

**INSIGHTS FROM A MULTI-OMICS INTEGRATION (MOI) STUDY IN OIL PALM
(*ELAEIS GUINEENSIS* JACQ.) RESPONSE TO SALINITY AND DROUGHT STRESSES**

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Abstract:

Oil palm (*Elaeis guineensis* Jacq.) is one of the World's most important oilseed crops. Together, palm oil and palm kernel oil, respond to about 35% of the global vegetable oil consumption. In Brazil, there are extensive areas suitable for oil palm cultivation outside the Amazon rainforest. Once in these alternative areas, the grower must use artificial irrigation to comply with oil palm's water requirements. The problem is that about one-quarter of the irrigated area in agriculture worldwide faces the problem of soil salinization, which negatively affects the productivity of traditional crops. Many research groups using distinct omics platforms nowadays to gain a deep understanding of plant response to biotic and abiotic stresses, hoping to develop strategies for supporting plant breeding initiatives to develop stress-tolerant superior varieties. In that context, our research group performed single-omics analysis (SOA) and Multi-Omics Integration (MOI) analysis of the metabolome, transcriptome, and proteome profiles of young oil palm plants submitted to very high salinity stress, as well as to water deprivation. SOA results showed the main biological processes, molecular function, and cellular components affected by these abiotic stresses in the leaves of young oil palm plants. MOI study revealed the pathways most affected by those stress conditions. Both, SOA and MOI studies, when analyzed alone or in combination, did reveal new insights into the early response of oil palm plants to these two abiotic stresses, pointing out genes, proteins, metabolites, and pathways directly affected by them.

Palavras-chave: Abiotic stress; metabolome; proteome; transcriptome; salt stress

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