GENETIC AND MOLECULAR ANALYSES OF RESISTANCE TO RUST DISEASES IN BARLEY

by

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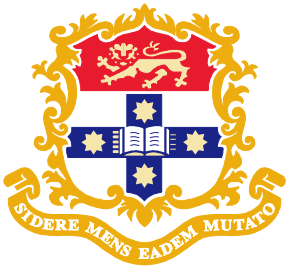

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Statement of authorship

This thesis contains no material which has been accepted for the award of any other degree or diploma in any university, and to the best of my knowledge, it contains no material previously published by any other person, except where due references are made in the text.

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“The reason of my liking to keep the marks for cleanness on plants, which have afterwards become rusty, is that I look upon lateness in becoming affected by it, as a measure of resistance to the parasite; and because I consider that individual plants may transmit to their progeny the valuable quality of resisting the parasite until a late stage of their lives, when it has less time for injuring the grain.”

Farrer, W. J. (1898). The making and improvement of wheats for Australian conditions. Agr. Gas. N.S. W. **9**: 131-168.

Dedicated to

All scientists who contributed to the current understanding of rust resistance in cereals

Summary

The responses of 92 barley genotypes to selected *P. hordei* pathotypes was assessed in greenhouse tests at seedling growth stages and in the field at adult plant growth stages to determine known or unknown resistances. On the basis of multipathotype tests, 35 genotypes were postulated to carry *Rph2*, *Rph4*, *Rph5*, *Rph12*, *RphCantala* alone or combinations of *Rph2* + *Rph4* and *Rph1* + *Rph2*, whereas 52 genotypes lacked detectable seedling resistance to *P. hordei*. Five genotypes carried seedling resistance that was effective to all pathotypes tested, of which four were believed to carry uncharacterised resistance based on pedigree information. Field tests at adult plant growth stages indicated that while 28 genotypes were susceptible, 57 carried uncharacterised APR to *P. hordei*. Pedigree analysis indicated that APR in the test genotypes could have been derived from three different sources. The resistant responses of seven cultivars at adult plant growth stages were believed to be due to the presence of seedling resistance effective against the field pathotypes.

Genetic studies conducted on 10 barley genotypes suggested that 'Vada', 'Nagrad', 'Gilbert', 'Ulandra (NT)' and 'WI3407' each carry one gene providing adult plant resistance to *P. hordei*. Genotypes 'Patty', 'Pompadour' 'Athos', 'Dash' and 'RAH1995' showed digenic inheritance of APR at one field site and monogenic inheritance at a second. One of the genes identified in each of these cultivars provided high levels of APR and was effective at both field sites. The second APR gene was effective only at one field site, and it conferred low levels of APR. Tests of allelism between resistant genotypes confirmed a common APR gene in all genotypes with the exception of 'WI3407', which based on pedigree information was genetically distinct from the gene common in 'Vada', 'Nagrad', 'Patty', 'RAH1995' and 'Pompadour'.

An incompletely dominant gene, *Rph14*, identified previously in an accession of *Hordeum vulgare* confers resistance to all known pathotypes of *P. hordei* in Australia. The inheritance of *Rph14* was confirmed using 146 and 106 F3 lines derived from the crosses 'Baudin'/ 'PI 584760' (*Rph14*) and 'Ricardo'/'PI 584760' (*Rph14*), respectively. Bulk segregant analysis on DNA from the parental genotypes and resistant and susceptible DNA bulks from F_3 lines using diversity array technology (DArT) markers located *Rph14* to the short arm of chromosome 2H.

Polymerase chain reaction (PCR) based marker analysis identified a single simple sequence repeat (SSR) marker, Bmag692, linked closely to *Rph14* at a map distance of 2.1 and 3.8 cM in the populations 'Baudin'/ 'PI 584760'and 'Ricardo'/'PI 584760', respectively.

Seedlings of 62 Australian and two exotic barley cultivars were assessed for resistance to a variant of *Puccinia striiformis*, referred to as *BGYR*, which causes stripe rust on several wild *Hordeum* species and some genotypes of cultivated barley. With the exception of six Australian barley cultivars and an exotic cultivar, all displayed resistance to the pathogen. Genetic analyses of six Australian barley cultivars and the Algerian barley 'Sahara 3771', suggested that they carried either one or two major seedling resistance genes to the pathogen. A single recessive seedling resistance gene, *Bgyr1*, identified in 'Sahara 3771' was located on the long arm of chromosome 7H and flanked by restriction fragment length polymorphism (RFLP) markers wg420 and cdo347 at genetic distances of 12.8 and 21.9 cM, respectively. Mapping resistance to *BGYR* at adult plant growth stages using a doubled haploid population derived from the cross 'Clipper'/'Sahara 3771' identified two major QTLs on the long arms of chromosomes 3H and 7H that explained 26 and 18% of total phenotypic variation, respectively. The QTL located on chromosome 7HL corresponded to the seedling resistance gene *Bgyr1*. The second QTL was concluded to correspond to a single adult plant resistance gene designated *Bgyr2*, originating from cultivar 'Clipper'.

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