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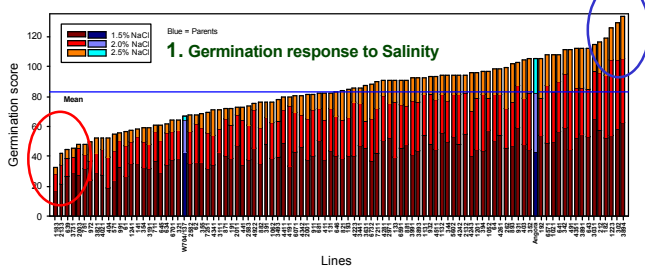
## Introduction

Salinity is among the most serious threats for crop production, especially in regions with unreliable or patchy rainfall patterns. Among the options available to sustain agricultural use of affected areas are genotypes sufficiently resistant to salinity to off-set the farmers' investment and to decrease famine hazards. Since most crops are salt sensitive, detailed knowledge of the traits involved in salinity resistance is imperative to successfully breeding tolerant varieties. The use of molecular trait markers could facilitate this process. Phenotyping of mapping populations under salt stress conditions and calculation of QTLs can detect markers linked to the genes responsible for salinity resistance.

## Conclusions

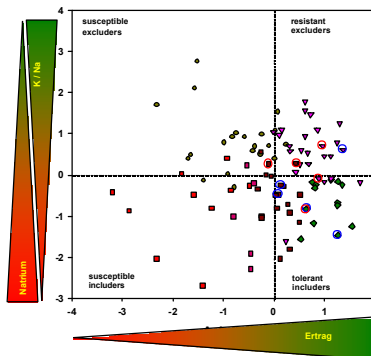
- Germination under saline conditions was related to QTLs
- QTLs originating from germination responses to salinity cannot reliably indicate resistance strategies realized in later development stages
- A QTL related to salt stress on the chromosome 3H present across development stages was related to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

## Results - Summary



1. Germination response to Salinity

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

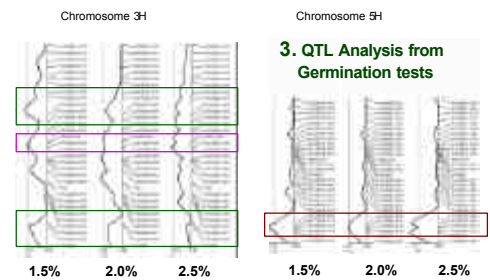


**1+3** Germination under saline conditions was related to QTLs detected on linkage groups 3H and 5H.

**2** PCA on yield components discriminated 4 groups of genotypes within the mapping population, namely tolerant and susceptible in-clusters and susceptible and resistant excluders.

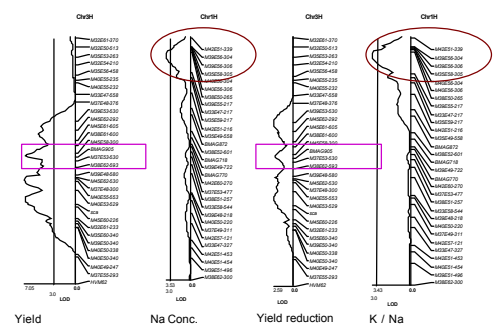
**1+2** The 4 best and the 4 worst performing lines from the germination test were found in the groups of tolerant in-clusters and resistant excluders.

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



3. QTL Analysis from Germination tests

4. QTL Analysis for selected traits from the field trial

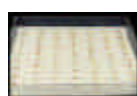


## Materials & Methods

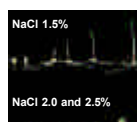
From the mapping population W766, a cross between the winter barley cultivars „Angora“ and „W704/137“, 95 DH lines and the parents were investigated at germination (climate chamber) and adult plant stage (field). QTL were analysed using the QGENE program (Nelson, 1997).

### Germination test – climate chamber

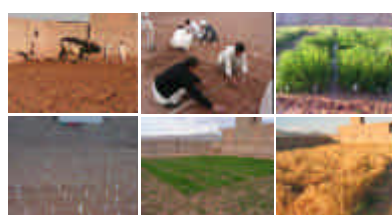
- Germination trays – filter paper
- 4 Salt levels (0, 1.5, 2, 2.5%)
- 10 seeds per treatment and line
- 20°C, 12h Photoperiod, 10 days
- Scoring of germination and seedling growth (Mano et al., 1996)



Germination tray



Scoring system



Field and Phytotron trials

### Salt tolerance validation – field trial

- Field trial, Herat, Afghanistan, Semi-arid, planted 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