Quantitative trait loci from two genotypes of oat (*Avena sativa* L.) conditioning resistance to *Puccinia coronata*

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Overview

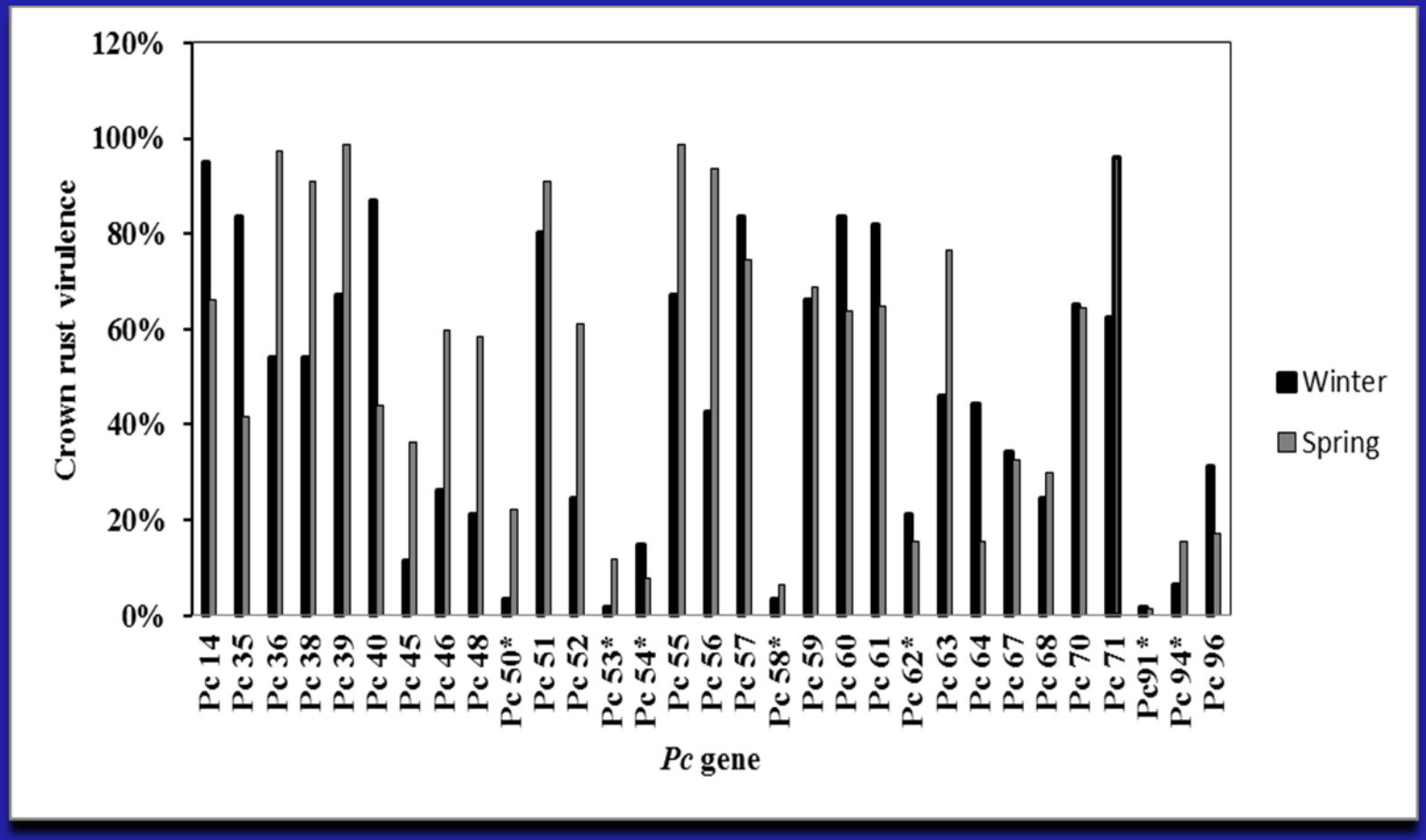
- Oat crown rust resistance in oat
  - Race specific resistance
  - Partial resistance (PR)
- Identifying crown rust QTL in three mapping populations
  - Populations
  - Methods
  - Results
- Implications and possibilities

