

Methods and strategies of bioinformatics search

The following sequences were used to search for homologues of genes encoding transcription factors (TFs) regulating leaf morphogenesis:

for WUS – CAA09986.1 (*Arabidopsis thaliana*) and WOX14 – NP_173493.2 (*Arabidopsis thaliana*),

for YABBY – AT1G08465.1 (*Arabidopsis thaliana* YAB2, arabidopsis.org), ATG86193.1 – *Huperzia selago*,

for KANADI – AT5G16560.1 (*Arabidopsis thaliana*, arabidopsis.org),

for C3HDZ – AT5G60690.1 (*Arabidopsis thaliana*, arabidopsis.org),

for ARP – AS1 protein sequence – ASYMMETRIC LEAVES 1 transcription factor from *Arabidopsis thaliana* (GenBank accession O80931.1), as well as the ARP homologue from *Selaginella kraussiana*, SkARP1 (XP_002962315.1).

Bioinformatic search was performed in NCBI, UniPort, China National GeneBank DataBase (CNGBdb), as well as arabidopsis.org was used. The search for protein homologues was performed using the tBLASTn and BLASTp algorithms available on the website of the National Gene Bank of China for OneKP database, Phytozome 13, CoGe and <https://www.hornworts.uzh.ch/en.html> for *Anthoceros* genome (Altschul et al., 1990; Lyons and Freeling, 2008; Lyons et al., 2008; Goodstein et al., 2012; OneKP, 2019; Li et al., 2020). MEME Suite 5.4.0 and HMMSCAN were also used to look at protein domains (Bailey et al., 2015; Potter et al., 2018). Amino acid sequences were downloaded in fasta format, combined into data set in Aliview (Larsson, 2014) and aligned using the Clustal-o (Clustal Omega) multiple alignment algorithm in SeaView (Version 5.0.4) (Gouy et al., 2021). The selection of evolution models for various data sets for different TFs was carried out automatically in the online version of IQTree (Trifinopoulos et al., 2016). For all tree reconstructions JTT+F+I+G4 evolutionary model was used. IQTree reconstructed the phylogeny of the identified proteins using the maximum likelihood (ML) method. Standard settings were used, and the number of bootstrap repetitions was set to 1000. To visualize the resulting phylogenetic trees, we used the TreeGraph2 program (Stöver and Müller, 2010). Branches with supports below 50 have been removed, so the trees show polytomies. Graphics were performed using Adobe Photoshop and Illustrator.

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