Genomics of nontuberculous mycobacteria in Hawai’i

The unique environment of Hawai’i influences the species and genomic diversity of NTM on the islands. Genomic analysis of clinical and environmental NTM isolates helps us to identify where in the environment clinically relevant species and genotypes reside. A goal of this research project is to identify and model clinically relevant exposures, using culture, genomic, and spatial information, in order to mitigate NTM exposures and disease risk.

Whole Genome Sequencing (WGS) to elucidate the complete genome of environmental and clinical NTM.

Clinical NTM samples and environmental samples and home Samples

Culture to identify if NTM is present.

Purify high quality NTM DNA.

Construct genomic libraries.

Next-generation sequencers and long read sequencers are used to determine the millions of base pairs per genome, followed by genomic and phylogenomic analysis.

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