Crown rust of oats

- Caused by *Puccinia coronata* f. sp. *avenae*
- Up to 20% reduction of seed quality and 40% yield losses – USA
- Management has relied primarily on the use of race specific crown rust resistance (*Pc*) genes derived from cultivated oat, *A. sativa*, wild oat *A. sterilis* and *A. strigosa*, and tetraploid *Avena* spp

Qualitative Resistance

- More than 96 *Pc* genes have been identified and many have been deployed, but resistance conferred by single *Pc* genes has been short lived



Martin Carson, 2011

Quantitative Resistance

- The use of PR to crown rust has been proposed as a means to improve the durability of resistance
- PR is characterized by reduction in pathogen reproduction despite a "susceptible infection type"
- PR could be pyramided with major genes for resistance only through marker assisted breeding, since major genes will mask the PR phenotype

Quantitative Resistance

- Several studies have reported QTL for partial resistance, but these QTL could not be assigned to specific chromosomes
- PCR-based markers were unavailable which slowed progress towards marker assisted breeding for crown rust resistance
- The recently developed SNP markers are advantageous because of their genome coverage, chromosome specificity, transferability between laboratories and amenability for genotyping using high throughput, automated scoring platforms

Identifying QTL for partial resistance to crown rust

- In a previous effort to identify PR in cultivated oat genotypes, several materials, including the cultivar 'CDC Boyer' and the breeding line 94197A1-9-2-2-2-5, consistently displayed PR at the adult stage

- CDC Boyer was developed by the University of Saskatchewan and 94197A1-9-2-2-2-5 is a breeding line developed by Dr. Greg Shaner at Purdue University from a cross with *A. sterilis*

- The objectives of this study were identify QTL for PR to crown rust in adult plants and identify candidate resistance genes by using the oat cDNA sequence data from which the SNP markers were developed

Material and Methods

Plant materials:

(1) Provena x CDC Boyer

(2) Provena x 94197A1-9-2-2-2-5

(3) CDC Boyer x 94197A1-9-2-2-2-5

Field evaluation:

(1) Louisiana State University 2009 and 2010

(2) St Paul, Minnesota 2009, 2010, and 2011

Disease assessment:

- Evaluated at the milk to early dough stage
- Recorded as the percent of diseased leaf area

Map construction and QTL analysis

Molecular marker analysis:

- ✓ iSelect SNP genotyping platform containing 5744 oat SNP markers

(1) Provena/CDC Boyer (PB) -148 RILs**:**

- 829 polymorphic markers were assigned to 50 LGs representing 20 chromosomes with a total map length of 1276.7 cM

