

Inheritance of adult plant resistance to leaf rust in four European winter wheat cultivars

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INTRODUCTION

Of the three rust diseases of wheat, leaf rust, caused by *Puccinia triticina* (*Pt*) is considered the most prevalent world-wide. The disease is best controlled through genetic resistance and more than 50 genes conferring resistance have been identified and catalogued³. The leaf rust pathogen, however, has a remarkable ability to overcome resistance through migration, mutation, recombination and selection, and as a consequence, most catalogued resistance genes have been rendered ineffective.

To achieve sustainable disease resistance, there is an ongoing need to search for, understand and manipulate new sources of resistance, particularly the adult plant resistance (APR) genes that have a reputation for longevity. This is supported by the fact that leaf rust APR genes *Lr34* and *Lr46* have continued to condition durable leaf rust resistance despite global deployment over an extended period of time. Despite the durability of *Lr34* and *Lr46*, it should not be assumed that *Pt* pathotypes with matching virulence will not appear in due course. Hence, over reliance on both of these genes is undesirable and there is a need to characterize and deploy cultivars with additional APR genes. Better knowledge of the genetic control of seedling and adult plant resistances (APR) can significantly expedite their efficient use in breeding programs.

Previous studies have reported high levels of APR to leaf rust in European winter wheats^{4,6}, including cultivars Armada, Lona, Mec and Pegaso. In this paper, we report the identification and genetic analysis of APR in these four winter wheats via classical genetic analysis and the use of molecular markers.

MATERIALS AND METHODS

The resistant parents, Armada, Lona, Mec and Pegaso, and the susceptible parents, Avocet-S and Cunderdin-sib along with the leaf rust differentials were tested at the seedling stage in the greenhouse with three *Pt* pathotypes 53-1,(6),(7),10,11 (PBI Accession No. 810043); 104-1,2,3,(6),(7),11 +*Lr37* (020281) and 10-1,3,9,10,11,12 (040120), and in the field (prevalent pathotypes 53-1,(6),(7),10,11 and 10-1,3,9,10,11,12). Pathotype nomenclature and the methods of sowing and inoculation are described in McIntosh et al³.

To determine the inheritance of APR, doubled haploid (DH) populations [Mec/Avocet (M/A), 152 lines; Pegaso/Avocet (P/A), 300 lines] or F₃ populations

[Armada/Cunderdin-sib (A/C), 102 lines; Lona/Cunderdin-sib (L/C), 110 lines] were developed and tested in field. The DH populations were screened in the greenhouse at the seedling stage with *Pt* pathotypes 104-1,2,3,(6),(7),11+*Lr37* as well as in the field at the adult plant stage. The F₃ populations were screened in the field at the adult plant stage only. Greenhouse screening was done on the basis of the infection type (IT) scale⁹ with slight modifications², such that ITs 3+ or higher were considered susceptible. For field screening, disease severity (percentage leaf area affected) and host response using the modified Cobb scale⁵ were recorded on three occasions at fortnightly intervals. Disease severities of 80S or higher were considered susceptible.

The recently developed molecular marker csLV34 that co-segregates with *Lr34*¹ and csLV46 that co-segregates with *Lr46* (unpublished, E.S. Lagudah personal communication) were applied on the parents to assess for the presence of *Lr34* and *Lr46*, respectively.

RESULTS

At the seedling stage, all parents showed high ITs to all three pathotypes, except Lona and Avocet, which showed low ITs (;12- and X+, respectively), very typical of *Lr13* with pt. 104-1,2,3,(6),(7),11+*Lr37* (Table 1).

Table 1. Leaf rust responses of parents tested in the greenhouse and the field

Parent	Infection type in greenhouse with pathotype			Field disease score*	Postulated genes
	A	B	C		
Armada	3+	3+	3+	20MS	APR
Mec	3+	3+	3+	20MR	APR
Pegaso	3+	3+	3+	0R	APR
Lona	3+	3+	X+	20MR	<i>Lr13</i> +APR
Avocet	3+	;	;12-	90S	<i>Lr13</i> + <i>LrM</i> +APR
Cunderdin	3+	3+	3+	100S	None

A = 53-1,(6),(7),10,11*; B = 10-1,3,9,10,11,12* C = 104-1,2,3,(6),(7),11+*Lr37*

* prevalent field pathotype

The cultivar Avocet also showed the low IT ; with pt 10-1,3,9,10,11,12. This indicated that the parents Armada, Mec and Pegaso lacked detectable seedling gene(s) or

possessed ineffective seedling gene(s) against the pathotypes tested, whereas Lona and Avocet were postulated to carry *Lr13*. Avocet also possesses an uncharacterized resistance gene temporarily designated as *LrM*, a gene similar to one present in cultivar Morocco (RF Park unpublished). In the field, Armada, Lona, Mec and Pegaso were resistant while Avocet and Cunderdin-sib were susceptible (Table 1).

The seedling responses of families of both DH populations to pt 104-1,2,3,(6),(7),11+*Lr37* implied the presence of a single gene, likely *Lr13* from parent Avocet. The adult plant response of the populations in the field implied a digenic inheritance for the A/C and L/C populations, trigenic inheritance for the P/A population, whereas the M/A population segregated for 2 to 3 genes (Table 2).

Application of the two molecular markers confirmed the presence of *Lr34* in Lona and Pegaso, and *Lr46* in Mec and Pegaso.

Table 2. Inheritance of leaf rust resistance in four winter wheat populations (pops)

Pop	Growth stage	No. of Genes	Genes	
			Involved	From
M/A	Seedling	1	<i>Lr13</i>	Avocet
	APR	≥2	<i>Lr46+UC</i>	Mec
P/A	Seedling	3	<i>Lr13</i>	Avocet
	APR	4	<i>Lr34+Lr46+UC</i>	Pegaso
L/C	Seedling	nt	<i>Lr13</i>	Lona
	APR	2	<i>Lr34+UC</i>	Lona
A/C	Seedling	nt	<i>None</i>	-
	APR	2	<i>UC</i>	Armada

nt = not tested; UC = uncharacterized

DISCUSSION

APR to leaf rust resistance was detected in all four cultivars, confirming previous studies^{4,6} and the genetic studies conducted demonstrated that the APR was conferred by 2 to 3 genes. Molecular markers suggested that at least one resistance locus in Lona and Mec is controlled by *Lr34* and *Lr46*, respectively. In Pegaso, of three APR genetic loci estimated from genetic analysis, two are likely controlled by *Lr34* and *Lr46*. It was also noted that cultivars Lona and Pegaso showed clear expression of leaf tip necrosis (*Ltn*), a morphological marker linked with gene *Lr34*⁸. Although this morphological trait is difficult to observe under Australian conditions⁷, it was very obvious in the case of Lona and Pegaso.

The remaining APR genes in these cultivars are unknown but are of great interest and value as they are potentially new. Further genetic studies are now underway to characterise these resistances in more detail. The M/A, P/A and L/C populations have been

genotyped for seedling gene *Lr13*, and putative lines lacking *Lr13* but possessing APR have been isolated to simplify future mapping studies. Marker assisted genotyping of the entire populations is underway to identify genotypes possessing *Lr34* and *Lr46*, to allow the populations to be partitioned for mapping using DArT markers. To gain a better understanding of gene expression, it is planned to test the populations at multiple international-locations at rust hot-spots.

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