Molecular marker-assisted selection

Population Development

Parental selection and hybridization

QTL Mapping

Linkage map construction
Phenotypic evaluation & QTL analysis

QTL Validation

Confirmation of position and effect of QTLs
Validation of QTLs in different genetic backgrounds
Fine mapping

Marker Validation & Selection

Testing of markers in important breeding materials

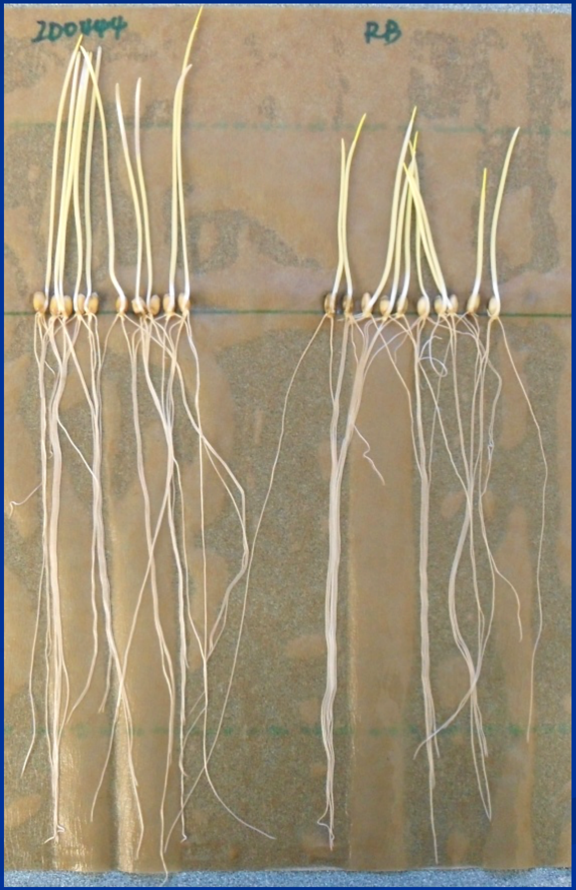
Parental Selection

- Yield productivity
- Coleoptile, root length and numbers
- Resistance to stripe rust and dwarf bunt
- Resistance to Fusarium head blight
- Resistance to hessian fly
- Desirable end-use quality
- Late maturity alpha amylase and PHS
- Water and nitrogen use efficiency

Type of Mapping Population

- Recombination inbred lines (RILs)
- Doubled haploid lines (DHLs)
- Nested RILs and DHLs
- Diverse germplasm
- Heterozygous inbred family (F5 or F6)
- Backcross-derived RILs and DHLs

RioBlanco x IDO444



RioBlanco **IDO444**

RioBlanco x IDO444 RILs

Year	Activities	Year	Activities
9596	F1 made	**0405**	F8:9, DArT
9697	F2 and F3 GH	**0506**	F8:9, Gp22, AB, GY, Q
9798	F4 GH	**0607**	F8:9, Gp22, RK and AR, GY, Q
9899	F5 field	**0708**	F8:10, 1-row, purify
9900	F6 GH	**0809**	F8:9, NSGC, purify, CL, Glu1, Q, SSR
0001	F7 GH	**0910**	F8:10, Gp15, BF, AB, GY, Q
0102	F8 field	**1011**	F8:11, Gp15, RK-GY, AB-GY+, Q, GH, SNP
0203	F8:9, INC, DB, Yr	**1415**	F8:12, Gp15 AB, 60 RILs, GY+
0304	F8:9, DB, Yr, NSGC	1516	F8:13, Gp15 60, GY+