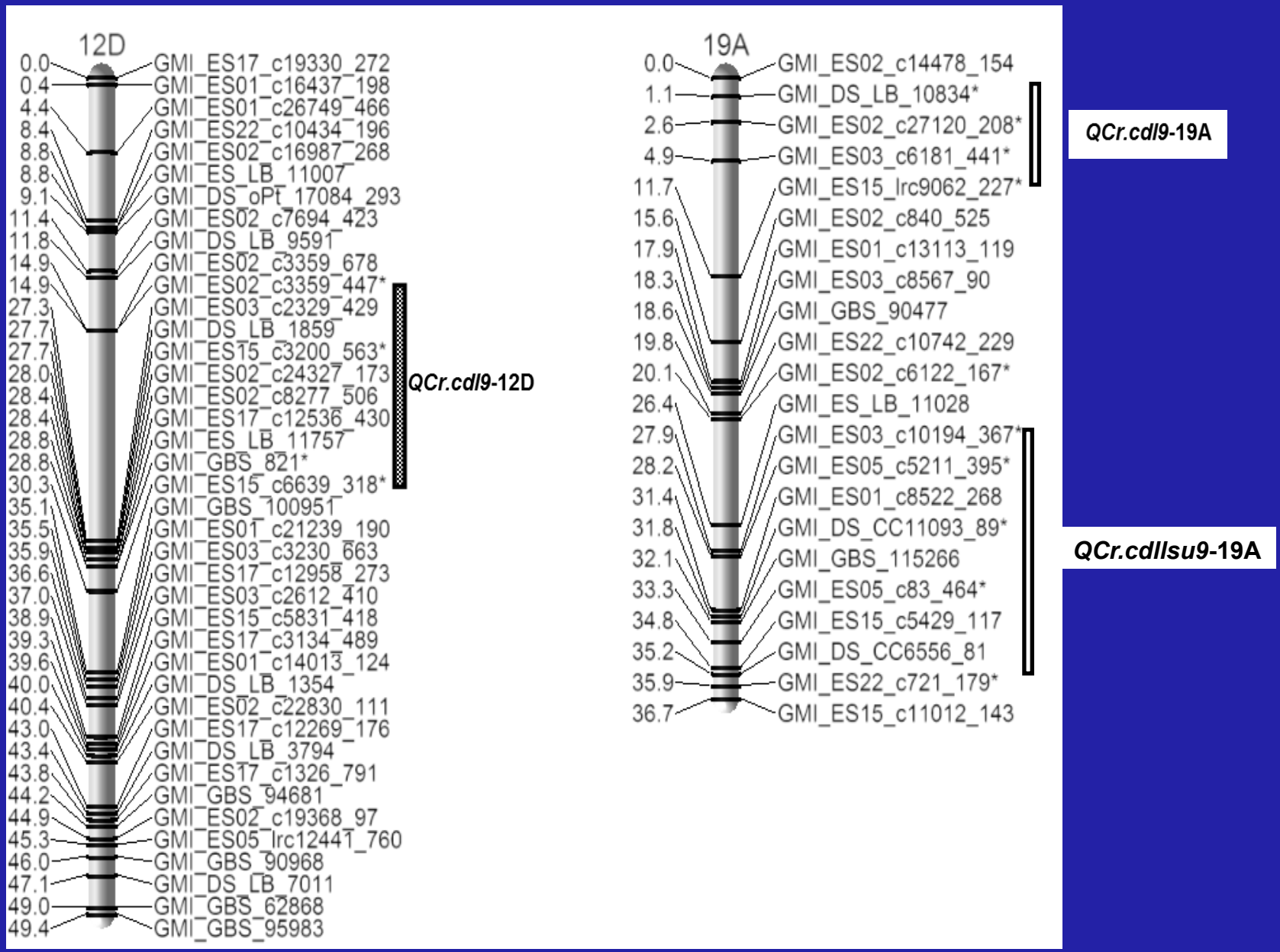
(2) Provena/94197A1-9-2-2-2-5 (P9) - 145 RILs**:**

- 954 polymorphic markers were assigned to 49 LGs representing 21 chromosomes with a total map length of 1130 cM

