

## Viruses of *Gremmeniella abietina*

Jarkko HANTULA<sup>a\*</sup> – Tero TUOMIVIRTA<sup>a</sup> – Juha KAITERA<sup>a</sup> –  
Victor CARRASCO-NAVARRO<sup>a</sup> – Stéphane VERVUURT<sup>a</sup> – Antti UOTILA<sup>b</sup>

<sup>a</sup>The Finnish Forest Research Institute, Vantaa, Finland

<sup>b</sup>Hyytiälä Forestry Field Station of Helsinki University, Korkeakoski, Finland

**Abstract** – Types and races of *Gremmeniella abietina* species complex cause Scleroderris canker on pine trees in Europe and North America. We have studied viruses of types A and B of *Gremmeniella abietina*.

In type A three different mycoviruses belonging to families *totivirus*, *partitivirus* and *mitovirus* occur. They were even observed to inhabiting a single mycelium. During early analyses of these viruses family *partitivirus* was the most common one. In more recent sampling *partitiviruses* and *totiviruses* were rare, but *mitoviruses* very common.

In type B we observed *totiviruses*, *mitoviruses* and a previously uncharacterized virus with high similarity to plant endornaviruses. The difference of viruses in types A and B supports our previous hypothesis that viruses do not move freely between the two Fennoscandian types of *G. abietina*.

A partial sequence, covering about 70 % of the complete genome, of putative *totivirus* of type B was determined. The dsRNA genome codes for putative coat and putative RNA dependent RNA polymerase (RdRp) and they were most similar to similar proteins of the *totiviruses* of *Spaeropsis sapinea* and *Helicobasidion momba*, respectively.

A complete sequence of a *mitovirus* from type B was determined. The putative RdRp was most similar to RdRp of a *mitovirus* from *Ophiostoma novo-ulmi*. The previously sequenced *mitoviruses* from type A had a relatively dissimilar RdRp. The putative start codon was in an AU-rich region surrounded by regions with a relatively high GC-content. Several previously observed secondary structures could be deduced from the nucleotide sequence, and sequence variations occurred at both ends.

The previously uncharacterized virus from type B was completely determined independently from two isolates. The dsRNA molecules (10374 and 10375 nucleotides) encoded for putative polyprotein possessing four conserved motifs coding for viral methyl transferase, DEAD/DEAH box helicase, viral RNA helicase and RdRp.

A population structure was determined for type A *mitoviruses* based on RT-PCR amplification and sequencing. It showed no genetic differentiation between the populations, suggesting that viruses are able to disperse freely between locations in southern Finland.

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\* Corresponding author: jarkko.hantula@metla.fi; P.O. Box 18, 01301 Vantaa, Finland