

عنوان مقاله:

Expression Analysis of Candidate Genes in Common Vetch (*Vicia sativa* L.) Under Drought Stress

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خلاصه مقاله:

Vicia sativa L., an annual winter growing leguminous plant, is a valuable source of protein and minerals for cattle. Drought is one of the key stress factors that influence plant growth and development. In order to investigate common vetch physiological and molecular responses under Normal irrigation (N) and two levels of drought stress [$S_1 = 30\%$ and $S_2 = 10\%$ Field Capacity (FC)], a greenhouse experiment was carried out on two genotypes, namely, Mahalimaraghe and F_1 , and some physiological traits [e.g. Relative Water Content (RWC), Electro Leakage (EL), total protein, chlorophyll (a, b), and carotenoid content] were measured and expression patterns of three genes (sod, aq1 and bzip) were evaluated by real-time quantitative RT-PCR analysis. Results showed that expression pattern of all three genes and physiological responses had significantly changed in response to the stress. The highest increase in the expression of each of the three genes was observed in Mahalimaraghe genotype in S_1 condition compared to N. In contrast, under S_2 condition compared to N, the highest increase in expression of the three genes was observed in genotype F_1 . In comparison of S_2 with S_1 , the highest changes in expression of all the three genes was observed in Mahalimaraghe genotype. All together, the obtained results may facilitate the understanding of molecular mechanism of *V. sativa* in response to drought stress, and also provide the basis of effective genetic engineering strategies for improving stress tolerance of *V. sativa*.

کلمات کلیدی:

Dought tolerance, Expression pattern, Gene expression, Molecular response, Osmotic adjustment

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