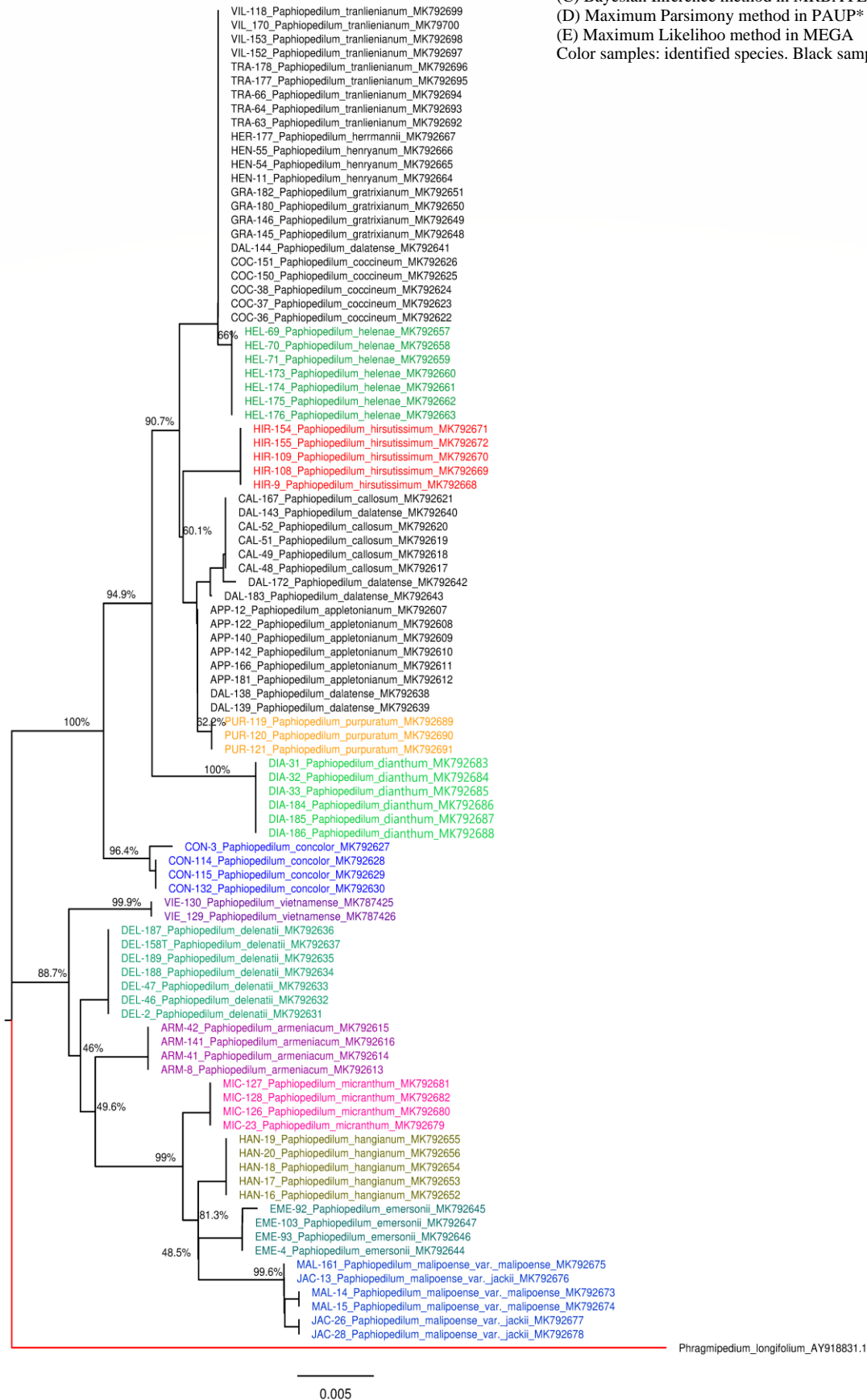
