

## vary with Development Stage in Field-grown Barley

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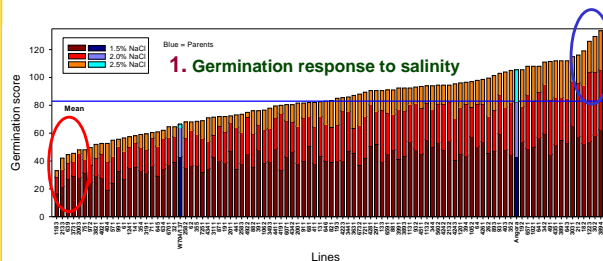
### Introduction

- 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.

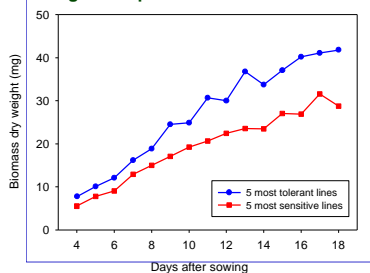
### Conclusions

- 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



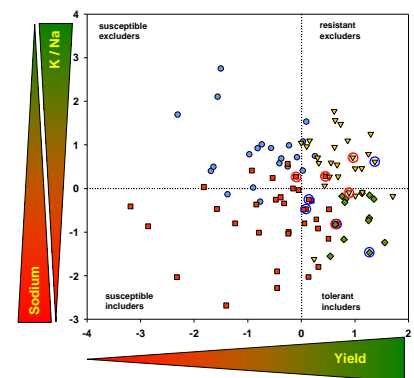
**1+4** Germination under saline conditions was related to QTLs detected on linkage groups 3H and 5H.

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

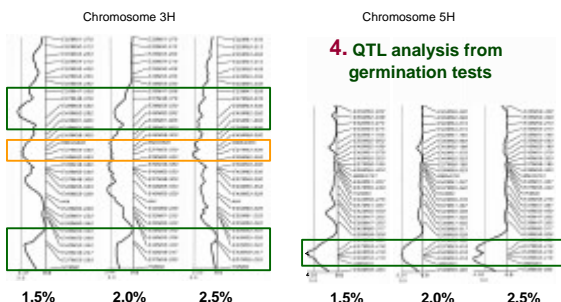
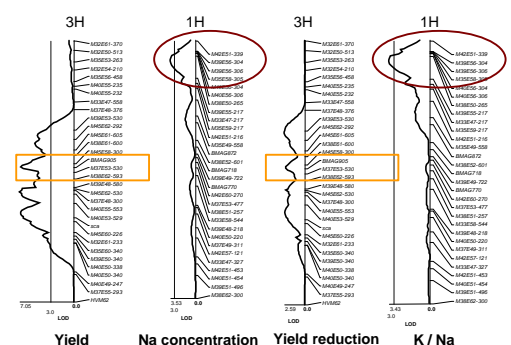
**1+2+3** The 5 best and worst performing lines from germination test, different at seedling stage also under non-stress conditions were found in the groups of tolerant inclusions and resistant excluders.

**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

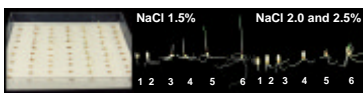
From the mapping population W766, a cross between the winter barley cultivars "Angora" and "W704/137", 95 DH lines and the parents were investigated at germination (climate chamber) and adult plant stage (field). QTL were analysed using the QGENE program (Nelson, 1997).

#### 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



Germination tray      Scoring system



#### Salt tolerance validation – field trial

- Field trial, Herat, Afghanistan, Semi-arid, sown in November
- 2 salt levels (0.6, 6.5 mS<sub>cm</sub><sup>-1</sup>)
- Randomized strip plot design
- Visual and destructive sampling in late vegetative stage (K, Na analyses)
- Yield, yield components at maturity