International Journal of Plant Breeding ©2008 Global Science Books

Characterisation of Seedling Resistance to Rust Diseases in Wheat Cultivars from Central Asia and the Caucasus

Kumarse Nazari[1,2] • Colin R. Wellings[1,3] • Robert F. Park[1] *

[1] The University of Sydney, Plant Breeding Institute Cobbitty, Private Mail Bag 11, Camden, NSW 2570, Australia
[2] Present address: International Center for Agricultural, Research in the Dry Areas (ICARDA), Tel Hadya, Aleppo, Syrian Arab Republic
[3] On secondment from NSW Department Primary Industries
Corresponding author: * **robertp@camden.usyd.edu.au**

ABSTRACT

The diseases stripe rust (caused by *Puccinia striiformis* f. sp. *tritici*, *Pst*), leaf rust (*P. triticina*, *Pt*), and stem rust (*P. graminis* f. sp. *tritici*, *Pgt*) are major threats to wheat production in the regions of Central Asia and Caucasus (CAC). Multi-pathotype tests on 32 winter wheat cultivars grown in CAC countries were used to characterise seedling resistance to *Pst*, *Pt*, and *Pgt* and where possible to postulate the identities of genes present. The most commonly postulated seedling stripe rust resistance gene was *Yr9* (eight cultivars). Evidence for the presence of *Yr1* (five cultivars), *Yr3+Yr4* (two cultivars), *Yr27* (one cultivar), and *Yr7+Yr9* (one cultivar) was also obtained. Twelve cultivars were seedling susceptible to all *Pst* pathotypes used, while the resistance of two cultivars could not be identified. Leaf rust resistance genes *Lr1*, *Lr2a*, *Lr3a*, *Lr3bg, Lr3ka*, *Lr13*, *Lr14a, Lr16*, and *Lr26* were postulated, present either singly or in combination in the cultivars. Of these, *Lr26* was the most common (nine cultivars) and *Lr13* was postulated frequently in combination with other *Lr* genes. Evidence was obtained for the presence of gene *LrB* in two cultivars, but this gene could not be differentiated clearly in this study. Stem rust resistance genes *Sr5*, *Sr7b*, *Sr8b*, *Sr9e*, *Sr9b*, *Sr11*, *Sr17*, *Sr30*, and *Sr31* were postulated in the cultivars either singly or in various combinations. Gene *Sr31* was the most common (10 cultivars), followed by *Sr8b* (six cultivars).

Keywords: gene postulation, leaf rust, multi-pathotype tests, *Puccinia*, stem rust, stripe rust, *Triticum*

INTRODUCTION

Despite the cultivation of improved high yielding and adapted wheat cultivars across large areas and different climatic zones, annual wheat production in many countries is often limited by biotic stresses that include rust diseases. Genetic resistance is regarded by many as the strategy of choice for the control of wheat rusts (Johnson 1988; McIntosh *et al.* 1995; Kolmer 1996). Conventional resistance breeding is environmentally safe, relatively easy to implement, and does not impose a direct added cost to farmers in low yielding production environments. Breeding for resistance to rusts has been successful in several national and international wheat breeding programs (McIntosh 1988; Rajaram *et al.* 1988; Singh *et al.* 2005).

Genetic diversity is a key element in plant breeding. Two methods have been used to determine the diversity of rust resistance genes in wheat cultivars: gene postulation (using multi-pathotype tests) and genetic analysis. Multi-pathotype tests apply the principles of the gene-for-gene hypothesis (Flor 1956; Person *et al.* 1962; Loegering 1985) to postulate rust resistance genes in host genotypes. This method has been used to postulate seedling resistance genes to all three rust diseases (e.g. McVey and Roelfs 1975; Roelfs and McVey 1979; Browder and Eversmeyer 1980; Dubin *et al.* 1989; Badebo *et al.* 1990; Singh and Rajaram 1991; Sharma *et al.* 1995; Singh *et al.* 2001; Oelke and Kolmer 2004).

