



Figure S3. Phylogenetic analysis of proteins conserved in BMV proviruses. The evolutionary history of the VP1/F-like, VP2/H-like and VP4/A-like proteins encoded by BMV proviruses was inferred by using the Maximum Likelihood method based on the Whelan and Goldman amino acid substitution model. Numbers at the branch-points represent bootstrap values (1000 replicates). The outgroups were chosen based on the BLAST analysis.