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Understanding the plant-microbe interaction molecular mechanisms for better exploitation of biocontrol agents to enhance sustainable agricultural practices

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Abstract

Trichoderma spp. are well-known bio-control agents which promote the plant growth and suppress the pathogen infection. The beneficial effects are attributed to the production of phytohormones, antibiotics, siderophores and secondary metabolites (SM). Trichodermin and Harzianum A, SMs have documented anti-fungal activities as well. *Tri5* gene encodes for trichodiene synthase (TS) contains a terpene fold and involved at the initial step of the biosynthetic pathway of these molecules. Furthermore, domain analysis of proteins from diverse organisms showed that the terpene fold has functional diversity with diverse applications in agriculture, medicine and applied biotechnology. These proteins can be classified into single and multi-domains based on their structures. It was observed that multi-domain proteins carry additional helices which may regulate the catalytic efficiency. Further, activity enhancing mutations with potentially higher catalytic activities were screened. In an offshoot to the above work, we have analyzed binding of Trichodermin with the 25S rRNA that constitutes the petidyltransferase centre (PTC). The trichodermin resistance protein (60S ribosomal protein L3) was reported to overcome the inhibitory effects of trichothecene compounds. Normal mode analysis and MD of trichodermin resistance protein and 25S consisting of PTC showed that the W-finger region of the protein may move towards 25S rRNA and may block the binding pocket of the trichodermin. These results may lead to develop strategies for higher TS activity and the mechanism of action of these molecules involved in plant-microbe interactions. These may be further exploited for enhancing the efficiency of these biotechnological agents used in sustainable agriculture.

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