## QTLs for salt tolerance in three different barley mapping populations

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### Introduction

Soil salinity is one of the crucial factors limiting crop production. Progression of salinisation of agriculturally arable land is mainly connected with mismanagement of water in irrigation systems, in particular under arid and semiarid climate conditions and global changes of water flow in the landscape. Selection of salt tolerant genotypes is necessary to ensure yield and to reclaim salt affected soils. The development of molecular marker(s) could facilitate the selection process. Phenotyping of mapping populations under salt stress conditions and calculation of QTLs are suitable instruments to detect markers that are responsible for tolerance/sensitivity. However, a quantitative inherited trait like salt tolerance requires a range of adaptations, with a whole host of genes interacting with each other to produce the visible phenotype.

### Materials and Methods

108 barley accessions from the Genebank Gatersleben (Germany) were tested at the germination stage under salt stress conditions. The plant material consists of spring barley

accessions from Pakistan (19), Tunisia (33), Libya (33), and winter barley accessions from Afghanistan (23), because these countries were known for problems with soil salinity.

Three different concentrations of sodium chloride solution (1.5%, 2.0% and 2.5%) and distilled water as a control were used to assess the salt tolerance. Ten seeds of each line and variant were tested on filter paper in plastic boxes. Seeds were transferred to climate chambers with a constant temperature of 20°C and a 12 hours light and 12 hours dark photoperiod. After ten days the plant material was scored with a modified scheme according to Mano et al. (1996) (Fig.1). In addition 92 DH lines of the Oregon-Wolfe-Barley (OWB), 72 DH lines of the Igri-Franka and 72 DH lines of the Steptoe-Morex mapping populations were tested in the same manner as described for the Genebank material, but with two replications. The scoring data were used to calculate QTLs with the QGENE programme of Nelson (1997).


Fig. 1: Scoring scheme for salt tolerance at the germination stage

**Results**

There are different levels regarding to salt tolerance within the Genebank accessions (Fig. 2).

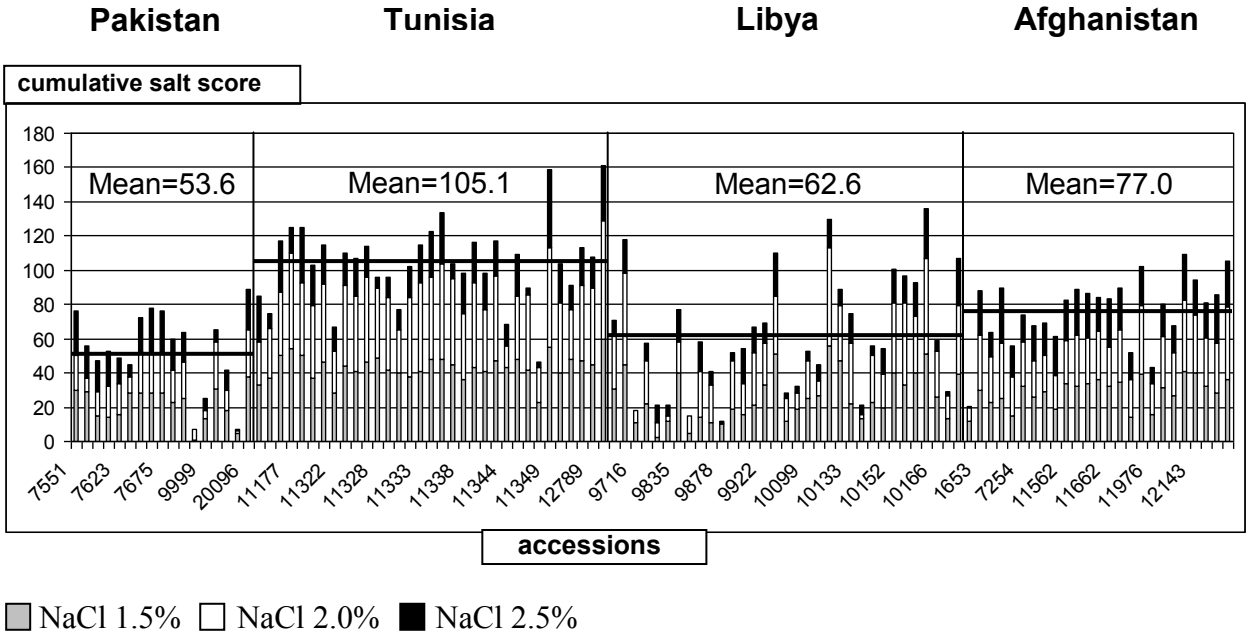


Fig. 2: Salt tolerance of barley accessions of the Gatersleben Genebank collection from four different countries at the germination stage

Barley accessions from Tunisia were characterised by a better growth under salt stress conditions than accessions from the other countries. The winter barley accessions from Afghanistan showed fewer differences in the stress response than accessions from Libya or Pakistan.

