Validation and Marker Assisted Selection of Three QTL Conditioning Fusarium Head Blight Resistance in Wheat

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Outline

- Introduction
- Materials & Methods
- Results
- Discussions


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Constraints that Greatly Limit the Development of Resistant Varieties

- Poorly adapted and partially resistant germplasm
- Multiple components of resistance
- Laborious and lack of cost effective selection system
- Confounding environmental effects

Breeding Constrains: resistance complexity

- Type I: Resistance to initial infection
- Type II: Resistance to spread of infection within a spike
- Type III: decomposition or non-accumulation of mycotoxin
- Schroeder & Christensen, 1963; Wang & Miller, 1988; Mesterhazy, 1995)

Disease Screening is Laborious and Costly Using Conventional Methods

MAS for FHB Resistance

- **MAS may be an alternative selection system for FHB resistance.**
- **Extensive efforts have been made previously to map QTL for type II resistance; but little is known about the significance and genetic control of other types of resistance.**
- **Over 18 chromosome regions have been reported; but few have been validated.**
- **Two QTL on 3BS and 5AS have large effect and are stable in several known resistance sources.**
- **One QTL on 3AS has a large effect in durum wheat (Chen et al., 2006), and in Frontana (Steiner et al., 2004) and in F201wheat (Shen et al., 2003).**
- **Little is known about the effectiveness of MAS of the three QTL in adapted backgrounds.**

Objectives of Current Study

- Validate and characterize the three QTLs for type I, type II, and type III resistance
- Elucidate the potential use of MAS for the three QTL in adapted backgrounds

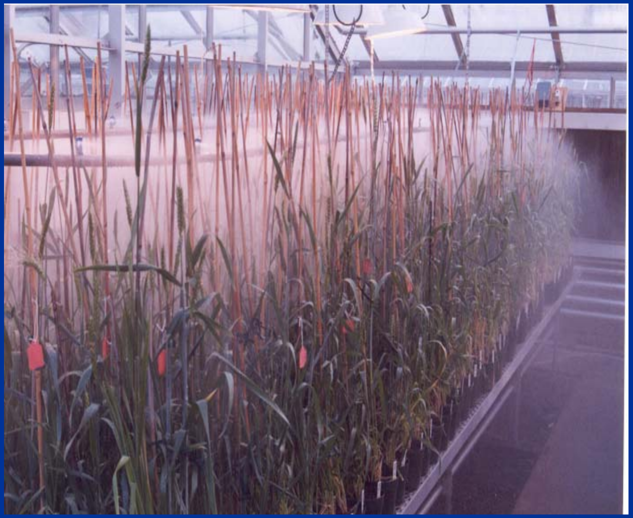
Materials & Methods

- Experiment I
  - 96 Doubled haploid lines derived from a cross between W14 and Pioneer2684
  - Two GH tests (2001 & 02) – floret inoculation
  - One field test (2004) – spraying inoculation

Materials & Methods

- Experiment II
  - Sixty SRW wheat lines
  - These lines were developed by a combination of top-crossing, backcrossing, and doubled haploid breeding methods
  - Two GH tests (severity) and two field tests (incidence, severity, and DON)

Floret Inoculation - Greenhouse



FHB Severity (%) – Type II resistance

At 21st day after inoculation

Measurement of DON content

↓

Shimadzu QP2010 GC/MS system

Spray-Inoculation: Field

FHB Incidence (%) – Type I resistance

FHB Severity (%) – Type I & II resistance

DON Content – Type III resistance

Data Analysis

- Linkage analysis - Mapmaker 3.0a, Lander et al., 1987
- QTL analysis – QTL Cartographer, Wang et al., 2004
  - Composite interval mapping (CIM)
  - A QTL was declared significant when LOD > 2.2
  - LOD (logarithm of odds) threshold was determined by permutation
- Regression Analysis (SPSS, $p < 0.05$)
- Homogeneous analysis-Duncan test

