Identification, characterization and mapping of a new leaf rust (Puccinia triticina) resistance gene in spring wheat (Triticum aestivum)

Boyce M1,2, Brule-Babel A1, Hiebert C2, McCallum B2

1Department of Plant Science, University of Manitoba; 2Cereal Research Centre, Agriculture and Agri-Food Canada

Introduction

- Leaf rust is the most common and widespread disease that affects wheat with average yield reductions between 5-15\% and epidemic losses of upwards of 65\%.
- 60+ leaf rust resistance genes identified to date, most of which confer race specific resistance.
- A series of near-isogenic wheat lines were developed in a Thatcher background, each with a single leaf rust resistance gene used for: world-wide virulence surveys, genetic studies of resistance genes, and host/parasite interaction experiments (Dr. Peter Dyck, Cereal Research Centre, AAFC, Winnipeg, Canada).
- After 2000, TDBG, a predominant race of leaf rust, demonstrated avirulence to some lines of the Tc-Lr1 near isogenic line (NIL) in a characteristic mesothetic infection type.
- The Tc-Lr1 NIL (RL6003) was demonstrated to contain an additional resistance gene in some lines which segregated independently of Lr1, this gene was temporarily designated LrCen.
- TDBG also demonstrates avirulence to the Tc-Lr14a and Tc-Lr20 NILs as well as Little Club, thought to be a universally susceptible cultivar.
- A doubled haploid population of Tc-LrCen/Sumai3- lr34 was developed to further study this gene.
- Preliminary phenotypic data on a diverse set of Canadian wheat lines indicate this gene may be widely distributed within the Canadian hard red spring wheat germplasm.

Objectives

1. To phenotypically characterize the leaf rust resistance gene, LrCen, derived from the Tc-Lr1 NIL.
2. To map the leaf rust resistance gene and identify usable markers for marker assisted selection.
3. Perform allelism testing with Lr14a (7B), Lr20 (7A) and Little Club.
4. Determine the distribution of LrCen within Canadian hard red spring wheat (CWRS) germplasm.

Materials and Methods

1. Phenotypic characterization of Tc-LrCen X Sumai3- lr34 DH population.

Results

Table 1. Phenotypic segregation of LrCen within the Tc-LrCen/Sumai3- lr34 DH population inoculated with race TDBG.

<table>
<thead>
<tr>
<th>Resistant lines</th>
<th>Susceptible lines</th>
<th>Expected ratio</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>108</td>
<td>84</td>
<td>1:1</td>
<td>0.081</td>
</tr>
</tbody>
</table>

Figure 1. Phenotypic reactions observed on seedlings from the Tc-LrCen/Sumai3- lr34 doubled haploid population inoculated with leaf rust race TDBG, avirulent to LrCen.

2. Mapping process

- Marker association
  - Flumine Infinium\# 90X SNP array
  - Filter SNP markers – GenesetStudio\#
  - Initial two-point linkage

- BLAST
  - Wheat survey sequence
  - Putative chr locations for SNPs

- Confirm and map location
  - Chr-specific SSR markers
  - Map using MapDisto\#

Figure 2. Preliminary linkage map created using MapDisto for SNP and SSR markers linked to LrCen.

Table 2. BLAST results for 133 linked SNP (Illumina Infinum assay) marker sequences against the Wheat Survey Sequence to determine the best putative chromosome location.

<table>
<thead>
<tr>
<th>BLAST match order for 7AL</th>
<th>Number of SNPs</th>
<th>Percent of linked SNPs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Best match</td>
<td>101</td>
<td>76%</td>
</tr>
<tr>
<td>Second best match</td>
<td>14</td>
<td>11%</td>
</tr>
<tr>
<td>Third or worse match</td>
<td>15</td>
<td>11%</td>
</tr>
<tr>
<td>No match</td>
<td>3</td>
<td>2%</td>
</tr>
</tbody>
</table>

Preliminary Conclusions

1. Preliminary marker data indicate a putative map location for LrCen on the long arm of chromosome 7A.
2. The Tc-Lr20 NIL appears to carry two genes, one of which appears to be LrCen. The relationship between these genes will be examined in future work.
3. Preliminary phenotypic infection data with race TDBG indicate LrCen is widely distributed within the Canadian hard red spring wheat germplasm.

References


Acknowledgements

I would like to acknowledge ARDI and the Willy Wiebe Fellowship for funding. I would also like to thank Mira Popovic, Jadwiga Budzinski, Mary Melscher, Maria Stomenzovu, and Epifania Austria for technical support.