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In Vitro Antagonism of Native Guatemalan Isolates of Trichoderma Harzianum and T. Viride for Biological Control of Rhizoctonia Solani

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Abstract

Rhizoctonia solani is a basidiomycete present in the soil that currently affects the production of potato crops in Guatemala's western highlands, causing the disease known as black scurf. The current classification of R. solani is based on the ability of the hyphae to merge and form an anastomosis group (AG), 13 AG being recognised so far. Due to the negative impacts of chemical disease control, a viable alternative is presented in usage of fungi from the genus Trichoderma as a biological control strategy. The research objective was to identify the AG of R. solani present in the western highlands of Guatemala through specific PCR. The potential of native isolates of T. harzianum and T. viride as biological control agents characterised by the molecular marker AFLP was also evaluated. Of the 78 isolates of R. solani, the groups $AG^{-3}PT$, AG-4-HG-II and AG-5 were identified with an incidence of 46.16%, 14.10% and 17.96%, respectively, while 17 isolates could not be assigned. Isolates of T. harzianum showed a higher average percentage inhibition of radial growth (PIRG) of R. solani (56.71 %) than T. viride (37.58 %) (p < .001). We determined that the phylogenetic groups of T. harzianum and T. virens are equally effective against the 3 AG identified, highlighting the benefit of using native isolates. We suggest using sequencing of the ITS region for the identification of unassigned isolates of R. solani through sequence comparison of NCBI genebank sequences and field evaluations to assess the efficiency of T. harzianum and T. viride native isolates.

Keywords: Anastomosis groups, genetic diversity, percentage inhibition of radial growth (PIRG)

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