RioBlanco x IDO444 RILs

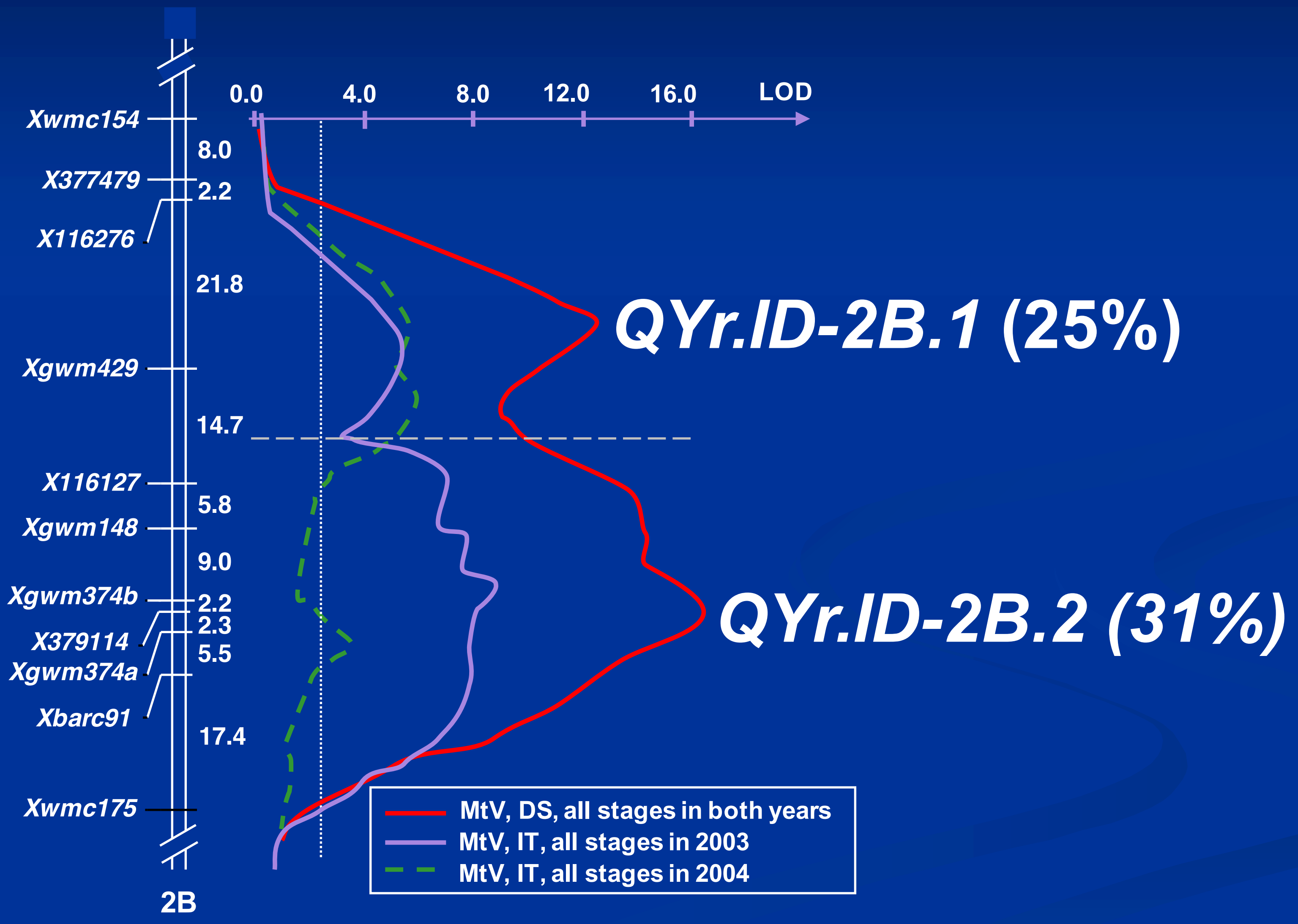
Genetic maps

- 96 microsatellite (SSR)
- 632 diversity array technology (DArT)
- Four sequence-tagged-site (STS)
- 9,000 single nucleotide polymorphism (SNP)

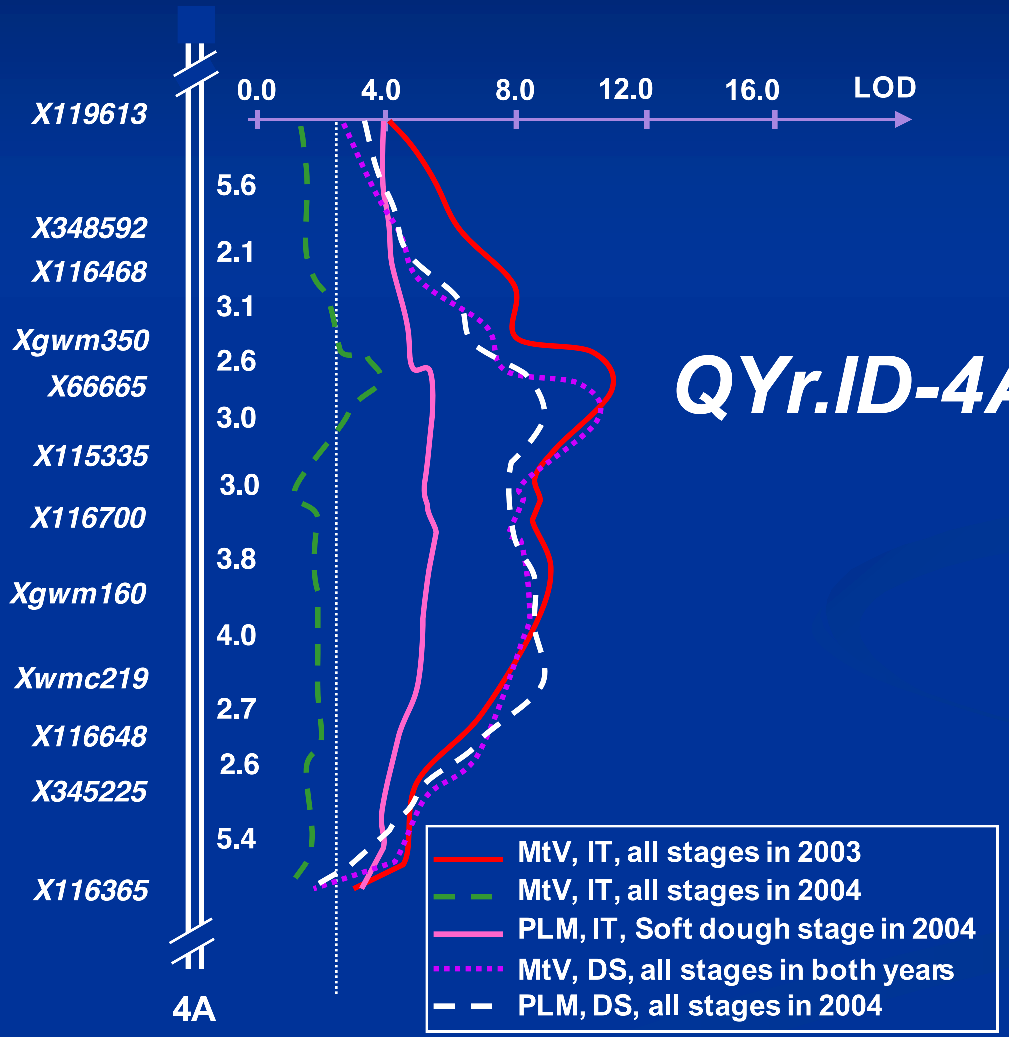
QTL mapping of HTAP resistance to stripe rust (*P. tritici*)

Chen et al., 2012 Crop Sci.

