

Quantitative proteome analysis of alfalfa in drought stress under the influence of *miR156*
(*Medicago sativa*)

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Medicago sativa is one of the most produced perennial forage crop and used as animal feed. Drought stress is a major form of abiotic stress affecting the productivity and annual yield of alfalfa. A small non coding RNA, *miR156* has role in drought tolerance, while regulating downstream *SPL* genes. The objective of this research was to study the whole proteome of *miR156OE* (A8) genotype of alfalfa under drought stress. In results, 3,000 proteins groups were identified using MaxQuant when searched against *Medicago truncatula* protein sequence database. Under control conditions, 68 proteins were upregulated in A8 and 84 proteins were downregulated, relative to EV (empty vector), whereas, under drought stress 610 proteins were upregulated and only 52 proteins were downregulated. Functional analysis using DAVID online tool showed enriched proteins are involved in biological and molecular processes like antioxidant response, response to stress, signal transduction and biosynthesis of secondary metabolites. Protein families related to signaling like MAPK, CDPK, PP2C, transcriptional regulators including bZIP and zinc finger proteins were found to be differentially regulated. The identified proteins families could be the potential targets of *miR156* in drought stress. This study provides a better understanding and an insight into the role of *miR156* in combating the drought stress in alfalfa at proteomic level.