GENOMIC SIGNATURES FOR VIRULENCE AND ANTIFUNGAL DRUG RESISTANCE DEVELOPMENT IN HIV-ASSOCIATED TALAROMYCES MARNEFFEI INFECTION

Project Summary
Talaromyces marneffei is a dimorphic fungus that causes an invasive fungal infection and a leading cause of death in patients with advanced HIV disease in Southeast Asia. The objective of this project is to identify genomic signatures for virulence and antifungal drug resistance development. The candidate will work with whole genome sequence data generated from 400 Talaromyces marneffei isolates coming from patients who participated in a treatment trial. The candidate will mine these genomes using a genome-wide association study (GWAS) approach to identify genes associated with important patient outcome data including mortality, rate of fungal clearance, treatment relapse, and antifungal treatment resistance. Ultimately this work may allow for improved treatment decision-making and identify genes of interest for drug development.

Timeline and desired outcomes
Week 1: Background reading, reproducibility training, introduction to analysis pipeline
Week 2-4: Identification of T. marneffei super-genome, setup pipeline with data subset
Week 5-6: Scale up to full dataset, gene-set enrichment analysis
Week 7-10: Preparing manuscript for publication

Expectations for intern
Candidates should be proficient in at least one of the common programming languages used in bioinformatics (Python, R, etc), have a strong interest in microbial genomics, specifically using pathogen genomics to elucidate pathogenicity, and excellent verbal and written communication skills. The ideal candidate will have experience with UNIX and in bioinformatics, computational biology, or related fields.

Supervisors
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