Gut Microbiota Colonization Process in HLA DQ2/DQ8-Positive Babies at-Risk of Celiac Disease

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BACKGROUND: It has been recently suggested that, beside genetic makeup and exposure to gluten, gut microbiota is involved in celiac disease (CD) pathogenesis.

AIM: To investigate the composition and temporal changes of the gut microbiota in newborns at risk of CD.

METHODS: Babies that are first-degree relatives of patients with biopsy-proven CD, and positive for HLA-DQ2 and/or DQ8 genotype were enrolled (N=16). Stool samples were collected at increasing time intervals up to 24 months of age. Fecal microbiota was analyzed by 454 pyrosequencing of barcoded 16S rRNA. CD serology was performed at the time of recruitment and for the length of the follow up.

RESULTS: Phylum level comparisons reveal low levels of Bacteriodetes, which were present in less than 1% in all samples. At the phylum level, GI microbial community appeared stable over time. Communities were dominated by Firmicutes and Actinobacteria. Genus level comparisons reveal that genera belonging to the phylum Firmicutes were the most predominant, but not equally distributed in each subject. Similarly to not at-risk newborns, Enterococcus, Streptococcus and Staphylococcus colonized earlier, but Streptococcus remained dominant at 18 months. At the genus level, GI microbial communities were temporarily unstable: after 18 months, most of the communities differed from those identified in not at-risk children.

CONCLUSIONS: The GI microbiota of CD at-risk infants appears to be different than that of non-predisposed children. The colonization process is very dynamics, with high degree of inter-subjects variation over time. Unlike non-predisposed children, the GI microbiota of CD at-risk infants does not stabilized towards an adult-like microbiota. Members of the phylum Bacteroides are absent from the GI microbiota up to 24 months, while they are predominant in non-predisposed children.