The rust diseases – stripe rust (caused by *Puccinia striiformis* West. f. sp. *tritici*, *Pst*), leaf rust (caused by *P. triticina* (formerly *Puccinia recondita* Roberge ex Desmaz. f. sp. *tritici* Eriks. & Henn.), *Pt*), and stem rust (caused by *P. graminis* Pers. f. sp. *tritici*, *Pgt*), are major challenges in breeding high yielding wheat cultivars in Central Asian and Caucasus (CAC) countries. Several epidemics of wheat rusts have been reported in the CAC region in recent years (Absattarova *et al.* 2002; Yahyaoui *et al.* 2002).

An understanding of the identity and diversity of resistance genes in cultivars grown in CAC countries will assist breeders in removing susceptible cultivars, in determining the identity of currently deployed resistance genes, and in introducing genetic diversity into breeding germplasm. In this study, 32 wheat cultivars from the CAC region were investigated for the presence of resistance to the three rust diseases at seedling growth stages.

MATERIALS AND METHODS

Pathogen

Eight characterised pathotypes of *Pst*, 12 pathotypes of *Pt*, and 10 pathotypes of *Pgt* (**Table 1**) were selected for multi-pathotype tests in order to maximise the ability to detect known seedling resistance genes. Pathotype nomenclature for *Pst* followed the system described by Johnson *et al.* (1972), and incorporated minor modifications made by Wellings and McIntosh (1990). The nomenclature of *Pt* pathotypes was based on the standard race designation (Johnston and Browder 1966) followed by the addition of Australian supplementary differentials as described by McIntosh *et al.* (1995). Stem rust pathotypes were similarly described based on standard race designation (Stakman *et al.* 1962) with additional Australian supplementary differentials (McIntosh *et al.* 1995).

Host materials

Host materials comprised 30 bread wheat (*Triticum aestivum* L.) and two durum wheat (*T. turgidum* L. *durum*) cultivars, representing locally adapted winter wheat germplasm from CAC countries, with the control differential genotypes for each pathogen included as controls. The names, pedigrees, and origins of the CAC cultivars are presented in **Table 2**.

Received: 14 April, 2008. Accepted: 16 June, 2008.

Original Research Paper

Table 1 Pathotypes of *Puccinia striiformis* f. sp. *tritici*, *P. triticina* and *P. graminis* f. sp. *tritici* used in multi-pathotype tests to postulate resistance genes in 32 wheat cultivars.

