

SOYBEAN AQUAPORINS: DIFFERENTIAL EXPRESSION, GENOME DISTRIBUTION AND STRUCTURE

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The major intrinsic protein (MIP) or aquaporins are channel-forming proteins with important roles in membrane absorption and movement of water and small solutes through biological membranes. Using well-known protein sequences of each plant aquaporin subfamily as seed sequence, we carried out a search for orthologs in soybean, revealing 11,288 reads in 102 clusters that, after anchoring in the soybean genome, enabled the location of 99 aquaporin coding genes, distributed in all soybean chromosomes. Such a high number of aquaporins reflects the polyploid nature of soybean. Among the transcripts identified by BLASTx tool, 44% referred to the subfamily PIP, 38% to TIP, 20% to NIP and 6% to SIP. Aquaporins were identified in 56 libraries, mostly associated with plant growth and development. Regarding the tissues with higher expression, a prevalence of transcripts in seeds (85.9%), roots (4.2%), hypocotyls (3.0%) and leaves (1.5%) were observed. Excluding alignments with sequences of soybean itself, the best alignments occurred with *Medicago truncatula*, *Cicer arietinum*, *Phaseolus vulgaris* and *Pisum sativum*, followed by ten other dicotyledonous species. Monocotyledons (rice and wheat) figured only in 10th and 12th places, despite the large number of sequences in databases, indicating strong evolutionary divergence between aquaporins of mono and dicots.