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

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science at the University of Southern Queensland

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2008

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 causes 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.

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Signature of Candidate Date

ENDORSEMENT

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Signature of Principal Supervisor Date

Acknowledgements

I would like to extend my sincere gratitude to my supervisors, Professor Mark Sutherland and Dr Anke Lehmensiek, for their guidance and support throughout the duration of my Post-graduate studies. Mark, your understanding, encouragement and support for my family has been awesome, no-one could ask for a better mentor and teacher. Anke, thank you for teaching me the "ropes" of QTL mapping and for your constant patience in the Lab, your efficiency and quality as a scientist is inspiring.

There are many other people I would like to thank, all of whom have made significant contributions to this research. Thankyou to Greg Platz and Dr Emma Mace from the Hermitage Research Station. I really enjoyed learning from you and I wish you both all the best in the future. Also, Thanks to Noel Knight and Rebecca Jolly, fellow students from USQ, and Terry Usher and Janet Barsby, from Hermitage Research Station, for their assistance and technical support with the phenotypic trials. I would also like to extend my gratitude to all the technical staff and others at USQ, in particular Bene Watson, Mo Boddington, Vic Schultz, Pat McConnell, Debbie White and Grant Daggard. You all made studying and working at USQ a pleasure and I wish you all the best in your future endeavours.

Heartfelt thanks to my Mum for planting and nurturing the seed that has grown into a love affair between me and all things science. The nights of watching Carl Sagan's "Cosmos" and days collecting rocks in the Atherton Tablelands laid the foundation for my desire to ask questions and find the answers. Thanks for always having faith in me, when most others didn't.

I could not have completed this thesis if not for my dearest husband, Bill. At times life has been very challenging for both of us, but we have faced those challenges head-on and we make an incredible team. Know that the most rewarding and precious moments in my life have been with you, you are a truly special person. I love the life we have made together and look forward to growing very old together.

Finally, I would like to thank my children, Jacynda and William, who make it all worthwhile.

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