

# Molecular mapping of resistance to Fusarium head blight derived from three *Triticum* species

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## INTRODUCTION

Due to yield and quality losses, especially the accumulation of mycotoxins in the grain, *Fusarium* head blight (FHB) remains a serious problem in wheat production. We report here about genetic analysis of FHB resistance derived from three *Triticum* sources: 1) *Triticum macha* (Georgian spelt wheat, 2n=42), 2) *Triticum dicoccum* (cultivated emmer, 2n=28) and 3) *Triticum dicoccoides* (wild emmer, 2n=28). Aim of this work was to unlock novel QTL for diversifying FHB resistance breeding.

## MATERIALS AND METHODS

### Plant material

Population 1: *T. macha* x Furore, 300 BC<sub>2</sub>F<sub>3,4</sub> lines,  
Population 2: *T. dicoccum*-line161 x Helidur, 120 BC<sub>1</sub>F<sub>5</sub> lines  
Population 3: *T. dicoccum*-line 161 x Floradur, 120 BC<sub>1</sub>F<sub>5</sub> lines  
Population 4: *T. dicoccoides* – Mt.Gerizim#36 x Helidur, 105 BC<sub>1</sub>F<sub>5</sub> lines

### Resistance evaluation

Populations 1, 2 and 3 were field evaluated for FHB severity using spray inoculations applying *F. graminearum* or *F. culmorum* conidia suspensions in 7 (or 8) experiments during 4 seasons similarly as described by Buerstmayr et al. (2003). Population 4 was single floret inoculated in one open field and four greenhouse experiments using *F. graminearum* similar to Gladysz et al. (2007).

### Genotyping and QTL mapping

The populations were genetically analysed using genome wide SSR and AFLP markers, linkage maps were constructed using CarthaGène (de Givry et al. 2004) and QTL analysis was done in QGene (Nelson 1997), with simple and composite interval mapping.

## RESULTS AND DISCUSSION

**Table 1:** QTL estimates for mean FHB severity (means over 7 experiments) in **population 1** (*T. macha* x Furore): chromosomal location, logarithm of odds (LOD) and percent of explained variance (VE) by simple interval mapping (SIM).

| Chrom. | Marker interval        | Resistance source | LOD>3 no of exp. | SIM  |    |
|--------|------------------------|-------------------|------------------|------|----|
|        |                        |                   |                  | LOD  | VE |
| 2A     | Xgwm296A - Xs12m14_5   | <i>T. macha</i>   | 6                | 6.2  | 9  |
| 2B     | Xs23m13_10 - Xgwm200   | <i>T. macha</i>   | 4                | 4.3  | 6  |
| 2B     | Xwmc317 - Xs24m19_6    | <i>T. macha</i>   | 7                | 7.9  | 11 |
| 5A     | <i>Q-locus (spelt)</i> | <i>T. macha</i>   | 7                | 18.7 | 25 |
| 5B     | Xs19m14_8 - Xs22m75_1  | <i>T. macha</i>   | 4                | 6.2  | 9  |



*Triticum macha*  
2n = 42

*Triticum dicoccoides*  
Mt.Gerizim#36  
2n=28

*Triticum dicoccum*  
Line 161  
2n=28

**Table 2:** QTL estimates for mean FHB severity (means over 8 experiments) in **population 2** (*T. dicoccum* x Helidur)

| Chrom. | Marker interval | Resistance source  | LOD>2.5 no of exp. | SIM |    |
|--------|-----------------|--------------------|--------------------|-----|----|
|        |                 |                    |                    | LOD | VE |
| 4B     | <i>RhtB1</i>    | <i>T. dicoccum</i> | 6                  | 14  | 41 |

**Table 3:** QTL estimates for mean FHB severity (means over 7 experiments) in **population 3** (*T. dicoccum* x Floradur)

| Chrom. | Marker interval        | Resistance source  | LOD>2.5 no of exp. | SIM |    |
|--------|------------------------|--------------------|--------------------|-----|----|
|        |                        |                    |                    | LOD | VE |
| 3B     | Xgwm493 - Xbarc133     | Floradur           | 4                  | 3.1 | 12 |
| 4B     | <i>RhtB1</i> - Xgwm888 | <i>T. dicoccum</i> | 3                  | 3.4 | 13 |
| 6B     | Xwmc398 - Xwmc397      | <i>T. dicoccum</i> | 2                  | 2.9 | 11 |

**Table 4:** QTL estimates for mean FHB severity (means over 5 experiments) in **population 4** (*T. dicoccoides* x Helidur)

| Chrom. | Marker interval     | Resistance source     | LOD>2.5 no of exp. | SIM |    |
|--------|---------------------|-----------------------|--------------------|-----|----|
|        |                     |                       |                    | LOD | VE |
| 3A     | Xgwm1121 - Xgwm720  | <i>T. dicoccoides</i> | 4                  | 4.8 | 20 |
| 3A     | Xgwm2 - Xgwm779     | <i>T. dicoccoides</i> | 2                  | 4.5 | 15 |
| 6B     | Xs13m24_6 - Xgwm626 | <i>T. dicoccoides</i> | 4                  | 6.4 | 26 |

## Summary

Several novel QTL for FHB resistance were discovered, all *T. macha* derived QTL are reported here for the first time. Interestingly, the largest QTL in *T. macha* appears associated with the *Q-locus* (spelt ear type) on 5A. In *T. dicoccum* a strong association between the semi dwarf allele *RhtB1b* and increased FHB susceptibility was evident, especially in the Helidur derived population. Resistance to fungal spread in *T. dicoccoides* was reproducibly associated with QTL on chromosomes 3A and 6B. The 6B QTL from *T. dicoccum* and *T. dicoccoides* are in a similar chromosomal segment.

## REFERENCES

- Buerstmayr H, Steiner B, Hartl L, Griesser M, Angerer N, Lengauer D, Miedaner T, Schneider B, Lemmens M 2003. Molecular mapping of QTLs for Fusarium head blight resistance in spring wheat. II. Resistance to fungal penetration and spread. *Theor Appl Genet* **107**:503-508
- De Givry S, Bouchez M, Chabrier P, Milan D, Schiex T 2005. Multipopulation integrated genetic and radiated hybrid mapping. *Bioinformatics* **21**:1703-1704
- Gladysz C, Lemmens M, Steiner B, Buerstmayr H 2007. Evaluation and genetic mapping of resistance to Fusarium head blight in *Triticum dicoccoides*. *Isr J Plant Sci* **55**:263-266
- Nelson JC 1997. QGENE: Software for marker-based genomic analysis and breeding. *Mol Breeding* **3**:239-245

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