

Co-infection of a Novel Mycovirus and its defective RNA Detrimental to Biocontrol Properties of *Trichoderma* spp.

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Purpose: *Trichoderma* spp. are a group of fungi commonly used as biocontrol agents for many plant diseases. This study aimed to analyze the full-length sequences of *Trichoderma harzianum* hypovirus 1 (ThHV1) and its defective RNA ThHV1-S, and to evaluate the possible effects of ThHV1 and ThHV1-S on the application of *Trichoderma* species for control of plant disease.

Methods: The genomes of ThHV1 and ThHV1-S were sequenced by using conventional methods. The horizontal transmission of ThHV1 and ThHV1-S was conducted by using the pairing culture technique. The mycoparasitism assays were conducted through dual-cultural test with *Botrytis cinerea*.

Results and Conclusions: The ThHV1 genome contained two Open Reading Frames (ORFs), namely ORF1 and ORF2. The start codon of ORF2 overlapped with the stop codon of ORF1 in a 43 nt long region. The polypeptide encoded by ORF2 of ThHV1 shared sequence similarity with those of betahypoviruses. Isolate T-70D carrying both ThHV1 and ThHV1-S showed abnormal biological properties, especially decreased mycoparasitism ability. Both ThHV1 and ThHV1-S could be vertically transmitted to conidia and horizontally transmitted to *T. harzianum* isolate T-68 and *T. koningiopsis* T-51, resulting in the decreased mycoparasitism ability of the derivative strains carrying both ThHV1 and ThHV1-S. However, the strains carrying ThHV1 alone were normal. ThHV1 was widely detected in *Trichoderma* spp. of China. Therefore, viruses in fungal biocontrol agents may also be a factor associated with the stability of their application.