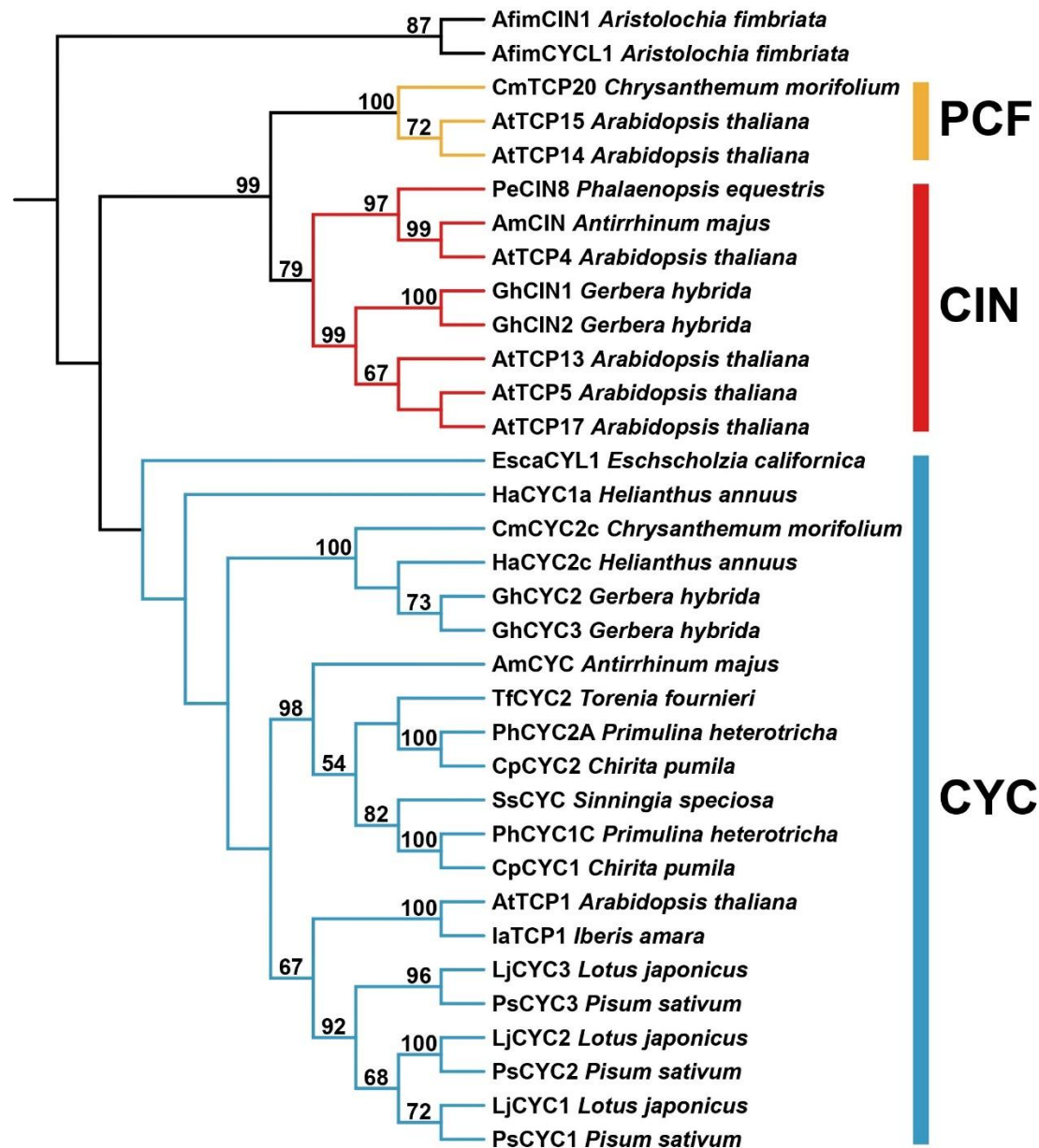




Supplemental Figure S1. Phylogenetic relationships among TCP genes mentioned in this review.

The phylogenetic tree was constructed using MEGA11 with the maximum likelihood method with 1000 bootstraps. The tree is divided into three major clades: PCF (marked in gold), CIN (marked in red), and CYC (marked in blue). Bootstrap support values are shown at each node. Only TCP genes with full-length amino acid sequences were used for analysis. Gene names and their corresponding species are indicated.