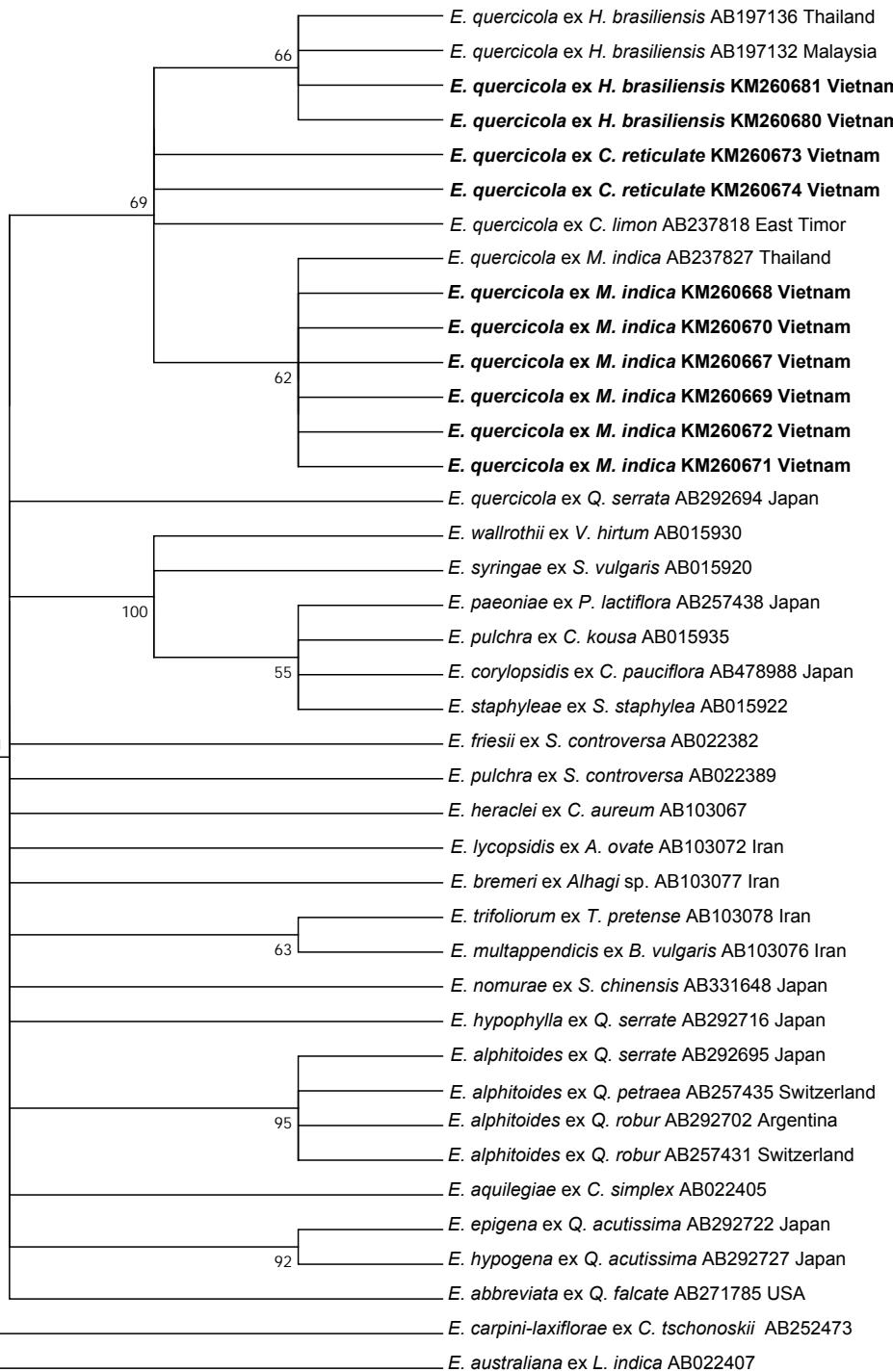


Supplemental Fig. 1. Evolutionary relationships of taxa of powdery mildew fungi damaging on mango in Vietnam based on ITS phylogenetic analysis: The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 0.34425480 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Tamura *et al.* 2004). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method (Kumar *et al.* 2016) and are in the units of the number of base substitutions per site. The analysis involved 34 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 524 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Felsenstein 1985).



Supplemental Fig. 2. Evolutionary relationships of taxa of powdery mildew fungi damaging on mango in Vietnam based on 28S phylogenetic analysis: The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 1.39955198 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Tamura *et al.* 2004). The evolutionary distances were computed using the Maximum Composite Likelihood method (Kumar *et al.* 2016) and are in the units of the number of base substitutions per site. The analysis involved 40 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 525 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Felsenstein 1985).