ABSTRACT

A molecular characterisation of fungi and fungal populations associated with cassava superelongation disease in the Caribbean

Shanice Mason

At present, one of the main pathogens affecting cassava is Sphaceloma manihoticola which causes cassava Superelongation disease (SED). The pathogen was first scientifically identified in the region in 2007 and 2008, in Trinidad and Tobago and Barbados, respectively. Symptoms of SED include, leaf and stem lesions, leaf deformation, defoliation, stem and petiole cankers and internode elongation. This pathogen is problematic to the growing cassava industry in the region as it can cause more than 80% yield loss. The main research aim of the study was to characterize S. manihoticola fungi and the fungal populations infecting cassava in the Caribbean by using both morphological and molecular analyses including a metagenomic approach. The pathogen was first isolated from diseased cassava leaf tissues from 7 locations in Barbados and fifty-three isolates suspected to be S. manihoticola were sub cultured for morphological characterization. DNA from these isolates was extracted to be amplified in a polymerase chain reaction (PCR) using ITS primers and the resultant amplicons were sequenced. Sequencing results identified the isolated pathogen as Auerobasidium spp. which shares a similar morphology to S. manihoticola in culture. For the mycobiome analysis, cassava leaf samples were taken from at least five sites in four Caribbean islands, Barbados, St. Vincent and the Grenadines, Trinidad and Tobago and Jamaica. DNA was extracted from the leaves and next generation sequencing of the internal transcribe spacer 1 and 2 (ITS 1 and ITS 2) were used to identify S. manihoticola and other fungal taxa associated with this pathogen. From the mycobiome analysis, S. manihoticola was absent in St. Vincent and the Grenadines, however it was found in high abundance in Trinidad and low abundance in Barbados and Jamaica. The mycobiome analysis also showed that the mycobiomes in each island were unique when it came to species that were found in high abundance and only 10% of the species were found in all four islands.

Keywords: cassava; superelongation disease; metagenomics; Sphaceloma manihoticola; pathogen