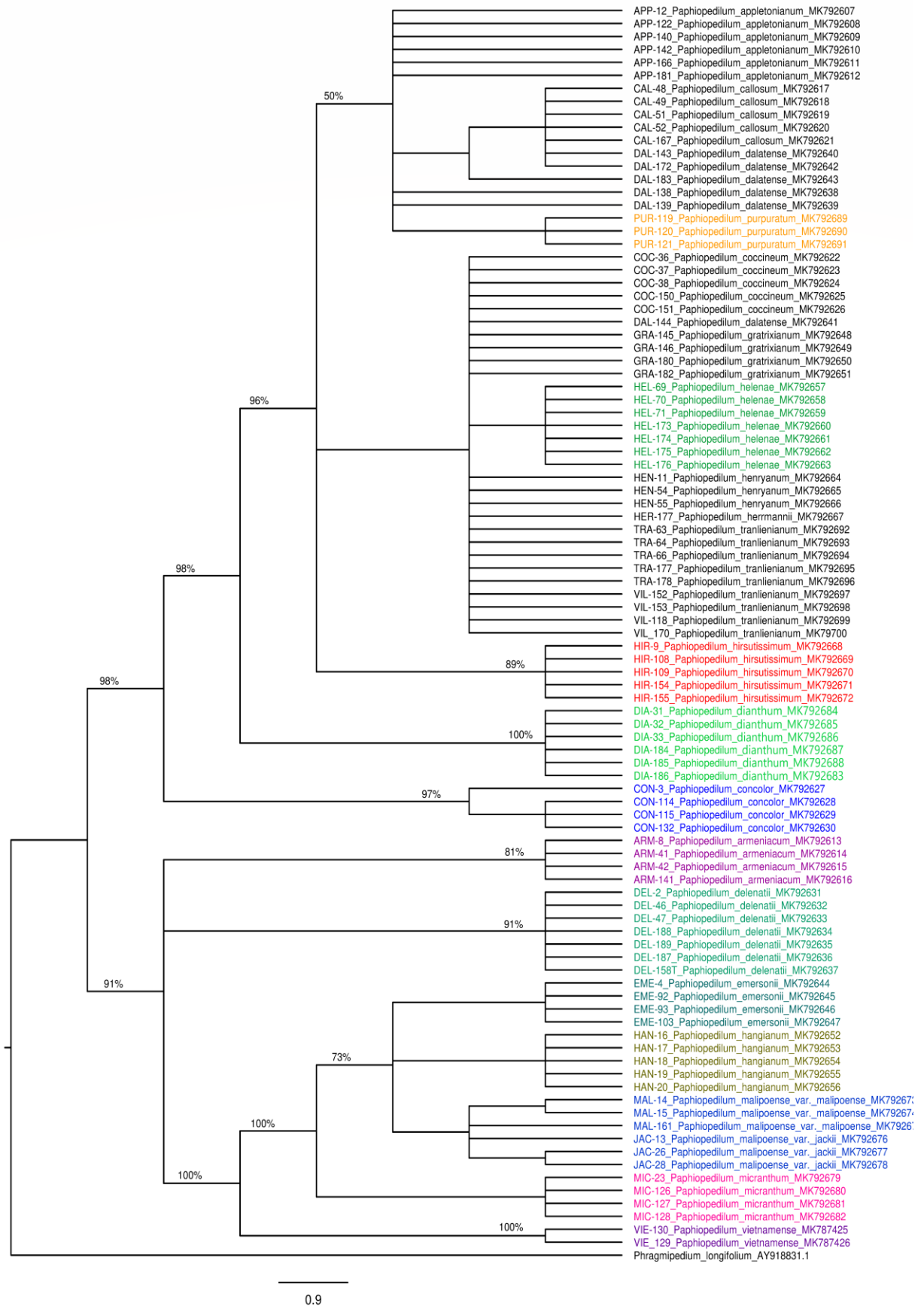


