

DETECTION OF QTLs LINKED TO FUSARIUM HEAD BLIGHT RESISTANCE IN ROMANIAN WINTER WHEAT

Matilda Ciucă*

ABSTRACT

Fusarium head blight (FHB) is one of the main diseases of wheat in Romania. Breeding for resistance to FHB is the most reliable method to control the field contamination and to reduce the detrimental effects of disease on yield, quality and contamination of kernels. Marker-assisted selection (MAS) is considered as a valuable tool in order to accelerate and increase genetic progress for resistance to FHB in wheat.

Our research was focused on detection of QTLs previously described as associated with resistance to FHB, based on evaluation of polymorphisms identified with specific SSR primers, in winter wheat breeding lines obtained at NARDI Fundulea.

Investigation of sixty lines using the primers for seven SSR markers (Xgwm and Xbarc), located on chromosomes 6B, 3B and 3A, revealed polymorphism possibly associated to FHB resistance in several F201R derivatives, but also in lines, with no known relation with F201R. Further investigations for confirmation of FHB resistance levels in these lines are necessary.

Primers for markers Xgwm 493 and Xgwm 533, located on chromosome 3BS, identified the same electrophoresis pattern with Sumai 3, in only one of 13 winter wheat lines, which had Sumai 3 among their parents.

The information about the presence of markers associated with FHB resistance in lines from the Romanian winter wheat breeding program can be used for pyramiding QTLs to further increase the level of resistance.

Key words: Fusarium head blight, FHB, QTLs, marker-assisted selection-MAS, winter wheat

INTRODUCTION

Fusarium head blight (FHB) is a wheat disease that causes serious yield losses and deteriorated grain quality in Romania. FHB is caused by several fungi from the genus *Fusarium*, among which *Fusarium graminearum* is predominant. As a result of natural occurrence, significant reduction of yield and quality, often associated with mycotoxin (secondary metabolites) contamination of kernels, are registered. Among the mycotoxins produced by pathogen strains of *Fusarium*, the most widespread is deoxynivalenol (DON, vomitoxin), with a harmful effect on humans and animals. DON is a significant factor affecting the food safety on the entire food chain.

Breeding for resistance to FHB is the most reliable method to control the field contamination and to reduce the detrimental effects of disease on yield, quality and contamination of kernels.

Breeding progress for resistance to FHB in wheat is much more difficult, as compared with other pathosystems, because of both the complexity of host resistance and the strong interference with environment. That's why, the

marker-assisted selection (MAS) is considered as a valuable perspective tool in order to accelerate and to increase genetic progress in breeding for resistance to FHB in wheat.

Resistance to FHB is complex, many genes controlling different aspects of the disease, such as resistance to initial infection (type I), resistance to the spread of the disease in the spike (type II) and resistance to the accumulation of mycotoxins such as deoxynivalenol (type III) (Gilbert and Tekauz, 2000; Somers et al., 2005).

Only few cultivars have been identified to have a relatively high level of FHB resistance (Buerstmayr et al., 2002; Saur, 1991; Shen et al., 2003; Snijders, 1990; Yang et al., 2005). These include the Chinese cultivar Sumai 3, the Brazilian Frontana, the Romanian F201R, and the Korean Chokwang.

Several research groups have identified a common set of FHB resistance QTLs in different crosses and genetic backgrounds (Anderson et al., 2001; Buerstmayr et al., 2002; Somers et al., 2003). Although, each identified QTL appears to explain only small amounts of the variation in infection, the effects appear to be additive. As a result, it seems essential to select for multiple genes in order to provide a sufficient level of resistance to FHB in wheat (Somers et al., 2003; Yang et al., 2003).

Our research was focused on detection of QTLs, previously described as associated with FHB resistance, in several winter wheat breeding lines obtained at NARDI Fundulea, through evaluation of polymorphism evidenced with specific SSR primers.

MATERIAL AND METHODS

Genotypes: 60 winter bread-wheat Romanian breeding lines, obtained at the National Agricultural Research & Development Institute Fundulea, were analyzed. The lines were selected from crosses involving F201R or Sumai 3, or showed various levels of FHB resistance in tests performed by M. Ittu in the Wheat Breeding Laboratory field.

* National Agricultural Research and Development Institute Fundulea, 915200 Fundulea, Călărași County, Romania
contact address: matilda72001@yahoo.co.uk

DNA isolation

Total DNA was isolated from leaves following the protocol proposed by Doyle & Doyle (1991).

