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Physiological and molecular response of young halophyte plants to salinity

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The extension of irrigated agriculture and the intense utilization of water resources in hot and dry countries lead to an inevitable appearance of salinity problems in soil and water. *Atriplex halimus* L. is a perennial native shrub of the Mediterranean Basin with an excellent tolerance to drought and salinity. Plants have developed a range of mechanisms to mitigate the effects of drought and salinity including sequestration of Na+ ions in the vacuole, synthesis and accumulation of osmolytes such as, proline, sugars and glycine betaine, which facilitate cell metabolism under stress conditions. Antioxidant metabolism also plays an important role in protecting plants from a wide variety of environmental stresses including drought, and salinity. In this study, a comparison was made in physiological, biological and molecular responses of two *Atriplex halimus* L. populations from contrasting environments: arid steppe and saline coastline to increasing levels of salt over a 6 week growth period. Results show a greater survival of the coastal population as well as greater accumulation of Na+ and K+ which is mirrored by higher induction of antiporter gene expression. Both proline and glycine betaine increased more significantly in the coastal population accompanied by greater induction of the CMO gene. Ascorbic acid content rose with increase in salt concentrations in both populations and catalase activity was strongly induced indicating an activation of ROS scavenging mechanisms both of which were more highly activated in the coastal population.

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Quantitative and qualitative characteristics of storage proteins of bread wheat with and without *1BL/1RS* translocation

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Significant part of wheat varieties has alien chromatin introgressions, including rye's genetic material. 1BL/1RS translocation has positive as well as negative selective traits. Varieties and biotypes of bread wheat with- and without 1BL/1RS translocation were differentiated by a complex of secalin bands in ω -zone, specific for rye. They were compared on total grain protein and its fractions content and qualitative characteristics of protein groups. Protein extraction was done according to Triboï, E. et.al., (2003) resulted to separating albumins and globulins, amphiphilic proteins, gliadins and glutenins. According to spectra of high molecular weight glutenin subunits of all samples have *Glu-1* quality score from 7 to 9. Genotypes without translocation were characterized by high intensity of bands with molecular mass 55.6 and 53.4 kDa, in the zone of low molecular weight glutenins and gliadins whereas samples with 1BL/1RS translocation have not such distinct components. Significant difference between genotypes without translocations on total seeds protein, amphiphilic and glutenin fractions content was not detected. At the same time wheat samples with 1BL/1RS translocation had higher content of amphiphilic proteins, which can be linked with the resistance of such forms to unfavorable stress factors of environment.

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