A Novel FHB-Resistance QTL with Uncertain Origin and its Introgression into Durum and Hard Red Spring Wheat

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Tetraploid wheat (*Triticum turgidum* L.) germplasm collections other than durum wheat

Sub species	No. of accessions	
	NSGC†	Received
T. turgidum ssp. *carthlicum*	97	93
T. turgidum ssp. *dicoccoides*	928	880
T. turgidum ssp. *dicoccum*	620	528
T. turgidum ssp. *paleocolchicum*	4	3
T. turgidum ssp. *polonicum*	80	77
T. turgidum ssp. *turanicum*	107	79
T. turgidum ssp. *turgidum*	457	453
Total	2,293	2,113

† USDA National Small Grains Collection (http://www.ars-grin.gov/cgi-bin/npgs/html/taxon.pl?410371)

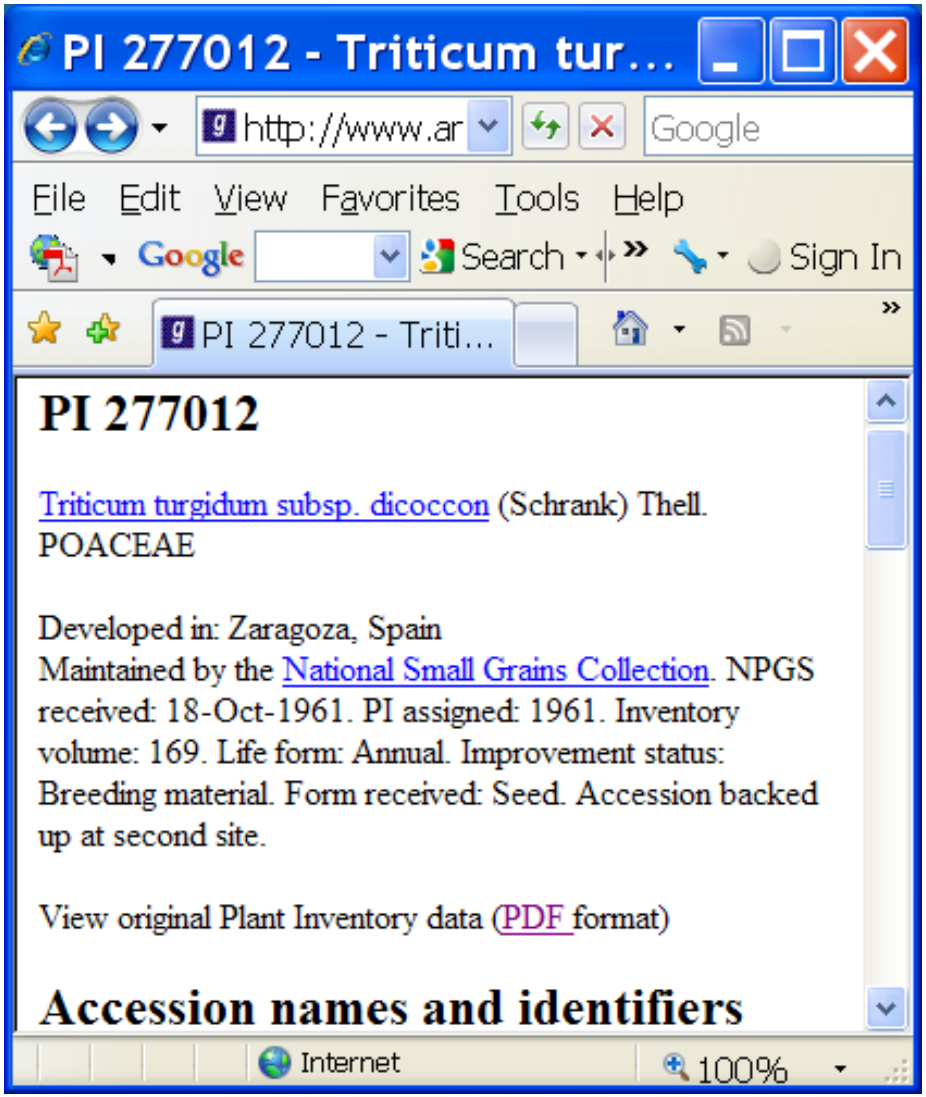
Reaction of "*T. turgidum* ssp. *dicoccum*" PI 277012 to FHB in greenhouse, 2008

Field Evaluation (Fargo, ND, 2010)