Pathogen/ Pathotype	Accession number[a]	Virulence
P. striiformis* f. sp. *tritici [b,c]		
1. 104 E137 A-	821559	*Yr2*, *Yr3*, *Yr4*, *YrSD*, *YrSu*
2. 104 E137 A+	821552	*Yr2*, *Yr3*, *Yr4*, *YrSD*, *YrSu*, *YrA*
3. 108 E141 A-	832002	*Yr2*, *Yr3*, *Yr4*, *Yr6*, *YrSD*, *YrSu*
4. 110 E143 A+	861725	*Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *YrSD*, *YrSu*, *YrA*
5. 111 E143 A-	881732	*Yr1*, *Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *YrSD*, *YrSu*
6. 111 E143 A-, Sk+	991710	*Yr1*, *Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr27*, *YrSD*, *YrSu*
7. 134 E16 A+	021510	*Yr6*, *Yr7*, *Yr8*, *Yr9*, *YrA*
8. 238 E143 A+	951504	*Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr9*, *YrSD*, *YrSu*, *YrA*
P. triticina [d,e]		
1. 122-1,3,4,(6),7,12	93-L-1	*Lr1*, *Lr2a*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr10*, *Lr14a*, *Lr15*, *Lr17a*, *Lr17b*, *Lr20,* (*Lr27+Lr31*)[f]
2. 104-1,2,3,(6),(7),9,11	970188	*Lr1*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr10*, *Lr14a*, *Lr16*, (*Lr17a*), *Lr20*, *Lr23*, *Lr26,* (*Lr27+Lr31*)
3. 104-1,2,3,(6),(7),11 +*Lr*37	020281	*Lr1*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr10*, *Lr14a*, *Lr16*, (*Lr17a*), *Lr20*, *Lr23*, (*Lr27+Lr31*), *Lr37*
4. 104-2,3,6,(7),9,12	840412	*Lr1*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr10*, *Lr14a*, (*Lr17a*), *Lr17b*, *Lr23*, *Lr27+Lr31*
5. 104-2,3,(6),(7),11	840045	*Lr1*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr10*, *Lr14a*, *Lr16*, (*Lr17a*), *Lr23*, (*Lr27+Lr31*)
6. 76-1,3,5,10,12	990423	*Lr2c*, *Lr3a*, *Lr3bg*, *Lr3ka*, *Lr10*, *Lr13*, *Lr14a*, *Lr17b*, *Lr20*
7. 10-1,2,3,4,12	720468	*Lr1*, *Lr2a*, *Lr2c*, *Lr10*, *Lr14a*, *Lr15*, *Lr17b*, *Lr20, Lr23*
8. 53-1,(6),(7),10,11	810043	*Lr10*, *Lr13*, *Lr16*, (*Lr17a*), *Lr20*, (*Lr27+Lr31*)
9. 64-(6),(7),(10),11	900053	*Lr1, Lr10*, (*Lr13*), *Lr16*, (*Lr17a*), (*Lr27+Lr31*)
10. 64-1,3,(9),12	710208	*Lr1, Lr2c*, *Lr10*, *Lr14a*, *Lr17b*, *Lr20*, (*Lr26*)
11. 26-1,3,12	640157	*Lr2c, Lr10*, *Lr14a*, *Lr17b*, *Lr20*
12. 122-1,2,3,5,7,12		*Lr1*, *Lr2a*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr3ka*, *Lr10*, *Lr14a*, *Lr17a*, *Lr17b*, *Lr20, Lr23*
P. graminis* f. sp. *tritici [g,h]		
1. 98-1,2,3,5,6	780129	*Sr5*, *Sr6*, *Sr8a*, *Sr9b*, *Sr9g*, *Sr11*, *Sr17*
2. 343-1,2,3,4,5,6	840837	*Sr5*, *Sr6*, *Sr8a*, *Sr9b*, *Sr11*, *Sr17*, *Sr36*
3. 343-1,2,3,5,6,8,9	890005	*Sr5*, *Sr6*, *Sr8a*, *Sr9b*, *Sr11*, *Sr17*, *Sr30*
4. 126-1,4,5,6,7,11	66-L-1	*Sr5*, *Sr6*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr15*, *Sr17*, *Sr36*
5. 34-1,2,3,4,5,6,7	74-L-1	*Sr5*, *Sr6*, *Sr7b*, *Sr8a*, *Sr9b*, *Sr9g*, *Sr11*, *Sr15*, *Sr17*, *Sr36*
6. 34-1,2,3,6,7,8,9	76-L-1	*Sr5*, *Sr6*, *Sr7b*, *Sr8a*, *Sr9b*, *Sr9g*, *Sr11*, *Sr15*, *Sr30*
7. 34-1,2,3,4,5,6,7,11	75-L-9	*Sr5*, *Sr6*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr9b*, *Sr9g*, *Sr11*, *Sr15*, *Sr17*, *Sr36*
8. 40-1,2,3,4,5,6,7,8,9,10,11	79-L-1	*Sr5*, *Sr6*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr9b*, *Sr9e*, *Sr9g*, *Sr11*, *Sr15*, *Sr17*, *Sr30*, *Sr36*
9. 34-1,2,7 +Sr38	010130	*Sr5*, *Sr6*, *Sr7b*, *Sr9g*, *Sr11*, *Sr15*, *Sr38*
10. 21-2,3,7,8,9	720032	*Sr7b*, *Sr9b*, *Sr9g*, *Sr11*, *Sr15*, *Sr30*

