

عنوان مقاله:

Proteomics analysis of canola seeds to identify differentially expressed proteins under salt stress

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خلاصه مقاله:

Seeds are an important part of the canola plant, and similar to other parts are affected by salt stress. Understanding the underlying mechanisms that take place in seeds of canola under salt stress is essential from the perspective of improving quality. In this study, we attempted to identify differentially expressed proteins of canola seeds in the Hyola³⁰⁸ cultivar under ۳۵۰ mM NaCl using two dimensional (۲D) gel electrophoresis. Effect of salt stress was significant on ۱۰۰-seed weight and number of seeds per plant ($p \leq 0.01$), and it changed the proteome of the seeds. From a total of ۵۴۸ reproducible protein spots, ۲۸ protein spots showed significant changes in abundance, of which seven spots showed downregulation. The "Gene Ontology" analysis classified differentially expressed proteins into six biological processes: oxidation-reduction (۲۸.۵%), response to abiotic stress (۲۸.۵%), response to hormones (۲۱.۴%), catabolic process (۲۱.۴%), nucleoside diphosphate phosphorylation (۱۷.۸%) and glycolytic process (۱۴.۲۸%). In conclusion, salt stress induced canola seeds to upregulate proteins that mostly involved in the antioxidant activity and .the proteins with nutrient reservoir activity

کلمات کلیدی:

Abiotic stress, Antioxidant Activity, Brassica napus, Proteomics, Two-dimensional polyacrylamide gel electrophoresis

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