Gut microbiome analysis of a diabetes mouse model raised at two separate facilities

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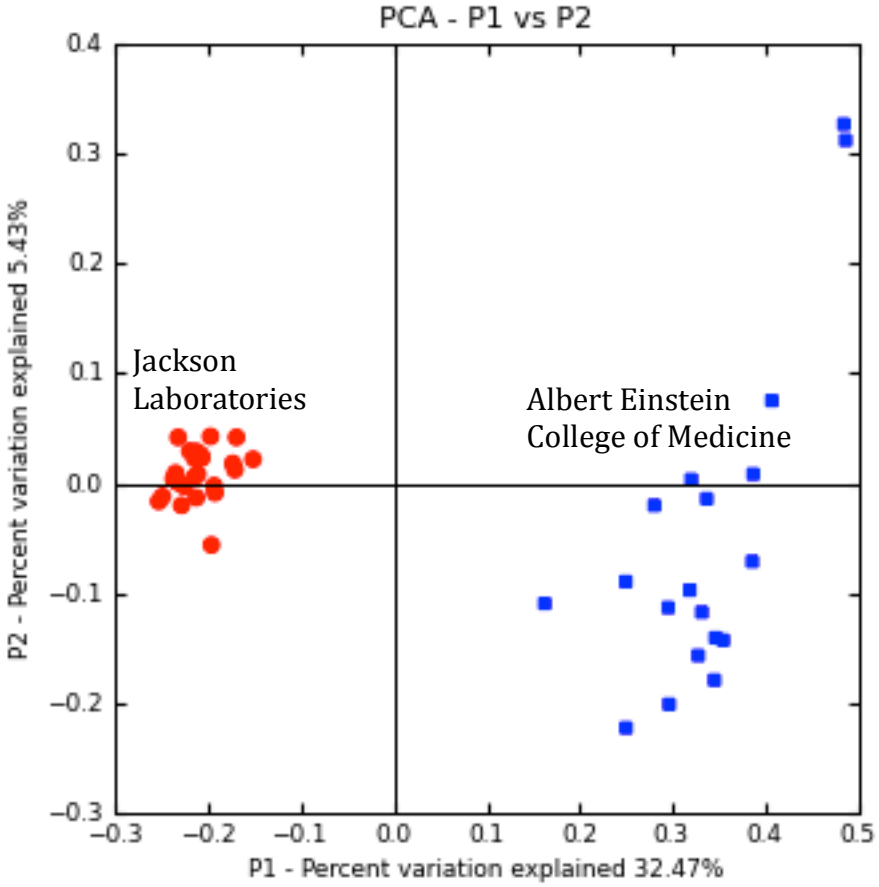
Summary:

This analysis was performed using samples collected from seven- to ten-week old male and female mice housed at either Jackson Laboratories or the Albert Einstein College of Medicine (AECM). AECM was represented by twelve samples, six *db/db* and six lean controls, taken from mice between seven and ten weeks of age, and Jackson Laboratories was represented by twenty-four samples, twelve *db/db* and twelve lean controls, taken from mice seven to eight weeks of age. In addition, AECM provided samples from six eight-week old mice of various designated genotypes, *B6-Awj*, *db3J*, and *Sir1*, which were also included in the analysis of overall community composition. DNA was extracted from fecal samples, and bacterial 16S rRNA genes were amplified by PCR with barcoded primers targeting the V1-V3 region of the 16S rRNA gene. PCR reactions were carried out in triplicate, and replicate amplicons were pooled, purified, and sequenced at the Environmental Genomics Core Facility at University of South Carolina using the Roche/454 pyrosequencing platform. To compare the overall diversity between samples, we used a commonly employed distance metric, UniFrac, which is based on the premise that bacterial communities that are related share an evolutionary history that is captured by a common phylogeny. Using this approach, we found that the microbial communities from mice within the same facility are more similar than those from mice with the same genotype but from different facilities.

Figure 1:



Bacterial diversity clusters by facility. The first two principal coordinates (PC1 and PC2) from the principal coordinate analysis of unweighted UniFrac are plotted for each sample. Each symbol represents a sample, colored according to the facility from which the mice came (red, Jackson Laboratories; blue, Albert Einstein College of Medicine). The variance explained by the PCs is indicated in parentheses on the axes.

