



**Figure S4.** Phylogenetic analysis of protein sequences of the 52 *Oeu*AQPs and the 79 *Oleur*AQPs with *Fraxinus excelsior*, *Arabidopsis thaliana* and *Populus trichocarpa* orthologs. Deduced amino acid sequences were aligned using ClustalW, and the phylogenetic tree was constructed using the Maximum Parsimony method. Maximum Parsimony analysis was conducted using the Subtree-Pruning-Regrafting algorithm. The number next to the branches represents bootstrap values  $\geq 50\%$  based on 5000 resampling. The distance scale denotes the number of amino acid substitutions per site. The AQP sequences from *O. europaea* var. *sylvestris*, *O. europaea* cv. Picual, *F. excelsior*, *A. thaliana* and *P. trichocarpa* are preceded by the prefixes Oeu, Oleur, Fraex, At, and Poptr, respectively. *Oeu*AQPs are mentioned in red, and *Oleur*AQP in bold. The name of each subfamily and subgroup is indicated next to the corresponding group. XIP\* and XIP\*\* correspond to XIP sequences from Rosids and Asterids, respectively. *Oeu*AQP accession numbers and sequences are listed in Table 1 and Figure S1. *Oleur*AQP, *Fraex*AQP accession numbers and sequences are listed in Figures S2 and S3, respectively.