PI 277012

Sumai 3

Grandin


PI 277012 - Triticum tur...
http://www.ar
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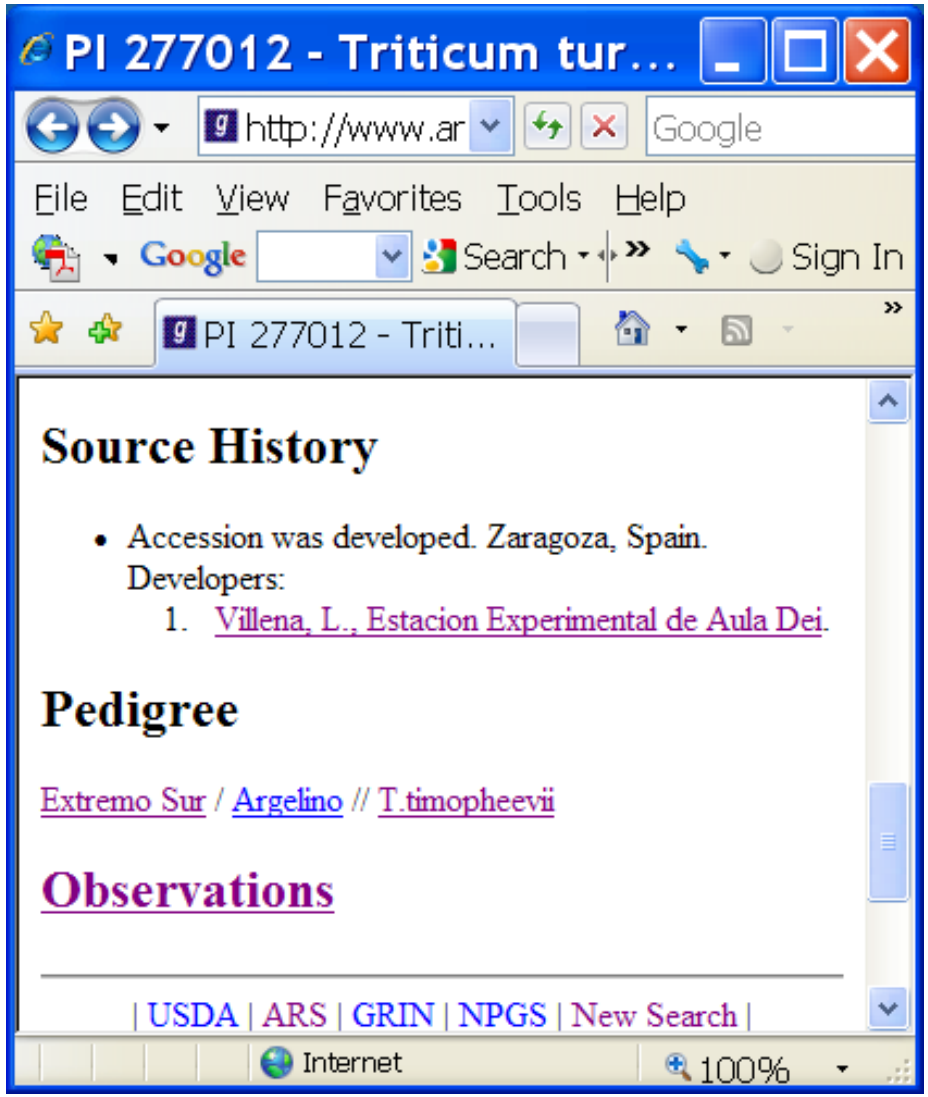
PI 277012 - Triti...
PI 277012
Triticum turgidum subsp. dicoccon (Schrank) Thell.
POACEAE
Developed in: Zaragoza, Spain
Maintained by the National Small Grains Collection. NPGS received: 18-Oct-1961. PI assigned: 1961. Inventory volume: 169. Life form: Annual. Improvement status: Breeding material. Form received: Seed. Accession backed up at second site.
View original Plant Inventory data (PDF format)
Accession names and identifiers
Internet
100%


