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

***Maria Buerstmayr*[1], *Karin Huber*[1], *Abdallah Alimari*[1], *Johannes Heckmann*[1], *Peter Jack*[2], *Christopher James*[2], *Marc Lemmens*[1], *Barbara Steiner*[1], *Hermann Buerstmayr*[1,3]**

BOKU-University of Natural Resources
and Applied Life Sciences, Vienna
Department IFA-Tulln, Institute for
Biotechnology in Plant Production
Konrad Lorenz Straße 20, A-3430 Tulln
Austria www.ifa-tulln.ac.at

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 $BC_2F_{3:4}$ lines,
Population 2: *T. dicoccum*-line161 x Helidur, 120 BC_1F_5 lines
Population 3: *T. dicoccum*-line 161 x Floradur, 120 BC_1F_5 lines
Population 4: *T. dicoccoides* – Mt.Gerizim#36 x Helidur, 105 BC_1F_5 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*	*T. macha*	6	6.2	9
2B	*Xs23m13_10 – Xgwm200*	*T. macha*	4	4.3	6
2B	*Xwmc317 - Xs24m19_6*	*T. macha*	7	7.9	11
5A	*Q-locus (spelt)*	*T. macha*	7	18.7	25
5B	*Xs19m14_8 - Xs22m75_1*	*T. macha*	4	6.2	9

ACKNOWLEDGMENTS

This work is financed by the Austrian Science Fund – FWF, project number: 17310-B05.

The research of IFA-Tulln is supported by the Government of Lower Austria

Abdallah Alimari is supported by a North-South Dialogue grant from the Austrian Academic Exchange Service

We gratefully thank **Clare Nelson** (Kansas State Univ.) for his support in mapping with CarthaGène.

We acknowledge **Jeannie Gilbert** (AG Canada, Winnipeg) for supplying the *T. dicoccum* line and **Tzion Fahima** and **Tami Krugman** (Univ. Haifa) for supplying the *T. dicoccoides* line.

We also sincerely acknowledge **Peter Jack** and **Christopher James** (RAGT, Cambridge, UK) for SSR genotyping of the *T. dicoccum* populations

1) Department IFA-Tulln, Austria. 2) RAGT Seeds, Cambridge, UK.
3) Author for correspondence: hermann.buerstmayr@boku.ac.at

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	*RhtB1*	*T. dicoccum*	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	*RhtB1 - Xgwm888*	*T. dicoccum*	3	3.4	13
6B	*Xwmc398 – Xwmc397*	*T. dicoccum*	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	*Xbarc67 – Xgwm779*	*T. dicoccoides*	3	5.6	22
6B	*Xs13m24_6 – Xgwm626*	*T. dicoccoides*	4	6.5	25

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 form *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