SSR analysis

PCR reaction was performed in 384 plates, containing 10 µl of a reaction mixture consisting of 1X buffer, 1,5 mM MgCl₂, 0,2 µM primer (SSR primer pairs developed by Röder et al. (1998) and Xbarc primer pairs developed by P. Cregan, Q. Song and associates - <http://wheat.pw.usda.gov/cgi-bin/graingenes>), 0,4U of Taq polymerase, 0,2 mM each dNTP and 20 ng of genomic DNA. The reaction mixture was denaturized at 94°C for 3 min.; followed by 35 cycles, each consisting of: 1 min. at 94°C, 1 min. at different annealing temperature (50°C, 55°C, 60°C), 2 min. at 72°C and a final extension step of 72°C for 10 min.

The polymorphism was revealed with LICOR system on 6% polyacrilamide gels, during our stay in IFA –Tulln, Austria.

RESULTS AND DISCUSSION

The lines and cultivars were screened with 30 microsatellites distributed across the genome, but only a few gave polymorphism and are presented here (Table 1).

The first group of microsatellites targeted the Sumai 3 resistance genes. A major QTL for Fusarium head blight (FHB) resistance, *Qfhs.ndsu-3BS*, derived from 'Sumai 3', which explained a large portion (25–60%) of the variation in FHB resistance, has been identified and verified by several research groups via molecular marker analysis (Liu et al., 2003).

Primer pairs for two microsatellite primers (Xgwm 493 and Xgwm 533), previously described as linked with the FHB resistance QTL on *3BS* (Anderson et al., 2001; Buerstmayr et al., 2002), were used to screen for polymorphism in lines derived from crosses with Sumai 3. Out of 13 lines derived from Sumai 3 (Table 1), only one line F 488 T1-01 presented the polymorphism linked to FHB resistance QTL, for both microsatellite markers (Figure 1).

This suggests that selecting for other traits followed in the winter wheat breeding program, without simultaneous selection for the presence of Sumai 3 FHB resistance gene *Qfhs.ndsu-3BS*, preferentially eliminated this gene.

The Romanian winter wheat line, Fundulea 201R (F 201R), was reported as having FHB resistance genes cumulated from cultivars NS732, Amigo and possibly other parents involved in its complex genealogy. It has no relation to any of previously described sources of resistance (Ittu et al., 2001). Shen et al. (2003) found four interval regions, located on chromosomes *1B*, *3A*, *3D*, and *5A* that conferred resistance to FHB in F 201R. The QTLs located on chromosomes *1B* and *3A*, contributed by F 201R, had large effects and were consistently expressed in three environments. The QTL that was located on the short arm of chromosome *3A*, near the centromere explained 13% of the phenotypic variation and was tightly linked to markers Xgwm 674 and Xbarc 67, which are 2.8 cM apart (Shen et al., 2003).

We evaluated F 201R and 15 lines obtained from crosses between F 201R and other Romanian winter wheat genotypes (Table 1), for polymorphism, using one pair of SSR primers previously described by Shen et al. (2003), for the marker Xbarc 67 on chromosome *3AS*. Our analyses with Xbarc 67 showed polymorphism in 10 lines, out of which 7 lines were derived from crosses with F 201R, while in three lines the origin of resistance to FHB could not be traced back to this line. This suggests that the FHB resistance QTL linked with Xbarc 67 might be widespread in the Romanian breeding germplasm.

Similar results were obtained in most lines with primers for SSR marker Xbarc19 located on *3A* chromosome, close to Xbarc 67 marker. We found polymorphism for this marker both in lines derived and not derived from F 201R (Figures 2 and 3). Further research should compare the reliability of markers Xbarc 19 and Xbarc 67 for the FHB resistance QTL on chromosome *3A*.

The marker Xgwm 508, located on chromosome *6B* identified polymorphism in Sumai3 and in 2 lines for which the source of resistance is not known. Further research should investigate the usefulness of this marker for FHB resistance.

The information about the presence of markers associated with FHB resistance in lines from the Romanian winter wheat breeding program can be used for pyramiding QTLs to further increase the level of resistance.

