

Population genomics reveals geographic structure in the charcoal rot fungus *Macrophomina phaseolina* from the US, Puerto Rico, and Colombia

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Macrophomina phaseolina is an important pathogen of crops worldwide. Charcoal rot caused by *M. phaseolina* can significantly reduce yield and seed quality in soybean and dry bean mainly in tropical and subtropical regions, but more recently in temperate zones as well. Little information is available on the population structure of *M. phaseolina*. Genomes of 96 *M. phaseolina* isolates from 13 states across the US, Puerto Rico, and Colombia, isolated from soybean and dry bean were sequenced to determine whether populations are structured by host, geographic distance or environmental differences. Sequencing was performed on an Illumina HiSeq 4000 with 150 bp paired-end reads to an average depth of 23X. Linkage disequilibrium analyses indicated that *M. phaseolina* isolates are predominantly clonal which is supported by its biology since *M. phaseolina* reproduces asexually. Inference on population structure revealed clustering of Puerto Rican and Colombian isolates from dry bean, while isolates from the US regardless of dry bean or soybean origin were assigned to a separate cluster and exhibited lower diversity. Limited genome-wide differentiation among populations by host origin was observed. To investigate the relative contributions of genetic distance and environmental differences to genetic differentiation between populations we used multiple partially constrained models (partial redundancy analysis). The candidate genes significantly associated with environmental variation were assembled to investigate their potential role in mediating adaptation in *M. phaseolina*.