



**Supplementary Figure 2:** Maximum likelihood phylogeny based on the amino acid sequences of the N-protein of barleria chlorosis-associated virus (indicated by solid circle markers) and selected members of the Tospoviridae family. The phylogeny represents the tree with the highest log likelihood and was generated in MEGA X using the best-fit (Le Gascuel) model with gamma distribution ( $n=4$ ). 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 sequence of Guaroa virus was used as an outgroup.