



Insights into *Populus* XIP aquaporins: evolutionary expansion, protein functionality, and environmental regulation

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Titre	Insights into <i>Populus</i> XIP aquaporins: evolutionary expansion, protein functionality, and environmental regulation
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Mots-clés	Aquaporin [17], Evolution [18], in situ hybridization [19], molecular physiology [20], <i>Populus</i> [21], XIP [22]
Résumé en anglais	<p>A novel category of major intrinsic proteins which share weak similarities with previously identified aquaporin subfamilies was recently identified in land plants, and named X (for unrecognized) intrinsic proteins (XIPs). Because XIPs are still ranked as uncharacterized proteins, their further molecular characterization is required. Herein, a systematic fine-scale analysis of XIP sequences found in flowering plant databases revealed that XIPs are found in at least five groups. The phylogenetic relationship of these five groups with the phylogenetic organization of angiosperms revealed an original pattern of evolution for the XIP subfamily through distinct angiosperm taxon-specific clades. Of all flowering plant having XIPs, the genus <i>Populus</i> encompasses the broadest panel and the highest polymorphism of XIP isoforms, with nine PtXIP sequences distributed within three XIP groups. Comprehensive PtXIP gene expression patterns showed that only two isoforms (PtXIP2;1 and PtXIP3;2) were transcribed in vegetative tissues. However, their patterns are contrasted, PtXIP2;1 was ubiquitously accumulated whereas PtXIP3;2 was predominantly detected in wood and to a lesser extent in roots. Furthermore, only PtXIP2;1 exhibited a differential expression in leaves and stems of drought-, salicylic acid-, or wounding-challenged plants. Unexpectedly, the PtXIPs displayed different abilities to alter water transport upon expression in <i>Xenopus laevis</i> oocytes. PtXIP2;1 and PtXIP3;3 transported water while other PtXIPs did not.</p>

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