



Supplementary Fig. 2. Phylogenetic tree inferred from P1 region of leek yellow stripe virus (LYSV) using the Bayesian method in the MrBayes program. Node value indicate percent of posterior probability (only $\geq 50\%$ are shown). Two isolates of onion yellow dwarf virus (OYDV; KJ451436 and NC_005029) were used as outgroup taxa. Labels in red indicate sequences obtained in this study.