

## **Identification of trichoderma species from wet paddy field soil samples**

### **Abstract**

Trichoderma species has gained immense economic importances because of their production of industrial enzymes and antifungal antibiotics, used as biocontrol agents, used in textile industry and as plant growth promoter. Thus, the correct identification of the species is necessary for its commercial demand. Preliminary identification of the species is usually based on its morphological properties, but the result is inadequate for species level identification. Molecular approaches using a single gene to multiple genes have applied for valid species identification. The main aim of this study is to characterize the genetic variability among twenty isolates of Trichoderma, obtained from wet paddy field soil. Data analysis of the internal transcribed spacer (ITS) regions of the rDNA and a partial sequence of the translation elongation factor 1-alpha (TEF1) were constructed in a phylogenetic analysis and were positively identified as *Trichoderma asperellum* (85%), *T. harzianum* (10%) and *T. reesei* (5%). The result confirmed the potential of molecular data in differentiating the species-specific level among all Trichoderma isolates.