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LIST OF ABBREVIATIONS

%	Per Cent
°C	Degree Celsius
µl	Microlitre
ADW	Autoclaved Distilled Water
AFLP	Amplified Fragment Length Polymorp
Approx.	Approximately
BCA	Biocontrol Agents
Bp	Base Pair
CWDEs	Cell Wall Degrading Enzymes
DNA	Deoxyribonucleic acid
dNTPs	Deoxynucleotide Triphosphates
EDTA	Ethylenediamine Tetra Acetic Acid
et al.	And Others
G	Gram
H_2O	Water
HCl	Hydrochloric Acid
HCN	Hydrogen Cyanide
IAA	Indole Acetic Acid
KCl	Potassium Chloride
M	Molar
MCL	Maximum Composite Likelihood
mg	Milligram
$MgCl_2$	Magnesium Chloride
ml	Milliliter
mM	Milli Molar

NaCl	Sodium Chloride
Ng	Nanogram
P	Phosphate
PAGE	Polyacrylamide Gel Electrophoresis
PCR	Polymerase Chain Reaction
PDA	Potato Dextrose Agar
PDB	Potato Dextrose Broth
RFLP	Restriction Fragment Length Polymorphism
SDS	Sodium Dodecyl Sulphate
TAE	Tris Acetic Acid EDTA Buffer
TE	Tris EDTA Buffer
TEF-1	Transcription enhancer factor-1
TSM	*Trichoderma* Selective Media
U	Units

ABSTRACT

Twenty-three isolates of *Trichoderma* species were isolated from 63 soil samples collected from different locations of the East Delta Region in Egypt. Bean was the most infection with pathogenic fungi followed by Faba Bean and Peas. *Trichoderma* isolates caused a remarkable reduction linear growth of three pathogenic fungi. *Trichoderma* isolates were found to be an effective biological control agent for three legumes crops from infection with pathogenic fungi. *Trichoderma* isolate G3 IQ2 recorded highly activity of as well as, isolate G5 PP1 recorded highly activity of β,1-3 Gluconase. Isolates G3 IQ2 and G4 IF2 recorded highly activity of Peroxidase While, isolate G6 SoR1showed highly activity of Polyphenoloxidase, isolate G3 IQ2 recorded highly activity of Catalase. The heritability estimates in broad sense were 90, 97, 98, 81, 71 and 98 for growth rate, Chitinase, B,1-3Gluconase, Peroxdase, Polyphenolox and Catalase, respectively. Which indicate that large additive effects are important in the determination of genetic behavior for these traits. Phylogenetic analysis of *Trichoderma* isolates ACTIN data set showed that, isolates obtained in this study were accommodated in 5 distinct clades, of which the first clade contained isolate (G4 IF2**)** grouped with *Trichoderma asperellum* (GJS 06-294). Whereas, the isolate (G6 SoR1) clustered with *T. viride* (Gr 22). The third isolate (G1 SA1) grouped with the two isolates (GJS 96-117 and CBS 979.70) of *T. koningii*. One isolate (G5 PP1) was identified as *T. hamatum* that accommodated with isolate (DAOM 167057). While, isolate (G2 NA) grouped with the *T. harzianum* isolate

(GJS 00-18). Phylogenetic analysis of *Trichoderma* isolates TEF1 data set showed that, the isolate (G2 NA) grouped with the *T. harzianum* isolates (CBS 226.95 and DAOM 222136). While, the isolate (G5 PP1) grouped with the two isolates (ER022 and ER033) of *T. hamatum*. The isolate (G3 IQ2) was accommodated with the LU809 isolate of *T. album*. The isolate (G6 SoR1) clustered with *T. viride* (CBS 586.95). The isolate (G1 SA1) grouped with the two isolates (GJS 89-122 and CBS 457.96) of *T. koningii*. The isolate (G4 IF2**)** grouped with *Trichoderma asperellum* (CHF 78). Our study suggested that, genetically development of *Trichoderma* isolates to plant growth promotion behind development to antagonism is very important to obtain super *Trichoderma* isolate.