Class Project Proposal

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Project title:

Mycoviral screening of meta transcriptomic data from Macrophomina phaseolina isolates

Introduction:

The fungus Macrophomina phaseolina is the causal agent of the charcoal rot disease, plants infected with this fungus suffer from wilting, damping-off, seedling blight. M. phaseolina can affect more than 500 species including both monocots and dicots (Ashby, 1927; Kaur et al., 2012; Sinclair & Backman, 1989; Singh, 1990).

Viruses that infect fungi are known as mycoviruses and are ubiquitous in the fungal kingdom (Ghabrial & Suzuki, 2009). They can exert phenotypic changes in the behavior of their fungal host which can reduce the severity of the disease, this effect is denoted as hypovirulence (Milgroom & Cortesi, 2004).

For the screening of mycoviruses traditional nucleic acid extraction has been used (Pearson et al., 2009). However, thank to the application of next generation sequencing technologies the discovery rate and characterization of mycoviruses has been enhanced (Kotta-Loizou, 2021). Therefore, in this project we aim to analyze NGS data to screen and characterize for fungal viruses.

Research questions:

Does the NGS data contains mycoviral signatures?

Methods:

Process raw sequencing reads

Use SPAdes assembly to generate contigs

Remove host associated reads from the files

Use BLAST using viral sequence datasets

Estimate viral abundance by normalizing the data using fragments per kilobase of transcripts per million fragments mapped (FPKM)

Generate a Sankey flow diagram using Sankeymatic

Generate maximum likelihood trees (IQ-TREE web server)

Expected outcomes:

We expect to find mycoviruses infecting the fungal pathogen, they might be novel sequences or already reported ones.

Evaluation of phylogenetic relationships of viruses screened.