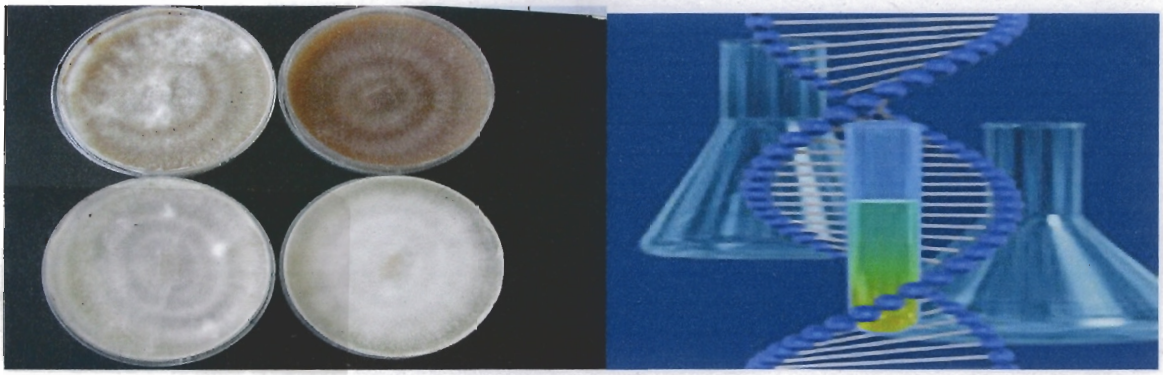
National University of Science & Technology

MOLECULAR IDENTIFICATION AND CHARACTERISATION OF *RHIZOCTONIA SOLANI* ISOLATES FROM ZIMBABWE



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ABSTRACT

The shift in the pathogenicity in infectious *R. solani* isolates prompted the investigation into the existence and level of genetic similarity between the originally known and originally discovered strains, in an attempt to gravitate towards the creation of an effective and environmentally friendly control measure. In this study, *Phytophthora nicotiana* was used as a negative control. The internal transcribed spacer region (ITS) ribotyping showed genetic relatedness between the isolates though it filed to discriminated between them. The Inter Simple Sequence Repeat (ISSR) generated data from the same isolates was able to discriminate among the isolates while maintaining some level of genetic similarity as shown by the mean genetic similarity coefficient of 0.7475± 0.0337 with a range of 0.40 to 1.0. The collective ISSR data yielded an overall amplified polymorphic band percentage of 44%, with an assay efficiency index (AEI) of 21, a mean polymorphism information content (PIC) value of 0.207 and an overall marker index (MI) value of 13.034 was also obtained.

The dendrogram generated from the collective ISSR data pictorially represented these similarity levels and produced five main clusters. The complimentary Principle coordinate analysis generated graph provided a pictorial spatial separation of the isolates and a more accurate clustering extent which produced six clusters. The multinucleate *R. solani* isolate denoted as R738 and the binucleate denoted as R773 showed a 1.0 level of similarity. It was, therefore, concluded that there was a high level of similarity between the two categories of disease causing *R. solani* isolates and that the ISSR marker system provided an efficient discriminatory tool for *R. solani* at the genetic level.