

Mapping Spot Blotch & Common  
Root Rot (Causal Agent: *Bipolaris  
sorokiniana*) Resistance Genes in  
Barley

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## Abstract

The fungal pathogen *Bipolaris sorokiniana* (teleomorph *Cochliobolus sativus*) causes the foliar disease spot blotch (SB) and the root disease common root rot (CRR). Spot blotch and CRR are serious disease constraints to barley production in warmer growing regions of the world, with estimated yield losses ranging from 30-70% from SB and 15-30% for CRR. Although chemical treatments may assist in controlling spot blotch infections, the most effective and environmentally sound means of control for each disease is breeding for varieties with natural resistance. In Australia, no commercially available varieties offer resistance to either SB or CRR. This study has sought to establish molecular markers that will be useful for selecting for resistance to each of these important fungal diseases.

Barley cultivars derived from the breeding line NDB112 have provided durable SB resistance in the North Dakota region of the USA for over 40 years. The robustness of this resistance had not been determined under Australian environmental conditions or with those *B. sorokiniana* pathotypes present within Australia. To elucidate the genetics of resistance, two seedling and two field trials were conducted on an ND11231-12/VB9524 (ND/VB) doubled haploid (DH) population (180 lines). A molecular map of the ND/VB population was curated in order to provide a firm basis for mapping of resistance loci. Composite interval mapping revealed that different gene combinations are effective at different stages of plant development. Seedling resistance was found to be conditioned by a major locus on the short arm of chromosome 7H and this region was validated in the related population ND11231-11/WI2875\*17. A minor quantitative locus on chromosome 5HS was detected in one of the two seedling trials. However, this region requires further investigation to confirm its association to SB resistance in this population. Field resistance to SB in adult plants was found to be associated with two major quantitative trait loci (QTL) on chromosomes 7HS and 3HS; and a putative third minor QTL on chromosome 2HS. The 7H region is common between seedling and field resistance and is the most important locus for the expression of resistance at both stages of plant

development. These findings largely concur with genetic studies of this trait in two-rowed barley germplasm in North American environments.

Common root rot is a difficult disease to phenotype for, and breeding programs will benefit from the identification of molecular markers linked to resistance. Data was provided from field trials of subsets of the population over four years. Using a novel approach combining the efficiency of bulked-segregant analysis with high-throughput Diversity Arrays Technology markers (BSA-DArT), CRR resistance was found to be conditioned by three putative QTL in an unmapped Delta/Lindwall population. QTL were identified on chromosomes 2HS, 4HS, and 7HS. To validate the trait-linkage associations between the DArT markers and the CRR QTL, microsatellite (SSR) markers known to map to the regions identified by BSA-DArT were used. The 2H and 4H regions were validated using marker regression of the SSR markers in most seedling trials, whereas the 7H QTL, which is proximal to the location of the SB resistance QTL in the ND/VB population, was detected in only one seedling trial.

The QTL identified in this study offer potential to combat the foliar and root diseases caused by this fungal pathogen. The chromosomal location of QTL for SB and CRR resistance have been found to differ in the ND/VB and D/L populations, which suggests that resistance to each disease is independently inherited. Further research is required to confirm the hypothesis that it is possible to combine resistance to both diseases into a single genotype. Such allelic combinations would provide elite germplasm that would benefit barley breeding programs world-wide.

## **Certification of Dissertation**

I certify that the ideas, experimental work, results, analyses, and conclusions reported in this dissertation are entirely my own effort, except where otherwise acknowledged. I also certify that the work is original and has not been previously submitted for any other award, except where otherwise acknowledged.

\_\_\_\_\_  
Signature of Candidate

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Date

### ENDORSEMENT

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Signature of Principal Supervisor

