Identification of Markers Associated With Barley Yellow Dwarf Virus Tolerance in Spring Oat and Their Utilization in Predictive Breeding

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Introduction

Spring oat (*Avena sativa* L.) historically has been an important cereal grain crop for human and livestock consumption, and although production has significantly declined through the 20th and early 21st century, oats are still recognized for their nutritional and health benefits. Barley Yellow Dwarf (BYD) is the most important viral disease of oat and causes economically significant yield losses worldwide.[1] BYD is caused by Barley Yellow Dwarf Viruses (BYDV) that are vectored by aphids. Until recently, molecular marker technology in oats has lagged behind corn and soybean and a newly developed SNP array using the Infinium Assay developed by Illumina has now allowed for more insight into tolerance to the disease.[2]

Objectives

The objectives of this study were to identify markers that are linked to quantitative trait loci (QTL) for barley yellow dwarf virus tolerance in two bi-parental recombinant inbred populations and to determine their use in predictive breeding.

Materials and Methods

- RIL Population 4 ($F_{5:8}$)
  - Tolerant parent: IL86-1156 (Ogle//Ogle/IL75-5743)
  - Susceptible parent: Clintland 64
  - 115 RILs
- RIL Population 5 ($F_{5:8}$)
  - Tolerant parent: IL86-6404 (IL75-5743/IL75-5662//IL81-1454)
  - Susceptible parent: Clintland 64
  - 177 RILs
- Tolerant parents share parent (IL75-5743) and grandparent (Coker 227)
- Phenotypic data from 2002, 2003, 2010, 2011 from the University of Illinois Small Grains Oat BYDV Nursery in Urbana, IL
  - Planted in 15 seed hills
  - Randomized Complete Block Design (RCBD)
  - 3 reps in 2002-2003 and 2 reps in 2010-2011
  - 3 ratings in 2002-2003 and 2 ratings in 2010-2011
- Plants inoculated with Bird Cherry-Oat Aphids (*Rhopalosiphum padi*) carrying BYDV-PAV-IL at the 2 to 3 leaf stage (Feekes GS 2)
- Rating performed on 0 – 9 scale[3,4]
  - 0 - completely healthy (no symptoms)
  - 9 - highly susceptible (stunting, completely blasted florets, leaf chlorosis)
  - Rated after flowering (Feekes 10.6)
- High Density Oat SNP Array
  - 6000 Single Nucleotide Polymorphisms (SNPs)
  - Infinium Assay developed by Illumina
  - ~1000 polymorphic SNPs between parents in each population

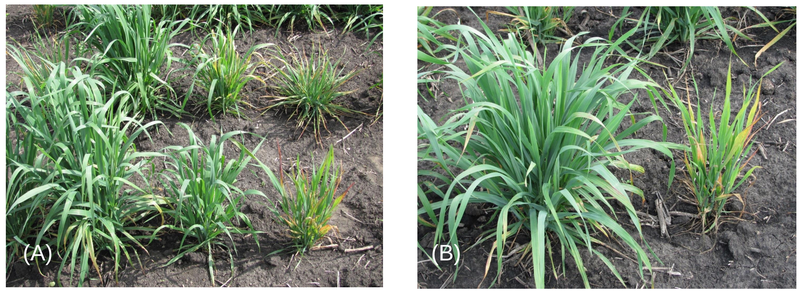

Figure 1. (A) Range of responses from oat (*Avena* sativa *L.)* to barley yellow dwarf virus (BYDV) from tolerant to susceptible (left to right). (B) Tolerant plant response compared to a susceptible response in oat to BYDV.