The diagrams of the salt score of the three tested mapping populations (Figure 3) present the mean of two replications. Within the OWB mapping population 24% of the lines performed better than the best parent REC and 49% of the lines were worse than the more sensitive parent DOM. No line of the Igri-Franka mapping population showed a better growth under salt stress conditions than the best parent Franka. Due to the little amount of seeds the parents of the Steptoe-Morex mapping population were not tested and therefore they are not included in the diagram. The Steptoe-Morex population showed the best growth under salt stress in comparison to the OWB and Igri-Franka mapping populations (Fig. 4).

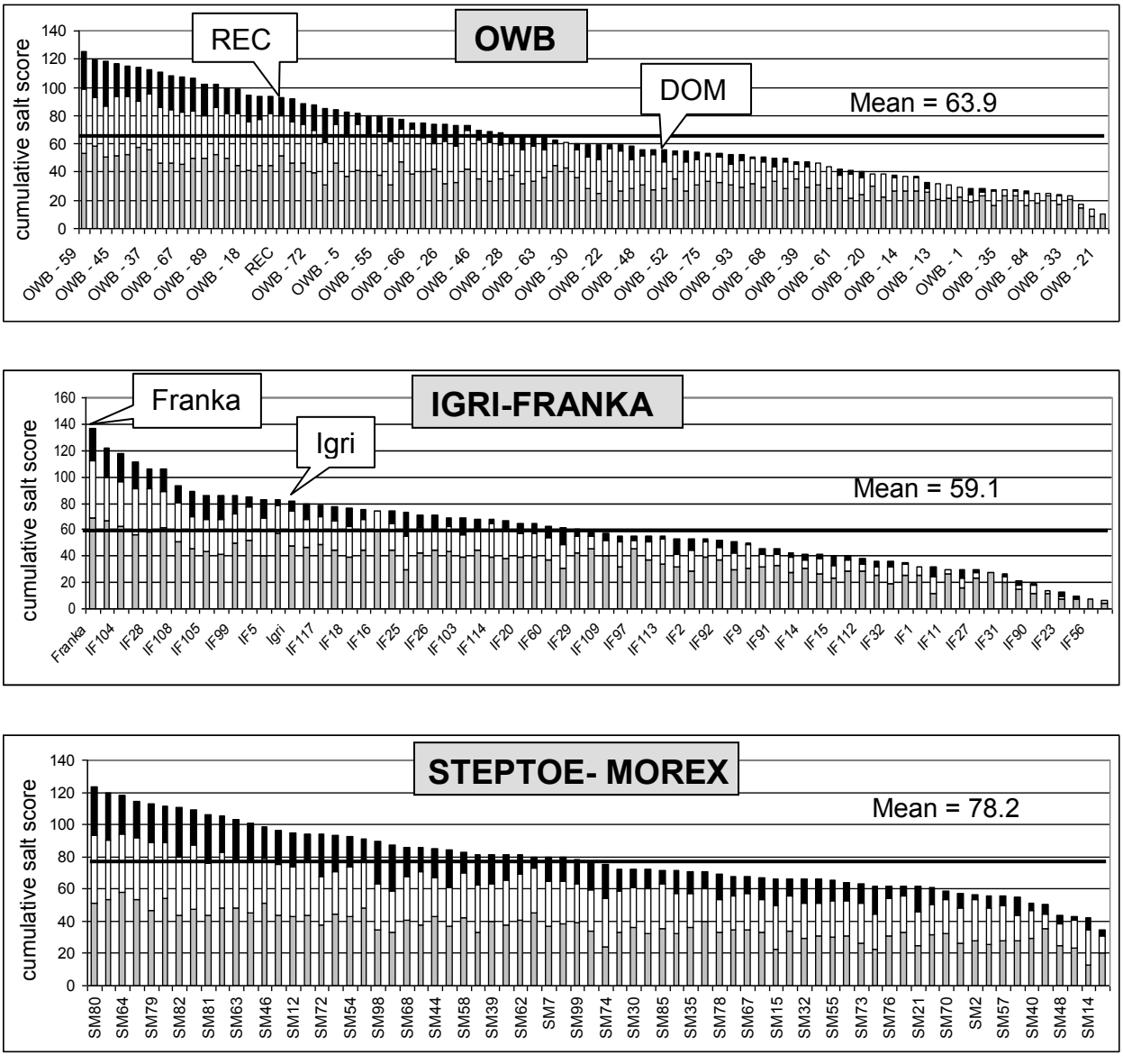
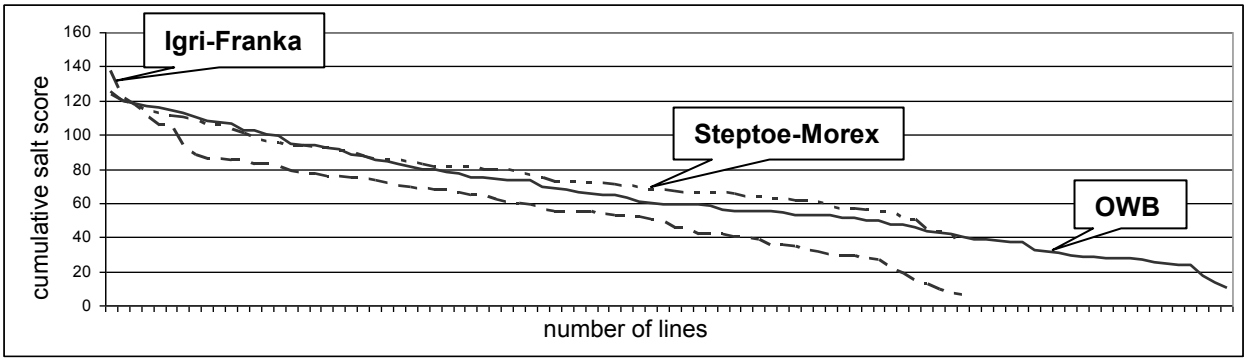


