

# The relationship of gut microbiota in standard and overweight children, before and after probiotic administration

Carter Linhardt<sup>1</sup>, Jonathan B. Clayton<sup>2</sup>, Suzie Hoops<sup>2</sup>, Syafinaz Nordin<sup>3</sup>, Dan Knights<sup>2</sup>

<sup>1</sup>Genetics, Cell Biology, and Development, University of Minnesota, Minneapolis, MN, <sup>2</sup>BioTechnology Institute, University of Minnesota, Minneapolis, MN, <sup>3</sup>Department of Medical Microbiology & Parasitology, UPM, Malaysia

## Abstract

The usage of probiotic foods and supplements has been widely considered part of a healthy diet by supplementing the gut microbiome with beneficial bacteria. Although the usage of probiotics is a common dietary accessory, there is limited reproducible evidence showing bacterial colonization, thus limiting long term effectiveness. We administered Yakult, a commercial probiotic composed of *Lactobacillus paracasei* strain Shirota, to overweight and standard weight school children in Malaysia. Using a crossover intervention study design, two groups of school children were administered the probiotic supplement or continued their typical diet in sequential 5-week intervention periods, separated by a 5-week washout period. Fecal samples were collected every five weeks over the course of the 15-week study period. The gut microbiome of each subject was analyzed using 16S rRNA gene sequencing. We observed significant differences in Lachnospiraceae, *Coprococcus*, *Roseburia*, *Pyramidobacter*, and *Bacteroides ovatus* between weight classes. However, differences in overall microbiome diversity between weight classes were not found to be significant. Subjects clustered according to their relative abundance of well-known genera *Bacteroides* and *Prevotella*, regardless of age, gender, or weight class. Overall, individual-to-individual variation overshadowed trends in gut microbiome composition associated with probiotic administration.

## Background

- Bioinformatics and computational microbiology are the collection and analysis of complex biological data
- Human microbiome is a collection of living microorganisms on and within our bodies
- Microbiota play important roles in our health
- Alpha and Beta diversity measure local diversity and abundance as well as regional differences, respectively

## Alpha Diversity

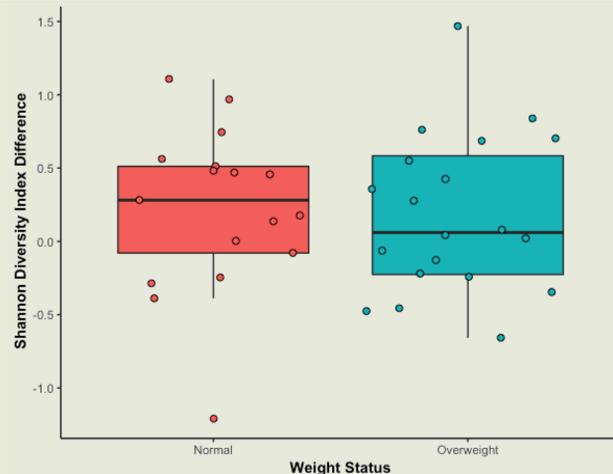
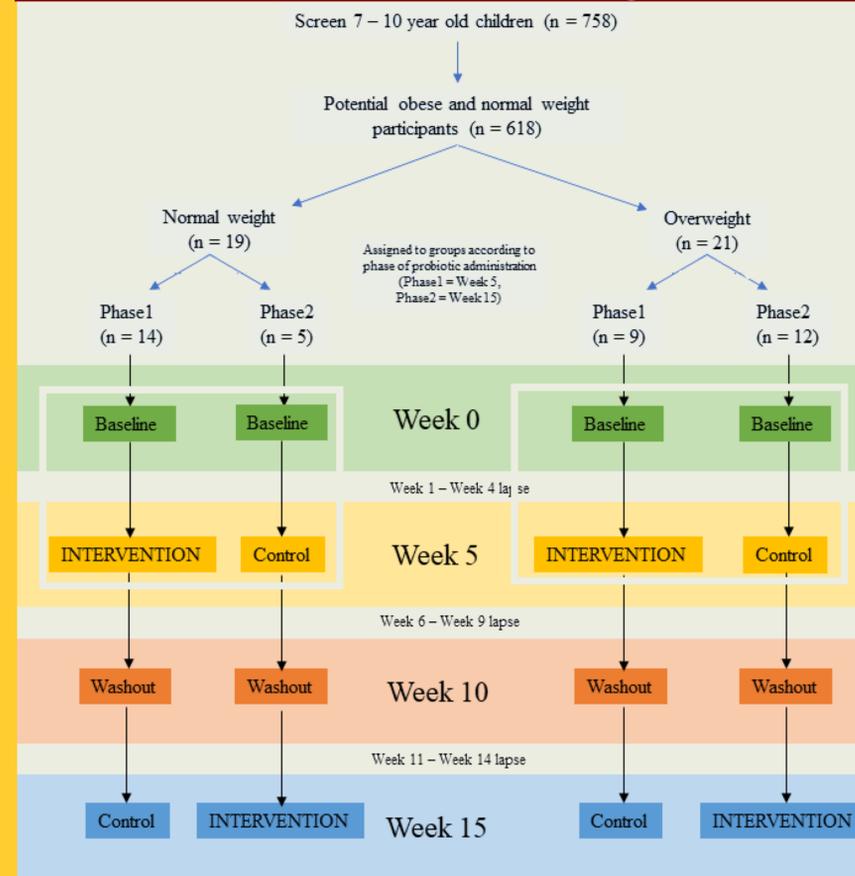


Figure 2: Difference of Shannon diversity index between before and after probiotic intervention, compared by weight status (n = 35). Significance was not found (p = 0.844).