RioBlanco x IDO444 RILs



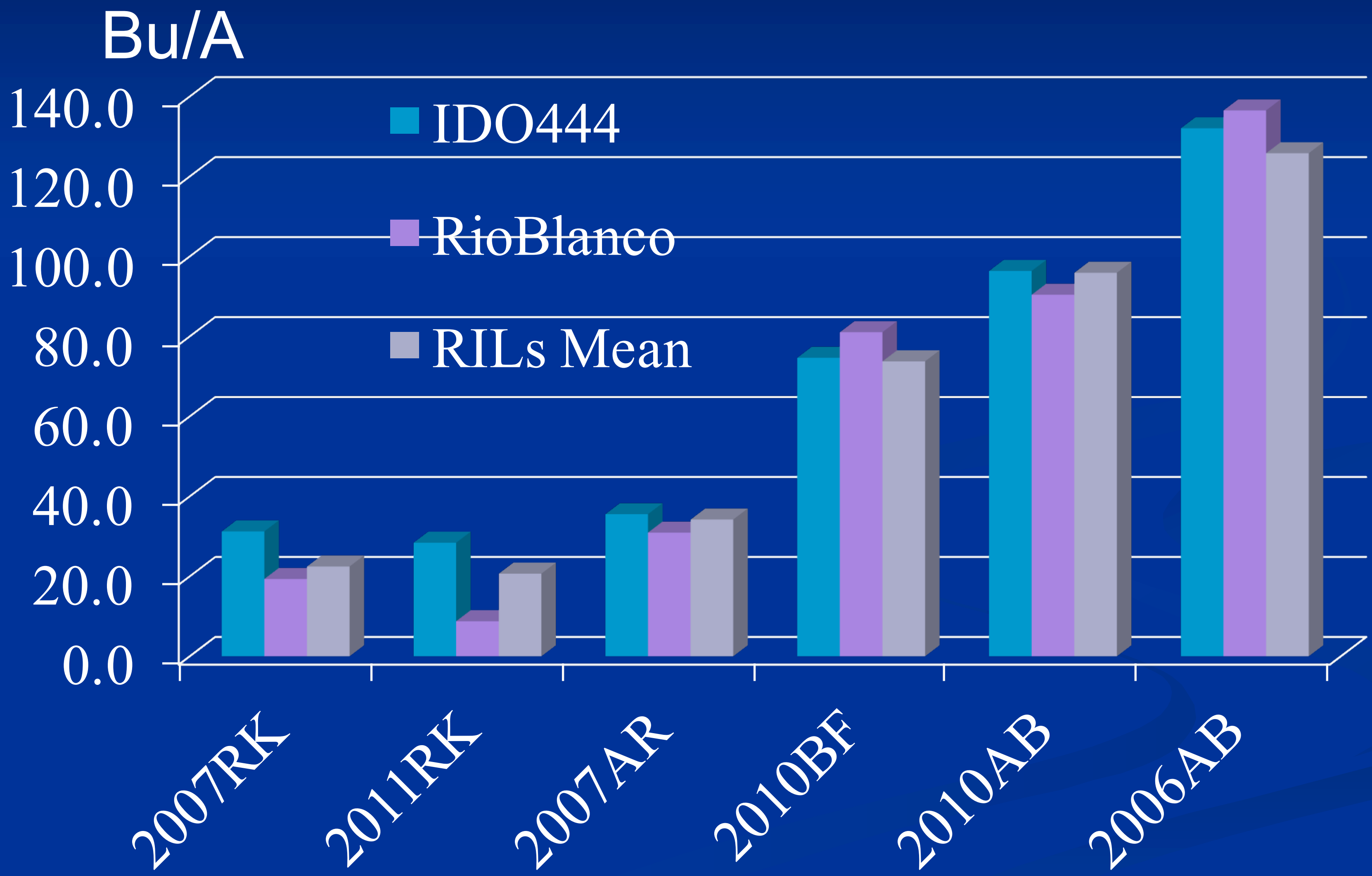
RioBlanco x IDO444 RILs



QYr.ID-4A (26%)

