

Differential responses to salinity of two olive tree cultivar are identified by modeling gene expression and mineral elements translocation.

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Soil salinity is a severe problem for the Mediterranean crop, which will increase in the 21st century. The olive tree is moderately resistant to salinity, with differences between varieties. Two cultivars with different tolerance to salinity, Leccino (susceptible) and Frantoio (tolerant), were treated with 120 mM of NaCl for 30 days. Gas exchanges were monitored throughout the treatment. The expression of *NHX*, *SOS1*, and *H⁺ ATPase*, and the hydrolytic activity of H⁺ ATPase were measured in the leaves. Furthermore, we analyzed the concentration of Na⁺, K⁺, Mn²⁺, Mg²⁺, and Ca²⁺ in the different plant organs. The gene expression, enzymatic activity, and gas exchange results were modeled using multiple linear models and mixed models. Both the cultivars significantly reduced the net photosynthesis and increased the water use efficiency after 30 days of treatment. Na⁺ was accumulated in the roots of both cultivars, and in the leaves of Leccino variety treated with NaCl. Plants treated with NaCl over-expressed the genes *NHX* and vacuolar *ATPase subunit E*, while the genes *SOS1*, *ATPase11*, and *ATPase8* were more expressed only in the Frantoio cultivar. The covariance between gene expression and element concentrations data was analyzed to identify significant interactions between cultivars and treatments.

Na⁺ accumulation in the roots of Frantoio was positively related to the accumulation of K⁺, Mn²⁺, Mg²⁺, and Ca²⁺ in the xylem, cortex, and leaves. The results suggest that the capacity of Frantoio to mobilize elements, together with the over-expression of key genes for Na⁺ management, could be a determinant for salinity tolerance.

Keywords: salt stress, *Olea europaea* L., ion pumps, calcium, multiple linear models.