PI 277012 - Triticum tur...
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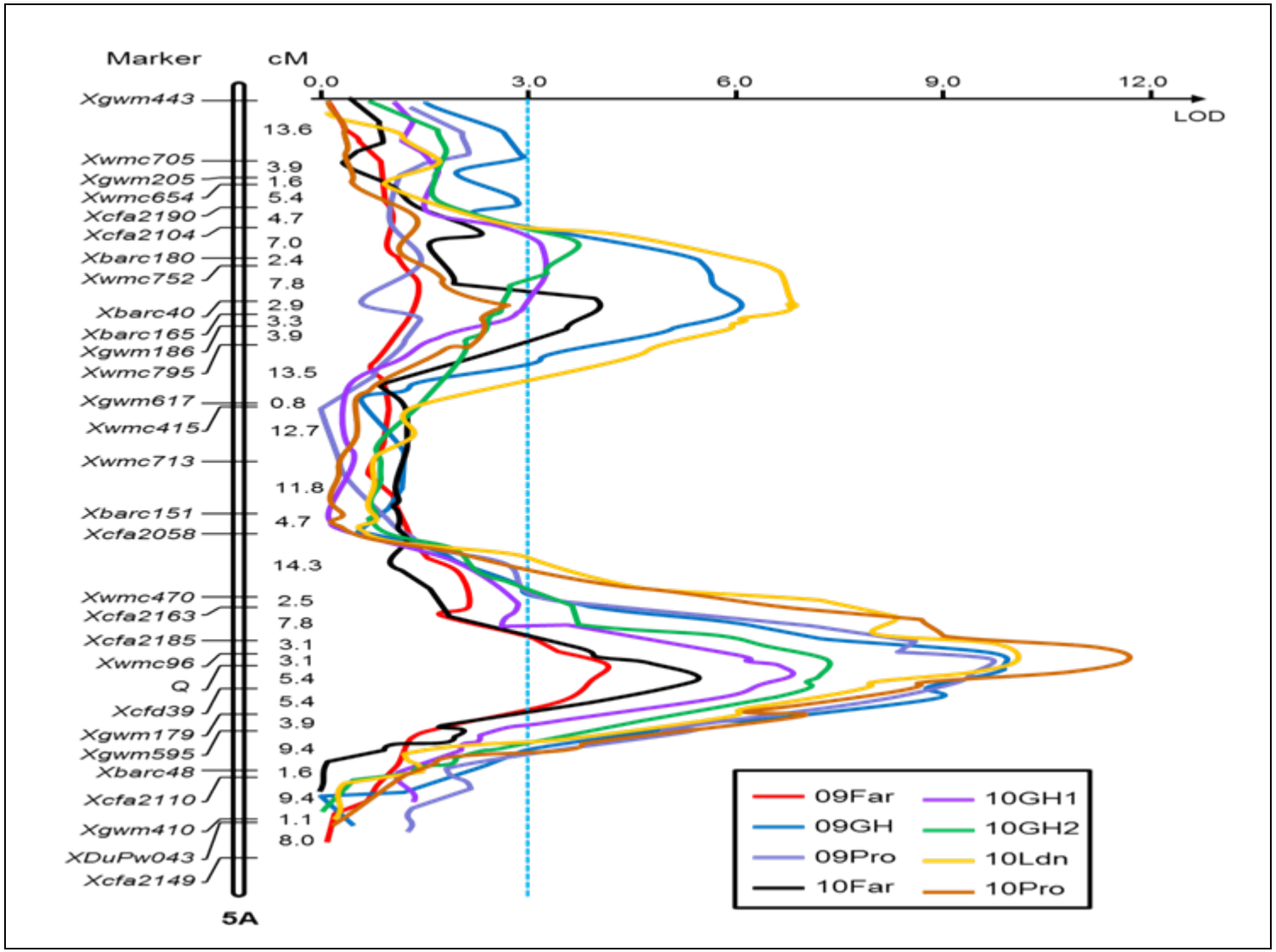
Source History
Accession was developed. Zaragoza, Spain.
Developers:
1. Villena, L., Estacion Experimental de Aula Dei.
Pedigree
Extremo Sur / Argelino // T.timopheevii
Observations
| USDA | ARS | GRIN | NPGS | New Search |
Internet
100%

Spike morphology of *T. turgidum* ssp. *dicoccum*

PI 298578 PI 254189 PI 355474 PI 190932 PI 276000 PI 352361 PI 276021 PI 330544 PI 352341 PI 355472 PI 355471 PI 277012

PI 277012 - Cytogenetic and genetic characteristics

- Somatic chromosome count: $2n = 42$
- HMW glutenin subunits: 1Dx2+1Dy12
- Chromosome pairing in F_1 hybrid with hard red spring wheat 'Grandin': 0.03 IV + 16.97 II (ring) + 3.34 II (rod) + 1.38 I (29 cells)
- Genomic *in situ* hybridization: *T. timopheevii* G-genome chromosome or large segments were not detected.
- Haplotype analysis: Not carry *Fhb1*