Mapping of Yield in Diverse Environments - 2011 field

Yield Performance of the Two Parents and RILs in the Six Environments



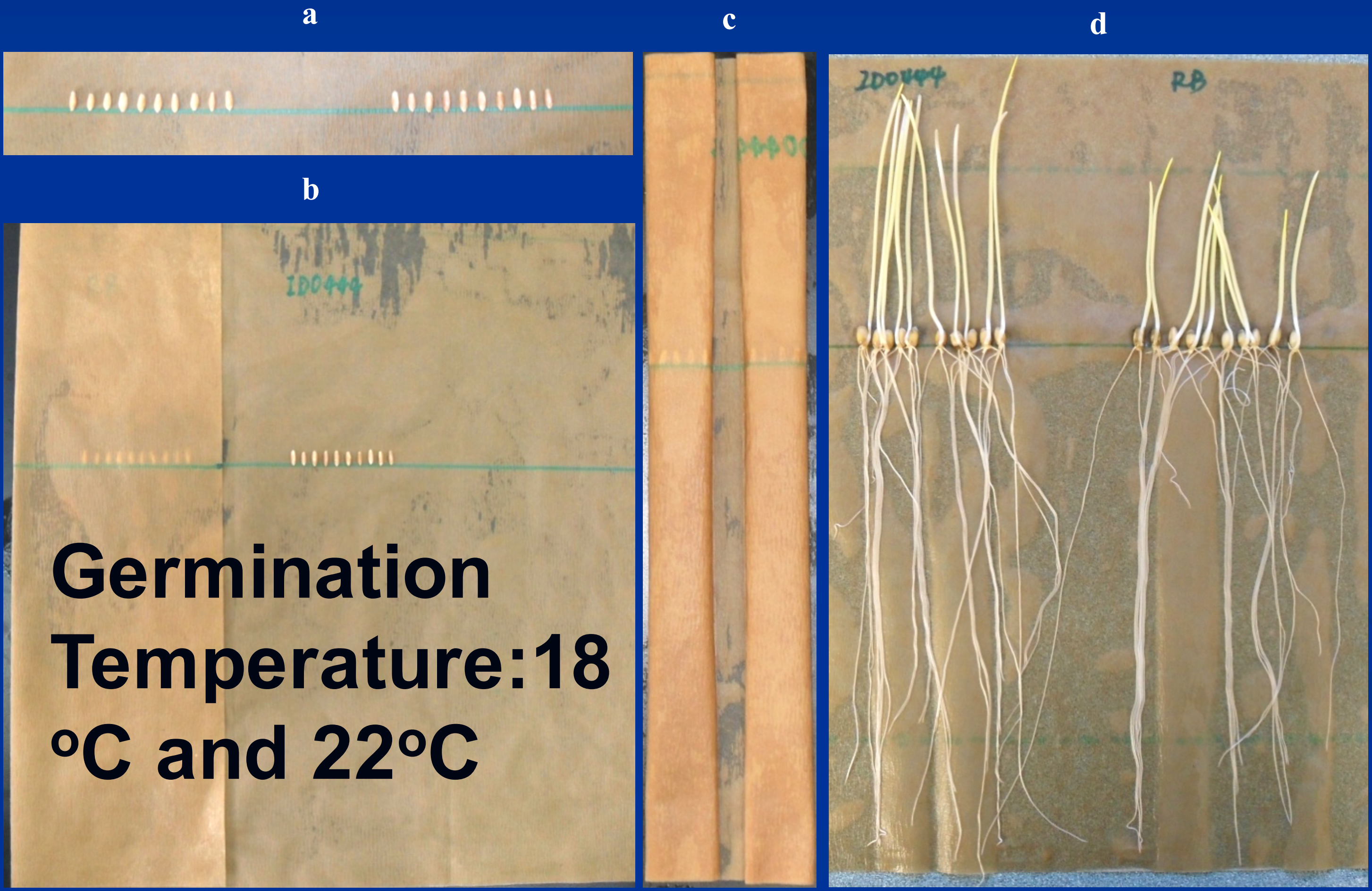
17 QTL on 14 Chr. Regions

QTL	Env.	Chr.	Position	Peak Marker	LOD	Add[a]	R^2 (%)
Q.Gy.ui-1A	10AB	1A-1	71.71	X115497	6.1	0.23	11
Q.Gy.ui-1B.1	11RK	1B-1	77.31	X304189	9.5	0.14	22
Q.Gy.ui-1B.2	11RK	1B-1	85.81	Xgwm264	9.6	0.15	22
	07RK	1B-1	91.21	IWA6787	3.7	0.10	8
	06AB	1B-1	92.21	IWA6787	4.8	0.25	9
	10AB	1B-1	92.21	IWA6787	3.2	0.17	6
	10BF	1B-1	93.21	IWA5976	3.4	0.14	7
	07AR	1B-1	93.91	IWA5976	4.3	0.09	9
Q.Gy.ui-2B.1	07AR	2B-1	45.71	X116276	3.9	0.08	8
Q.Gy.ui-2B.2	06AB	2B-2	8.31	IWA6453	4.0	-0.23	8
Q.Gy.ui-2D	07AR	2D	74.71	X119684	2.9	0.07	6