[a] Accession number allocated to cultures in the Plant Breeding Institute Cereal Rust Collection.
[b] Pathotype designations as outlined by Johnson *et al.* (1972) and Wellings and McIntosh (1990)
[c] Tested for pathogenicity on differential genotypes carrying the resistance genes: *Yr1, Yr2, Yr3, Yr4, Yr5, Yr6,Yr7, Yr8, Yr9, Yr10,Yr15, Yr17, Yr27, Yr32, YrSD, YrSu, YrND, YrSP, YrA*
[d] Pathotype designations as outlined by McIntosh *et al.* (1995)
[e] Tested for pathogenicity on differential genotypes carrying the resistance genes: *Lr1*, *Lr2a*, *Lr2b*, *Lr2c*, *Lr3a*, *Lr3bg*, *Lr3ka*, *Lr9*, *Lr10*, *Lr11*, *Lr13*, *Lr14a*, *Lr15*, *Lr16*, *Lr17a*, *Lr17b*, *Lr19*, *Lr20*, *Lr21*, *Lr23*, *Lr24*, *Lr25*, *Lr26*, *Lr27+Lr31*, *Lr28*, *Lr29*, *Lr30*
[f] Parentheses indicate partial virulence
[g] Pathotype designations as outlined by McIntosh *et al.* (1995)
[h] Tested for pathogenicity on differential genotypes carrying the resistance genes: *Sr5,Sr6*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr9b*, *Sr9e*, *Sr9g*, *Sr11*, *Sr13*, *Sr15*, *Sr17*, *Sr21*, *Sr22*, *Sr24*, *Sr26*, *Sr30*, *Sr31*, *Sr32*, *Sr35*, *Sr36*, *Sr38*

Inoculation, disease assessments and gene postulation

Postulation of seedling resistance genes was carried out in seedling tests. Eight to 10 seeds per cultivar were examined with each pathotype. Seedlings were raised in disease free rooms at 17–20°C for 10–12 days and inoculated once the first leaf was fully expanded and the second leaf had partly emerged. Urediniospores, suspended in mineral oil (Shellsol TK®), were atomised over seedlings using a hydrocarbon propellant pressure pack. Seedlings inoculated with *Pst* were incubated in a dark room at 8–10°C for 24 hours in trays filled with tap water and covered with polythene hoods (Wellings and McIntosh 1990). Seedlings inoculated with *Pt* were incubated at 15–20°C for 24 hours in a dark room in which mist was provided by an ultrasonic humidifier (Park *et al.* 2000). Seedlings inoculated with *Pgt* were incubated for 48 hours under natural light at 18–22°C in trays filled with tap water and covered with polythene hoods (McIntosh *et al.* 1995).

Seedling infection types (IT) were recorded 14–17 days after inoculation for *Pst* (Wellings *et al.* 1988), 9–12 days after inoculation for *Pt* (Park *et al.* 1995), and 14–16 days after inoculation for *Pgt* (Park 1996) using the "0", ";" (fleck), "1" to "4" infection type (IT) scale of Stakman *et al*. (1962) as modified by McIntosh *et al*. (1995). Marked differences in ITs within a test cultivar were interpreted to indicate genetic heterogeneity for resistance and were recorded using a comma (,) to separate phenotypes, with the most common IT noted first. For *Pst*, ITs of "3" to "4" were considered high (Wellings 1986; McIntosh *et al.* 1995). For *Pt* and *Pgt*, ITs "0" to "3" were regarded as low IT and ITs "3^{+}" and "4" as high IT (McIntosh *et al.* 1995; Singh *et al.* 2001). The identities of seedling resistance genes present in the lines were postulated by comparing the pattern of phenotypic responses across the pathotype arrays in relation to control genotypes.

RESULTS

Stripe rust

The IT responses for differential cultivars with known resistance genes inoculated with eight *Pst* pathotypes are presented in **Table 3**. The pathotypes used allowed the postulation of genes *Yr1*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr9*, *Yr27* and *YrA*. Cultivars were grouped according to similar responses to the pathotype arrays.

Resistance Group 1 (*Yr-RG1*). Cultivars Zhetysu, Erythrospermum 350, Zernokormonaya 50, Karlygash, Sapaly, Naz, Bogarnaya 56, Lutescens 72, Mirabashir 128, Steklovidnaya 24, Kyzyl Dan and Erythrospermum 13 displayed high ITs of "33^{+}" and "3^{+}" to all *Pst* pathotypes, indicating that they did not possess any resistance genes effective against the eight pathotypes used in the present study.

