

vary with Development Stage in Field-grown Barley

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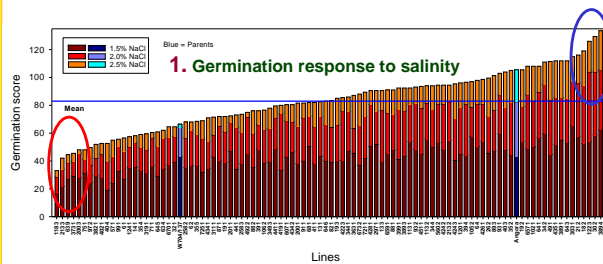
Introduction

- Since most crops are salt sensitive, detailed knowledge of the traits involved in salinity resistance is imperative to successfully breeding tolerant varieties.
- Investigation of mapping populations under salt stress conditions is a prerequisite to combine phenotype with genotype information.
- Calculation of QTLs at different stages of plant development can detect markers linked to the genes responsible for salt tolerance.
- Test of QTLs with respect to other abiotic stress conditions is necessary to assess combined / alternative effects.
- The use of molecular trait markers as "screening-tool" would facilitate the selection of adapted genotypes and hence support the breeding progress.

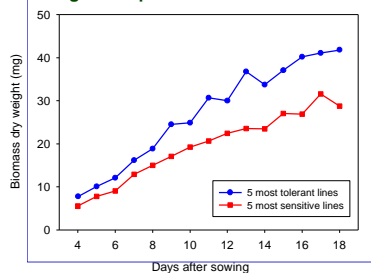
Conclusions

- Germination under saline conditions was related to QTLs
- QTLs originating from germination responses to salinity cannot reliably indicate resistance strategies realized in later development stages
- A QTL related to salt stress on the chromosome 3H present across developmental stages was related to yield in full-grown plants, probably indicating a gene location related to translocation of carbohydrates.

Results - Summary



2. Seedling development under non-stress conditions



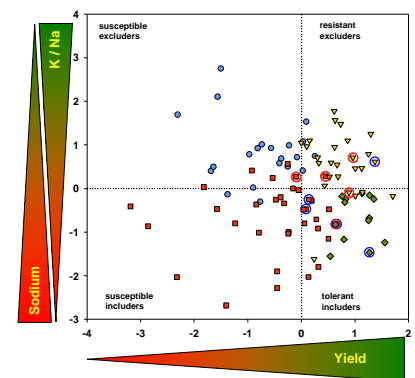
1+4 Germination under saline conditions was related to QTLs detected on linkage groups 3H and 5H.

3 PCA on yield components discriminated 4 groups of genotypes within the mapping population, namely tolerant and susceptible inclusions and susceptible and resistant excluders.

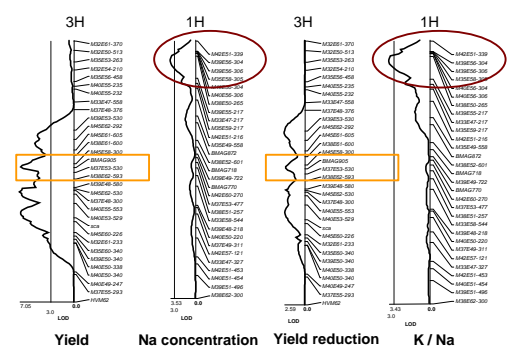
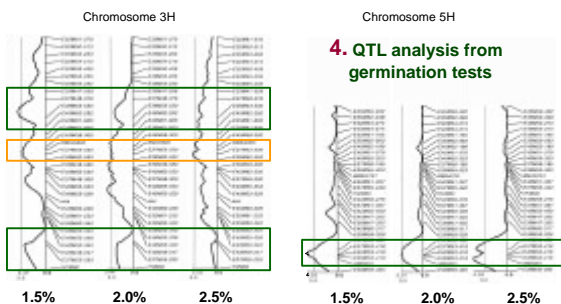
1+2+3 The 5 best and worst performing lines from germination test, different at seedling stage also under non-stress conditions were found in the groups of tolerant inclusions and resistant excluders.

5 A QTL related to Na uptake that was not identified from germination test was found on chromosome 1H in the field trial.

3. Principal Component Analysis of salt effects on yield components from the field trial



5. QTL analysis for selected traits from the field trial

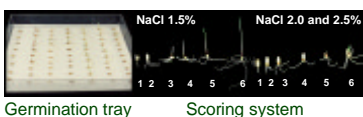


Materials & Methods

From the mapping population W766, a cross between the winter barley cultivars "Angora" and "W704/137", 95 DH lines and the parents were investigated at germination (climate chamber) and adult plant stage (field). QTL were analysed using the QGENE program (Nelson, 1997).

Germination test - climate chamber

- Germination trays - filter paper
- 4 salt levels (0, 1.5, 2.0, 2.5%)
- 10 seeds per treatment and line
- 20°C, 12h photoperiod, 10 days
- Scoring of germination according to a scheme of Mano et al. (1996)



Seedling test - climate chamber

- Germination trays - filter paper
- 5 most tolerant / sensitive lines
- 4 days after sowing - hydroponics
- 50% aerated Hoagland - solution
- 20°C, 12h photoperiod, 14 days
- Assessment of shoot and root dry weight



Salt tolerance validation – field trial

- Field trial, Herat, Afghanistan, Semi-arid, sown in November
- 2 salt levels (0.6, 6.5 mS_{cm}⁻¹)
- Randomized strip plot design
- Visual and destructive sampling in late vegetative stage (K, Na analyses)
- Yield, yield components at maturity