17 QTL on 14 Chr. Regions, cont.

QTL	Env.	Chr.	Position	Peak Marker	LOD	Add[a]	R^2 (%)
Q.Gy.ui-3B.1	06AB	3B-1	10.61	X116345	6.1	0.28	12
Q.Gy.ui-3B.2	10BF	3B-2	156.01	Xbarc229	3.4	-0.15	8
Q.Gy.ui-4B	10AB	4B	62.51	XRhtB1	8.3	-0.27	16
Q.Gy.ui-5A.1	07RK	5A-1	19.41	IWA8154	3.5	0.13	8
Q.Gy.ui-5A.2	10AB	5A-1	65.91	Xgwm156	2.8	0.16	6
Q.Gy.ui-5B.1	07RK	5B-2	25.11	IWA6946	2.8	-0.08	6
Q.Gy.ui-5B.2	10BF	5B-2	54.61	IWA5620	4.2	-0.15	8
Q.Gy.ui-6B	10AB	6B-2	57.01	IWA7625	2.9	0.15	5
	10BF	6B-2	60.31	Xbarc136	2.6	0.12	5
Q.Gy.ui-7A.1	10BF	7A-4	37.41	IWA7430	3.6	-0.14	7
Q.Gy.ui-7A.2	10AB	7A-5	0.01	X408088	4.3	-0.20	8
Q.Gy.ui-7B	07AR	7B-1	0.01	IWA8177	5.3	-0.10	11

Assessing and Mapping of Coleoptile and Root Length and Numbers



Germination Temperature:18 °C and 22°C

QTL for coleoptile and root
Crop Science, 2011

Traits	No. of QTL	Chromosome	R^2 (%)	h_B^2(%)
CL	2	4B, 6B	9 - 67	71 – 81
RL	2	4B	9 - 26	25 - 66
RN	5	2B, 4B, 7A, 5A, 5B, 7B	7 - 11	59 - 81

Effect of *RhtB1* on coleoptle and root lengths (mm), number of roots

Traits	RhtB1a	DF	RhtB1b	DF	Diff.	*P*
CL18	8.10	86	6.23	73	1.87	< 0.001
CL22	8.16	86	6.11	73	2.05	< 0.001
LR18	16.98	86	17.64	73	-0.66	< 0.01
LR22	19.20	86	19.73	73	-0.53	< 0.01
RN18	3.19	86	3.36	73	-0.17	< 0.01
RN22	3.21	86	3.44	73	-0.22	< 0.01
TRL18	43.06	86	46.28	73	-3.21	< 0.001
TRL22	49.56	86	56.09	73	-6.52	< 0.001
Height	88.21	86	80.65	73	7.56	< 0.001

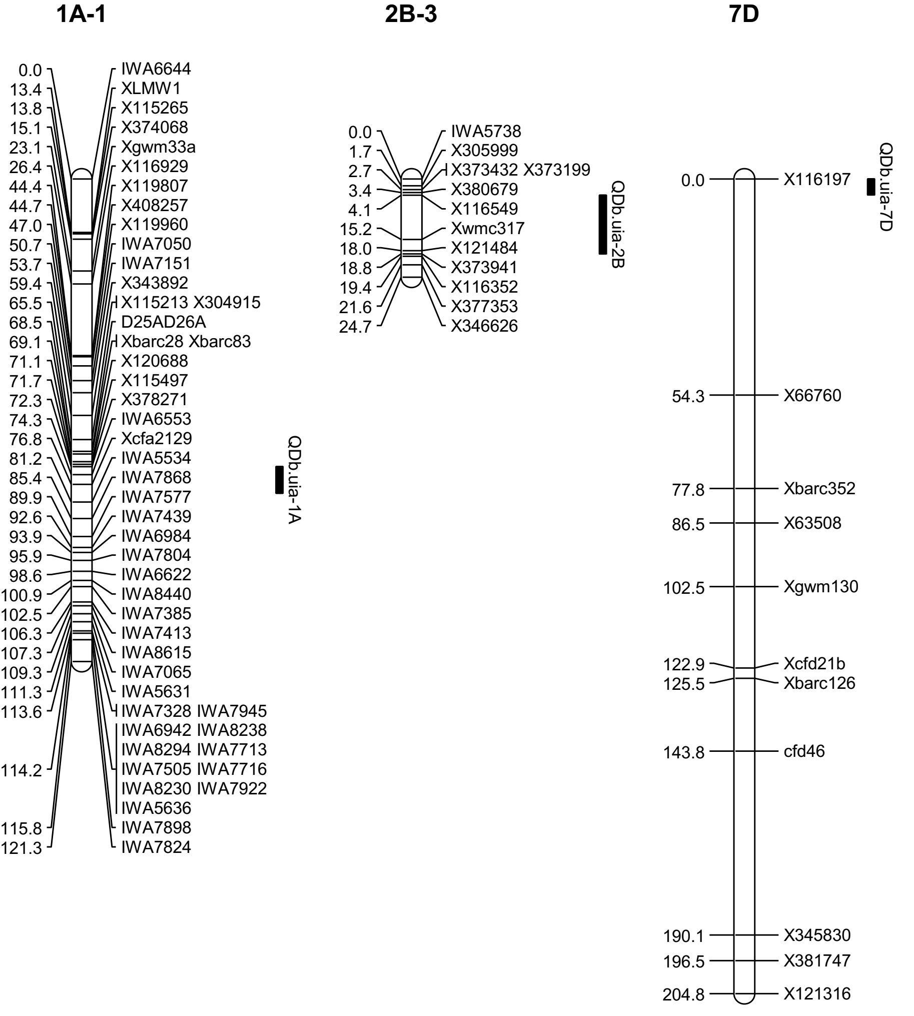
Effect of RhtB1 on yield (bu/a)