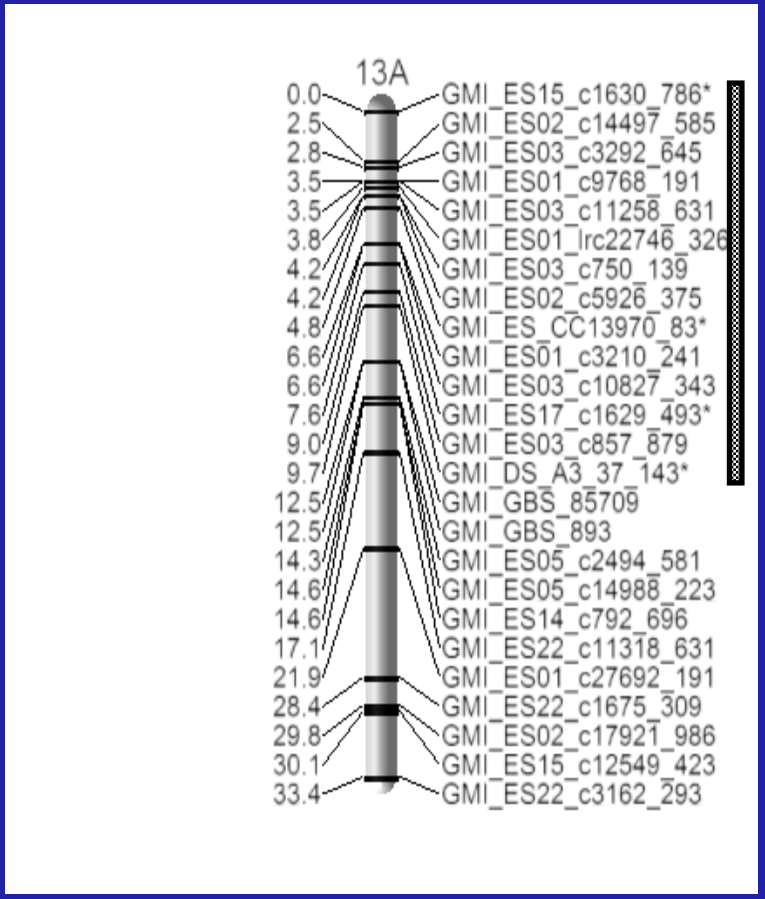
(3) CDC Boyer x 94197A1-9-2-2-2-5 (B9) - 80 RILs**:**

- Out of 1119 polymorphic markers, 287 were used assigned to 21 chromosomes with a total map length of 1119.8 cM

