

Figure S1: Phylogeny obtained by bayesian inference analysis of the combined ITS, EF1-α, and TUB sequence alignment of Diplodia species. BI posterior probability support values above 90 % (**bold**) and ML bootstrap support values above 70 % are shown at the nodes. Strains analysed in this study are emphasised in **bold**. Branches that are crossed by diagonal lines are shortened by 50 %.



Figure S2: Agarose gel electrophoresis (1 % w/v) of dsRNA extracted from fungal tissue of NW-FVA 1581 and NW-FVA 1706. M, GeneRuler 1 kb plus ladder (Thermo Fisher Scientific). The sizes of the marker are given on the left.



Figure S3: Sequence of DfFV1b with annotated peptides identifies by protein sequencing.



Figure S4: Sequence of DfPV1, segment 2 with annotated peptides identified by protein sequencing.

**Appendix B**

Table S1: Sequences of oligonucleotides used in this publication.

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| Number # | Name | Sequence 5‘ – 3‘ |
| 1 | Partitivirus-RNA-I-REV | TTCGGGCTTACGCGTGAATCC |
| 2 | Partitivirus-RNA1-II-FW | ATCGGTCTCTTCGATCGG |
| 3 | Partitivirus-RNA2-REV-NEU | AACTTTCCAGGCATCGGC |
| 4 | Partitivirus-RNA2-II-FW | TTCGTTGGAGGGTTAACGCG |
| 5 | Partitivirus-RNA3-I-REV | TCTTAACGCTTCGTCGTACGG |
| 6 | Partitivirus-RNA3-II-FW | TTCCTCGAAGCTCACAACTCGG |
| 7 | Partitivirus-RNA1-I-Detection-FW | TTCGCCTTTGGATCCCACCC |
| 8 | 1581/1706-FV-Det-FW | TTGTGCGTTAAGCACGCCGC |
| 9 | 1581/1706-FV-Det-REV | TTCCTCTCGAGGTGCAAAGCC |
| 10 | 1706-I-REV | ACACTCAGGGACCCCTTATGG |
| 11 | 1706-II-FW | ATGCTTCCGATGTTCCTCCC |
| 12 | 1581-5-rev-neu | GAGTAGTGGGTGATCAGGG |
| 13 | 1581-II-FW | TTCATGCTTCCGATGTCCCTCC |