Fig. 3: Salt tolerance of OWB, Igri-Franka and Steptoe-Morex mapping populations at the germination stage




– – – –Igri-Franka, — · · — Steptoe-Morex, ——— OWB mapping population

Fig. 4: Comparison of the three different barley mapping populations with respect to salt tolerance

Main QTLs for the growth under salt stress conditions were found on linkage group 5H and 7H for the OWB, on 3H for the Igri-Franka and on 5H for the Steptoe-Morex mapping populations. Both QTLs for the OWB on 5H and 7H and the QTL for the Steptoe-Morex mapping population were located in the centromere region. The QTL for the Igri-Franka population was located on the short arm of linkage group 3H.

**Discussion**

Linkage group 5 of *Triticeae* possesses clusters of QTLs and major loci controlling plant adaptation to the environment (Cattivelli et al. 2002). In both spring barley mapping populations OWB and Steptoe-Morex investigated here, QTLs related to growth under salt stress conditions were found on linkage group 5H. In addition for the OWB population a main QTL on linkage group 7H was detected. In OWB the detected QTLs became more distinct with increasing salt concentration (Weidner and Börner, 2005). Mano and Takeda (1997) found the most effective QTLs for salt tolerance at different loci on chromosome 5H in two barley mapping populations. In Steptoe-Morex QTLs were located near the centromere region, which confirms our findings for the same population and in line with our results for OWB. The third mapping population investigated in the present study is based on a cross between the winter barley Igri and the spring barley Franka. The main QTL on linkage group 3H is in line with other findings of the winter barley mapping population W766 (data not published).

According to Mano and Takeda (1997) additional QTLs with minor effects for germination speed under salt stress conditions were detected on chromosomes 3H and 7H for Steptoe-Morex and Harrington-TR306, respectively. According to Munns (2002), salt and water stress tolerance during a time frame from germination to a few days into the seedling stage, depends upon hormonal regulation. Expressed by a good growth regardless of the real impact of plant stress it seems to correspond with good plant vigour during the germination stage. The theory of a special kind of plant vigour may be based on hormonal regulation is supported by another experiment about pre-harvest sprouting (Lohwasser et al. 2006, present Newsletter) investigating the OWB mapping population. The stress conditions differed from salt stress, but scoring criteria was the growth of the plantlets after seven days and the main QTL was located in the same region as for salt stress.

Good plant vigour is a prerequisite to escape from unfavourable environment conditions. Further investigations are necessary to detect the genes which protect the plants at later developmental stages against salt stress because of high salt concentrations inside the plant.

Finally it should be mentioned that all three mapping populations are saturated with expressed sequence tag (EST) based markers (Kota et al. 2001, Thiel et al. 2003, Varshney et al., unpubl. data). Besides determining the position within the genome one may detect genes with known function, controlling the traits of interest.

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