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

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Materials and Methods

- **RIL Population 4 (F₄)**
  - Tolerant parent: IL86-1156 (Ogle/Ogle/IL75-5743)
  - Susceptible parent: Clintland 64
  - 115 RILs
- **RIL Population 5 (F₄)**
  - 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-PAVIL at the 2 to 3 leaf stage (Feekes GS 2)**
- **Rating performed on 0 – 9 scale:**
  - 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 marker set developed by Illumina
  - ~1000 polymorphic SNPs between parents in each population

Results

- Broad continuous distribution for BYDV rating was observed across both populations and across all years (Figure s 1 and 2).
- QTL were identified on chromosomes: 1C, 3C, 5C, 15A, 19A, 9D, 12D (Table 1).
- Population 5 had multiple specific QTL not present in Population 4.
- SAS v9.2 (SAS Institute, Cary, NC)
- 6000 Single Nucleotide Polymorphisms (SNPs)
- Critical LOD threshold values set at 3.05 for RIL population 4
- Critical LOD set at 3.12 for RIL population 5

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 crosses between tolerant populations to determine their use in predictive breeding.
- Improving the quality of crosses can lead to more efficient progress for tolerance 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.

Analysis

- **Phenotypic Evaluation**
  - PROC MIXED.
  - PROC UNIVARIATE.
  - PROC GLM
- **Linkage mapping and QTL analysis**
  - MapQTL Genomics 5.1 (SAS Institute, Cary, NC)
  - Composite interval mapping
  - LOD threshold values determined using 1000 permutations
  - Critical LOD threshold values set at 3.12 for RIL population 4
- Framework map used

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.

<table>
<thead>
<tr>
<th>Population</th>
<th>Chromosome</th>
<th>cM</th>
<th>Linked Marker</th>
<th>LOD</th>
<th>Additive Effect (%)</th>
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</thead>
<tbody>
<tr>
<td>4</td>
<td>1C</td>
<td>7.6</td>
<td>GMI_ES_c1017091_292</td>
<td>5.34</td>
<td>-1.80</td>
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<tr>
<td></td>
<td>3C</td>
<td>27.9</td>
<td>GMI_Ds_c11800_254</td>
<td>16.84</td>
<td>-0.96</td>
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<tr>
<td></td>
<td>5C</td>
<td>81.3</td>
<td>GMI_GBS_9676</td>
<td>3.06</td>
<td>-0.37</td>
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<td></td>
<td>19A</td>
<td>20.4</td>
<td>GMI_ES5/05_c3073</td>
<td>0.40</td>
<td>-0.60</td>
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<tr>
<td>5</td>
<td>1C</td>
<td>116.7</td>
<td>GMI_ES_IL_7284</td>
<td>6.51</td>
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<td>3C</td>
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<td>GMI_Ds_c11800_254</td>
<td>38.40</td>
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<td>19A</td>
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<td>GMI_ES_17_c360_817</td>
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<td>9D</td>
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<td>12D</td>
<td>90.7</td>
<td>GMI_ES17_c1268_176</td>
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<td>-0.28</td>
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Literature Cited