Straining to understand the microbiome?

High-throughput, low cost microbe StrainID and analysis with Shoreline Biome

Hosted by the laboratory of Dr. David Hafler, MD Dept of Immunobiology and Neurology

> September 30, 2019 12:15 pm-1:15 pm Yale School of Medicine 300 George Street, 3rd Floor Room 354 New Haven, CT 06511

Pizza and refreshments will be served



Dr. Mark Driscoll, Co-founder and Chief Scientific Officer Shoreline Biome, LLC

Strain level profiling is needed for a complete understanding of how microbial communities influence human health. Microbiome profiling of rRNA gene amplicons is a well-understood method that is rapid and inexpensive, but standard short read 16S rRNA gene methods generally cannot differentiate closely related strains. WGS/shotgun microbiome profiling is a high resolution alternative, but with decreased throughput and increased sequencing costs and analysis burden. In addition, many of the commercial kits fail to lyse those difficult gram-positive bacteria such as Firmicutes, require extensive hands on time and rely on harsh bead beating methods that damage DNA. Data will be presented demonstrating a novel, non-bead beating lysis method combined with a unique, contiguous ~2500 bp 16S-23S amplicon containing essential internally transcribed spacer-region sequences that are a rich source of variability crucial for differentiating closely related bacterial strains. When StrainID amplicons are run on the PacBio Sequel, the combination of robust lysis, comprehensive PCR primer pools, a 16S-23S amplicon product, and long read Athena database one can enable differentiation of closely related strains within and across samples. using a simple, rapid, cost effective approach.

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