

# A New Method to Study the Human Microbiome

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We are outnumbered; trillions of non-human microbes live on and within our bodies. Combined they consist of 3.3 million genes while the human genome has only 23,000 genes. The human microbiota plays an important role in health including cancer, obesity, diabetes, infectious disease, liver disease, autoimmunity, allergies, and even mental health. Hypothesis: Using novel methods that increase speed and decrease cost, the microbiome can be sequenced and analyzed. Methods: An iterative multiphase approach was used to screen the gut and oral microbiomes from multiple individuals. Phase 1 used a commercial kit to analyze the gut microbiota from three sisters. Phases 2 and 3 used a mouthwash collection method. Samples were collected daily from student researcher (longitudinal analysis), and over the same time frame for a broader population (cross-sectional analysis). Data was analyzed using local and cloud-based algorithms. Results: Bacteria were identified at various taxa level. 31 samples were screened. Medically relevant bacteria like *Mycobacterium tuberculosis* were identified in multiple samples and streptococcus in every sample. Unique genera like *Methanobrevibacter* (linked to athletic performance) were identified in low frequencies. Specifically, *S. mitis* is a candidate for applications such as drug delivery. Conclusion: It is possible to monitor one's microbiome with mouthwash collection method, sequencing on an Oxford Minion, and analyzing data with cloud-based software. The cost and time for sample collection and analysis are \$2.00 and 1 day respectively. Taken together, my results indicate a useful and cost-effective way to monitor one's microbiome and can be applied directly to personal health.

## Awards Won:

Drexel University: Full tuition scholarship \$200,000