

Publication

Developmental and Environmental Regulation of Aquaporin Gene Expression across Populus Species: Divergence or Redundancy?

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Aquaporins (AQPs) are membrane channels belonging to the major intrinsic proteins family and are known for their ability to facilitate water movement. While in *Populus trichocarpa*, AQP proteins form a large family encompassing fifty-five genes, most of the experimental work focused on a few genes or sub-families. The current work was undertaken to develop a comprehensive picture of the whole AQP gene family in *Populus* species by delineating gene expression domain and distinguishing responsiveness to developmental and environmental cues. Since duplication events amplified the poplar AQP family, we addressed the question of expression redundancy between gene duplicates. On these purposes, we carried a meta-analysis of all publicly available Affymetrix experiments. Our in-silico strategy controlled for previously identified biases in cross-species transcriptomics, a necessary step for any comparative transcriptomics based on multispecies design chips. Three poplar AQPs were not supported by any expression data, even in a large collection of situations (abiotic and biotic constraints, temporal oscillations and mutants). The expression of 11 AQPs was never or poorly regulated whatever the wideness of their expression domain and their expression level. Our work highlighted that PtTIP1;4 was the most responsive gene of the AQP family. A high functional divergence between gene duplicates was detected across species and in response to tested cues, except for the root-expressed PtTIP2;3/PtTIP2;4 pair exhibiting 80% convergent responses. Our meta-analysis assessed key features of aquaporin expression which had remained hidden in single experiments, such as expression wideness, response specificity and genotype and environment interactions. By consolidating expression profiles using independent experimental series, we showed that the large expansion of AQP family in poplar was accompanied with a strong divergence of gene expression, even if some cases of functional redundancy could be suspected.

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