Env.	**RhtB1a**	**RhtB1b**	**1a - 1b**	***P***
06AB - IR	124.5	127.0	-2.5	NS
07AR - D	34.5	33.9	0.6	NS
07RK - D	23.1	21.7	1.4	NS
11RK - D	25.9	25.4	0.4	NS
11AB - D	34.3	36.5	-2.3	NS
11AB - IR	96.9	103.9	-7.0	<0.05
10AB - TD	70.3	77.7	-7.4	<0.001
10BF - TD	77.4	81.7	-4.3	<0.01

Role of RhtB1 and Rht-D1 dwarfing genes in wheat

- Increase yield in hexaploid wheat – green revolution
- Reduce coleoptile length
- Increase number of roots and root length

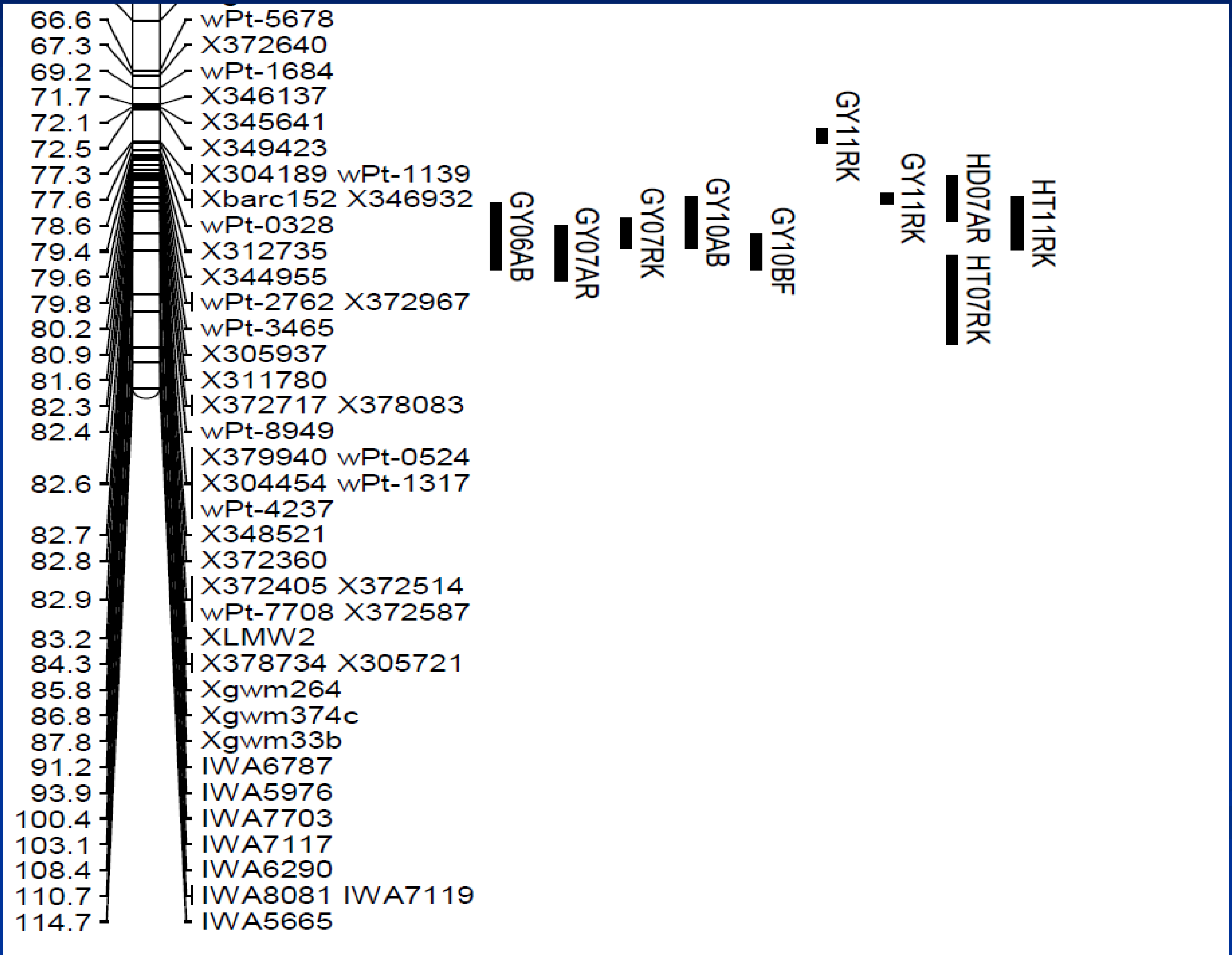
QTL for Dwarf Bunt



Validation

- Use additional population
  - IDO835 x Moreland DHLs
  - UI Silver x Shaan89150 DHLs
  - UI Platinum x SY Capstone DHLs
  - UI Stone x Alturas RILs
  - UI Platinum x LCS Star
- Fine mapping
  - HIFs

