

QTL Analysis for Salt Tolerance in Barley

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Introduction

Soil salinity, often combined with overgrazing, threatens vast areas of agriculturally productive land, particularly in semi-arid regions. Barley is potentially tolerant to salinity and is an important food and fodder crop. Given the appropriate genotypes, reclamation of degraded soils could be envisaged using barley pastures.

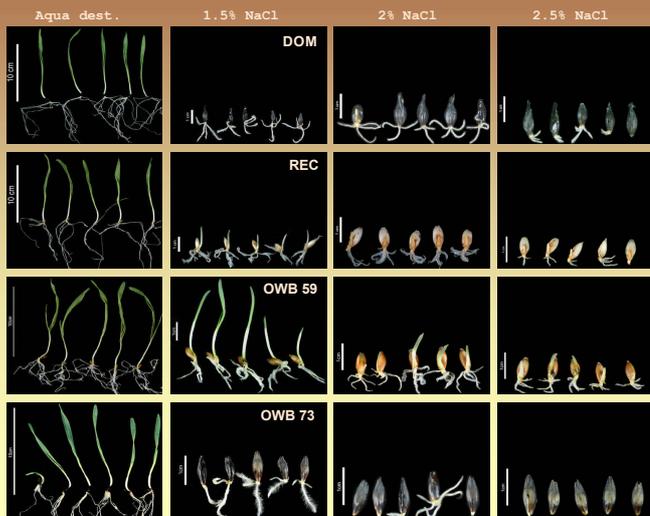
The objective of this study was to identify the genetic basis of salt tolerance traits in barley (*Hordeum vulgare* L.) using as a start the Oregon Wolfe Barley (OWB) mapping population and number of Afghan barley cultivars.

Germination and early seedling growth were used to evaluate the salinity tolerance expression in the mapping population. QTL analysis was used to identify chromosome regions related to those traits.



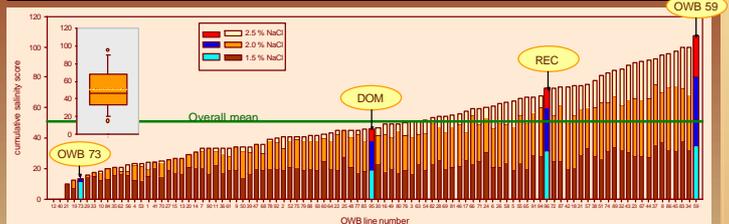
Methodology

The marker saturated Oregon-Wolfe barley mapping population (94 lines + 2 parents) was subjected to 4 different concentrations of NaCl solution (0, 1.5, 2, 2.5%) for ten days. Seed was sown in seeding trays containing 10 grains per line in climate chambers (20°C, 100% rH, 12h PP). Salinity responses of 10 individual seedlings were scored after ten days for leaf and root development on a scale from 1 (poorest) to 6 (best). Results were correlated with markers using the QGene program of Nelson (1997) resulting in the identification of QTLs for salinity tolerance in the germination stage.

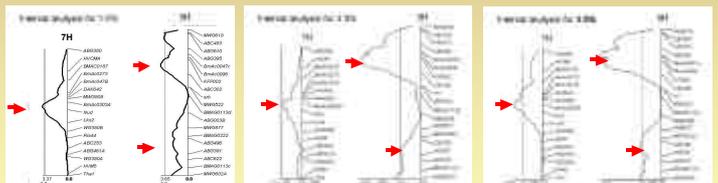


Results & Discussion

Germination and early seedling growth in response to different levels of salinity differed strongly among the lines of the OWB population. At low salt concentrations almost all lines germinated. With increasing NaCl concentration germination rate decreased. About 20% of the lines performed better than the REC parent and about 35% performed worse than the DOM parent.



Three chromosome regions were found to correlate with salinity evaluation scores of the OWB population. Two on chromosome 5H and one on chromosome 7H (red arrows in figure below.) The likelihood for QTLs related to salinity tolerance on the centromere region of chromosome 5H increased with the salt concentration (LOD scores at the specific regions). The increase of the LOD score on chromosome 7H at higher salt concentration was less.



QTLs for salt tolerance at germination have been described for the Harrington / TR306 population on chromosomes 1H and 5H and for the Steptoe / Morex population on chromosomes 4H, 5H and 6H (Mano et al. 1997). In contrast to Mano et al. who found QTLs on chromosome 5HL, we located the QTLs in the centromere region of chromosome 5H, between the molecular markers BmAc0047 and ABC302 (LOD=9.66) which accounted for 41% of the total variance. In line with earlier reports, QTLs found on the chromosome 7H were located at the centromere region.

Outlook

- Identification of chromosome regions carrying traits for resistance or tolerance to salinity in barley will allow to test of a large number of accessions for specific traits with little experimental effort.
- In our quest for barley cultivars suitable for the target country Afghanistan, adapted to semi-arid conditions and resistant to salinity, the QTL analyses shown here will help identify suitable cultivars from local germplasm.
- The QTLs identified in this study will be validated for the vegetative and reproductive stage in a field trial in Afghanistan under saline and non-saline conditions including Afghan barley varieties.
- Results will be used to select Afghan barley genotypes, resistant to salinity that can be developed further to serve as multi-purpose crop to feed either humans or livestock.

Contact at DTT 2004



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Pictures from the OWB population were obtained from: http://wheat.pw.usda.gov/ggpages/OWB_gallery/index.htm and IPK Gatersleben

References

Mano Y and Takeda K (1997). Mapping quantitative trait loci for salt tolerance at germination and the seedling stage in barley (*Hordeum vulgare* L.). *Euphytica* 94: 263-272.
Nelson JC (1997) QGENE: software for mapping - based genomic analysis and breeding. *Mol Breed* 3: 239-245.

