

CHARACTERIZATION OF THE RESPONSE OF *GLIRICIDIA SEPIUM* (JACQ.) STEUD. TO SALINE STRESS THROUGH THE USE OF PROTEOMIC AND METABOLOMIC

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Abstract:

Gliricidia sepium (Jacq.) Walp., a legume, is a medium-sized multipurpose plant originally from Central America. At an economic level, *gliricidia* can improve water infiltration, increase the soil's water retention capacity, reduce erosion, and restore the soil's quality. This species can adapt to very high levels of salt stress (≥ 20 dS m⁻¹). Soil salinity is an environmental limiting factor for plant biomass production worldwide, and one-quarter of the irrigated area in agriculture has a problem with salinity stress. Our research group performed a comprehensive analysis to characterize the metabolomic and proteomic profiles in the leaves and roots of *gliricidia* under salinity stress, aiming to identify those metabolic pathways, metabolites, and proteins affected by this stress. Groups of five and a half-month-old *gliricidia* plants were kept under control conditions or subjected to saline stress (27 dS/m of electric conductivity) for 2 (short-term stress) or 55 (long-term stress) days. The samples got separated into leaf and root data and organized as follows: all in treatments data set (control and stressed plants at 2 and 55 DAT); age effect - AE (samples from the control plants at 2 and 55 days after treatment - DAT, only metabolomics); short-term stress - STS (the control and the stressed plants at 2 DAT); long-term stress 1 - LTS1 (control and stressed plants at 55 DAT); and long-term stress 2 - LTS2 (the stressed plants at 2 and 55 DAT, only metabolomics). Each data set had five and three biological replicates per treatment for metabolome and proteome analysis, respectively. Based on the results from the metabolome component of this study, it was possible to postulate that the accumulation of lignin and some phytosterols, as well as lysine biosynthesis-but not degradation, play a role in promoting the adaptation response of *gliricidia* plants to a very high level of salinity. The number of proteins found in the STS was much lower than in the LTS in both organs. The differential expression analysis revealed three groups of proteins, those present only in the control plants, those in the stressed, and those in both. The functional annotation analysis revealed a prevalence of proteins from Genetic Information Processing and Carbohydrate metabolism groups in both tissues of salt-stressed plants; and in both scenarios. The integration of the results from both omics platforms used is underway.

Palavras-chave: *Gliricidia*; Integratomic; Metabolomic; Proteomic; Salt stress.

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