Chromosomal regions associated with CR resistance in PB population



Chromosomal region associated with CR resistance in P9 population



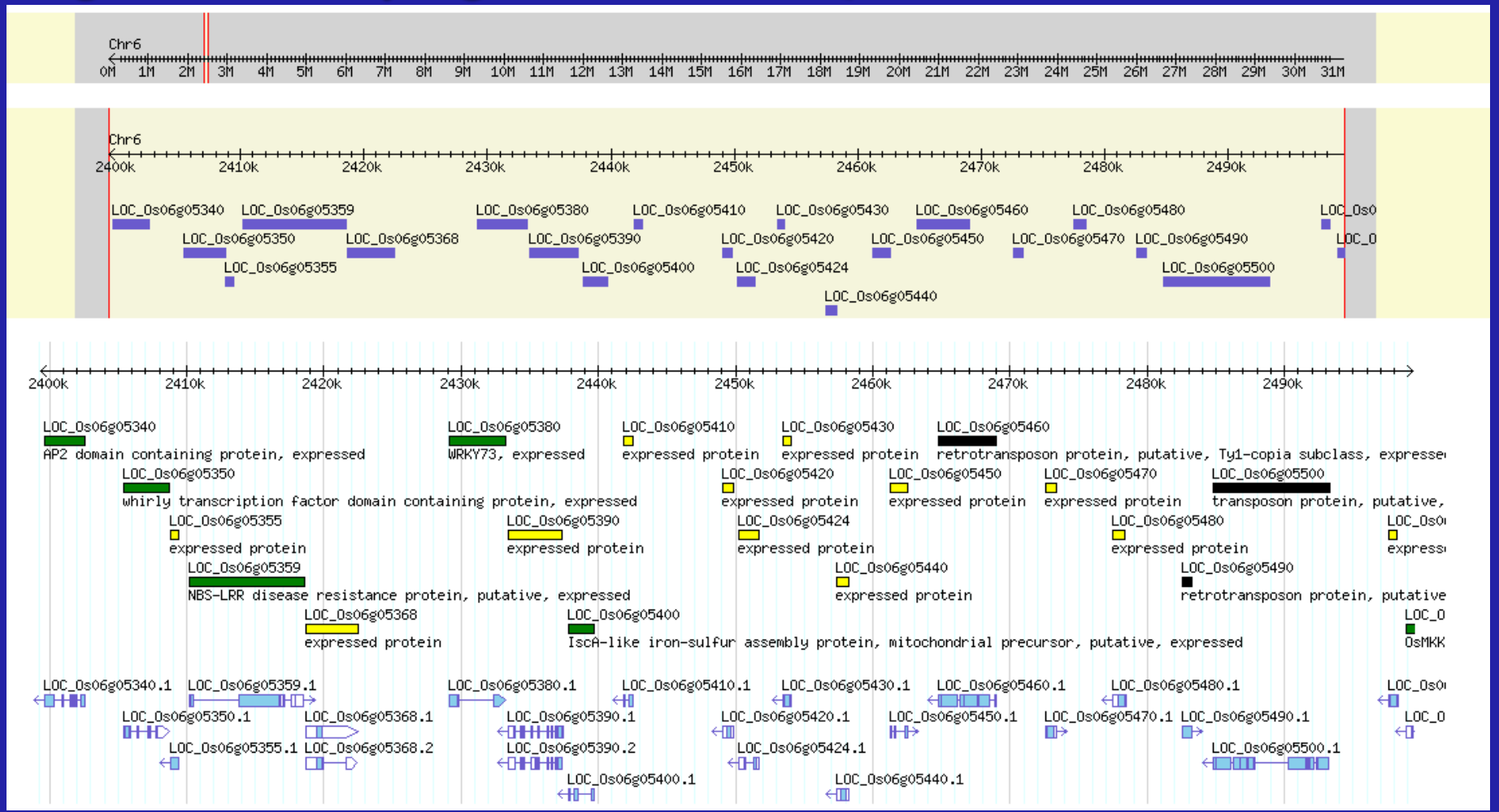
***QCr.cdl11*-13A**

Results

Population	QTL	Marker	Chromosom	Environmen	LOD	R^2 (%)	Additive effec
Provena x CDC-Boyer	*QCr.cdl9-19A*	GMI_DS_LB_10834	19A	CDL-09	3.6	11	-3.9
		GMI_ES02_c27120_208	19A	CDL-09	3.3	10	-3.8
		GMI_ES03_c6181_441	19A	CDL-09	4.9	15	-4.1
		GMI_ES15_lrc9062_227	19A	CDL-09	4.1	13	-3.9
		GMI_ES02_c6122_167	19A	CDL-09	4.5	14	-4.1
		GMI_ES03_c10194_367	19A	CDL-09	3.5	11	-3.6
		GMI_ES05_c5211_395	19A	CDL-09	5.1	16	-4.4
		GMI_DS_cc11093_89	19A	CDL-09	6.5	20	-4.7
		GMI_ES05_c83_464	19A	CDL-09	5.9	18	-4.5
	QCr.cdllu9-19A	GMI_ES22_c721_179	19A	CDL-09	3.7	11	-3.7
		GMI_ES02_c6122_167	19A	LSU-09	3.7	12	-4.2
		GMI_DS_cc11093_89	19A	LSU-09	3.0	10	-3.7
		GMI_ES05_c83_464	19A	LSU-09	3.3	10	-3.9
		GMI_ES02_c3359_447	12D	CDL-09	3.2	10	-3.4
	QCr.cdl9-12D	GMI_ES15_c3200_563	12D	CDL-09	3.1	10	-3.2
		GMI_GBS_821	12D	CDL-09	3.3	11	-3.3
		GMI_ES15_c6639_318	12D	CDL-09	3.0	10	-3.3
Provena x 94197A1-9-2-2-	*QCr.cdl11-13A*	GMI_ES15_c1630_786	13A	CDL-11	11.2	33	-7.9
		GMI_ES01_lrc22746_326	13A	CDL-11	12.0	35	-8.0
		GMI_ES_CC13970_83	13A	CDL-11	8.8	27	-7.2
		GMI_ES17_c1629_493	13A	CDL-11	7.0	22	-6.5
		GMI_DS_A3_37_143	13A	CDL-11	5.8	19	-6.0
CDC Boyer x 94197A1-9-2	*QCr.cdl11-13A*	GMI_ES15_c1630_786	13A	CDL-11	10.4	53	-12.9
		GMI_ES17_c3808_324	13A	CDL-11	9.7	50	-12.5
		GMI_ES05_c14988_223	13A	CDL-11	5.3	32	-10.1
		GMI_ES22_c11318_631	13A	CDL-11	4.7	29	-9.8
		GMI_ES01_c27692_191	13A	CDL-11	4.6	28	-9.9
	QCr.cdl09-13A	GMI_ES15_c1630_786	13A	CDL-09	3.5	19	-6.1
		GMI_ES17_c3808_324	13A	CDL-09	3.4	18	-6.0