1	2	3	4	5	6	7	8	9	10
45	F00356 G8-104	Unknown	-	-	-	-	-	-	-
46	F00399G2-11	Unknown	-	-	-	-	-	+H	-
47	F00628 G34-1	Unknown	+	-	-	-	-	+!	+!
48	F01156 G3-1	Unknown	-	-	-	-	-	-	-
49	F01400 G1-2	Unknown	-	-	-	-	-	+!	+!
50	F01429 G4-1	Unknown	-	-	-	-	-	+!	+!
51	F01461 G3-2	Unknown	-	-	-	-	-	+!	+!
52	F01459 G4-1	Unknown	-	-	-	-	-	+!	+!
53	F02083 GP-3	Unknown	-	-	-	-	-	-	-
54	F02122 GP1	Unknown	-	-	-	-	-	-	-
55	F02211 G2-1	Unknown	-	-	-	+!	-	-	-
56	F96831 G6-1001	Unknown	-	-	-	-	-	-	-
57	F98039 G5-10INC-1	Unknown	-	-	-	-	-	-	-
58	F99051 G3-3INC2	Unknown	-	-	-	-	-	-	-
59	F99146 G1-101	Unknown	-	-	-	-	-	-	-
60	F99419 G4-1A1 1-1	Unknown	-	-	-	-	-	-	-

Note:

Polymorphism linked to FHB resistance:	Symbol:
- present;	+
- absent	-
- present, genotype heterozygote	+H
- polymorphism, other position	+ ?
- present, resistance source not Sumai 3 or F 201R	+!
- present, polymorphism different from Sumai 3	-/+

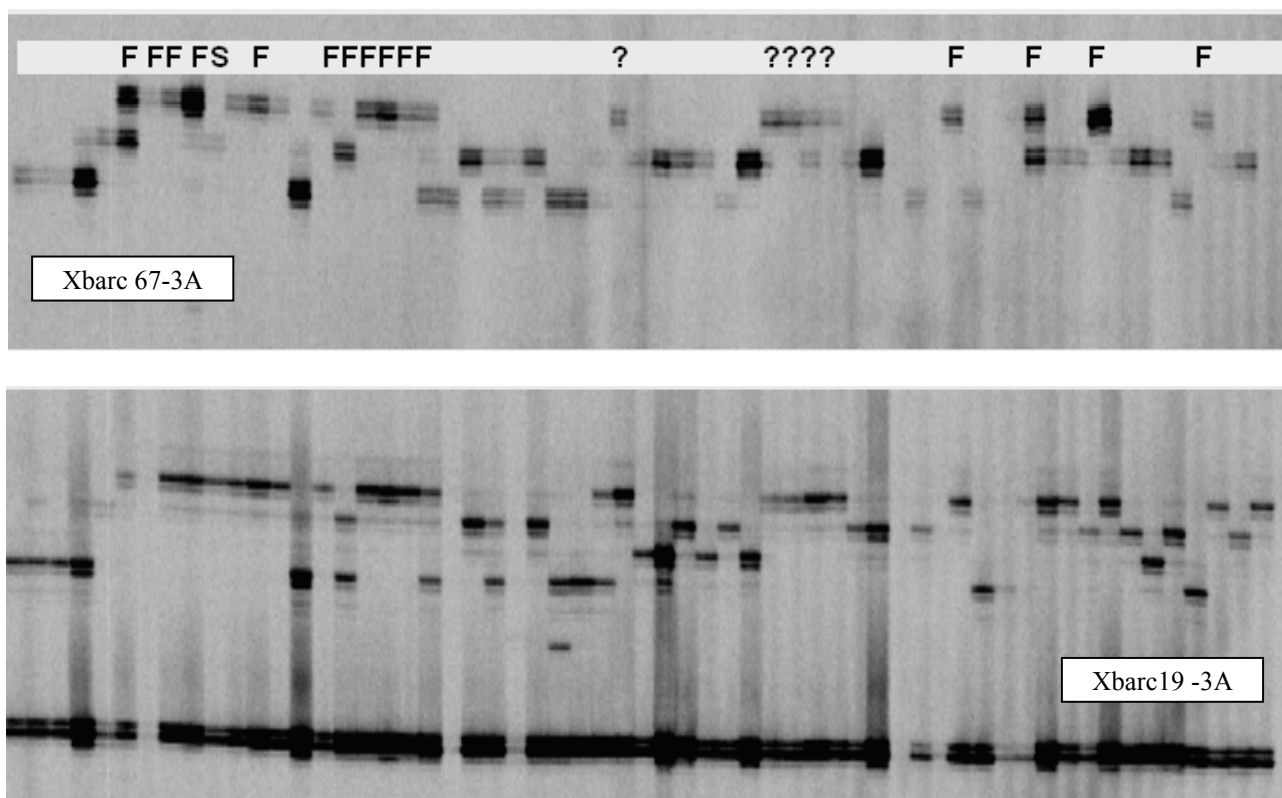


Figure 1. Electrophoresis pattern obtained with primers for microsatellite markers Xbarc 67 and Xbarc 19: F-F 201R and progenies; S- Sumai 3; ?- source unknown.