**Figure S4. Phylogenetic trees of 21 Vietnamese *Paphiopedilum* species based on *matK* region using different methods.**

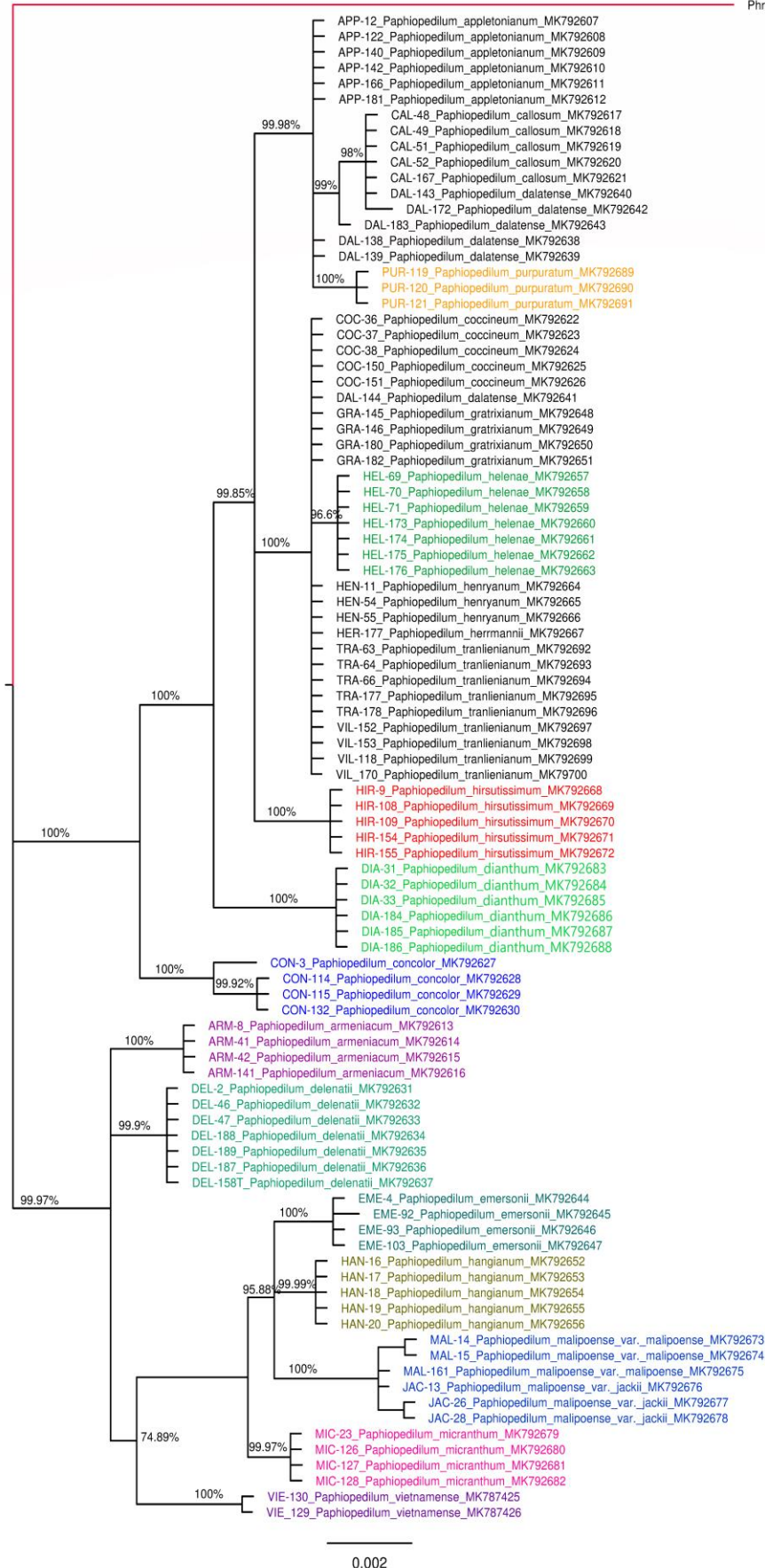
- (A) Neighbor-joining method in MEGA  
 (B) Maximum Likelihood method in PAUP\*  
 (C) Bayesian Inference method in MRBAYES  
 (D) Maximum Parsimony method in PAUP\*  
 (E) Maximum Likelihood method in MEGA  
 Color samples: identified species. Black samples: unidentified species)

