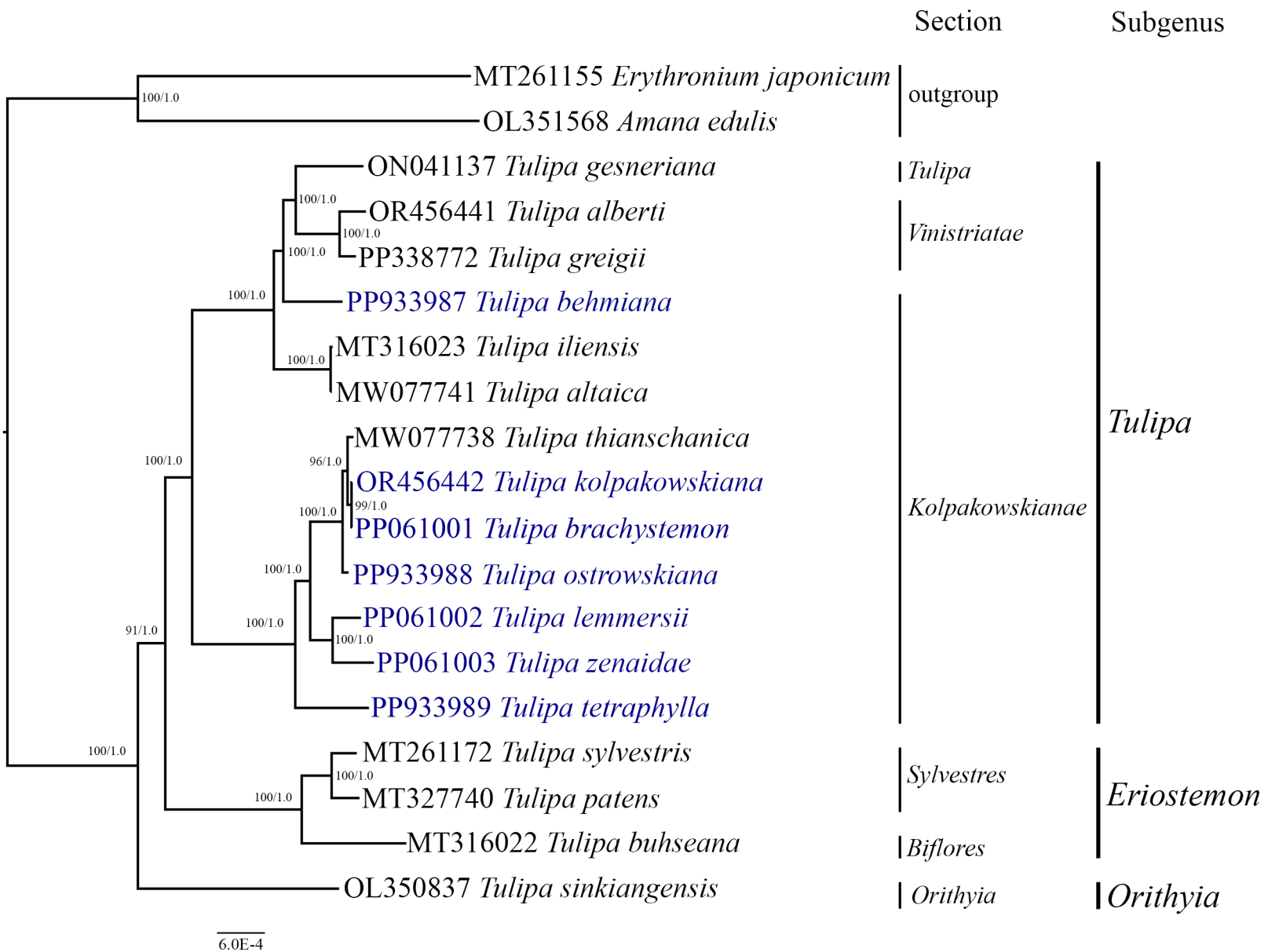


Phylogenetic tree reconstructed using sequences of 80 protein-coding genes from 17 *Tulipa* species and two outgroup species, employing Maximum Likelihood (ML) and Bayesian Inference (BI) methods. The numbers at the branch nodes represent ML bootstrap/BI posterior probability values. The species analyzed in this study are highlighted in blue.