Principal Coordinate Analysis of Unweighted UniFrac

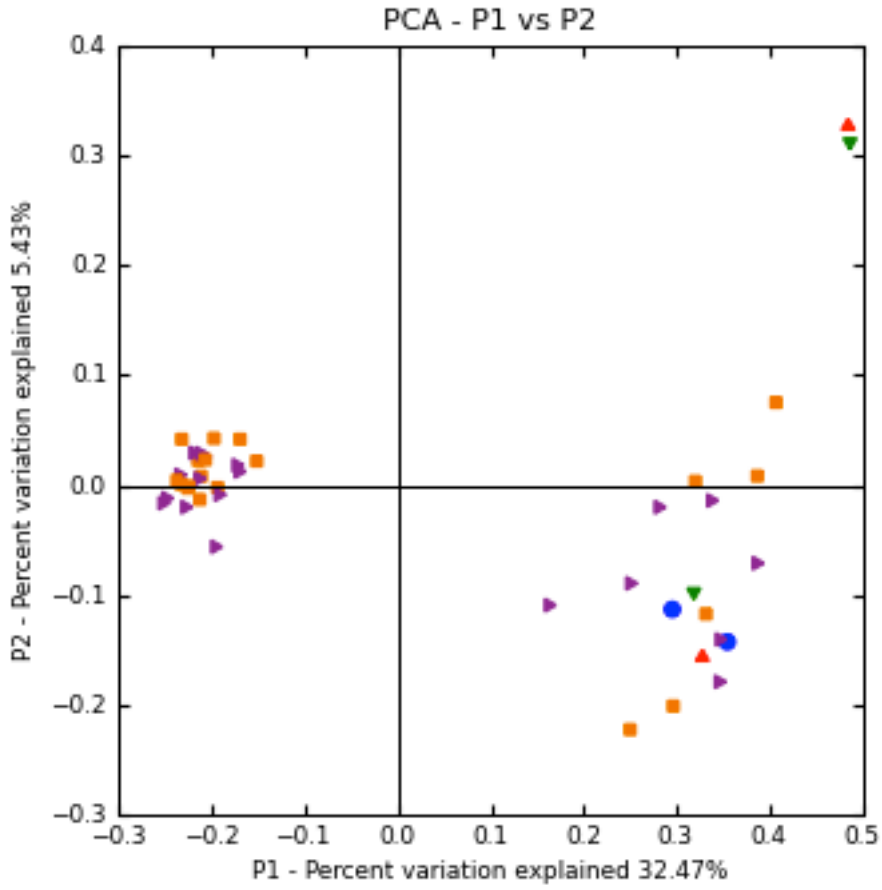


Figure 2: Bacterial diversity does not cluster by genotype. The first two principal coordinates (PC1 and PC2) from the principal coordinate analysis of unweighted UniFrac are plotted for each sample. Each symbol represents a sample, colored by according to genotype (red, B6Awj; green, db3J; blue, Sir1; orange, control; purple, dbdb). The variance explained by the PCs is indicated in parentheses on the axes.

Principal coordinate analysis reveals distinct clustering of samples dependent upon the facility where the mice were raised, but not genotype, indicating that the environment is affecting overall community composition far more than genotype (Figures 1, 2). Furthermore, samples from within the same facility do not show distinct clustering by genotype. To investigate the possibility of effects on the competitive balance of the existing populations, we assessed the relative abundances of bacterial genera within the mouse microbiotas and used the statistical software R to perform an ANOVA on these data using a generalized linear model, factoring in genotype, facility, and gender. There is no statistically significant difference in the specific abundance of any detected OTU (operational taxonomic unit) dependent upon genotype, at either the phylum or genus level. However, the specific abundances of several OTUs differ based on facility, including the genera *Rikenellaceae*, *Lachnospiraceae*, and *Ruminococcaceae*. Further tightly controlled experiments will be required to determine whether microbiome composition is a factor causing the discrepancies between phenotypes reported by the different facilities. Future experiments should control factors including but not limited to facility, diet, cage, age and gender.