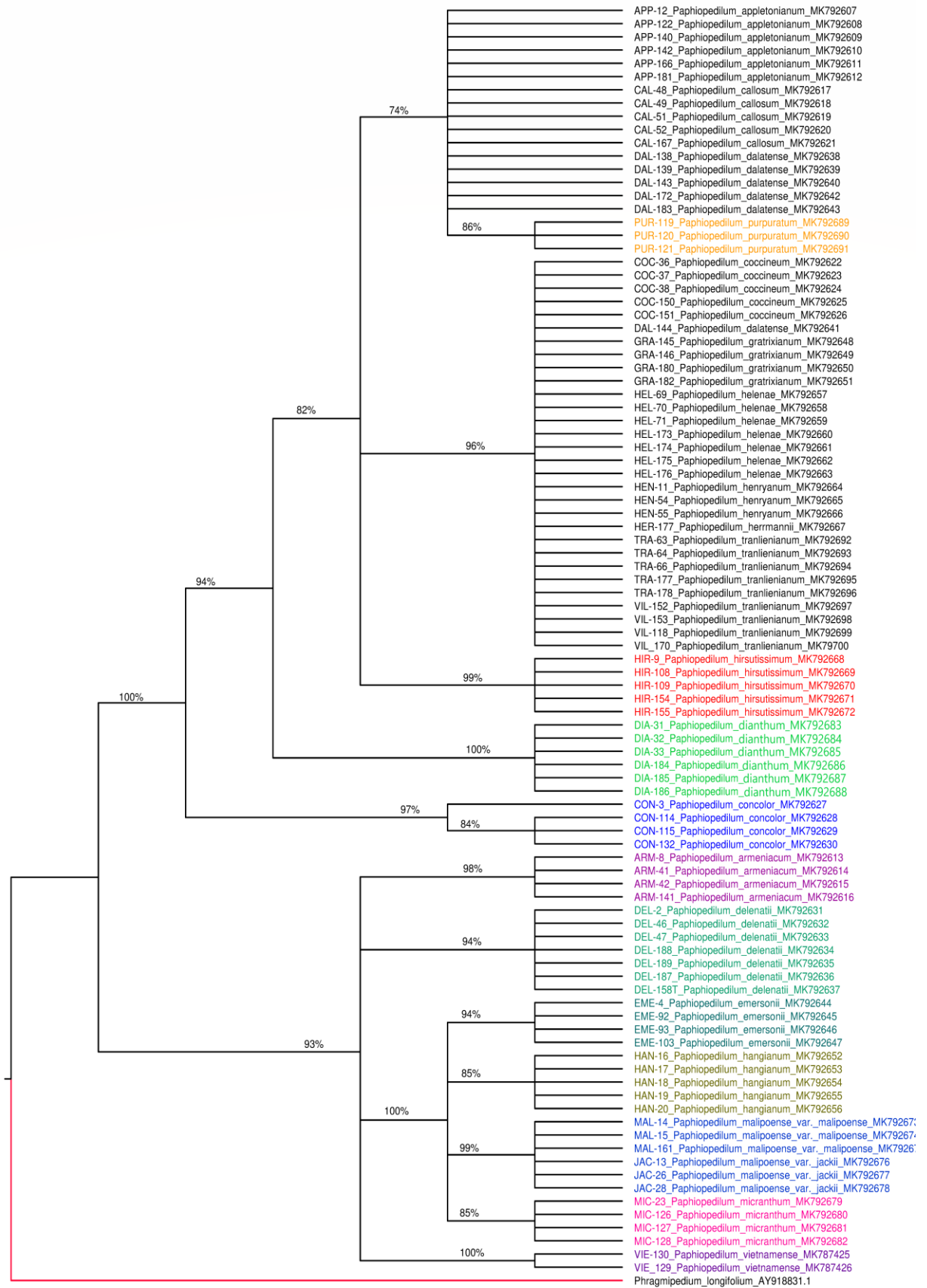


**A. Neighbor-joining method in MEGA**



## B. Maximum Likelihood method in PAUP\*

