COMPOSITION AND DYNAMIC CHANGES OF GUT MICROBIOTA IN HLA DQ2/DQ8 POSITIVE BABIES AT RISK OF CELIAC DISEASE: PRELIMINARY RESULTS

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BACKGROUND
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, the major protein component of wheat, rye and barley, is the main environmental factor. Gluten proteins provoke the disease as the high protein content is relatively resistant to proteolytic digestion in the intestinal tract with consequent abnormal 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 after many years after the first gluten exposure.

The involvement of intestinal colonization in the maturation of immune responses is well characterized in animal models, showing that both the intestinal associated immune system and systemic immunity mature on intestinal colonization in the first year of life. The involvement of intestinal colonization in the maturation of immune responses is well characterized in animal models, showing that both the intestinal associated immune system and systemic immunity mature on intestinal colonization in the first year of life. Environmental and genetic factors contribute to the pathogenesis of CD.

STUDY DESIGN

METHODOLOGY

Aims

- To describe colonization pattern of HLA DQ2/DQ8 positive infants at risk of CD and identify microbiota alterations as predictive marks of gluten tolerance.

METHODS

- Short samples were collected at 7, 30 days and 6, 10, 12, 18 and 24 months of age.
- DNA extraction
- 16sRNA amplification and 454 pyrosequencing of barcoded 16s rRNA genes
- Quantitative PCR assay from total bacteria and Bacteroidetes age.
- NMR spectrometry analysis of fecal samples
- CD xerography (AGA IBD, AIAG, AIAG, AIAG, AIAG, AIAG, AIAG, Total AIAG)

RESULTS

Phylogenic tree

Phylogenic trees reveal the striking low levels of Bacteroides, which are present at less than 1% in all samples (Figure 1).

In not at-risk children, Bacteroides do colonize and establish in the GI in the first year of life. At the phylogenic level, GI microbial communities appears somewhat stable over time.

Phylogenic tree comparison of DQ2/DQ8 positive untreated cases and other children

Phylogenic tree comparison of group A and B by 16s rRNA analysis shows that the GI microbial communities do not appear to be stable over time and no difference is detectable in the two groups of the microbial community composition, the Principal Component Analysis (PCA) plot of NMR spectrometry shows a similar spectrum in three group B babies. The metabolites analysis shows a consistent microbial function and a clustering by time points.

CONCLUSIONS

The GI microbial communities do not appear to be stable over time and no difference is detectable in the two groups of the microbial community composition. The metabolite analysis shows a consistent microbial function and a clustering by time points.

REFERENCES


Figure 1

Phylogenic tree comparison of DQ2/DQ8 positive untreated cases and other children

Figure 2

Phylogenic tree comparison of group A and B by 16s rRNA analysis shows that the GI microbial communities do not appear to be stable over time and no difference is detectable in the two groups of the microbial community composition. The metabolite analysis shows a consistent microbial function and a clustering by time points.