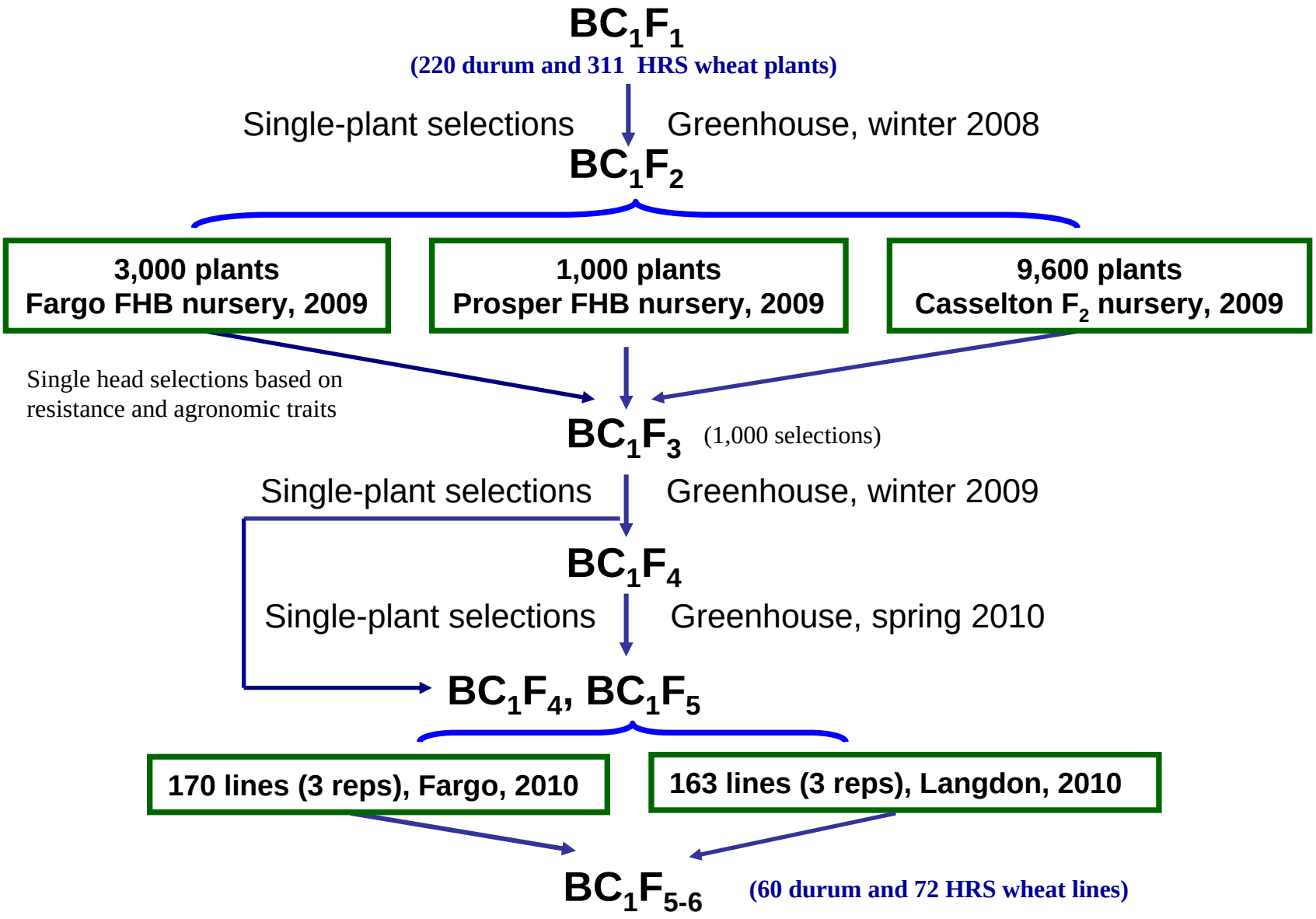
Two FHB resistance QTLs identified on chromosome 5AS and 5AL based on 130 doubled haploids from the cross between PI 277012 and 'Grandin'.