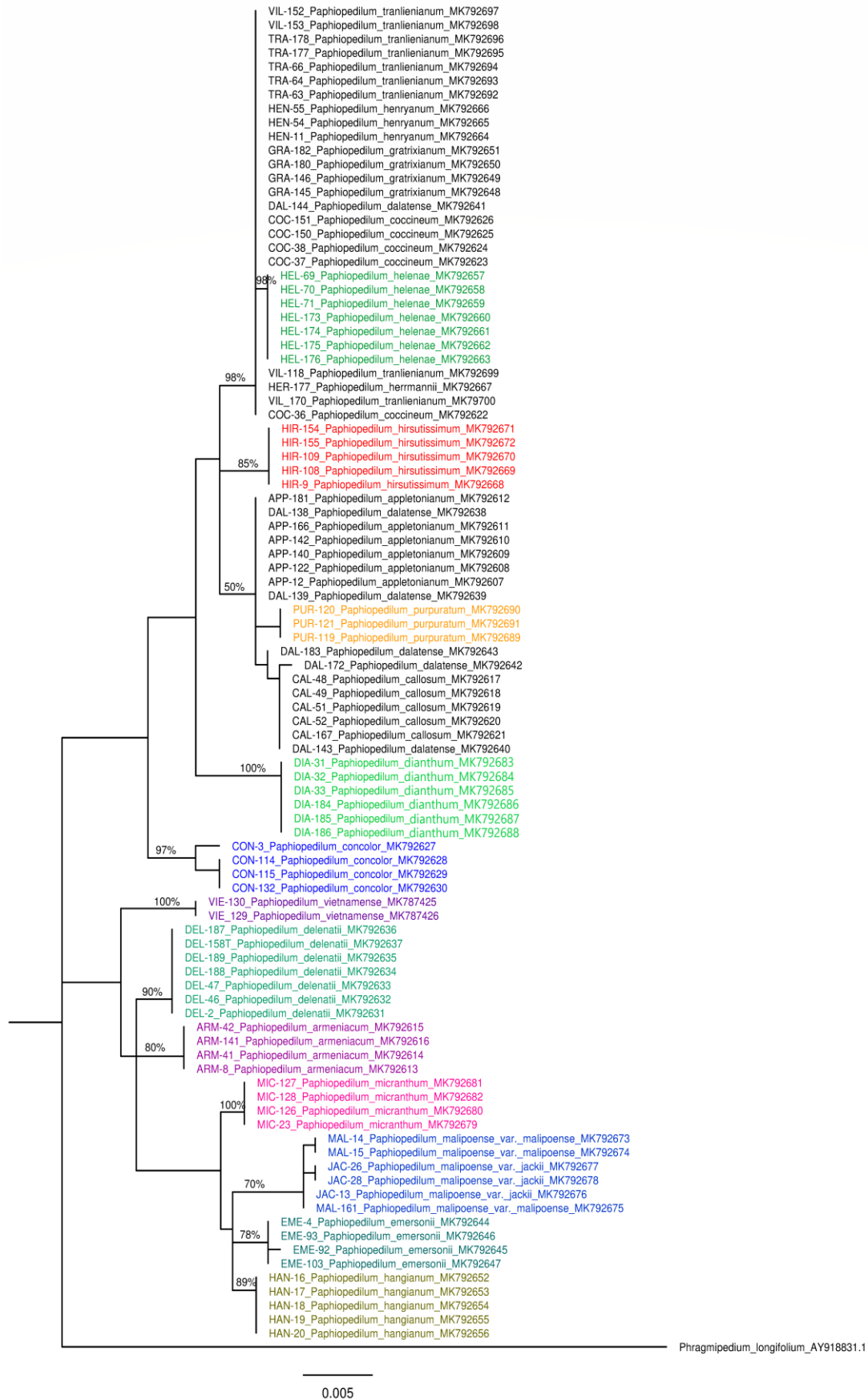




0.8

D. Maximum Parsimony method in PAUP\*





## E. Maximum Likelihood method in MEGA