

IDENTIFICATION OF TWO NEW QTL FOR FHB RESISTANCE IN A HARD RED SPRING WHEAT CULTIVAR 'PARSHALL'

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Abstract

The intensive use of the Chinese Sumai3 as the major resistance source for FHB has narrowed the variation of the allelic forms in many wheat breeding programs. Therefore, the aim of our study was to investigate new genetic regions in the North Dakota (ND) spring wheat cultivars. A population with 110 RIL, called (PR), was generated from the cross between 'Parshall' and 'Reeder', a moderate resistant and a susceptible cultivars released by the ND State University, respectively. PR population was evaluated for FHB resistance for the three years (2010-2012) under field conditions at three different locations in the USA. In addition, two years (2011-2012) of greenhouse experiments were performed to validate field data. Several FHB resistance traits including incidence (INC), severity (SEV), FHB-index (NDX), deoxynivalenol (DON), and FHB-damaged kernel (FDK), and heading date (HD) were assessed. Our results revealed that out of 65 QTL; 39 QTL had significant major effect. Three QTL (*QFHB.2AL*, *QFHB.3AL1* and *QFHB.3BL3*) were stable across at least three year x location environments. Likewise, four QTL (*QFHB.4AL2.a*, *QHD.4AL2.b*, *QFHB.4BS* and *QFHB.6BL*) were stable and had major effect across at least four environments. Most importantly, the *QFHB.4BL2.a* QTL was stable under nine environments controlling four different FHB-related traits including SEV and FDK. Our data also demonstrated that Parshall acquired novel chromosomal regions for FHB resistance. Such new regions may contain allelic forms that help increase/widen and bridge the narrow allelic variation existed in FHB resistance traits. These alleles could be implemented in national and international genome wide selection (GWS) and molecular assisted breeding (MAB) programs. Finally, Parshall pyramids many genomic regions that were associated with high-yield and quality end-uses, and other agronomic, including drought tolerance that can improve wheat production

FHB Screening

Population and Phenotyping:

- 110 (PR) RILs developed from Parshall (FHB-resistant) × Reeder (FHB-susceptible).
- **FHB Incident (INC):** percentage of infected spikes per entry → for 4-environments.
- **FHB Severity (SEV):** percentage of diseased spikelets on the infected spick (Disease spread) → for 6-environments.
- **FHB DON Analysis:** DON concentration is run by gas chromatography and/or mass spectroscopy methods → for 3-environments
- **FHB FDK:** Percent of damaged kernels based on 200 kernels → for 2-environments
- **Heading dates (HD):** Number of days, from planting until the growth stage Feekes 10.5 → for 5-environments.

Mapping and QTL Analysis

- PR population was genotyped using 9K-SNP-Illumina (USDA, wheat genome enhancement lab, Fargo, ND, USA) combined with DaRT (<http://www.triticcate.com.au>).
- 481 polymorphic combined SNP & DaRT markers mapped to 44 linkage groups belonging to 19 chromosomes (Table 2).
- Total genetic distance=597.1 cM (2.35 cM/marker loci).

Table 1: Identified QTL for FHB resistance and related traits in the hard red spring wheat cultivar 'Parshall'.

