



**Supplementary Figure 3:** Maximum likelihood phylogeny based on the amino acid sequences of the RNA-dependant RNA polymerase of barleria polero virus 1 (indicated by solid circle markers) and selected members of the Luteoviridae family. The phylogeny represents the tree with the highest log likelihood and was generated in MEGA X using the best-fit (Jones-Taylor-Thornton) model. Bootstrapping was applied (1000 replicates) and the percentage of trees in which the associated taxa clustered together is shown next to the branches. Bootstrap percentages lower than 50 are not shown. The cognate amino acid sequences of two enamoviruses were used as outgroups.