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“Reconcile land system changes
with planetary health”

Comparing phenotyping systems for salinity tolerance in quinoa (*Chenopodium quinoa*) across phenological stages

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Abstract

Salinisation of agricultural land poses a substantial threat to global food security. Quinoa (*Chenopodium quinoa*), a drought and salt-tolerant crop from the Andes, provides highly nutritious seeds and exhibits a broad genetic diversity. It is adapted to marginal environments and provides opportunity to sustainably diversify cropping systems in saline and arid regions. Consequently, identifying quinoa accessions adapted to saline soils and elucidating the respective tolerance mechanisms are critical to improve quinoa breeding for marginal environments. Phenotyping for salinity tolerance under field conditions is challenging due to heterogeneous soil conditions, cost- and labour requirements. Phenotyping therefore often relies on simpler systems and younger plant stages, and the relevance to field conditions remains unclear.

We screened 100 quinoa accessions for their response to salinity in a hydroponic system compared to a soil-based pot system in the greenhouse: In the hydroponic system, plants were grown in nutrient solution for 15 days (to the six-leaf stage) and subjected to 300 mM NaCl for 14 days. In the soil system, plants were grown in individual pots until 10-leaf stage and exposed to 400 mM NaCl for 14 days. In both experiments, leaf greenness, chlorophyll fluorescence and stomatal conductance were assessed before sampling. Plants in the hydroponic experiment were then harvested for biomass of roots and shoots, plants in the greenhouse were left to grow and harvested after seed maturity. For both experiments, Na⁺ and K⁺ content and osmolality of roots and leaves were assessed. As a measure for salt tolerance, a salt tolerance index was calculated based on the maintenance of biomass and seed yield under salinity, between control and treatment group.

Salinity tolerance was found to differ between accessions in both experiments and related to various physiological parameters, depending on the accession. Tolerance rankings were not uniform between phenotyping systems, implying methods need to be carefully chosen. The results serve as a basis for investigating the efficiency of phenotyping in different systems for selection purposes and lay a foundation for further investigation of the underlying molecular mechanisms of salinity tolerance in quinoa.

Keywords: Abiotic stress, phenotyping, quinoa, salinity