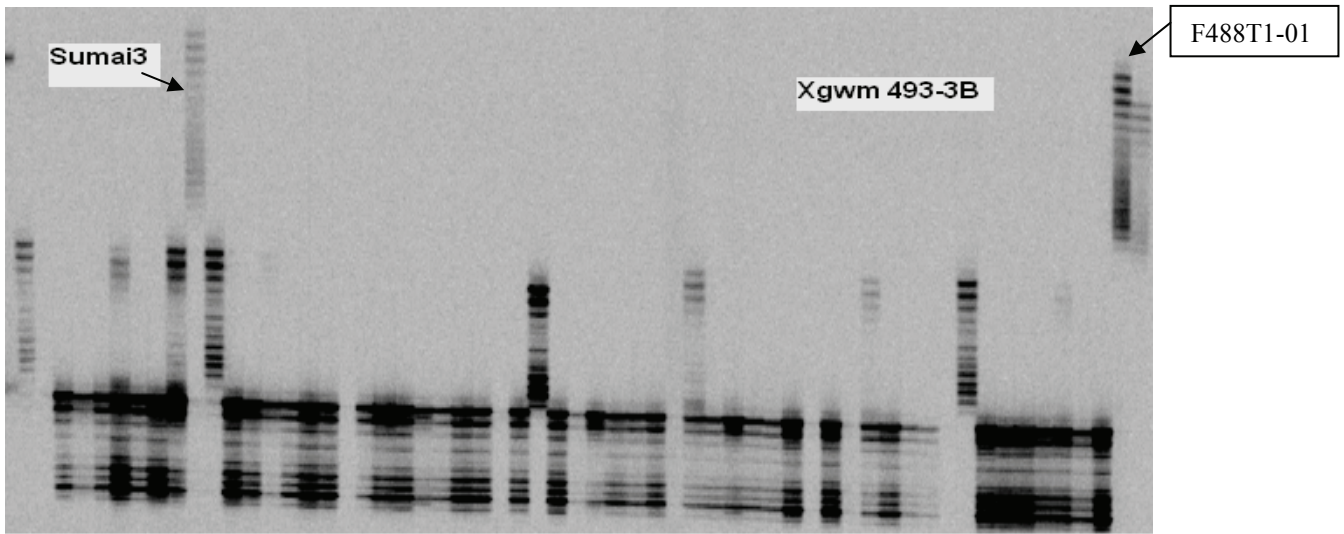


Figure 2. Electrophoresis pattern obtained with SSR primers for Xgwm 493

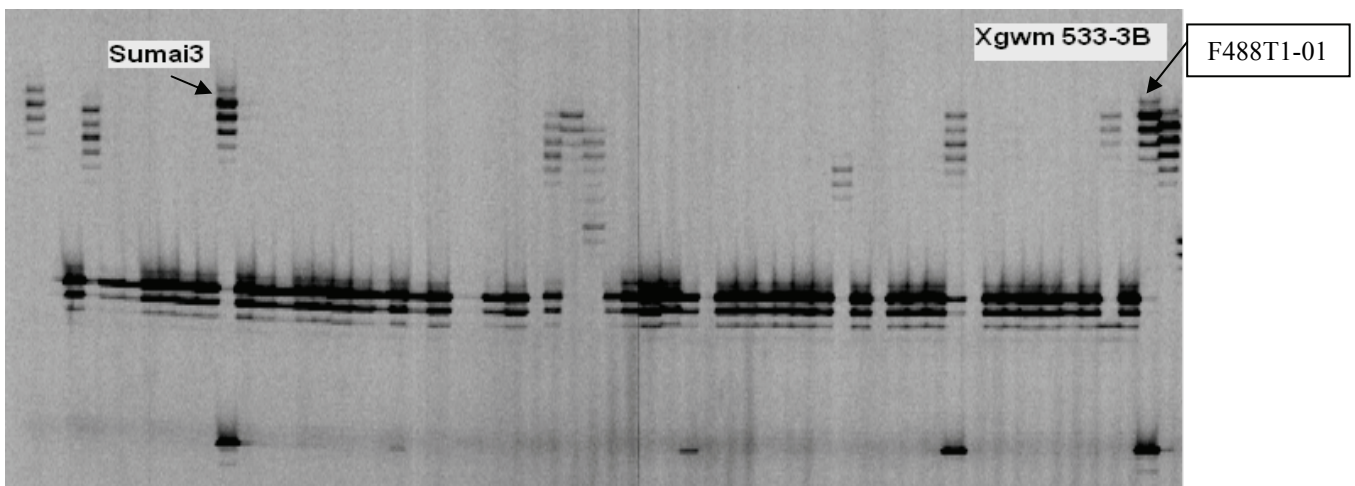


Figure 3. Electrophoresis pattern obtained with SSR primers for Xgwm 533

REFERENCES

- Anderson, J.A., Stack, R.W., Liu, S., Waldron, B.L., Field, A.D., Coyne, C., Moreno-Sevilla, B., Mitchell Fetch, J., Song, Q.J., Cregan, P.B., Froberg, R.C., 2001. DNA markers for Fusarium head blight resistance QTL in two wheat populations. *Theor. Appl. Genet* 102:1164-1168.
- Buerstmayr, H., Lemmens, M., Hartl, L., Doldi, L., Steiner, B., Stierschneider, M., Ruckebauer, P. (2002). Molecular mapping of QTLs for Fusarium head blight resistance in spring wheat. I. Resistance to fungal spread (Type II resistance). *Theor. Appl. Genet* 104:84-91.
- Doyle, J.J., Doyle, J.L., 1991. Isolation of plant DNA from fresh tissue. *Focus* 12, No.1: 13-15.
- Gilbert, J., Tekauz, A., 2000. Review: recent developments in research on Fusarium head blight in Canada. *Can. J. Plant Path* 22:1-8.
- Ittu, M., Săulescu, N.N., Ittu, G., 2001. Progress in breeding for scab resistance in Romania on wheat. 183-187. In National Fusarium Head Blight Forum Proceedings, Cincinnati. 10-12 Dec. 2000.
- Liu, S., Anderson, J.A., 2003. Marker assisted evaluation of Fusarium head blight resistant wheat germplasm. *Crop Science* 43:760-76
- Röder, M. S., Korzun, V., Wendehake, K., Plaschke, J., Tixier, M. H., Leroy, P., and Ganal, M. W., 1998. A microsatellite map of wheat. *Genetics* 149: 2007-2023.
- Saur, L., 1991. Sources of resistance to head blight caused by *Fusarium culmorum* in bread wheat and relative species. *Agronomie* 11:535-541.