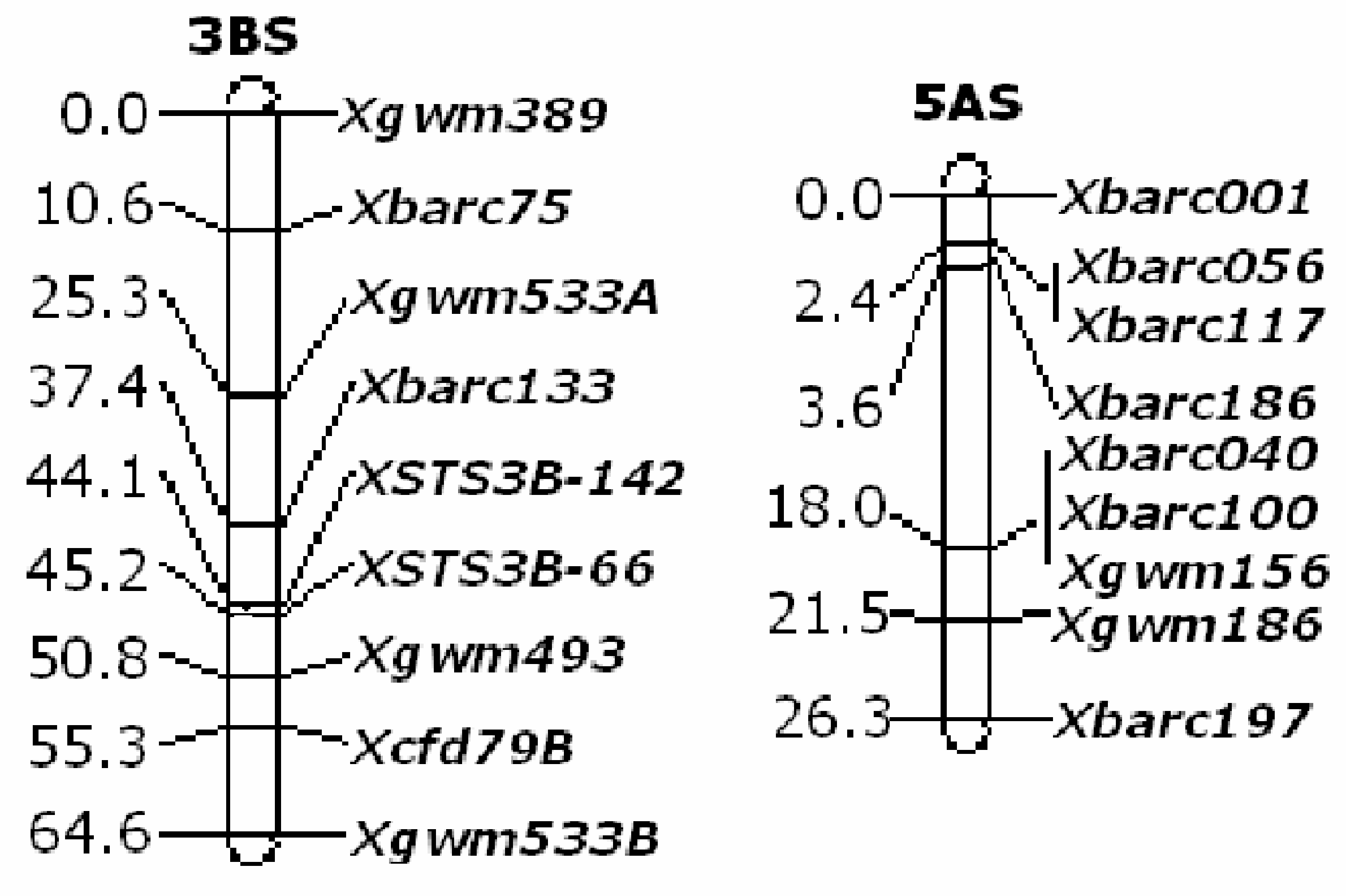
Results & Discussions

- Validation of the three QTL in the first population
- Genetic characterization of the three QTL in the two populations
- Strategy for MAS of the three QTL

Marker Validation – 23 SSR + 2 STS

3BS	5AS	3AS
gwm389	barc001	barc045
barc075	barc117	gwm002
gwm533	barc056	gwm032
barc133	barc186	gwm674
STS3B142	barc040	barc019
STS3B66	barc100	barc067
gwm493	gwm156	wmc428
cfd079	barc186	wmc264
	barc197	
Liu et al., 2006; Chen et al., 2006	Hermann et al., 2004; Chen et al., 2006	Shen et al., 2003; Somers, et al., 2005; Chen et al., 2006

