

# Genomics of nontuberculous mycobacteria in Hawai'i



Clinical NTM samples  
*and*



Environmental samples  
and home Samples

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.



Culture to  
identify if NTM is  
present.



Purify high quality  
NTM DNA.

Construct  
genomic libraries.

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



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