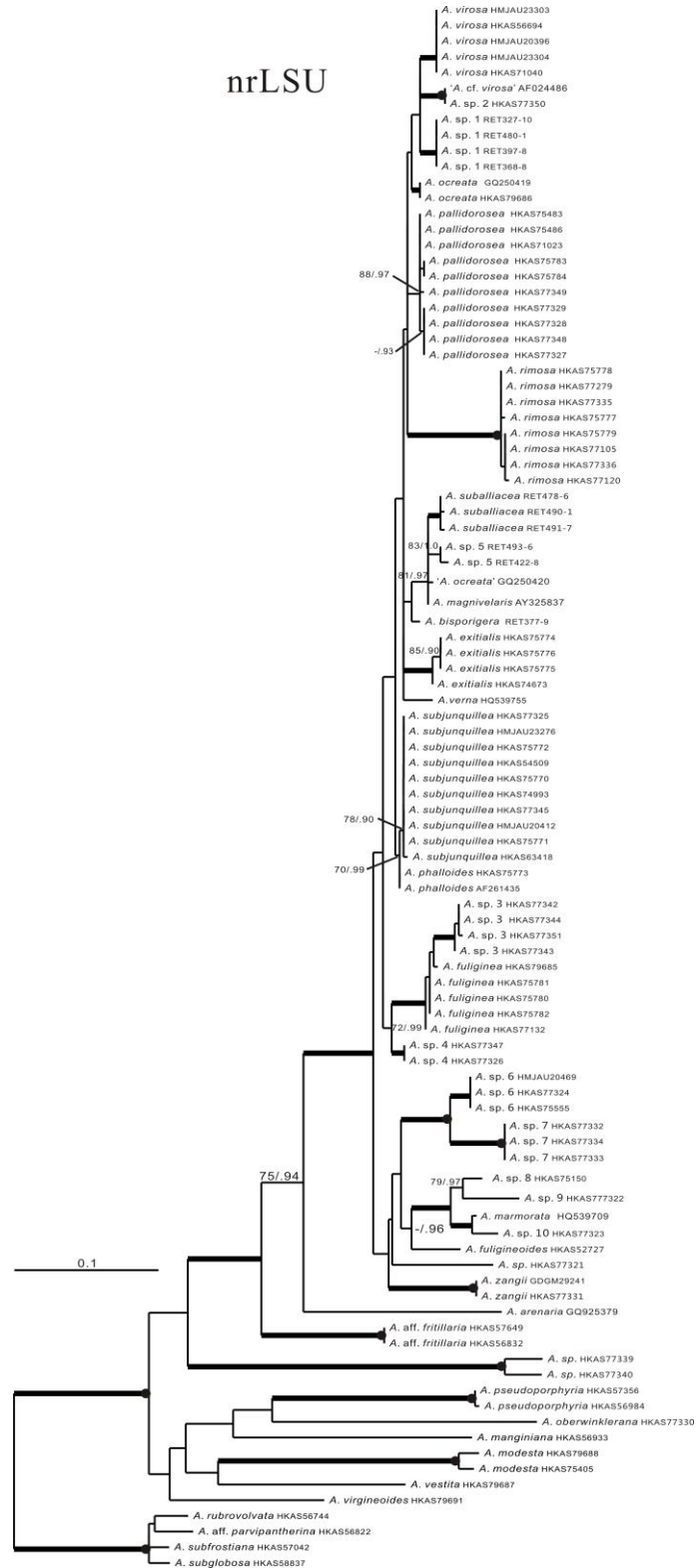
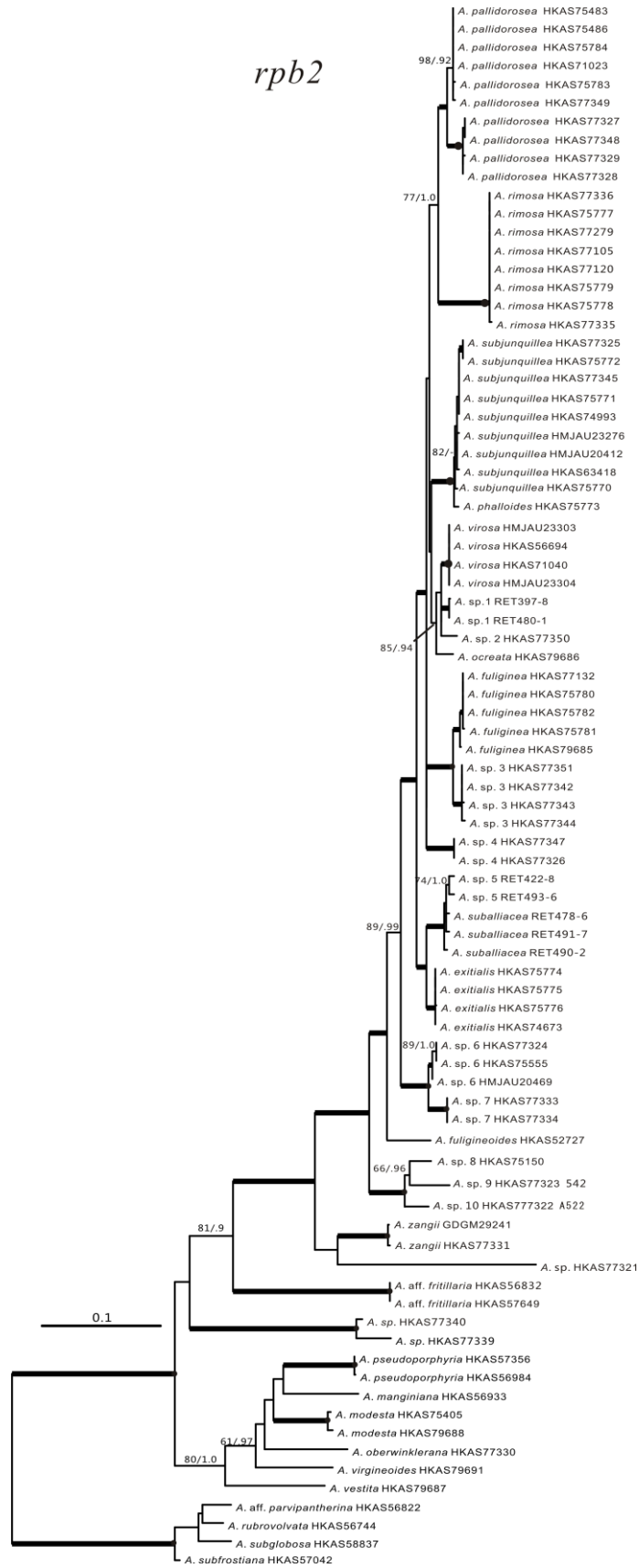
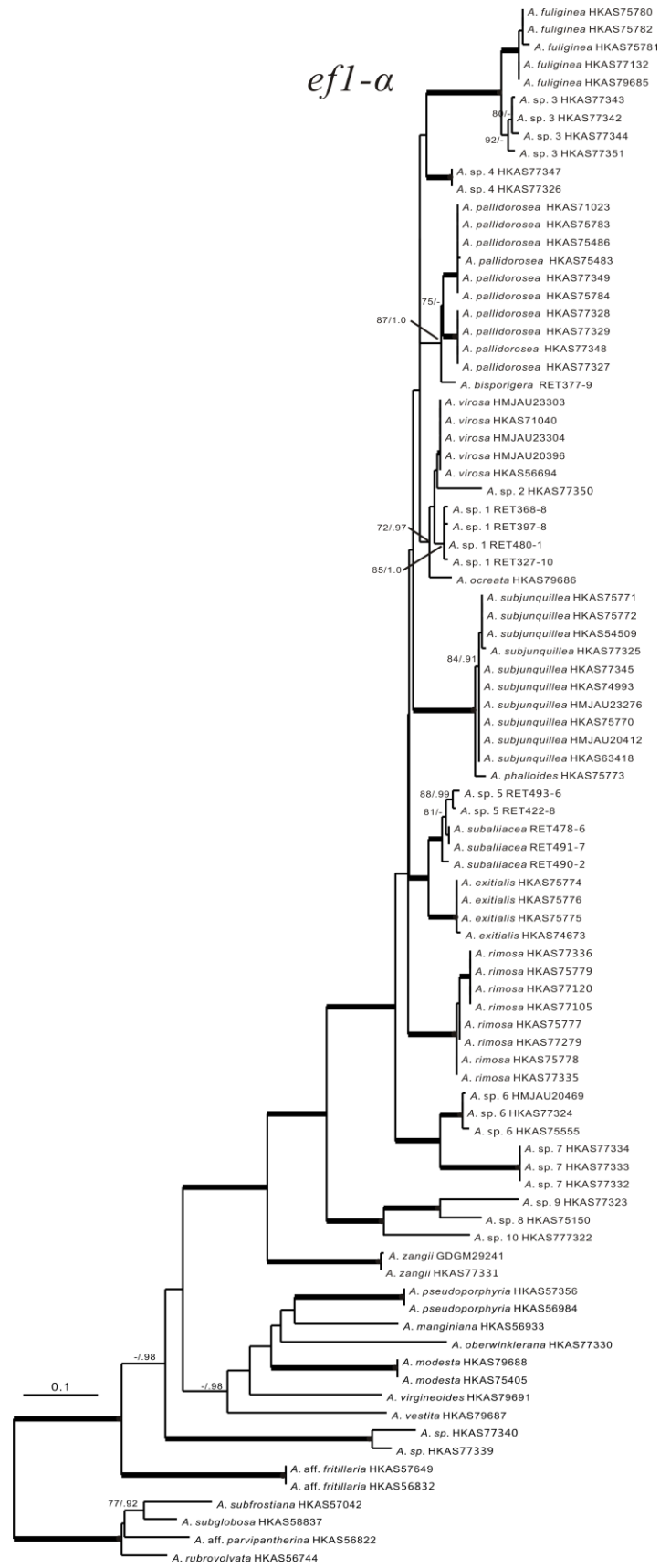


**Figure S1** Phylogenetic trees inferred from maximum likelihood (ML) analysis with branch support obtained by ML and BI analyses based on nrLSU, *rpb2*, *ef1- $\alpha$*  and  *$\beta$ -tubulin*, respectively. Only maximum likelihood bootstraps (LB) over 70% and Bayesian posterior probabilities (PP) over 0.90 are reported on the branches. Thickened branches indicate LB between 90%-100% and PP between 0.95-1.0. Thickened branches with dots on the root nodes represent 100% LB and 1.0 PP.







*β-tubulin*