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Disclaimer

Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

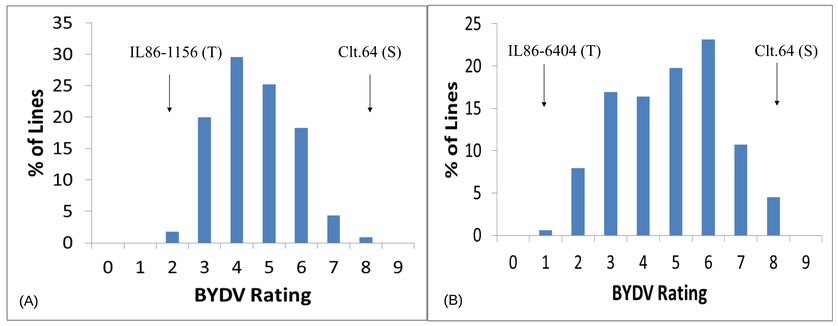

Figure 2. Frequency distributions of RIL population 4 (A) and RIL population 5 (B) for barley yellow dwarf virus (BYDV) rating averaged across four years of phenotypic data. Population 4 (115 RILs) was developed from the cross between the tolerant (T) IL86-1156 and the susceptible (S) Clintland 64. Population 5 (177 RILs) was developed from the cross between the tolerant IL86-6404 and the susceptible Clintland 64.

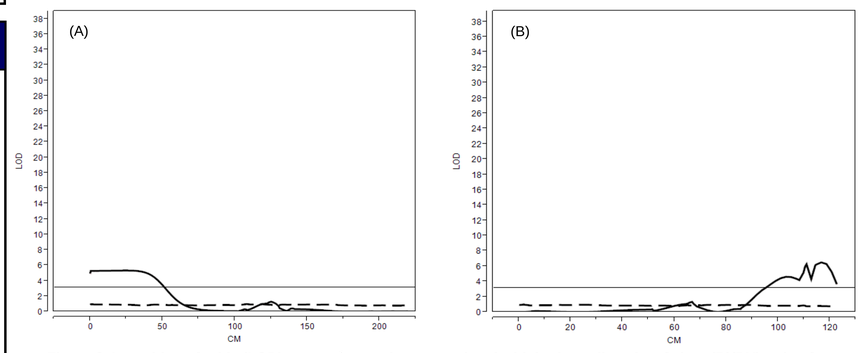

Figure 3. Logarithm of odds (LOD) scores for markers associated with barley yellow dwarf virus (BYDV) rating for population 4 (A) and 5 (B) on chromosome 1C

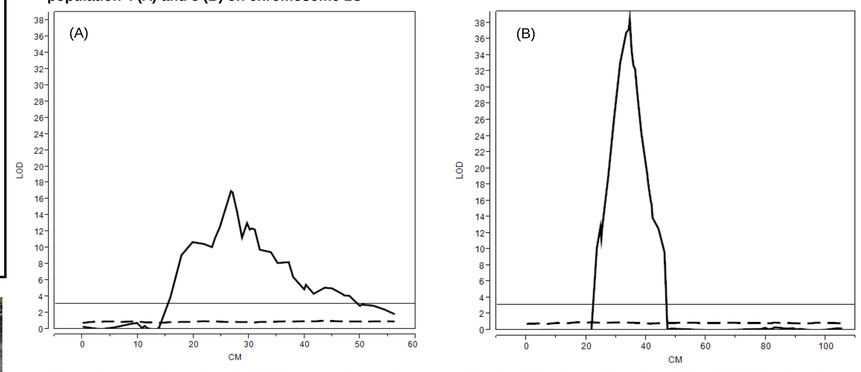

Figure 4. Logarithm of odds (LOD) scores for markers associated with barley yellow dwarf virus (BYDV) rating for population 4 (A) and 5 (B) on chromosome 3C