Double haploid (DH) and backcross populations from crosses between PI277012 and hard red spring (HRS) wheat cultivars

Pedigree	Generation	No. of plants
Grandin/PI277012//Grandin	BC_1F_1	69
Glenn/PI277012//Howard	F_1	50
Reeder/PI277012//Reeder	BC_1F_1	66
Reeder/PI277012//Russ	F_1	15
Russ/PI277012//Russ	BC_1F_1	111
Total		311

Backcrosses and three-way crosses between PI277012 and ND durum wheat cultivars

Pedigree	Generation	No. of Plants
Ben/PI 277012//Ben	BC_1F_1	34
Ben/PI 277012//Maier	F_1	11
Divide/PI 277012//Divide	BC_1F_1	39
Divide/PI 277012//Ben	F_1	10
Lebsock/PI 277012//Lebsock	BC_1F_1	42
Lebsock/PI 277012//Ben	F_1	13
Mountrail/PI 277012//Alkabo	F_1	14
Mountrail/PI 277012//Ben	F_1	9
Mountrail/PI 277012//Divide	F_1	11
Mountrail/PI 277012//Maier	F_1	15
Mountrail/PI 277012//Lebsock	F_1	22
Total		220



(Marker genotyping, disease evaluations, 2nd round introgression, winter 2010)

Introgression of FHB resistance from PI 277012 to durum and spring wheat

Reeder/P12//Reeder (BC_1F_5) Russ/P12//Russ (BC_1F_5) Divide/P12//Divide (BC_1F_3)

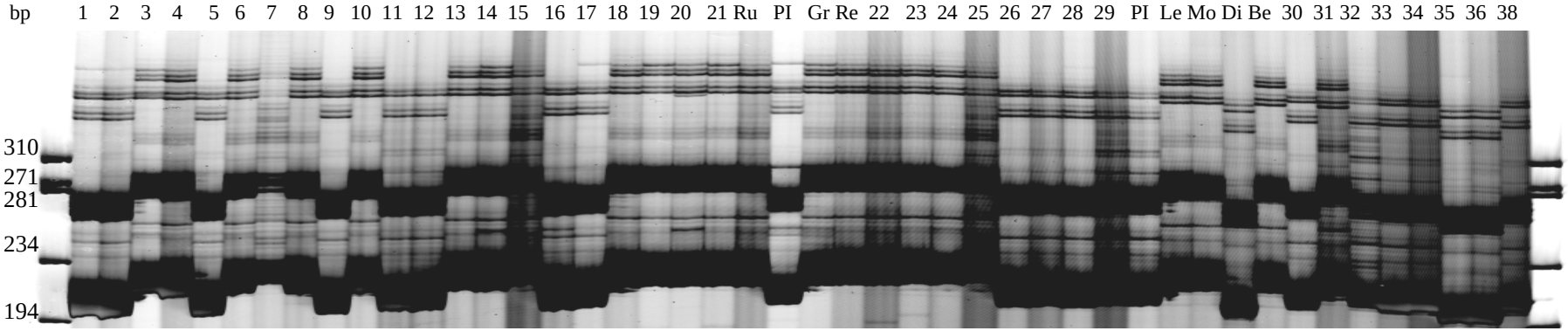
Russ/PI 277012//Russ (BC_1F_5) **Russ**

Mountrail/PI 277012//Divide (F_4) **Divide**

Markers analyzed in BC_1F_{5-6} lines from backcrosses of PI 277012 (PI) with durum wheat (DW) and HRS wheat (SW) cultivars.

Line No.	1	2	3	4	5	6	9	10	11	12	13	14	16	17	18	19	20	21	26	28	29	30	27	32	33	34	38	PI	SW	DW
Xgwm129	2	**1**	2	**1**	**1**	2	**1**	2	**1**	**1**	2	2	**1**	**1**	2	**1**	2	2	2	2	2	0	**1**	**1**	**1**	2	**1**	**0**	2	2
Xwmc752	2	**1**	2	**1**	**1**	2	**1**	2	**1**	**1**	2	2	**1**	**1**	2	**1**	2	2	2	**1**	**1**	**1**	**1**	**1**	**1**	2	**1**	**1**	2	2
Xbarc40	**1**	**1**	2	2	**1**	2	**1**	2	**1**	**1**	2	2	**1**	**1**	2	2	2	2	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	2	2
Xbarc165	**1**	2	2	2	2	2	**1**	2	**1**	**1**	2	2	2	2	2	2	2	2	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	2	2
Xwmc795	**1**	h	h	h	h	h	**1**	h	h	**1**	h	h	h	h	h	h	h	0	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	2	2
Xcfa2185	h	h	h	h	h	h	h	h	h	h	h	h	h	h	h	h	h	h	1	2	2	h	h	2	2	2	2	**1**	2	2
Xgwm96	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	2	2	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	2	2	**1**	2	2	2	2	**1**	2	2
Xcfd39	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	**1**	2	2	2	**1**	**1**	**1**	2	2	2	**1**	2	2
Xgwm179	2	2	2	2	2	2	2	2	2	2	2	2	2	**1**	2	2	2	2	h	2	**1**	**1**	**1**	2	2	0	2	**1**	2	2