QTL	TRT	LOC	MRK	Pos	CI	Add	LOD*	R ² %	Perm-LOD
<i>QFDK.1AL</i>	FDK	S10	wPt-6853-wPt-0432	3.0-3.5	3.1-6.7	4.3	3.3**	13	2.5-3.6
<i>QFHB.1AL</i>	INC,FDK	P11,S12	wPt-4065-wPt-7215	17.5-18.0	6.7-18.4	1.2	3.1***	9.0-12.0	2.2-3.5
<i>Q.SEV.1BS.a</i>	SEV	G12	wPt-4366-wPt-0328	5.5	3.1-6.9	-3.8	2.6*	10	2.6-3.4
<i>Q.SEV.1BS.b</i>	SEV	G12	wPt-3465-wPt-2762	8.0	7.1-9.5	7.9	2.9*	12	2.6-3.4
<i>QFHB.2AL</i>	FDK,HD	S10,S12,NDH	wPt-665330-wsnp_Ex_c6660_11526924	0.0-14.5	0.0-24.7	±0.4-4.7	2.6-4.2***	10.2-16.0	2.2-3.6
<i>QINC.2AS.a</i>	INC	M10	wsnp_Ex_c11560_18632777-wPt-4533	1.5	0.9-3.2	-3.7	2.5*	10	2.2-3.0
<i>QINC.2AS.b</i>	INC	M10	wPt-4533-tPt-1041	6.0	3.2-12.3	14.8	5.8****	21.8	2.2-3.0
<i>Q.FHB.3AL1</i>	SEV,FDK	P11,G12,GHS	wsnp_Ex_rep_c67349_65914945-wsnp_RFL_Contig4273_4946890	0.0-0.5	0.0-1.0	2.5-4.1	2.2-4.5****	9.0-17.0	2.5-3.6
<i>QFHB.3AL2</i>	SEV,DON	G12,S10	wPt-744743-wPt-9154	0.0-1.5	0.0-3.2	-0.5-4.0	3.0**	12	2.5-3.5
<i>QFHB.3AL3</i>	SEV,FDK	G11,S10	wPt-5173-wPt-9049	11.5-14.0	8.8-14.4	±3.3-4.0	2.8*	11	2.5-3.6
<i>QSEV.3AL4</i>	SEV	GH	wsnp_Ex_c26887_36107413-wsnp_Ex_c4923_8767234	14.0	0.0-20.5	-3.8	3.4**	13	2.5-3.6
<i>QFDK.3BL1</i>	FDK	S10	tPt-1759-wPt-10130	3.0	2.8-3.3	-2.7-3.6	2.4-4.1****	10-15.7	2.5-3.6
<i>QDON.3BL2</i>	DON	P11	wPt-4933-wPt-667746	1.0	0.6-3.8	-0.21	2.7**	11	2.2-3.1
<i>QFDK.3BL2</i>	FDK	G12	wPt-7037-wPt-2439	6.0	5.4-6.3	-4.4	3.0**	12	2.6-3.6
<i>QFHB.3BL2</i>	SEV,NDX	C11	wPt-0401-wPt-5295	9.0	8.9-9.4	1.1	2.9**	11	2.5-3.5
<i>QFDK.3BL3</i>	FDK	S10,GH	wPt-3327-wsnp_Ex_c6445_11200449	9.0-10.0	0.0-10.8	±2.4-5.4	2.0-3.2**	8.0-13.0	2.5-3.6
<i>QFHB.3BL3</i>	INC,SEV,FDK	P10,AI,S10	wsnp_ID_c6974_8084752-wsnp_Ku_c15149_23666345	19.0-22.5	14.1-25.2	1.2-5.2	2.3-3.6**	9.0-14.0	2.4-3.6
<i>QFHB.3BS1</i>	SEV,HD	P12,G11	wsnp_Ex_c7108_12222660-wsnp_Ex_c2325_4355706	1.5-3.0	0.0-3.0	±3.6	3.4**	13.3	2.5-3.6
<i>QFDK.3BS2</i>	FDK	G11,GH	wsnp_Ex_c16919_25506076-wPt-742337	10.0	9.4-12.3	3.3-4.02	2.0-3.1**	8.0-12.1	2.6-3.7
<i>Q.SEV.3DS</i>	SEV	P10	wPt-741536-wPt-742314	0.0	0.0-0.5	2.9	2.9*	12	2.5-3.3