Fig.1. Genetic Maps of W14



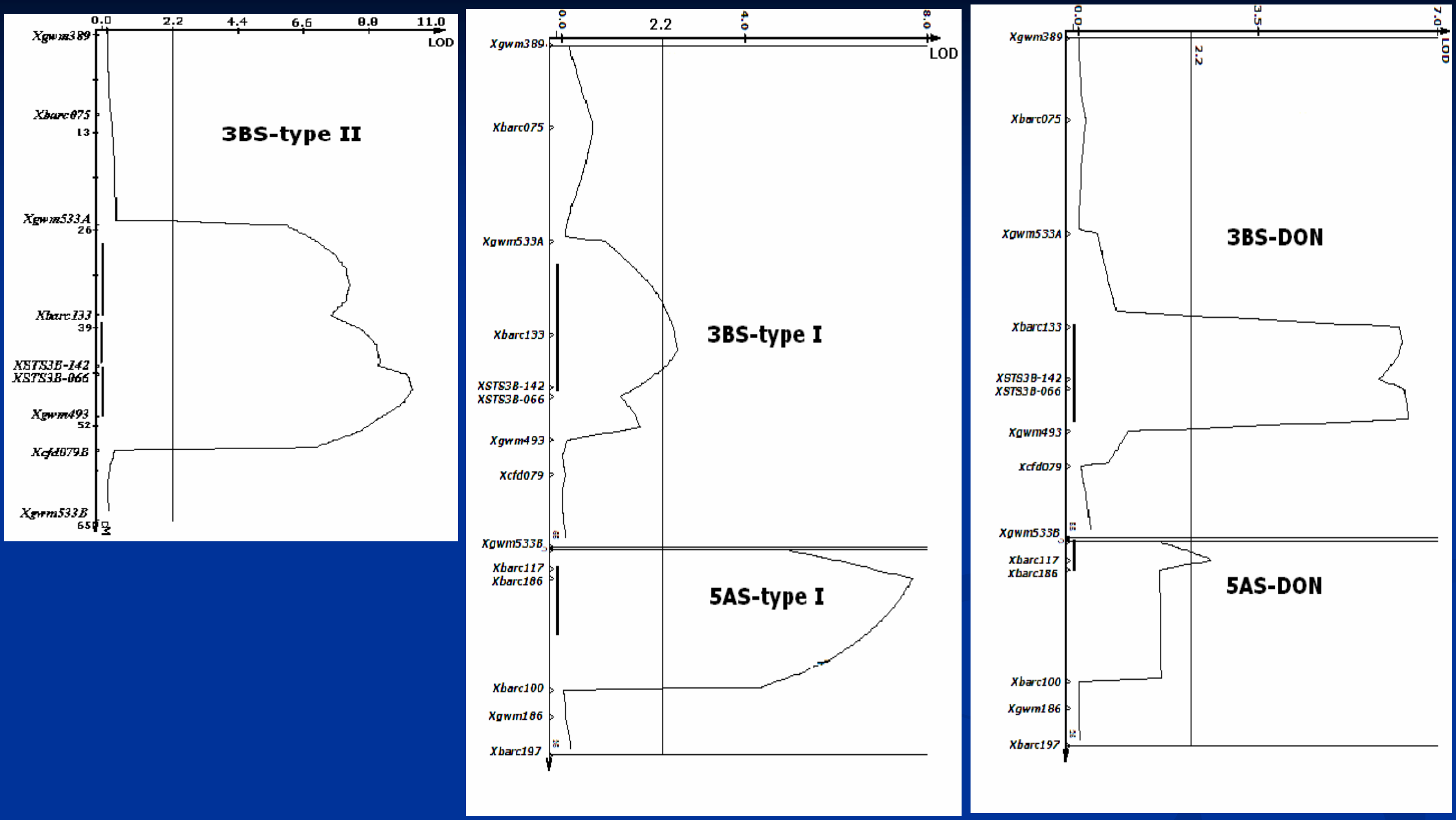


Fig. 2. Likelihood map for type I, II and III resistance QTL

Table 3. Putative QTL for type I, II, and III

QTL-markers		Type I		Type II		Type III	
QTL	Closest marker	LOD	R^2	LOD	R^2	LOD	R^2
3BS	Xgwm533A			7.1	0.28		
3BS	Xbarc133	2.5	0.09	7.3	0.26	6.3	0.24
3BS	XSTS142	1.7	0.06	7.8	0.28	6.4	0.24
5AS	Xbarc117	7.7	0.29			2.6	0.09

Table 4. Homogeneous analysis among four haplotypes of two QTL for type I, II, and III resistance in DH population.