Xbarc40



1-21: Russ/PI//Russ (BC_1F_6); Ru: Russ; P: PI 277012 (PI); Gr: Grandin; Re: Reeder; 22-23: Grandin/PI//Grandin (BC_1F_6); 24-26 and 28-30: Reeder/PI//Reeder (BC_1F_6); Le: Lebsock; Mo: Mountrail; Di, Divide; Be: Ben; 27and 32-34: Lebsock/PI//Lebsock (BC_1F_5); 35-36: Mountrail/PI//Divide (BC_1F_5); 38: Ben/PI//Ben BC_1F_5).

Disease severity and marker validation of BC_1F_6 lines from backcross of Russ to PI 277012

Line	Pedigree	Ht (cm)	Hd	FHB (%)	QTLs
10FAR2282-1	Russ/PI 277012//Russ	82.0	48.3	21.0	5AS, 5AL
10FAR2290-2	Russ/PI 277012//Russ	94.2	54.0	15.9	5AS, 5AL
10LDN553-2	Russ/PI 277012//Russ	101.5	50.8	21.2	5AS, 5AL
10FAR2383-1	Russ/PI 277012//Russ	98.5	56.8	27.4	5AS, 5AL
10FAR2450-1	Russ/PI 277012//Russ	77.0	46.0	7.0	5AS, 5AL
10LDN563-3	Russ/PI 277012//Russ	94.8	50.3	26.2	5AL
10LDN584-2	Russ/PI 277012//Russ	110.0	53.3	28.4	5AL
10FAR2357-1	Russ/PI 277012//Russ	91.3	54.5	17.0	5AL
10LDN580-2	Russ/PI 277012//Russ	111.7	53.3	15.4	5AS
10LDN585-2	Russ/PI 277012//Russ	109.3	52.0	23.9	5AS
PI 277012		108.0	60.5	10.7	
Sumai3		105.0	57.0	12.6	
Grandin		81.0	56.0	62.6	

Ht, plant height; Hd, days to heading; FHB (%), average disease severity from 2010 field nurseries in Fargo & Langdon, ND.

Disease severity and marker validation of Marker validation of BC_1F_5 lines from backcross of durum to PI 277012 (P12)

Line	Pedigree	Ht (cm)	Hd	FHB (%)	QTLs
10FAR2778-1	**Lebsock/P12//Lebsock**	**88.0**	**57.5**	**32.3**	**5AS, 5AL**
10LDN198-1	Lebsock/P12//Lebsock	87.0	62.3	57.5	5AS
10LDN211-2	Lebsock/P12//Lebsock	95.0	60.7	31.6	5AS
10LDN214-2	Lebsock/P12//Lebsock	99.7	58.7	25.3	5AS
10FAR2866-2	Mountrail/P12//Divide	95.0	59.7	61.4	5AS
10FAR2873-2	Mountrail/P12//Divide	102.6	61.7	52.0	5AS
10LDN210-2	Ben/P12//Ben	87.5	59.5	42.5	5AS
Sumai3		105.0	57.0	12.6	
PI 277012		108.0	60.5	10.7	
Grandin		81.0	56.0	62.6	
Divide		102.3	60.0	73.5	

Ht, plant height; Hd, days to heading; FHB (%), average disease severity from 2010 field evaluations in Fargo and Langdon, ND.

Current Work and Future Plans

- The durum line and five HRS wheat lines with both 5AS and 5AL QTLs will be further improved for agronomic performance by 2nd round of introgression by one more backcross with cultivars.
- These lines will be supplied to U.S. durum and wheat breeding programs. A small amount of seed samples will be available by February, 2011.
- The 5AS and 5AL QTLs in HRS wheat lines will be pyramided with *Fhb1* and other two QTLs mapped on 5A from *T. monococum* and *T. timopheevii.*
- The 5AS and 5AL QTLs in durum will be pyramided with *Fhb1* and three mapped QTLs (3AS, 6BS and 7AL) derived from wild emmer (3AS, 6BS and 7AL).
- Saturation mapping of chromosomal interval harboring 5AL QTL.

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