## Experimental Design



\*\*\* INTERVENTION = Probiotic administration in the past 4 week lapse  
Control = No probiotic administration from past 4 weeks

Figure 1: Intervention of probiotic Yakult to Malaysian children. Administration occurred between weeks zero and five in phase-1 and weeks ten and fifteen for phase-2.

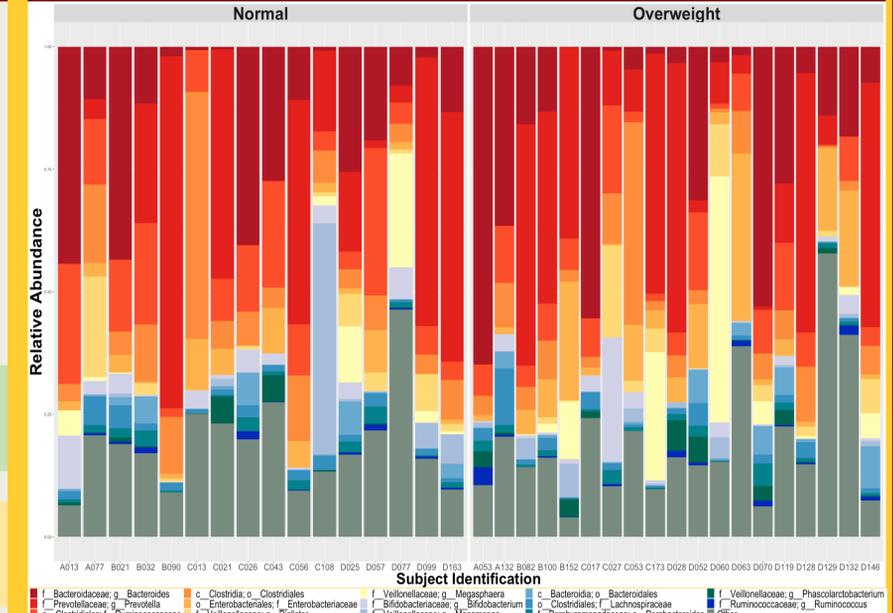
## Results

- Significant differences were found for Lachnospiraceae, *Coprococcus*, *Roseburia*, *Pyramidobacter*, and *Bacteroides ovatus*, between weight groups
- Individuals showed predominance for *Prevotella* or *Bacteroides*, independent of other factors. These genera are dominant in humans and influence the gut microbiome
- Individual to individual trends overshadow probiotic intervention changes, which shows the highly dynamic property of the human microbiome

## Future Directions

- Replication of the experiment with more frequent sampling
- Additional Metadata testing across more varied populations such as: country, age and diet

## Taxa Summary Before



## Taxa Summary After

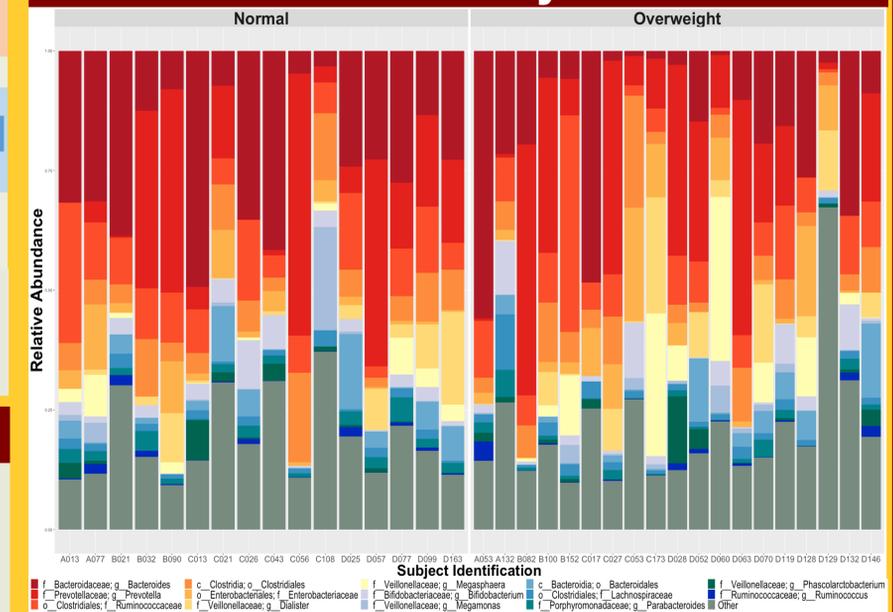


Figure 3: The relative abundance of taxa before and after probiotic administration according to weight group (n = 35). The probiotic Yakult was administered daily for five weeks between the sampling

## Acknowledgements

College of  
Biological Sciences  
UNIVERSITY OF MINNESOTA  
Driven to Discover<sup>SM</sup>

