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From transcriptomics to the field - improving screening for salinity tolerance in quinoa (*Chenopodium quinoa*)

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Abstract

Salinisation of agricultural land poses a threat to global food security. Quinoa (*Chenopodium quinoa*) is a salt-tolerant crop, which provides highly nutritious seeds and exhibits a broad genetic diversity and adaption to saline and arid environments. Identifying quinoa accessions adapted to salinity and elucidating the respective tolerance mechanisms is critical to improving quinoa breeding for marginal environments. Phenotyping for salinity tolerance in field conditions is challenging due to heterogeneous soil conditions, unpredictable extreme weather events, cost- and labour requirements. Phenotyping therefore often relies on small-scale systems and younger plant stages, with relevance to field conditions remaining unclear. In this study, we screened 150 quinoa genotypes for their response to salinity in a soil-based pot experiment in the greenhouse and conducted transcriptomic analyses on leaf samples of 29 contrasting genotypes. Additionally, 6 genotypes were investigated in a multi-year field experiment in Uzbekistan. Physiological parameters, such as stomatal conductance, leaf ion contents and osmolality were assessed after the treatment period and plants were harvested after seed maturity. 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. The screening revealed differences in salinity tolerance across genotypes and suggests K+-dynamics and shoot water relations in early stress phases are important traits for seed biomass maintenance. Transcriptome analyses provide insights into the underlying molecular pathways. Also, genotypes which had a high salt tolerance index in the greenhouse pot experiment also performed well in saline field conditions, suggesting the screening system in the greenhouse indeed had relevance for plant performance in the field. The presented results will help identify genetic markers for physiologically important traits for salinity tolerance in quinoa and facilitate selection of genotypes for breeding quinoa for saline environments.

Keywords: Abiotic stress, phenotyping, quinoa, salinity

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