<i>QFHB.4AL2.a</i>	INC,SEV,NDX	P12,S10,AI,M10,AN	wsnp_Ku_rep_c68565_67614479-wsnp_Ku_c45197_52288542	0.0-1.5	0.0-4.1	±1.5-4.1	2.8-6.1****	11.0-23.0	2.3-3.6
<i>QHD.4AL2.b</i>	HD	C11,L11,P12,M10,NDH	wsnp_Ku_c45197_52288542-wPt-7427	4.5-10.0	4.1-10.4	0.4-0.9	2.2-4.0***	9.0-15.4	2.5-4.0
<i>QFHB.4BL2.a</i>	SEV,NDX,FDK,HD	P10,C11,L11,M10,S11,S12,Fields,AN,NDH	wPt-6149-wPt-7569	6.0-18.5	0.0-20.9	0.5-6.7	2.2-8.8****	9.0-31.0	2.2-4.0
<i>QFHB.4BL2.b</i>	FDK,DON	P11,S10	wsnp_CAP12_c1101_569783-wsnp_RFL_Contig4416_5179910	21.0-22.0	20.9-22.8	0.5-11.8	3.0-3.6****	12.7-14.2	2.2-3.6
<i>QSEV.4BL3</i>	SEV	G12	wsnp_Ku_c5210_9290700-wsnp_Ex_c4685_8377545	21.5	0.0-26.1	-6.1	4.0****	15	2.6-3.4
<i>QFHB.4BS</i>	DON,HD	P10,M10,NDH,G11,S11	wsnp_Ex_c13357_21054802-wsnp_Ex_c6739_11646407	2.0-18.5	0.0-18.7	-0.4-0.7	2.2-6.2****	9.1-23.0	2.4-3.7
<i>QDON.5AL</i>	DON	S11	wsnp_Ra_rep_c69221_66574260-wsnp_Ex_rep_c70343_69286072	15.5	0.0-15.7	-0.6	4.9****	19	2.5-3.4
<i>QHD.5AL</i>	HD	C11	wsnp_Ex_c4666_8349206-wsnp_Ku_c30743_40542247	16.5	15.7-22.7	-0.8	3.0**	11.7	2.6-4.0
<i>Q.FHB.5AL</i>	SEV,NDX,DON	S12,G11	wsnp_ID_c1796_2496653-wsnp_Ex_c19647_28632894	27.5-31.5	22.7-31.5	±0.5-1.6	2.1-3.7****	8.7-14.4	2.5-3.6
<i>QFDK.6AL</i>	FDK	S10	wsnp_RFL_Contig420_4824600-wsnp_Ex_c42447_49025091	2.0	1.0-2.5	4.5	3.7****	14.4	2.6-3.6
<i>QDON.6AS</i>	DON	SD	wPt-731413-wPt-733115	7.5	2.7-11.9	0.4	3.0**	12	2.5-3.5
<i>QFHB.6Bc</i>	DON,HD	SD,ND	wsnp_Ku_c7002_12116034-wPt-6247	3.5-8.0	0.0-12.7	0.4	2.2-2.8*	9.0-11.0	2.5-3.5
<i>QFHB.6BL</i>	DON,HD	S11,P10,M10,C11	wPt-743231-wPt-1048	19-21.5	16.0-21.9	0.8-0.43	2.7-3.6****	10.8-14.1	2.4-4.0
<i>QFHB.6BS1</i>	SEV,NDX	P12	wPt-7203-wsnp_CAP12_c1388_706924	5.5-6.0	2.0-6.6	-4.1	2.2	9	2.5-3.8
<i>Q.FHB.6BS2</i>	SEV,NDX	P11	wPt-743078-wPt-7576	1.5	0.0-4.5	-2.8	4.1****	16	2.5-3.4
<i>Q.FHB.7AL1</i>	SEV,HD	P10,M10	wPt-7785-wPt-1928	0.0-0.5	0.0-0.3	2.2	2.7*	8.0-11.0	2.5-3.7
<i>QFHB.7AL2</i>	SEV,NDX	S12	wsnp_RFL_Contig2136_1423367-wPt-664237	0.0	0.0-9.6	-1.5	3.0**	12	2.5-3.6
<i>QFDK.7AL3</i>	FDK	G12	wPt-744715-wPt-744937	15.5	0.0-15.8	-5.8	4.3****	16.3	2.6-3.6
<i>QINC.7AL4</i>	INC	P11	wPt-4721-wPt-0275	02.5	0.0-21.3	-5.6	5.5****	20.7	2.5-3.5

