

QTLs for salt tolerance: Comparison of barley mapping populations

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Expected growth of the world population from 6.5 billion to 9.1 billion in 2050 requires a duplication of the food production within the next decades. Currently 40% of the world's food production is realised on 17% of the cropland which is under irrigation, but 1-2% of this area is lost every year by secondary salinisation. The „White death“ in the form of desertification of agricultural arable land due to salt is the most serious threat for the nutrition of mankind. There is a demand to breed salt tolerant crops, because most of them are sensitive. QTL analysis using functional molecular marker maps permit detailed information about both location and function of genes involved in the polygenic inherited trait salt tolerance. This information could facilitate marker validation as pre-requisite for marker assisted selection of adapted plant material with respect to a directed breeding of tolerant cultivars.

Three barley mapping populations (Oregon-Wolfe-Barley, Steptoe-Morex and Igri-Franka) were subjected to salt stress at germination stage in climate chambers (20°C, 12h photoperiod, 10 days). 94, 73 and 73 DH lines were tested, respectively, under four salt concentrations (0 to 2.5% NaCl). Ten seeds per line and

treatment in two replications were scored from 1 to 9 according to a modified scheme of MANO et al. (1996). QTLs were analysed using a functional molecular marker map comprising >500 EST-based markers (KOTA et al. 2001, THIEL et al. 2003, VARSHNEY et al., unpubl. data) and the QGENE program (NELSON, 1997).

QTLs with main effects for germination under salt stress conditions were located at the same regions on chromosomes 5H for Steptoe-Morex and OWB for all concentrations of sodium chloride solution. Minor effects were observed for Igri-Franka with respect to 1.5% sodium chloride. Main QTLs for the Igri-Franka population were detected on chromosome 3H. Minor effects were found in comparable regions for Steptoe-Morex and OWB. Chromosome 4H shows additional minor QTLs at different salt levels for both Steptoe-Morex and Igri-Franka.

Homoeologous group 5 chromosomes of *Triticeae* clusters for QTLs and major loci controlling plant adaptation to environment (CATTIVELLI et al. 2002), which is in accordance with our findings for various levels of salt stress. How-

ever, the location of main QTLs for salt stress response is different between spring and winter type mapping populations. The Oregon-Wolfe-Barley and Steptoe-Morex populations are spring type and QTLs are located on 5H. The Igri-Franka population is winter type and main QTLs were detected on 3H which was found for another winter type mapping population, too. This result indicates a separation of the gene pools used for breeding purposes.

References

- CATTIVELLI, et al., 2002: Chromosome regions and stress-related sequences involved in resistance to abiotic stress in *Triticeae*. *Plant Mol Biol* 48:649-665.
- KOTA, et al., 2001: Application of DHPLC for mapping of single nucleotide polymorphisms (SNPs) in barley (*Hordeum vulgare* L.). *Genome* 44, 523-528.
- MANO et al., 1996: Varietal variation in and effects of some major genes on salt tolerance at the germination stage in barley. *Breeding Science* 46:227-233.
- THIEL, et al., 2003: Exploiting EST databases for the development and characterization of gene-derived SSR markers in barley (*Hordeum vulgare* L.). *Theor. Appl. Genet.* 103, 411-422.
- NELSON, J.C., 1997: QGENE: software for mapping - based genomic analysis and breeding. *Mol Breed* 3:239-245.

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