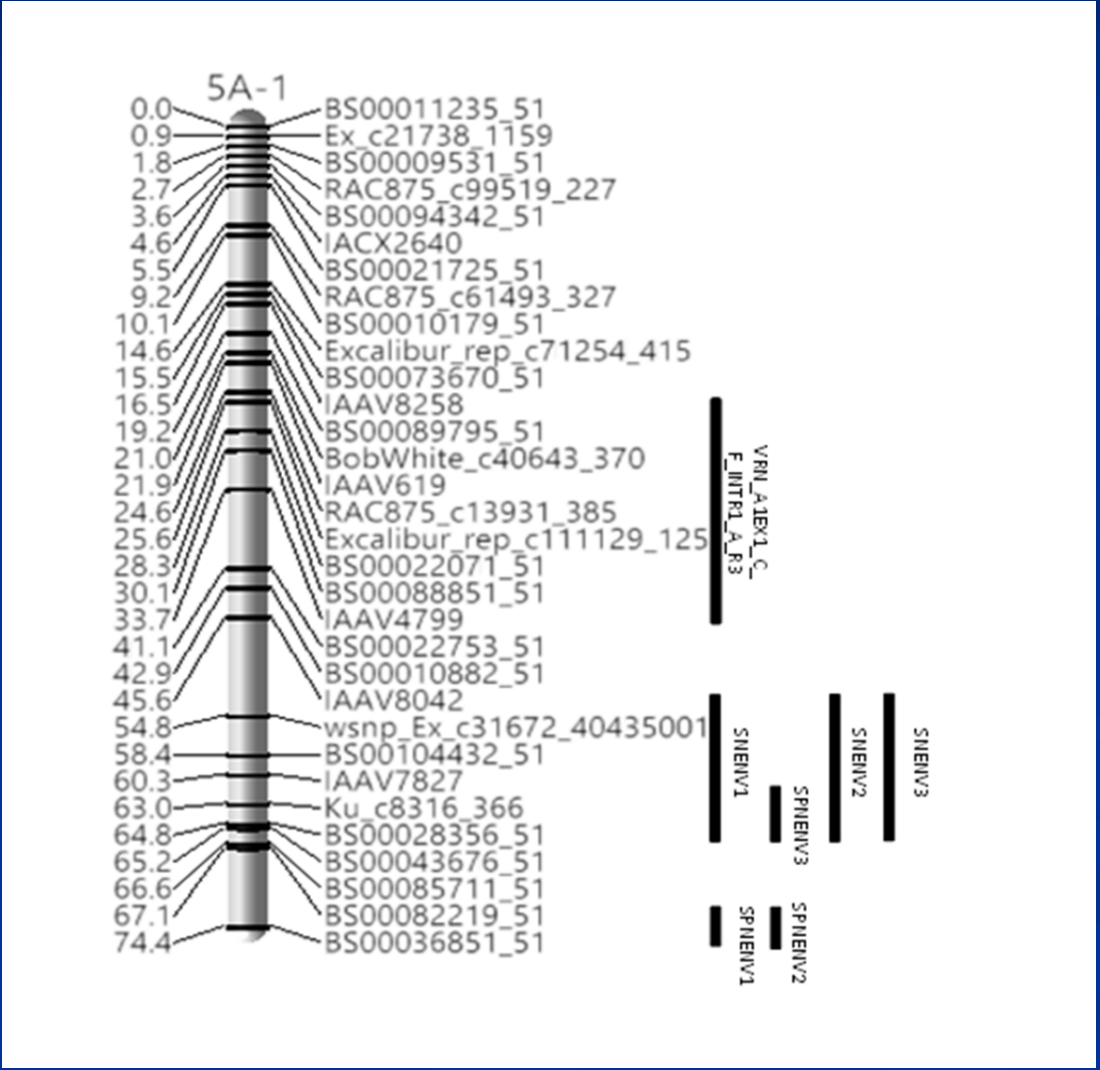
Q.Gy.ui-1B.2


66.6 wPt-5678
67.3 X372640
69.2 wPt-1684
71.7 X346137
72.1 X345641
72.5 X349423
77.3 X304189 wPt-1139
77.6 Xbarc152 X346932
78.6 wPt-0328
79.4 X312735
79.6 X344955
79.8 wPt-2762 X372967
80.2 wPt-3465
80.9 X305937
81.6 X311780
82.3 X372717 X378083
82.4 wPt-8949
82.6 X379940 wPt-0524 X304454 wPt-1317 wPt-4237
82.7 X348521
82.8 X372360
82.9 X372405 X372514 wPt-7708 X372587
83.2 XLMW2
84.3 X378734 X305721
85.8 Xgwm264
86.8 Xgwm374c
87.8 Xgwm33b
91.2 IWA6787
93.9 IWA5976
100.4 IWA7703
103.1 IWA7117
108.4 IWA6290
110.7 IWA8081 IWA7119
114.7 IWA5665
GY06AB
GY07AR
GY07RK
GY10AB
GY10BF
GY11RK
GY11RK
HD07AR
HT07RK
HT11RK

