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## Genome analysis of bio-control fungus *Trichoderma harzianum* and the biosynthesis of peptaibols alamethicin

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*Trichoderma harzianum* has strong ability for encoding secondary metabolites, which contribute a lot for its bio-control function. peptaibols alamethicin is a family of antibiotics isolated from *T. harzianum* and was found significantly suppress against various *Fusarium* fungi. Unfortunately, little was known about its biosynthetic genes and pathway to data. In this study, we assembled the high-quality genome of *Trichoderma harzianum* T29, which consists of 72 scaffolds, with total size of 32 Mb and the 1.5 Mb N50 value. A total of 10773 gene models were predicted in the genome. We predicted 36 secondary metabolite gene clusters in T29 genome and the function of some secondary metabolite related genes were identified by homologous deletion. We further identified a serial of genes from THBJ\_06541 to THBJ\_06568, including core enzymes, modifying enzymes and transporter enzymes coded for the biosynthesis of alamethicin. To verify the biosynthesis pathway of peptaibols alamethicin, we disrupted PKS (paD) in the cluster by homologous recombination and found the peptaibols alamethicin were disappeared in  $\Delta$  paD. These results will provide theoretical guidance for understanding the mechanism of *T. harzianum* against *Fusarium* fungi.

### Biography

Jian Ling has been engaged in the research of plant pathology in Institute of Vegetable and Flower Research in Chinese Academy of Agricultural Sciences (CAAS) since 2008. His main researches are focused in analyzing the molecular mechanism of the interaction between crops and pathogens, using genomics and metabolomics, and developing the safe and efficient biocontrol technology against *Fusarium* wilt and root knot nematode.

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