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GWAS: laccase expression in *Ceratocystis albifundus**

Genome-wide association studies (GWAS) have been applied to various organisms, including fungi. These studies have successfully identified gene regions associated with traits such as pathogenicity and virulence. The plant pathogen *Ceratocystis albifundus* is infecting non-native *Acacia mearnsii* trees and has recently been found to infect native cultivated *Protea cynaroides* plants in South Africa, resulting in severe economic losses. Isolates collected from Southern and Eastern Africa have shown differences in their genetic composition. Since multicopper oxidase, that catalyze a wide range of substrates from phenols to non-phenolic compounds are known to influence the outcome of plant-pathogen interactions. This study aimed to identify genomic regions associated with laccase production of these isolates using the GWAS approach. The single nucleotide polymorphisms (SNPs) across the whole genome sequences of the population were identified, and associations between fungal laccase production and SNPs were tested using a mixed linear model. A putative multicopper oxidase coding gene that harbored SNP was found to be significantly associated with laccase production (FDR p-value < 0.05). We will also perform pathogenicity trials to establish the role of *C. albifundus* on native and non-native hosts. This study will provide insight into the biology of the fungal pathogen and provide a platform for further molecular analysis. Further investigation of fungal laccase functionality will be investigated by the knockout study.

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Yes

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