

STRONG CHILDREN'S RESEARCH CENTER

Summer 2017 Research Scholar

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ABSTRACT

Title: Immunoglobulin A (IgA) Coated Bacteria in Infant Stool Microbiota Used as a Biomarker for Immune System Development between Old Order Mennonite and Rochester Populations – A Pilot Study

Background: According to the World Allergy Organization, the prevalence of allergic disease in the industrialized (developed) world has continuously risen over the past 50 years¹. The “Hygiene Hypothesis” attempts to explain this rise by associating increased allergic disease prevalence with misdirected immune system caused by a lack of microbial exposure in newborns and infants. Our lab’s recent and continuing study aims to compare immune system development within infants from two communities: Old Order Mennonites of the Penn Yan, NY area (OOM) and the residents of urban/suburban Rochester, NY (ROC). When compared to the general population, OOM seldom report being affected by allergic conditions such as asthma, hay fever, and food allergy thus, they can be labelled as low-risk for allergic disease². This low risk is thought to be attributed to the farm-life lifestyle, which exposes them to a large amounts and diversity of microbes. Therefore, we hypothesize that the diet, lifestyle, and microbial exposure of OOM newborns and infants lead to the development of a much more robust immune system than the Rochester general population.

Objective: This project aims to compare 1) the diversity of IgA coated microbiome and 2) the initial appearance of IgA coated bacteria OTUs in stool samples of infants from populations of both the OOM and Rochester communities.

Methods: Collection of ROC (n=4) and OOM (n=4) samples occurred at two time points/visits post-delivery: between 0-1 month and between 4-12 months. We then used IgA-SEQ (flow-cytometry-based bacterial cell sorting followed by 16S rRNA sequencing) in order to identify and categorize distinct bacteria OTUs. Data were analyzed using the QIIME package.

Results: Our pilot data show that 1) alpha diversity of total microbiome significantly increases in both ROC and OOM infants; 2) diversity of IgA non-coated bacteria in ROC outpaces OOM; 3) diversity of IgA coated bacteria is higher in OOM and outpaces ROC. LEfSe analysis showed that specific IgA+ bacteria OTUs colonize in OOM more quickly than in ROC. Additionally, in the LEfSe analysis of specific bacteria OTUs, it was found that some OTUs that colonize OOM at the first visit appear to colonize ROC only at the second visit, suggesting a sequential development of the microbiome that is faster in OOM.

Conclusion: These preliminary results demonstrate that OOM and ROC microbiome consists of distinct subpopulations of bacterial taxa, with OOM showing a more robust development of IgA coated microbiome. This may reflect their higher rates of breastfeeding providing IgA coated bacteria to the infant gut and/or a faster development of infants’ own IgA production. Larger numbers of samples have been processed and are being currently sequenced.

References:

1. Pawankar R, Canonica GW, Holgate ST, Lockey RF. White Book on Allergy 2011-2012 Executive Summary. World Health Organization.
2. Martina, C.; Looney, R.; Marcus, C.; Allen, M.; Stalhlut, R. "Old Order Mennonites in New York Have Low Prevalence of Allergic Disease". *Annals of Allergy, Asthma, & Immunology*. 2016; 117, 562-63.