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Date

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## Table of Contents

<u>1. Introduction and Literature Review.....</u>	<u>1</u>
<u>1.1 Barley: History, Origin and Breeding.....</u>	<u>1</u>
<u>1.2 Major Limitations on Crop Production.....</u>	<u>4</u>
<u>1.3 Spot Blotch and Common Root Rot.....</u>	<u>4</u>
<u>1.3.1 The Fungal Organism.....</u>	<u>5</u>
<u>1.3.2 Infection and Symptoms.....</u>	<u>7</u>
<u>1.3.2.1 Spot Blotch.....</u>	<u>8</u>
<u>1.3.2.2 Common Root Rot.....</u>	<u>9</u>
<u>1.3.3 Disease Cycle and Management.....</u>	<u>10</u>
<u>1.4 The Nature of Plant Disease Resistance.....</u>	<u>11</u>
<u>1.4.1 Current Resistance Status.....</u>	<u>13</u>
<u>1.5 Selecting for Resistance.....</u>	<u>13</u>
<u>1.5.1 Phenotypic Screening Methods for Spot Blotch Resistance.....</u>	<u>13</u>
<u>1.5.2 Phenotypic Screening Methods for Common Root Rot Resistance. .</u>	<u>14</u>
<u>1.5.3 Molecular Markers.....</u>	<u>15</u>
<u>1.5.3.1 Linkage Maps.....</u>	<u>16</u>
<u>1.5.3.2 Mapping Populations.....</u>	<u>17</u>
<u>1.5.3.3 Identification of Polymorphisms and Marker Systems.....</u>	<u>18</u>
<u>1.5.3.3.1 Simple Sequence Repeats.....</u>	<u>19</u>
<u>1.5.3.3.2 Expressed Sequence Tags.....</u>	<u>20</u>
<u>1.5.3.3.3 Single Nucleotide Polymorphisms (SNPs).....</u>	<u>20</u>
<u>1.5.3.3.4 Diversity Array Technology.....</u>	<u>20</u>
<u>1.5.3.4 Bulk Segregant Analysis.....</u>	<u>21</u>
<u>1.5.3.5 Marker Genotyping.....</u>	<u>22</u>
<u>1.5.3.6 Linkage Analysis of Markers.....</u>	<u>22</u>
<u>1.5.4 Spot Blotch Resistance in Barley.....</u>	<u>25</u>
<u>1.5.5 Common Root Rot Resistance in Barley.....</u>	<u>26</u>





3.2.3 QTL Analysis.....	56
3.2.4 Epistatic Interactions Between QTL.....	56
3.2.5 Fine Mapping with SSRs.....	56
3.2.6 DNA Extraction and Quantification.....	57
3.2.7 Validation Analysis.....	58
3.3 Results.....	59
3.3.1 Map Curation.....	59
3.3.2 QTL Identification and Analysis.....	64
3.3.2.1 Seedling Resistance.....	64
3.3.2.2 Adult Plant Resistance.....	65
3.3.3 Epistatic Interactions between QTL.....	72
3.3.4 Fine Mapping of Chromosome 3H.....	75
3.3.5 Validation Analysis.....	76
3.4 Discussion.....	77
3.4.1 Map Curation.....	77
3.4.2 QTL Analysis.....	78
3.4.2.1 Identification of Seedling Resistance QTL.....	78
3.4.2.2 Identification of Field Resistance QTL.....	80
3.4.3 Validation of ND11231-12 derived QTL.....	81
4. Common Root Rot Resistance.....	84
4.1 General Introduction.....	84
4.2 Materials and Methods.....	85
4.2.1 Plant Materials.....	85
4.2.2 Bulk Segregant Analysis and Diversity Array Technology.....	85
4.2.3 Identification of Regions Associated with Common Root Rot Resistance.....	87
4.2.4 Confirmation of Regions with SSR Markers.....	87
4.3 Results.....	88

4.3.1 Response to Infection.....	88
4.3.2 Identification of Genomic Regions Associated with Common Root Rot Resistance.....	89
4.3.3 Confirmation of Regions with SSR Markers.....	95
4.4 Discussion.....	96
5. General Discussion.....	99
5.1 Spot Blotch Resistance.....	100
5.1.1 The ND11231-12 - derived resistance QTL.....	100
5.1.1.1 The 7H resistance QTL.....	100
5.1.1.2 The 3H QTL for Field Resistance.....	102
5.1.2 The VB9524 - derived resistance QTL.....	104
5.1.3 Other resistance alleles in the ND11231-12/VB9524 population .....	104
5.2 Common Root Rot Resistance.....	105
5.3 Future Directions.....	106
5.4 Conclusions.....	107

