Detection of novel specialized metabolites produced by *Bacteroides vulgatus*

**Abstract**
Gut colonization by the microbe *Bacteroides vulgatus* has been linked to type II diabetes in humans. Diabetes can cause serious health consequences by causing the body to resist insulin or by inhibiting its production. The long-term goal of our research is to determine how specialized metabolites produced by *B. vulgatus* impact the human microbiome to better treat chronic diseases like diabetes. In this study, we sought to establish a pipeline to detect unique molecules made by *B. vulgatus* and gain a better understanding of *B. vulgatus* biology as it relates to human health. To do this, we coupled Matrix Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF) mass spectrometry with iDBac and Mass-Up, programs for analyzing metabolite data. We selected *B. vulgatus* mutants from a transposon library and generated mass spectra of their metabolites. We then analyzed the data to infer the relationships between multiple *B. vulgatus* strains based on their metabolite profiles. So far, this analysis indicates we can rapidly identify *B. vulgatus* transposon mutants that produce small molecules with unique masses using this pipeline. So far, we have screened ~1400 transposon mutants in triplicate and identified 284 mutants with altered metabolite profiles. In doing so, we have validated Mass-Up’s utility for metabolite screening of transposon mutants, as well as identified strains for follow-up studies. In addition to screening additional mutants, we intend to analyze strains with altered metabolite profiles to link genes to molecule production to explore *B. vulgatus* physiology and its potential impact on the host.

**Results**
- Established a methodology for rapidly profiling metabolite production of *B. vulgatus* using MALDI-TOF MS
- Collected mass spectra from 1440 mutant strains in triplicate
- Significantly improved the quality of mass spectra
- Detected 284 potentially altered metabolites in mutant library
- Working to identify genes linked to metabolite production

**Future work**
- Cross reference masses with publicly available mass spectrometry data to search for potential molecule matches
- Conduct LC-MS/MS on mutants with altered metabolite profiles to obtain accurate metabolite masses and identify metabolites
- Fluorescence- and phenotype-based coculture screen to identify chemically mediated microbial interactions

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