Sequence homology

- Availability of rice genome database as well as oat SNP sequences serve as valuable tools to identify candidate genes underlying the detected QTL



The syntenic relationships between the significant markers on 13A and the Rice, Brachypodium and Sorghum genomes

Marker	Ch	Rice gene	Brachy gene	Sorghum gene
GMI_ES_CC13970_83	13A	**LOC_Os06g10560**	**Bradi1g46280**	Sb10g006800
GMI_DS_A3_37_143	13A	**LOC_Os06g27830**	Bradi4g10940	-
GMI_ES15_C1630_786	13A	-	**Bradi1g51130**	-
GMI_ES01_LRC22746_326	13A	-	**Bradi1g46960**	-
GMI_ES17_C1629_493	13A	-	-	-

- Four of the SNPs showed significant sequence homology to loci on chromosome 6 of rice. This region of rice chromosome 6 shows extensive orthology with several SNP markers on chromosome 13A of oat. Within this region, there are 7 candidate genes for resistance. Six of these are NBS-LRR genes and one is a LRR receptor kinase gene.

The syntenic relationships between the significant markers on 19A and the Rice, Brachypodium and Sorghum genomes

Marker	Ch	Rice gene	Brachy gene	Sorghum gene
GMI_ES14_C2285_377	19A	LOC_Os12g43630	Bradi4g00910	Sb08g022770
GMI_ES02_C27120_208	19A	LOC_Os12g04940	Bradi4g26590	Sb05g002755
GMI_ES15_LRC9062_227	19A	LOC_Os11g10070	Bradi4g22770	Sb05g006520
GMI_ES03_C16306_411	19A	LOC_Os10g37710	Bradi3g31440	Sb01g049530
GMI_ES15_C5429_117	19A	LOC_Os10g40200	Bradi3g32830	Sb01g029750
GMI_ES05_C83_464	19A	LOC_Os10g40510	Bradi3g50900	Sb01g050360
GMI_DS_LB_955	19A	**LOC_Os01g59580**	**Bradi2g52970**	Sb09g026141
GMI_ES03_C10194_367	19A	**LOC_Os01g57066**	**Bradi2g51700**	-
GMI_ES_LB_11028	19A	**LOC_Os01g62870**	Bradi3g37330	Sb03g039770
GMI_ES03_C6181_441	19A	-	-	-
GMI_ES05_C2066_503	19A	-	Bradi4g20900	Sb05g006890
GMI_ES01_C16071_418	19A	-	-	-

- Three of these markers showed significant sequence homology to loci on chromosome 1 of rice. Within this region, there are 5 candidate genes for resistance.

The syntenic relationships between the significant markers on 12D and the Rice, Brachypodium and Sorghum genomes

Marker	Ch	Rice gene	Brachy gene	Sorghum gene
GMI_ES02_C3359_447	12D	LOC_Os04g56620	Bradi5g24930	Sb06g031680
GMI_ES15_C6639_318	12D	LOC_Os04g39270	Bradi5g12870	Sb06g019430
GMI_ES15_C3200_563	12D	-	-	-
GMI_GBS_821	12D	-	-	-

- These markers spanned a 17350 Kb region on chromosome 4 of rice, which is a homologous to chromosome 12D of oat
- Using the genome browser, 8 candidate genes for resistance were identified within this region. Five of these are NBS-LRR genes, two are RPP genes, and one is a RPM gene

Future Work

- Validate these QTL and identify tightly linked markers for MAS
- Find candidate resistance genes underlying this QTL which may facilitate synteny-based positional cloning of disease resistance genes from the two parents


Thank you
Questions?