

TRANSCRIPTOME-WIDE ANALYSIS OF AQUAPORINS AND THEIR RESPONSES IN *GLIRICIDIA SEPIUM* UNDER HIGH LEVEL OF SALINITY STRESS

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Abstract:

Considering that the human population will probably reach 10 billion people by 2050, many efforts are underway to increase biomass production sustainably. This challenge becomes even more challenging since it must occur while the plants are affected by several biotic and abiotic stresses. Salinity is one abiotic stress that severely affects agriculture, especially in arid and semi-arid regions. Aquaporins (AQPs) are transmembrane proteins with a role in transporting water and other small molecules across cellular membranes. Regulation of AQP activity and gene expression are seen as a part of the adaptation mechanisms to stress conditions, including salt stress. *Gliricidia* (*Gliricidia sepium* (Jacq.) Kunth) is a multipurpose tree belonging to the Fabaceae family that can withstand various adverse conditions. Our previous studies not only mapped the distinct types of responses to salinity stress in this species - tolerance and adaptation - but also identified the metabolic pathways most affected by this stress. To further characterize this adaptation response, and considering that *gliricidia* does not have a published genome, our research group generated a reference transcriptome for *gliricidia* using RNA-seq data from plants under control and stress conditions. The reference transcriptome has a total of 90.581 proteins with complete ORFs, and the initial annotation analysis used the BlastKOALA tool. A reference transcriptome-wide analysis looking for aquaporins identified 81 ORFs coding for orthologs of aquaporins, with only eight having a differential expression profile, two up- and six down-regulated due to the salt stress. The two up-regulated aquaporins belong to the PIP (Plasma membrane intrinsic proteins) subfamily of aquaporins, and the six down-regulated to both the NIP (Nodulin-26 like intrinsic proteins) and the PIP subfamily. The role of aquaporins in plants is the regulation of water transport across the membrane when the water flow needs to be adjusted or in situations where flow is critically low. Most PIPs are in plasma membranes and localized in organs characterized by experiencing large fluxes of water (vascular tissues, guard cells, and flowers). NIPs have lower water permeability and are permeable to small organic solutes and mineral nutrients. Under stress, the phosphorylation of NIPs increases, showing a role in salt stress responses and in maintaining plant water balance. The list of aquaporins differentially expressed in *gliricidia* under salinity stress is undergoing further characterization to understand the role of such types of proteins in the adaptation response.

Palavras-chave: Abiotic stress; Water transport; Transcriptomics; Salt stress;

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