Genetic Variability and Relationships among Seventeen *Trichoderma* Isolates to Control Dry Root Rot Disease Using RAPD Markers

Kuruba Gopal[a,*], Yasodam Sreenivasulu[a], Venati Gopi[a], Gundala Prasadbabu[a], Teruvai Bharat Kumar[b], Puchakayala Madhusudhan[a], Shaik Khayum Ahemed[a], and Sellappa Gounder Palanivel[c]

[a] All India Co-ordinated Research Project on Tropical Fruits (Citrus), Citrus Research Station, Acharya N. G. Ranga Agricultural University, Tirupati – 517502, Andhra Pradesh, India. E-mail: gopalkurub@yahoo.co.in

[b] Department of Biotechnology, Sri Vidya Niketan College of Engineering and Technology, Tirupati, Andhra Pradesh, India

[c] Department of Microbiology, J. J. College of Arts and Science, Pudukkottai – 622404, Tamil Nadu, India

* Author for correspondence and reprint requests

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Trichoderma spp. has been identified as potential antagonist of *Fusarium solani*, which is causing dry root rot of *Citrus*. A random amplified polymorphic DNA (RAPD) marker was used to estimate the genetic variation among 17 isolates of *Trichoderma*. These isolates were characterized using 20 random primers of the OPM series, out of which 16 primers gave a total of 145 DNA fragments, showing 91.8% polymorphism. The genetic distance between each isolate was calculated, and cluster analysis was used to generate a dendrogram showing the relationship among them. The isolates grouped into two major clusters, the first major cluster consisted of TCT_{14}, TCT_{17}, TCT_{13}, TCT_{12} and TCT_{16}. The remaining isolates in the second major cluster separated in two sub-clusters; the first cluster consisted of TCT_4, TCT_{10}, TCT_2, TCT_3, TCT_8, TCT_6, TCT_9, and the second sub-cluster consisted of TCT_1 TCT_{15} TCT_5, TCT_{11}, and TCT_7. The similarity matrix indicated that TCT_6 and TCT_{13} were genetically distinct as they showed only 22.6% similarity followed by TCT_5 and TCT_{16}; TCT_6 and TCT_{16} (25%), while the isolates TCT_4 and TCT_{10} were found to be genetically similar, as 66.7% similarity was observed between the isolates followed by 61.3% similarity between the TCT_2 and TCT_4 isolates.

Key words: Fusarium solani, Dry Root Rot Disease, *Citrus*