Bacterial conjugative elements from human gut metagenomic assemblies suggest structural differences between cohorts

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Background

- Conjugative elements can carry clinically relevant metabolic pathways such as antimicrobial resistance and bile salt metabolism (1).
- Previous research on bacterial conjugation in the human gut has focused on integrative and conjugative elements (1).

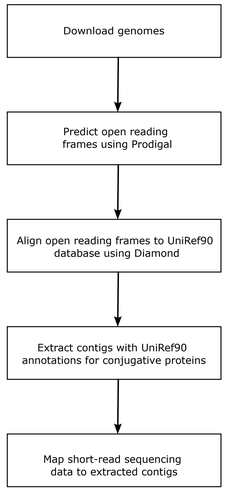
Research Objectives

- Identify conjugative systems from assemblies of short-read sequencing data and from a reference genome set.
- Quantify the relative abundances of the identified conjugative systems and compare between cohorts.

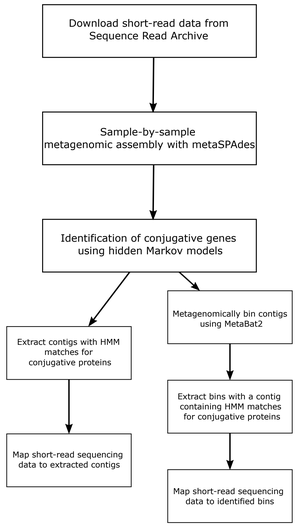
Methods

Two separate approaches were taken:
Approach #1: Search for conjugative systems in a human gut metagenome set and compare abundances across 8 cohorts
Approch #2: Assemble short-read sequencing data and search all assembled contigs for conjugative systems and compare between 2 cohorts used for assembly

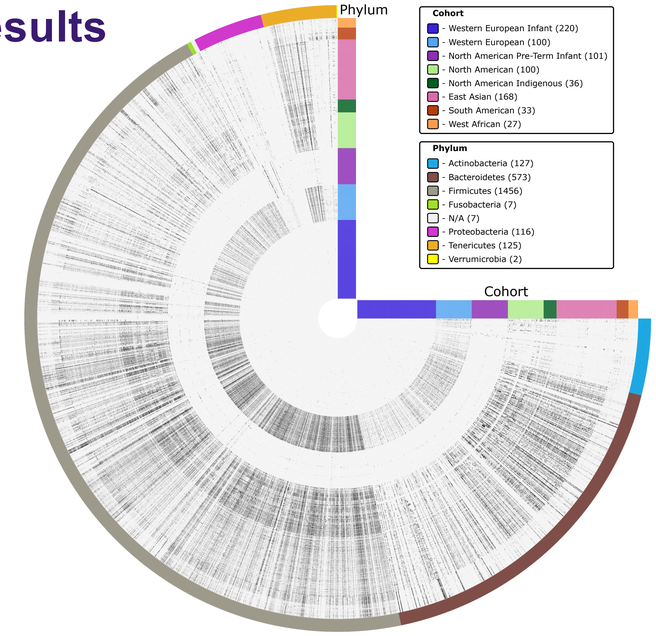
Approach 1: Use metagenome database to search for conjugative systems



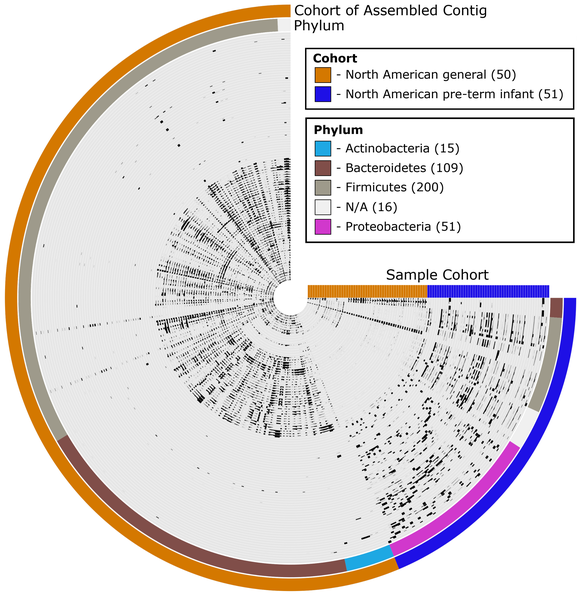
Approach 2: Assemble raw reads and search assemblies for conjugative systems



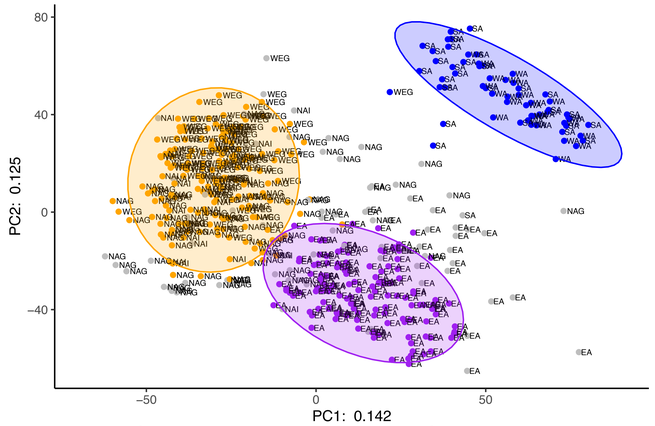
Results



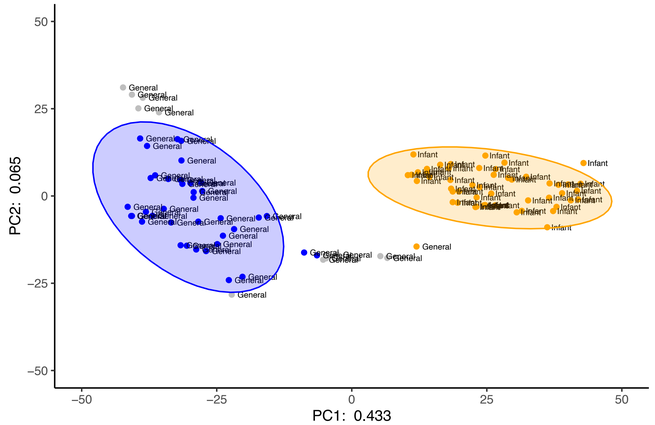
From conjugative systems identified from the genomes set, striking patterns can be observed. The intensity of the cells on the above cladogram represent the abundance of the individual conjugative system in a specific sample. Overall, it appears that there are few to no conjugative systems in the infant cohorts.



From conjugative systems identified from assembled short-read data, differences between a general North American and North American pre-term infant datasets are readily apparent. Conjugative systems appear to be private to either cohort. Notably there is a diversity of pre-term infant conjugative systems not captured by the genome set.



Abundances of conjugative systems identified in the genome set result in clustering of cohorts on the principal components.



Abundances of conjugative systems identified in the assemblies of short-read data result in clustering of cohorts on the principal components.

Discussion

- Abundances of conjugative systems are discriminatory between cohorts.
- Like the microbiota (2), infants have a distinct array of conjugative systems in comparison to adults.
- Reference human gut microbiome sets may be biased against the inclusion of infant conjugative systems.

References

1. Jiang X, Hall AB, Xavier RJ, Alm EJ. Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. PLoS One. 2019;14:e0223680.
2. Milani C, Duranti S, Bottacini F, Casey E, Turroni F, Mahony J, et al. The first microbial colonizers of the human gut: Composition, activities, and health implications of the infant gut microbiota. Microbiol Mol Biol Rev. 2017;81.

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