- Shen, X., Ittu, M., Ohm W.H., 2003. Quantitative trait loci conditioning resistance to Fusarium Head Blight in wheat line F 201R. *Crop Science* 43: 850-857.
- Snijders, C.H.A., 1990. Genetic variation for resistance to Fusarium head blight in bread wheat. *Euphytica* 50:171-179.
- Somers, D. J., Fedak, G., Savard, M., 2003. Molecular mapping of novel genes controlling Fusarium head blight resistance and deoxynivalenol accumulation in spring wheat. *Genome* 46: 555-564.
- Somers, D. J., Thomas, J., DePauw, R., Fox S., Humphreys, G., Fedak, G., 2005. Assembling complex genotypes to resist Fusarium in wheat (*Triticum aestivum* L.). *Theor. Appl. Genet* 111: 1623-1631.
- Yang, Z.-P., Gilbert, J., Somers, D.J., Fedak, G., Procnier, J.D., McKenzie, R., 2003. Marker-assisted selection of Fusarium head blight resistance genes in two doubled-haploid populations of wheat. *Mol. Breeding* 12 (4):309-317
- Yang, J., Bai, G., Shaner, E.G., 2005. Novel quantitative trait loci (QTL) for Fusarium head blight resistance in wheat cultivar Chokwang. *Theor. Appl. Genet* 111: 1571-1579.

Acknowledgements. This work is part of the project Biotech 4545/ 2004-2006, founded by The National Center for Programs Management - Romania. We gratefully acknowledge Dr. Hanne ØSTERGÅRD, Risø National Laboratory, Denmark, Dr. Maria Finckh, University of Kassel, Germany, coordinators of COST Action 860 for the received funds and Prof. Hermann Buerstmayr from Institute for Plant Biotechnology-IFA Tulln, Austria, for the perfect organization, guidance and support of the STSM, carried in January 2006. Also, the author wishes to express thanks to the Wheat Breeding team of NARDI Fundulea for providing the lines analyzed in this work and information, and to Dr. Mariana Ittu for all support and constructive comments.