QTL, name of QTL; TRT, FHB traits. LOC, locations; MRK, flanking markers; Pos, position; CI, Confidence intervals; Add, additive effect; LOD, logarithmic likelihood; *, significance levels at 0.05, 0.01, 0.001 and 0.0001 of permutation test; R²%, percentage of phenotypic variation (PV); Perm-LOD, threshold LOD values generated by permutation test. INC, incidence, SEV, severity, DON, deoxynivalenol, FDK, *Fusarium* damaged kernels, HD, heading dates; A, All combined homogeneous environments of the specified trait; P, prosper; C, Carrington; G, greenhouse; L, Langdon; S, SD; M, MN; Field, all combined field data; 10, the year 2010; 11, the year 2011; 12, the year 2012.

Results

QTL analysis for FHB traits and heading dates (Table 1):

- Composite interval mapping (CIM) using QTL CARTOGRAPHER identified = 6 for INC (type 1); 18 for SEV (type 2); 6 for NDX; 10 for DON (type 3); 14 for FDK (type 4), and 11 QTL for HD.
- The PV explained by individual QTL = 09-21.8% for INC; 08-25% for SEV; 10.6-30.9% for NDX; 08-23% for DON; 08-16.3% for FDK; and 09-18.8% for HD. All QTL had significant major effect (PV>10%) except for *QFHB.6BS1*.
- Four major consistent QTL (4AL2, 4BL2, 4BS, and 6BL) for INC,SEV,NDX,DON,FDK and HD were detected in more than 5 environments explaining 09 to 31% of PV.
- The QTL (*QFHB.4BL2.a*) for SEV,NDX,FDK, and HD was detected in 9 environments out of total 13 combined years/locations environments.

