

## Abstract

Diet variations have been prevalent among societies around the globe, be it by choice or inherited from culture. According to the CDC, in recent years it was found that 17.1% of those 20 years and older in the United States were on a special diet, most commonly for weight loss<sup>1</sup>. The purpose of this study is to determine what, if any health and wellbeing markers can be identified from a significant change in diet accompanied by gut microbiome changes. The participant, a healthy individual in her early twenties, originally omnivorous, followed a strict vegan diet for a six-week period. Urine, blood, and fecal samples were collected before and during the study. Metadata included measured vital signs such as blood pressure, heart rate, weight, BMI and subjective reports as well as information regarding bowel movements and urinations. The participant recorded these various measures in a daily log. Fecal samples were sent to an outside sequencer for 16S rRNA sequencing in order to determine bacterial composition in the gut. Using QIIME2 and R programs, the metadata collected along with the resulting sequences were analyzed. Results indicate presence of a positive association between the microbiota present and overall health and wellbeing markers. Although correlations were found, there remain ways to further study the effect of the gut microbiome on overall wellness. Future research may include investigations into whether these fluctuations in the microbiota causative of the recorded impacts on wellbeing markers are.

# Rationale

The approach of individualizing medicine is a fairly newly accepted practice. Organizations such as they Mayo Clinic are known and have been for years for their use of this approach which as led to the ill all over the world seeking their assistance. Why would you want a generalized approach to your health when you can have one tailored to your own body? This study utilizes an individualized approach to study the participant's health and well-being changes during and after a significant change in diet. The Vegan diet was chosen due to its increasing popularity and its extreme differences from the diet of the participant before the study.

# Methods

### **Study Design**

Dietary intervention methods incorporating both discovery and hypothesis-based scientific exploration.

#### **Participation**

The participant of this study is a 22-year-old white, female student from the United States with no pre-existing physical or psychological medical conditions.

#### **Dietary Intervention**

The subject will follow the Vegan diet for the six weeks of the study. The Vegan diet is void of all animal products including, meat, eggs, dairy, and honey.

### **Sample Collection**

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*Fecal* samples were collected weekly for analysis of the gut microbiome.

<u>Blood</u> samples were collected biweekly for metabolic, lipid, and vitamin analysis.

<u>Urine</u> samples were collected daily for analysis of color, concentration, and content.

A variety of metadata was also collected multiple times during each day of the study including vitals, weight, energy levels, and other descriptors.





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## Results

### **Samples Used for Analysis**

• A variety of different bodily samples were collected from the participant throughout the study. Fecal (n=7), urine (n=43), and blood (n=3) samples were obtained from the participant for use in the determination of the significance of the vegan diet on both the gut microbiome and human health.

### **Sample Quality**

• As per the report, samples ranged from roughly 200,000 to 300,000 reads and 65-94 Mbases. All samples had greater than 71% of bases with a quality score of greater than 30 with all samples having a mean quality score of 31.23 to 31.64.

#### Filtering

- Due to the limited number of fecal samples collected for analysis, and their high Phred scores, all sequenced sampled were kept for further analysis.
- A standard 10 bp were removed from the 5' end in processing.





e ID	Morphology	Gram Reaction	Metabolic Role in Gut	Associated Diseases
er	Appearance of pairs or chains of spherical or tear drop shaped cells, generally a small and large body <sup>6</sup>	Negative / Variable <sup>6</sup>	Carbohydrate fermentation, formic and butyric acid production <sup>6</sup>	IMIDs (Crohn's, Ulcerative Colitis, MS, and Rheumatoid Arthritis) <sup>6</sup>
octerium	Non motile and rod shaped <sup>7</sup>	Positive <sup>7</sup>	Butyric acid production <sup>7</sup>	IBD, Colorectal Cancer, Obesity, Celiac <sup>7</sup>
occus	Cocci form pairs or chains <sup>8</sup>	Positive / Variable <sup>8</sup>	Degradion of complex polysaccharides into nutrients <sup>8</sup>	IBD, Parkinson's, Celiac, Arthritis
cterium	Clubbed or branching rods with some species exhibiting swollen coccoid forms <sup>9</sup>	Positive / Variable <sup>9</sup>	Digest dietary fiber and produce vitamins <sup>10</sup>	Ulcerative colitis, IBD, Diarrhea, Other Infections of the Intestine <sup>10</sup>

Table 6 summarized the bacterial genus' present over the course of the study. See table 4 for their estimated percentage of presence during collection of each of the samples.

# Conclusions

Faecalik

Rumino

Bifidoba

- Although there is more than one factor that contribute to microbiome changes, this study focuses on the changes produced by diet variation, specifically, those associated with the vegan diet. • Just as the metadata may impact the microbiome, the microbiome may impact the metadata as well. For this reason, correlation is all that can be observed accurately with this method.
- Results indicate presence of a positive association between the microbiota present and overall health and wellbeing markers. Although correlations were found, there remain ways to further study the effect of the gut microbiome on overall wellness.
- The ability to perform more accurate testing, and analysis based solely off an individual's own characteristics and create an individualized treatment plan is a great asset to the medical community.

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