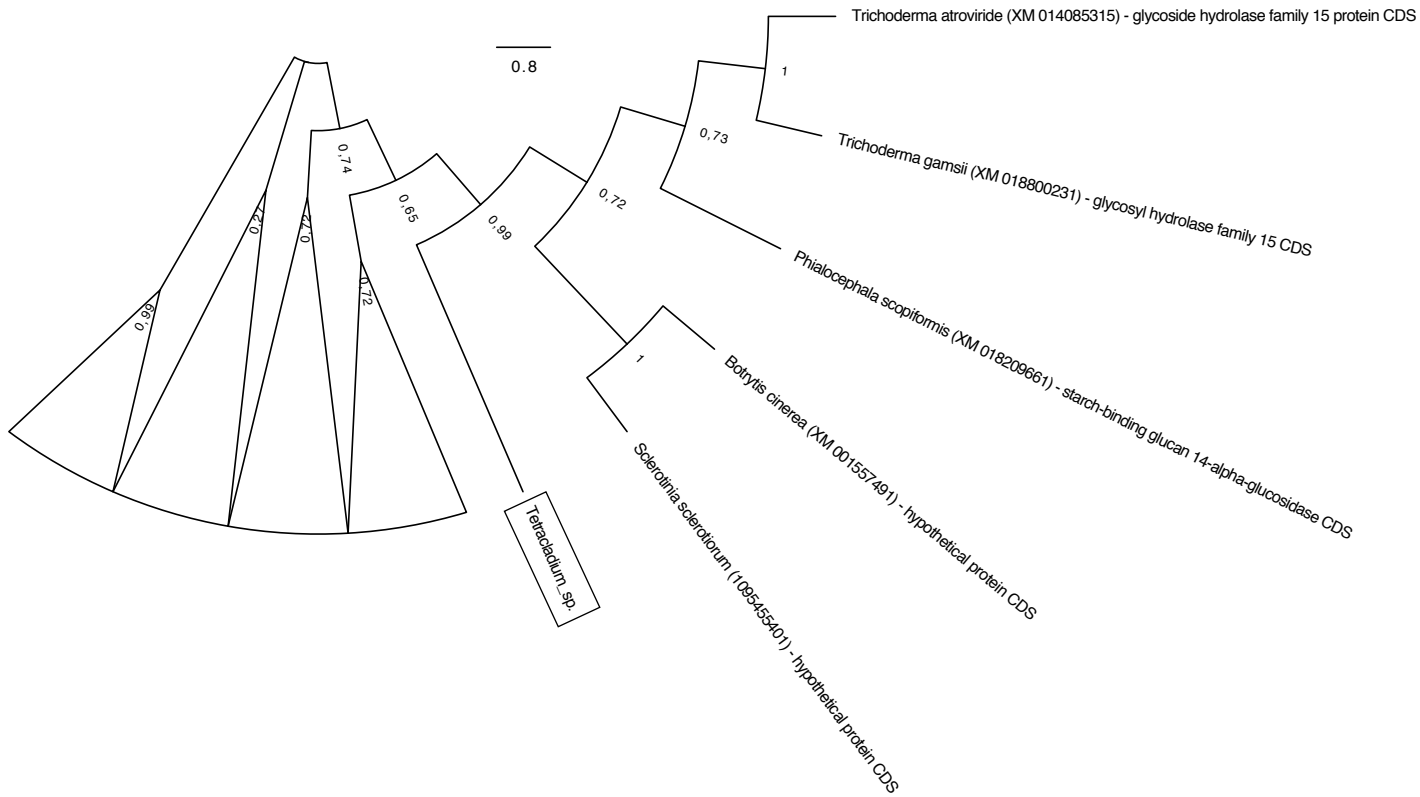
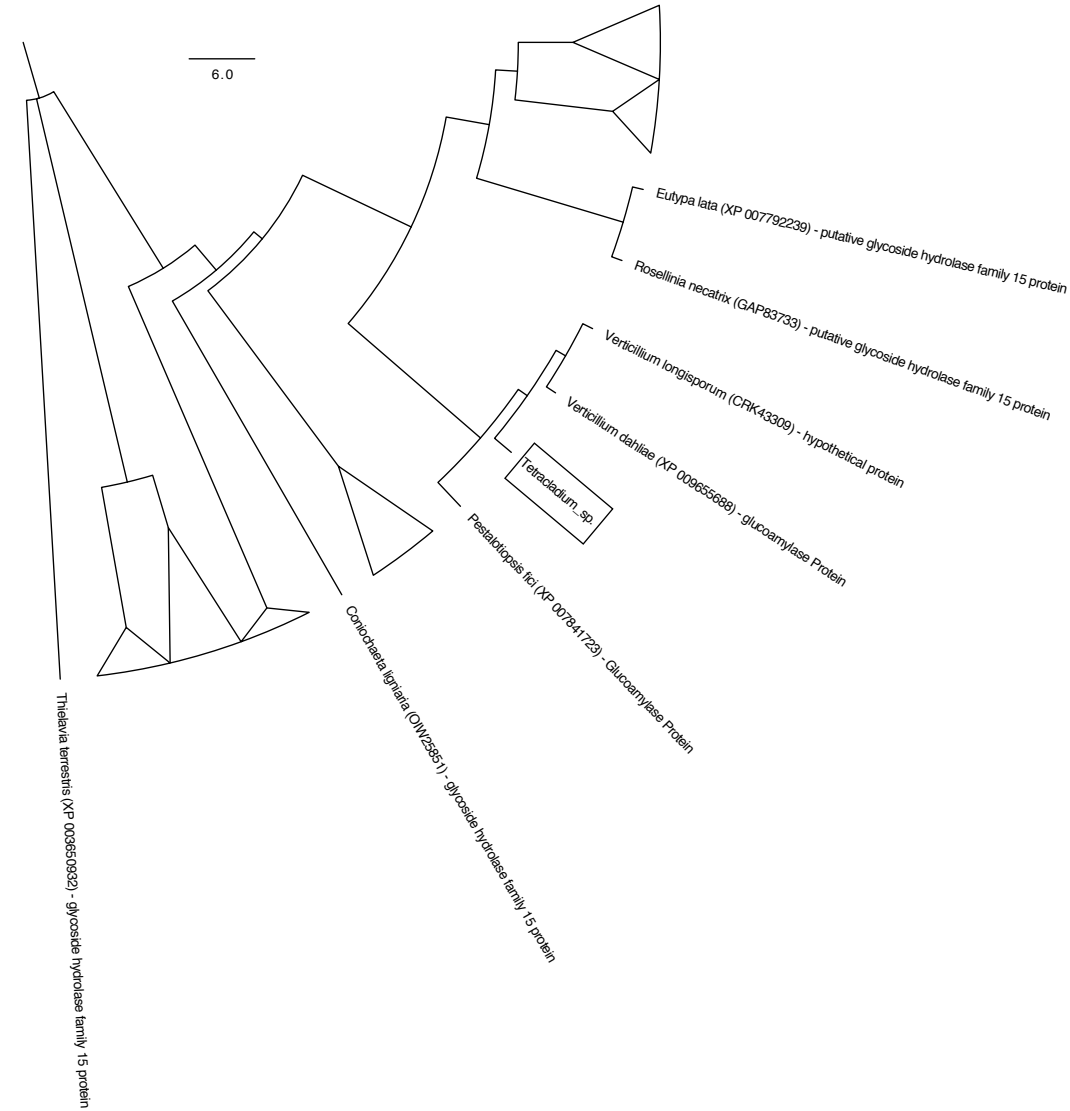


A



B



Supplementary Material 4. Molecular Phylogenetic analysis by Maximum Likelihood method. A, Based on the encoding nucleotide sequences; B, Based on the translated sequences. All positions with less than 95% site coverage were eliminated, that is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. Evolutionary analyses were conducted using MEGA7. Box, Sequences from *Tetracladium* sp.