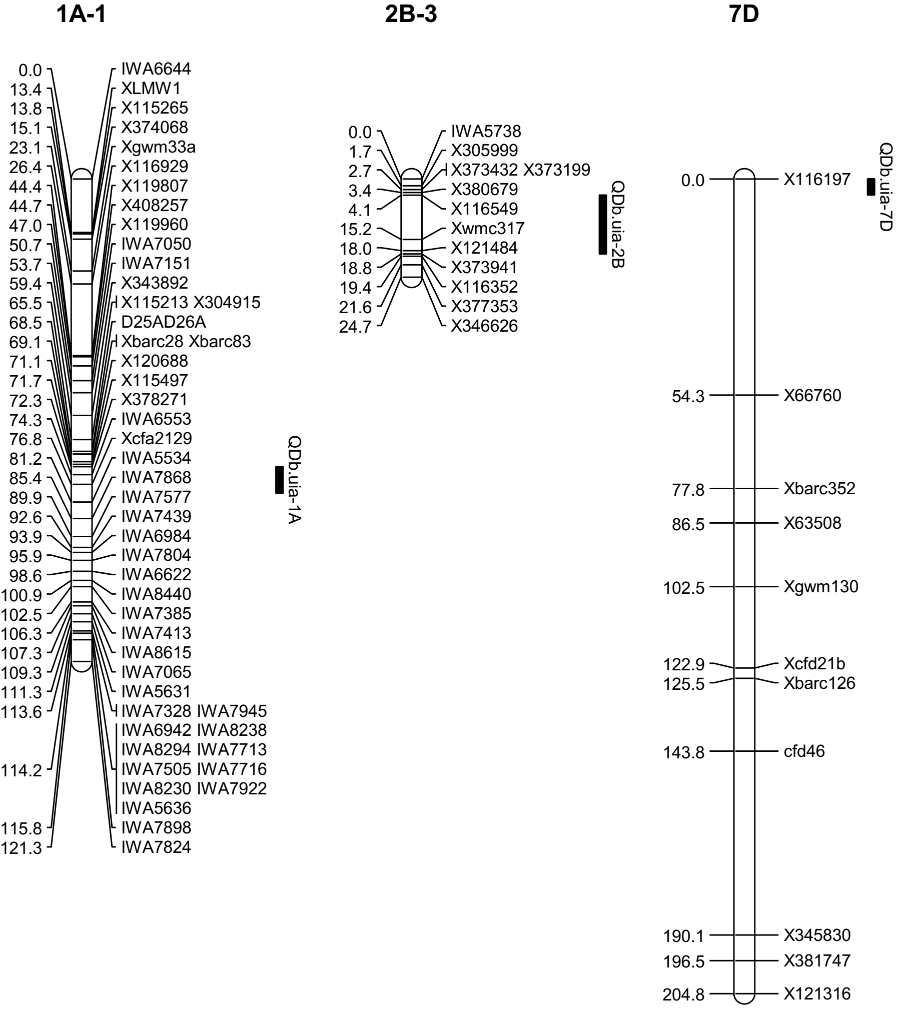
Selecting Heterozygous Families

Line	G264	G374	G33	SPN	FN	SN	KN
F5-IDO444	187	219	98	117.0	47.4	15.4	39.6
F5-RB	183	222/236	102	134.0	43.3	14.4	26.3
RB-659	187	222/236	98/102	114.2	46.0	15.4	35.3
RB-611	183/187	219	98	119.7	47.3	15.7	38.6
RB-485	183	219	98/102	127.0	48.4	16.1	40.1
RB-709	183	219	98/102	145.0	43.9	14.5	38.8
RB-567	187	219/222/236	98				
RB-759	183/187	219	98/102				
RB-633	187	219/222/236	102				
RB-761	183	219/222/236	98/102				
RB-825	183/187	219/222/236	102				
RB-589	183/187	219/222/236	98				

Q.SN.ui-5AL


5A-1
0.0 BS00011235_51
0.9 Ex_c21738_1159
1.8 BS00009531_51
2.7 RAC875_c99519_227
3.6 BS00094342_51
4.6 IACX2640
5.5 BS00021725_51
9.2 RAC875_c61493_327
10.1 BS00010179_51
14.6 Excalibur_rep_c71254_415
15.5 BS00073670_51
16.5 IAAV8258
19.2 BS00089795_51
21.0 BobWhite_c40643_370
21.9 IAAV619
24.6 RAC875_c13931_385
25.6 Excalibur_rep_c111129_125
28.3 BS00022071_51
30.1 BS00088851_51
33.7 IAAV4799
41.1 BS00022753_51
42.9 BS00010882_51
45.6 IAAV8042
54.8 wsnp_Ex_c31672_40435001
58.4 BS00104432_51
60.3 IAAV7827
63.0 Ku_c8316_366
64.8 BS00028356_51
65.2 BS00043676_51
66.6 BS00085711_51
67.1 BS00082219_51
74.4 BS00036851_51
VRN_A1EX1_C_F_INTR1_A_R3
SNENV1
SPNENV3
SNENV2
SNENV3
SPNENV1
SPNENV2

QTL for Dwarf Bunt



Fine Mapping of 1BL and 5AL

Year	Activities
1617	Replant F5 to get F6, select 1000 F5:2 in each HIF in RB444 Select HIFs from 500 F4 heads in PSDH
1718	GY for 4 x 1000 F5:2 from RB444 GY for 4 x 1000 F4:2 from PSDH
1819	Fine mapping of QTLui.Gy-1BL Fine mapping of QTLui.SN-5AL
1920	New marker development
2021	MAS
2122	QTL cloning
2223	QTL cloning

Marker-Assisted Pyramiding

Line	Class	FHB1	H25	YR36	GPC	GluD1	GluA3a	BKV1A
IDO586	HWS		+			+	+	
Lassik	HRS	+		+	+	+		+
Jefferson	HRS					+	+	+
New	HWS	+	+	+	+	+	+	+
New	HRS	+	+	+	+	+	+	+