STRONG CHILDREN'S RESEARCH CENTER
Summer 2019 Research Scholar

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ABSTRACT

Title:
Comparison of Infant Fecal *Bifidobacterium spp.* and *Bifidobacterium longum subsp. infantis* Proportions Between Cohorts at High and Low Risk for Allergy

Background:
Interest in the infant gut microbiome has recently come of age as these early colonizers help set the stage for proper host immune system development. Gut microbiome diversity is considered to be important for priming the infants' mucosal and systemic immunity. The prevalence of food allergies among children under the age of 18 has greatly increased by 18% from 1997 to 2007[1,2]. However, fewer than 1% of the Old Order Mennonites (OOM) in Penn Yan, the Yates County (Finger Lakes), have food allergies, asthma or other allergic diseases[2]. We chose to study *Bifidobacterium* and *Bifidobacterium longum subs. infantis (B.infantis)* because low levels of human milk oligosaccharides (HMOs), which are main substrate for *Bifidobacteria*, were shown to correlate with development of allergies in infants[2]. Moreover, lacto-*N*-neotetraose, a specific HMO component, was shown to provide a selective advantage to *B. infantis* in a gnotobiotic mouse model.[3]

Methods:
Total *Bifidobacteria spp.* and *B. infantis* in DNA extracts of infant (age range 14-198 days) stool samples from Old Order Mennonites (OOM) and Greater Rochester (ROC) communities were tested and compared across similar age groups. The total bacterial 16S ribosomal RNA gene (16S) copies of infant stool samples was quantified using SYBR-based qPCR analysis. TaqMan probe-based primer sets were used to quantify *Bifidobacteria spp.* and *B. infantis* normalized to total 16S copies in each sample. Total of 87 samples were tested (57 OOM; 30 ROC).

Results:
Total *Bifidobacterium* and *B.infantis* 16S normalized levels are significantly lower in ROC compared to OOM samples, p= 0.02386 and p=0.0001, respectively. There was significant difference between the *Bifidobacteria* 16S normalized levels among 1-100 days-old groups between the ROC and OOM communities (p=0.0429) and no significant difference among 100-200 days-old groups (p= 0.2994). The *B. infantis* 16S normalized levels within the same age groups is significantly lower in ROC compared to OOM for 1-100 days (p=0.0011) and no significant difference among 100-200 days (p=0.0571).

Conclusion:
Early infant fecal samples show in OOM community at low risk for allergies have higher *Bifidobacteria* and *B. infantis* proportions than Rochester community at higher risk for allergies. Lower levels of HMOs in breastmilk were found to correlate with development of allergies, and HMOs are a substrate for *Bifidobacteria*. Therefore, lower *Bifidobacteria spp.* and *B. infantis* levels may indirectly indicate HMO levels and potential risk of allergy development. It requires follow-up studies to determine the mechanism by which *Bifidobacteria* directly affect allergy development. The differences in microbiota may be due to lifestyle related with various microbiome exposures, such as large families and long period of breastfeeding and/or breastmilk components, such as HMOs and microbiome.

References:

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