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ONLINE

## LABEL-FREE QUANTITATIVE PROTEOMICS OF POPCORN ROOTS REVEALS MAJOR METABOLIC PATHWAYS ASSOCIATED TO ALUMINUM TOLERANCE

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### RESUMO

Aluminum toxicity is one of the most important abiotic stresses that affect crop production worldwide. To date, there are no reports of large-scale proteomic analysis of maize in response to Al<sup>3+</sup> ion. To investigate the post-transcriptional regulation in response to Al toxicity, we performed a comparative proteomics analysis in roots of two Al-contrasting popcorn inbred lines and an Al-tolerant commercial hybrid during 72 h under Al-stress and quantified its metabolites in roots and shoots. A total of 489 differentially accumulated proteins (DAPs) were identified in the Al-sensitive (L60), 491 in the Al-tolerant (L133), and 277 in the commercial hybrid. Among them, 120 DAPs were co-expressed in both Al-tolerant genotypes. Bioinformatics analysis indicated starch and sucrose metabolism, glycolysis/gluconeogenesis, and carbohydrate metabolism as significant biochemical processes regulated in response to Al toxicity. The up-accumulation of sucrose synthase in L133 may be an important player in the increasing of sucrose content and starch degradation to enhance popcorn tolerance to Al-stress. The increase of glucose content in roots under stress, and its unchanged content in shoots suggests that roots maintain the osmotic homeostasis of cells serving as an energetic resource under stress, suggesting that glucose metabolism might be dependent on the glycolysis cycle in Al-stress condition. Up-accumulation of citrate synthase suggests a key role in the detoxification process in the L133, and malate and fumarate can help in the detoxification process but are not the main players in the Al-tolerance in popcorn. Previous transcriptomic data was integrated with this proteomic data indicating that Al tolerance response presents a complex regulatory network into the transcription and translation dynamics of popcorn roots development. These results highlight new players involved in the systemic plant response to Al<sup>3+</sup> and help to understand the dynamic of plant-Al interaction in the root system and its contribution to Al-tolerance.

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**PALAVRAS-CHAVE:** Abiotic stress, Aluminum toxicity, Label-free proteomics, Biochemical pathways, Zea mays

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