## List of Tables

<a href="#"><u>Table 1-1. Comparison of common marker types used in cereal breeding (adapted from Korzun, 2003)</u></a>	<a href="#"><u>19</u></a>
<a href="#"><u>Table 2-2. Variance components used to calculate heritability for reaction to the spot blotch disease</u></a>	<a href="#"><u>42</u></a>
<a href="#"><u>Table 2-3. Means, standard deviations and skewness for spot blotch phenotypic trials</u></a>	<a href="#"><u>43</u></a>
<a href="#"><u>Table 2-4. Pearson's correlation between independent seedling and field trials</u></a>	<a href="#"><u>46</u></a>
<a href="#"><u>Table 2-5. The segregation ratios of spot blotch resistant and susceptible progeny and broad-sense heritability at the seedling and adult plant stages (ratio values of resistant: susceptible progeny represent the mean of the replicated trials)</u></a>	<a href="#"><u>47</u></a>
<a href="#"><u>Table 3-6. Summary of map curation, comparing the original map by Emebiri et al. (2005) with the curated map</u></a>	<a href="#"><u>64</u></a>
<a href="#"><u>Table 3-7. Summary of QTL identified using QTL Cartographer for spot blotch resistance seedling and field resistance in DH population ND11231-12/VB9534</u></a>	<a href="#"><u>71</u></a>
<a href="#"><u>Table 3-8. QTL identified for spot blotch resistance using QTL Network program</u></a>	<a href="#"><u>72</u></a>
<a href="#"><u>Table 4-9. Lines selected for BSA from the Delta/Lindwall population. Disease Severity, taken as a percentage of Timgalen, represents the average rating from trials in 2002, 2003 and 2004 (2005 data was not available to use for constructing the bulks)</u></a>	<a href="#"><u>86</u></a>
<a href="#"><u>Table 4-10. DArT analysis of bulked DNA</u></a>	<a href="#"><u>90</u></a>
<a href="#"><u>Table 4-11. Marker regression of SSR markers confirming regions identified by BSA and DArT analysis</u></a>	<a href="#"><u>95</u></a>

## List of Figures

<a href="#">Figure 1-1. Worldwide distribution of barley showing levels of production in different regions (map taken from Gramene, 2005).....</a>	<a href="#">2</a>
<a href="#">Figure 1-2. Distribution map of major barley growing regions in Australia (map taken from Barley Australia, 2005). .....</a>	<a href="#">3</a>
<a href="#">Figure 1-3. Worldwide cereal cropping systems where <i>Bipolaris sorokiniana</i> infections have been detected (adapted from Kumar et al., 2002). Highlighted regions depict distribution of disease occurrence.....</a>	<a href="#">6</a>
<a href="#">Figure 1-4. Light microscope image showing conidia of <i>Bipolaris sorokiniana</i> (magnification = x1000; image taken from the Danish Research Centre for Organic Farming, 2005).....</a>	<a href="#">7</a>
<a href="#">Figure 1-5. Spot blotch symptoms on mature barley plants (photo: J. Bovill).....</a>	<a href="#">8</a>
<a href="#">Figure 1-6. Symptoms of common root rot of barley. Diseased plants show the characteristic infection of the sub-crown internode (arrow) and poor root development. Image reproduced with permission from K. Moore (NSW DPI).....</a>	<a href="#">9</a>
<a href="#">Figure 2-7. Infection rating scale of seedling infection responses to the spot blotch disease.....</a>	<a href="#">39</a>
<a href="#">Figure 2-8. Infection rating scale for field screening for spot blotch (scale adapted from Fletch and Steffenson, 1999).....</a>	<a href="#">40</a>
<a href="#">Figure 2-9. Frequency of infection responses to the spot blotch disease at the seedling stage. Arrows represent mean parental scores (ND11231-12 = ND; VB9524 = VB). .....</a>	<a href="#">45</a>
<a href="#">Figure 2-10. Frequency of infection responses to the spot blotch disease under field conditions. Arrows represent mean parental scores (ND11231-12 = ND; VB9524 = VB).....</a>	<a href="#">46</a>
<a href="#">Figure 2-11. Progression of the spot blotch infection in the field at two week intervals (rating 1-3). The red line represents the normal distribution curve.....</a>	<a href="#">48</a>
<a href="#">Figure 3-12. Revised genetic linkage map of the doubled haploid population ND11231*12/VB9524. ....</a>	<a href="#">60</a>

Figure 3-13. QTLs identified by composite interval mapping of seedling and field trials using the program QTL Cartographer. Horizontal red, purple and blue lines represent thresholds for suggestive, significant, and highly significant QTL respectively. The additive effect [a(H1)] of the QTL are also shown – a positive additive effect indicates that the QTL was inherited from the VB parent; a negative effect indicates that the QTL is inherited from the ND parent.....67

Figure 3-14. Mean disease severity of seedlings of doubled-haploid lines with the 7H QTL present and absent. ....73

Figure 3-15. Mean disease severity of doubled-haploid lines with combination of alleles for seedling resistance.....74

Figure 3-16. Mean disease severity of doubled-haploid lines with combination of alleles for field resistance.....75

Figure 4-17. Frequency of average adult infection responses to CRR. Disease severity is expressed as a percentage of the susceptible cultivar Timgalen. Arrows indicate average parental scores (D= Delta, L=Lindwall).....88

Figure 4-18. Normalised difference graphs of DArT-BSA genome scan identifying regions associated with CRR resistance in the Delta/Lindwall RI population. A normalised difference (plotted on y-axes) >100 is considered significant.....91