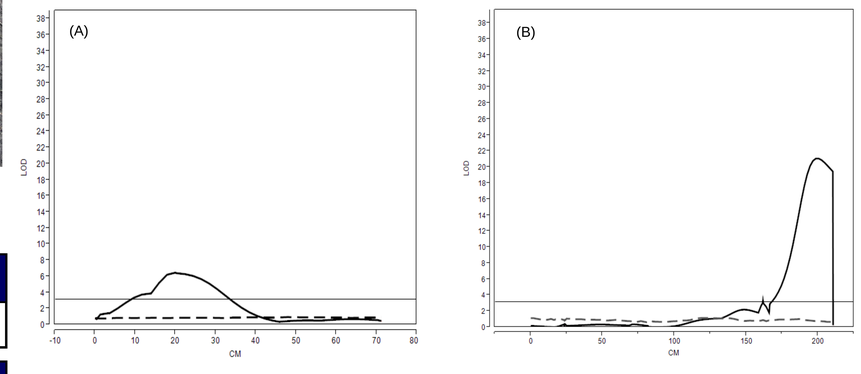

Figure 5 . Logarithm of odds (LOD) scores for markers associated with barley yellow dwarf virus (BYDV) rating for population 4 (A) and 5 (B) on chromosome 19A

Analysis

- Phenotypic Evaluation
  - SAS v9.2 (SAS Institute, Cary, NC)
    - PROC MIXED.
    - PROC UNIVARIATE,
    - PROC GLM
- Linkage mapping and QTL analysis
  - JMP Genomics 5.1 (SAS Institute, Cary, NC)
    - Composite interval mapping
    - LOD threshold values determined using 1000 permutations
    - Critical LOD threshold values set at 3.05 for RIL population 4
    - Critical LOD set at 3.12 for RIL population 5
    - α = 0.05
    - Framework map used[2]

Results

- Broad continuous distribution for BYDV rating was observed across both populations and all years (Figure s 1 and 2).
- QTL were identified on chromosomes: 1C, 3C, 5C, 15A, 19A, 9D, 12D (Table 1).
- QTL significant across both populations were located on chromosomes 1C, 3C, 5C and 19A however the QTL on 1C appears to be different depending on the population.
- The QTL on chromosome 19A was found to be similar between the populations with the two markers being in close linkage.
- Population 5 had multiple specific QTL not present in Population 4 on chromosomes 15A, 9D and 12D.
- The QTL on chromosome 3C was the most significant QTL observed and explained the most phenotypic variation, almost 50% in population 4 and 65% in population 5.
- The three QTL shared between the two populations appear to have large effects.

Table 1. Summary of significant quantitative trait loci (QTL) for barley yellow dwarf virus tolerance in oat recombinant inbred line (RIL) populations derived from two tolerant by susceptible crosses.

Population	Chromosome	cM	Linked Marker	LOD	Additive Effect	R^2 (%)
4	1C	24.4	GMI_ES_cc11019_290	5.34	-1.40	16.6
	3C	27.0	GMI_DS_cc1800_254	16.84	-0.96	49.7
	5C	81.3	GMI_GBS_9676	3.06	-0.37	11.7
	19A	20.4	GMI_ES05_c3073	6.40	-0.60	22.9
5	1C	116.7	GMI_ES_LB_7284	6.51	-0.45	16.4
	3C	34.5	GMI_DS_cc1800_254	38.40	-1.15	65.3
	5C	58.3	GMI_ES15_c2810_658	4.69	-0.29	12.1
	15A	0.3	GMI_DS_opt_12128_39	3.64	-0.25	9.6
	19A	200.5	GMI_ES_17_c360_817	21.08	-1.30	39.4
	9D	71.0	GMI_ES14_c2753_587	4.14	-1.19	10.8
	12D	90.7	Gmi_ES17_c12269_176	4.23	-0.28	11.0

Conclusions

- The shared QTL appear to be important regions conveying BYDV tolerance (1C, 3C, and 19A) (Figures 3 – 5).
- Although the QTL on chromosome 3C was the most significant and explained the most variation, it did not have the largest effect compared to the other shared QTL.
- The markers associated with significant QTL can be used in predictive breeding via partition trees to help aid in the selection of BYDV tolerant parents by crossing lines with undesired alleles at these markers to lines containing the proper alleles.
- Improving the quality of crosses can lead to more efficient progress for tolerance to BYD.

Literature Cited

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