	Haplotypes			Mean Data			
	3BS	5AS	No. of	Greenhouse, 2001&02		Field, 2004	
	M1,M2	M1	Lines	II	III	I	I & II
1	+	+	24	14.5a	2.8a	43.9a	10.9a
2	+	-	22	17.1a	3.9a	65.9bc	15.3bc
3	-	+	15	24.8b	15.2a	53.7ab	14.2ab
4	-	-	15	41.3c	56.3c	78.2c	20.1c

A to c represents homogeneous subsets conducted by Duncan test at $p < 0.05$.

Marker Validation – 23 SSR + 2 STS

3BS	5AS	3AS
gwm389	barc001	barc045
barc075	barc117	gwm002
gwm533	barc056	gwm032
barc133	barc186	gwm674
STS3B142	barc040	barc019
STS3B66	barc100	barc067
gwm493	gwm156	wmc428
cfd079	barc186	wmc264
	barc197	

Table 1. Comparison of Coefficients of Determination (R^2 x 100) of three QTL on three components of FHB resistance in two populations (A and B)

QTL	FHB Field Incidence (%)		FHB Field Severity (%)		FHB DON Content (ppm)		FHB Greenhouse Severity (%)	
	A	B	A	B	A	B	A	B
3BS	10.0	23.8	17.4	26.8	26.5	-	40.5	5.0
5AS	31.6	21.0	16.5	14.4	8.5	-	-	5.5
3AS	-	29.2	-	18.5	-	-	-	4.9
All markers	42.9	52.2	33.5	42.4	36.3	-	43.5	10.9

3BS: Barc133, STS3B-142; 5AS: Barc117, Barc186; 3AS: Wmc428, WMC264

MAS of Three Components of FHB Resistance – Experiment II

QTL	No. of Lines	Type I Field Incidence (%)	Type I & II Field Severity (%)	Type III Field DON (ppm)	Type II Greenhouse Severity (%)
3BS+3AS +5AS	**11**	**46 a**	**14.8 a**	**1.0 a**	**9.1 a**
3BS	**7**	**64 b**	**21.0 b**	**1.1 ab**	**13.1 ab**
5AS	**8**	**64 b**	**23.6 bc**	**1.2 ab**	**14.9 b**
3AS	**5**	**47 a**	**19.9 b**	**1.1 ab**	**19.6 c**
none	29	**78 c**	**27.6 c**	**1.7 b**	**13.7 b**

Elite Lines with One to Three QTL in VT Wheat Breeding Program

QTL	Lines
3BS+3AS+5AS	VA04W-389, VA04W-628, VA04W-631
3BS +5AS	VA04W-433
3AS + 3BS	VA02W-555, Massey, VA01W-476
3BS	VA04W-563, VA04W-592
5AS	VA04W-474, VA00W-38
3AS	VA04W-515
none	VA02W-713, VA04W-439

Summary Remarks

- This study targeted three main components of FHB resistance through validation and MAS of three major QTL on 3BS, 5AS, and 3AS chromosome regions.
- The 3BS QTL is a major one having larger effect than the 5AS and 3AS QTL for type I, II, and III (DON) resistance.
- Pyramiding of 3BS with 5AS and 3AS would improve overall FHB resistance.

Remarks cont.,

- **Ideal haplotype of the three QTL is comprised of six favorable marker alleles, two on 3BS (barc133 & STS142), two on 5AS (barc117 & barc186), and two on 3AS (wmc428 & wmc264).**
- **Elite lines having desirable marker haplotype will provide breeding programs with a source of unique and adapted FHB resistant parents and some of the lines also may have potential for release as cultivars.**

Ongoing Research Applications

Marker-assisted breeding for improved FHB resistance in VT wheat breeding program

- Parental profiling of multiple FHB resistance QTL in addition to 3AS, 3BS, and 5AS
- Early generation selection of multiple QTL
- Haplotyping of various QTL in advanced lines

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