Showcasing the functional profile of murine fecal samples using whole metagenomic and metatranscriptomic data together

Molly Zeller (zeller2@wisc.edu), University of Wisconsin, Madison, **Molly Zeller**, University of Wisconsin Madison Biotechnology Center

Metagenomic and metatranscriptomic sequencing has provided a means to explore microbial species and genes at resolutions previously unobtainable. Broadly available, short-read sequencing platforms provide sequence data with low error rate, high throughput, and low cost. Despite these advantages, their use in metagenomic research has demonstrated contextual limitations including fragmented assemblies and misclassifications. Recent improvements in long-read sequencing have provided an affordable, high quality alternative to short-read metagenome approaches. Our previous work demonstrated long-read platforms result in the same, or better, outcomes as short-read sequencing at a comparable cost. Here, we aim to demonstrate that long-read platforms result in more complete metagenomic and metatranscriptomic information and in turn using both metagenomic and metatranscriptomic data can showcase the functional profile of the microbial community present in a sample. Information obtained from multiple genomes has a potential to infer the microbiome's functional capability, but alone cannot describe spatio-temporal patterns of gene expression that occur normally or in response to variable environmental stimuli. Studying in conjunction the metagenome and metatranscriptome will capture microbial gene expression patterns thus providing a means to disentangle the potential (gene) and realized (transcript) composition of bacterial metabolism. To evaluate the suitability of shotgun metagenomics combined with metatranscriptomics to assess the concordance of gene content with transcriptional content, we utilized fecal samples from individual mice. Half of the mice are wildtype B6 mice and the other half are mice with the aryl-hydrocarbon receptor (AHR) gene knocked out. AHR is involved in the regulation of biological responses to planar aromatic hydrocarbons. In addition to looking at the microbial composition of the fecal samples, detection of host transcripts should differ between the two host types. Our data is publicly available with the intent to promote bioinformatic tool development for metagenomic/transcriptomic studies based on long read technologies.