

**Supplementary file 9.** Expanded phylogenetic trees of PAC domains from Bryophytes to *A. trichopoda* (Tree I) and from *A. trichopoda* to Brassicales (Tree II).

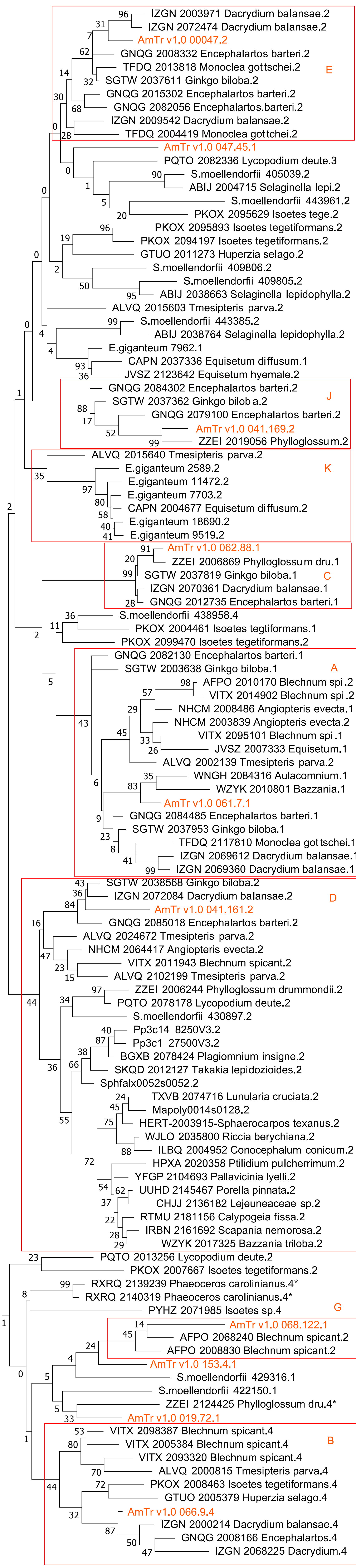
Calculations have been performed using PROMALS3D (<http://prodata.swmed.edu/promals3d/promals3d.php>) for sequence alignment according to secondary structures and MEGA7 (<https://www.megasoftware.net/>) for phylogenetic tree building using the Maximum Likelihood statistical method with 500 bootstraps.

The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model [Jones *et al.* 1992]. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA7 [Kumar *et al.* 2016].

Tree I (page 2). The tree with the highest log likelihood (-9717.26) is shown. The analysis involved 116 amino acid sequences. There were a total of 58 positions in the final dataset.

Tree II (page 3). The tree with the highest log likelihood (-14586,02) is shown. The analysis involved 197 amino acid sequences. There were a total of 60 positions in the final dataset.

Jones DT, Taylor WR, Thornton JM (1992) The rapid generation of mutation data matrices from protein sequences. Computer Applications in the Biosciences 8: 275-282  
Kumar S, Stecher G, Tamura K (2016). MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 33: 1870-1874



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Tree II