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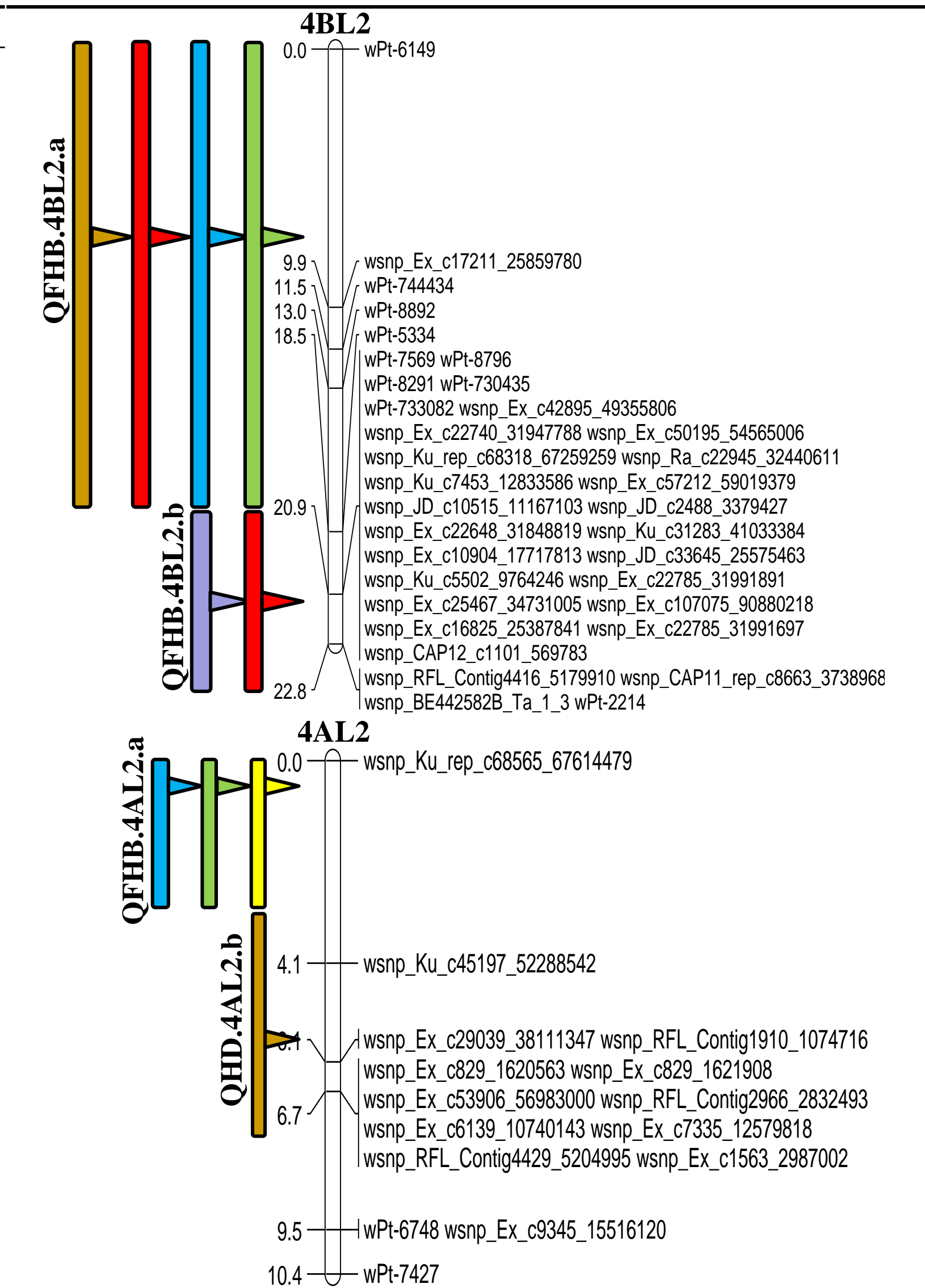


Fig. 1. Chromosomal map for major and consistent QTL identified on 4AL2 and 4BL2 in (PR) population. (QTL intervals shown as (lines); QTL positions shown as (Triangles); QTL for INC, SEV, NDX, DON, FDK, and HD were shown in (Yellow, Blue, Green, Purple, Red, Brown) respectively).

Table 2: Number of chromosomes, groups, markers, unique loci, cumulative distance and the average distance between two loci.

Chrm.	GP	MRK	DIST	UL	AVDIST
1A	2	18	27.1	15	1.8
2A	2	16	37.5	10	3.75
3A	4	22	45.4	14	3.24
4A	3	34	31.6	19	1.66
5A	1	17	42.9	7	6.13
6A	2	12	15.1	9	1.68
7A	4	42	74.5	23	3.24
Total A	18	161	274.1	97	2.83
1B	1	19	10.7	11	0.97
2B	1	12	2.6	10	0.26
3B	5	75	57.6	28	2.06
4B	4	51	85.2	18	4.73
5B	3	20	52	15	3.47
6B	4	26	46	21	2.19
7B	1	30	37.7	13	2.9
Total B	19	233	291.8	116	2.52
1D	0	0	0	0	0
2D	1	16	8.8	9	0.98
3D	1	25	1.9	8	0.24
4D	0	0	0	0	0
5D	2	12	2.7	9	0.3
6D	1	10	3	5	0.6
7D	2	24	14.8	10	1.48
Total D	7	87	31.2	41	0.76
Total Genome	44	481	597.1	254	2.35

CHRM, Chromosome. GP, number of groups in each chromosome. MRK, number of markers in each chromosome. UL, unique loci. DIST, cumulative kusambi distance in each chromosome. AVDIST, average distance between every two marker loci.