Genomic Analysis of Nontuberculous Mycobacteria (NTM)

Presented by:
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Genomic and Computational Approaches to Nontuberculous mycobacteria
Host-Pathogen-Environment Interactions

Human – Pathogen Interactions

Human

Pathogen

Environment
Next Generation Sequencing

Next Generation sequencing enables the rapid and robust sequencing of whole bacterial genomes.
Genomic Analysis Pipeline

Bacterial Preparation

Genomic DNA isolation

Genomic Library Construction

Next Generation Sequencing and Genomic Analysis

We release and make sequence data available to the public through the National Center for Biotechnology Information (NCBI Bioproject)
Phylogenomics of Brazilian epidemic isolates of Mycobacterium abscessus subsp. bolletii reveals relationships of global outbreak strains. Davidson RM, Hasan NA, de Moura VC, Duarte RS, Jackson M, Strong M. Infection Genetics and Evolution Sep 18;20C:292-297. 2013
Genome sequencing of *Mycobacterium abscessus* isolates from patients in the United States and comparisons to globally diverse clinical strains.

In cases of limited genomic diversity among species (as appears to be the case for *M. chimaera*), WGS will enable much more precise and accurate comparisons, where other methods would not provide adequate resolution.

Other typing approaches: MLST – Multilocus sequence typing, PFGE- pulse field gel electrophoresis, VNTR – Variable Number Tandem Repeat, RAPD – Randomly Amplified polymorphic genotyping, Rep-PCR – repetitive sequence PCR, MST - multispacer sequence typing
Phylogenomic Comparison between select *M. chimaera* (n=19) and MAC isolates (n=3).
2 tiered phylogenomic comparison of *M. chimaera*
## Genomic Relatedness of Strains

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<tr>
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<th>Mean SNPs</th>
<th>N</th>
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<tr>
<td>Within Heater/Cooler Study (HC) M. chimaera</td>
<td>2.67</td>
<td>3</td>
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<tr>
<td>Between HC and non-HC M. chimaera</td>
<td>867</td>
<td>48</td>
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Perform **Whole Genome Sequencing (WGS)** and compare sequence information from *M. chimaera* isolates in the US, Canada, and Europe, including environmental, hospital, patient, and non-related strains (to assess genomic diversity, refine genomic interpretation, and identify putative markers).

We at National Jewish Health welcome referral of clinical and environmental isolates of NTM, specifically *M. chimaera*, to populate this project and further aid the FDA and CDC to get to the bottom of this public health issue.