Viruses of *Gremmeniella abietina*

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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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