rRNA genes

Quantitative PCR assay from Bacteroides and Bacteroidales

CD sepsdogy: AGA IgA Ab, AGA IgA Ab, AGA IgA Ab, AGA IgA Ab, AGA IgA Ab, Tوت (3A)

Quantitative PCR assay from Bacteroides and Bacteroidales

at the time of recruitment and for the length of the follow-up.

Results

Figure 1. Figure 2. Table 1. Sample collected.

Phylum-level comparison

Genus-level comparison

Table 1. Sample collected.

RESULTS

Phylum-level comparison reveal the striking low levels of Actinobacteria, which are present at less than 1% in all samples (Figure 1).

At the phylum level, GI microbial communities appears somewhat stable over time.

The GI microbiota of CD at treatment is highly dynamic, with high degree of intra-individual variation. At the genus level, the communities do not look like that of not at risk children (Figure 2).

Figure 1. Figure 2.

CONCLUSIONS

The low numbers of CD at-risk infants appears to be different than that of non-pre-disposed children. The colonization process is very dynamic, with high degree of intra-individual variation over time.

Unlike non-pre-disposed children, the GI microbiota of CD at-risk infants does not stabilize towards an adult-like microbiota. Members of the phylum Bacteroides are absent from the GI microbiota up to 24 months, while they are pre-disposed in non-children.

REFERENCES