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QTLs for Salt Resistance Vary with Development Stage in Field-Grown Barley

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Abstract

Salinity is among the most serious threats for crop production, especially in regions with unreliable rainfall patterns. To sustain agricultural use of affected areas, genotypes are needed that are sufficiently resistant to salinity to offset the farmers' investment and decrease famine hazards. Detailed knowledge of the traits involved in salinity resistance is imperative to successfully breeding tolerant varieties. Molecular trait markers could facilitate this process. Phenotyping of mapping populations under saltstress conditions and computation of QTLs can detect markers closely linked to the genes responsible for salinity resistance. The winter barley mapping population W766 ('Angora' × W704/137) was subjected to saltstress at germination in climate chambers (IPK, Germany, 100 lines, 4 salt concentrations 0–2.5% for 10 days, germination score 1–9 of 10 replications and from the vegetative stage to maturity in a field trial (Herat, Afghanistan, 100 lines, 12.04.-05.05., 2 treatments, EC = 0.8 and 3.2 mS cm⁻¹, 3 replications). Aboveground biomass was sampled 21 days after salt application and at maturity. Dry matter, K and Na concentrations were measured at the vegetative stage and yield components were determined at maturity. QTLs were calculated using the QGENE software. Germination under saline conditions was related to QTLs on linkage groups 3H and 5H confirming earlier results for the OWB and Steptoe-Morex mapping populations. Evaluation of salt responses in yield components using principal component analysis discriminated 4 groups of genotypes within the mapping population, namely tolerant and susceptible includers and susceptible and resistant excluders. From the germination test, the five best and worst performing lines were found in the groups of tolerant includers and resistant excluders, respectively. Thus, QTLs originating from germination responses to salinity cannot reliably indicate resistance strategies realised in later developmental stages. A QTL related to sodium uptake not identified from the germination test was found on chromosome 1H in the field trial. However, one QTL responding to saltstress on chromosome 3H was found in both development stages and was related to yield and yield reduction in the later developmental stages, probably indicating a gene location related to translocation of carbohydrates. Studies are ongoing to further corroborate these findings.

Keywords: Afghanistan, development stage, yield components

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