Yr-RG2. Cultivars Krasnovodopadskaya 25 and Oktyabrina 70 were postulated to carry *Yr1* (Table 4). The typical low IT "0;" for cultivars Vugar, Melanopus 223, and Yuzh-

Table 2 Name, pedigree, country of origin and seedling rust resistance genes postulated in 32 wheat cultivars examined in the present study

Cultivar	Pedigree	Country	Resistance genes		
			Yr	***Lr***	***Sr***
Mirabashir	Pobellon-67 (Mexico) / Shark (selection from Azerbaijan landraces)	Azerbaijan	*Yr3*, *Yr4*	*?*	*Sr9b*, *Sr11*
Vugar[a]	Not known	Azerbaijan	*Yr1+*	*?*	*Sr9e**[b]
BDME 9	Ymh/Tob//Mcd/3/Lira	Turkey/ Tajikistan	*Yr3*, *Yr4*	*Lr14a*	*Sr17*, *Sr11*
Turkmenbashi	Selection from Ak Bugday	Turkmenistan	*Yr7*, *Yr9*	*Lr26*, *Lr3bg*	*Sr31+*
Satheni 332	M-574-51/ M-408 (cross between mutants)	Armenia	missing	-[c]	missing
Ani 352	Kenia-226/Armyanka- 60	Armenia	*Yr9*, *Yr27*	*Lr13*, *Lr16*	*Sr31+*
Ani 435	Not known	Armenia	*Yr9+*	*Lr26**[d]	*Sr31**
Ani 591	Not known	Armenia	*Yr9+*	*Lr26*	*Sr31*
Lalvar	Krasnodar line/ Erevani-4	Armenia	*Yr9+*	*Lr13*, *Lr26*	*Sr31+*
Lori 292	Not known	Armenia	*Yr27*	*Lr26**	*Sr31**
Tilek	Intensivnay/ Albidum 202/2/Donskoy polykarlik	Kyrgyzstan	*?*	-	*Sr8b+*
Melanopus 223[a]	Odesskaya yubileinaya/Oviachik 65	Kyrgyzstan1	*Yr1+*	*Lr3a*, *Lr13?*	*Sr8b?*
Zhetysu	Almatinskaya p-k/Kharkovskaya-38	Kazakhstan	-	*Lr13**	*Sr8b*, *Sr5*
Erythrospermum 350	Ferrugineum-356(Bezostaya-1/Mutant Kaz.126)/Erithr.8068	Kazakhstan	-	-	*Sr8b*, *Sr5*
Zernokormonaya 50	Bogarnaya-56/K-47100(Rom)	Kazakhstan	-	*Lr3a*, *Lr16?*	-
Karlygash	G-276402/B-56//Dneprovskaya-521/3/Dakota	Kazakhstan	-	*Lr16*	*Sr11*
Sapaly	Bogarnaya-56/Albidum-114//Krupnokolosaya	Kazakhstan	-	*Lr3a*	-
Naz	G-7451/Kyrgizskaya-3/Besostaya-1/Kavkaz	Kazakhstan	-	*Lr16*	*Sr5+*
Bogarnaya 56	Yubileinaya Osetii/Amphydiploid-LB-1//Bezostaya-1	Kazakhstan	-	*Lr3a*, *Lr13?*	*Sr8b*
Krasnovodopadskaya 25	Krasnovodopadskaya 49/Bi-ma/Besostaya-1	Kazakhstan	*Yr1*	*Lr3a*, *Lr13?*	*Sr8b*
Mtskhetskaya 1	TAST/SPRW//ZAR	Georgia	*Yr9+*	*Lr26*	*Sr31*
Lutescens 72	Lutescens 62/ Kauka	Kyrgyzstan	-	-	*Sr5*, *Sr7b*
Ekinchi	Selection from a Hungarian variety	Azerbaijan	*Yr9*	*Lr13*, *Lr26*	*Sr31*
Mirabashir 128	Bezostaya-1/C-273 (Pakistani line)	Azerbaijan	-	*Lr3a*, *Lr16?*	*Sr9b*, *Sr11*
Nairi 131	Lutescens-93/mixture of varieties	Armenia	*Yr9+*	*Lr26*	*Sr31*
Steklovidnaya 24	Bogarnaya-56/Teploklyuchenskaya-2//Rostovchanka	Kazakhstan	-	*Lr3a*, *Lr13?*	*Sr5*
Kyzyl Dan	Krasnovbodopadskaya 210/Kavkaz	Kyrgyzstan	-	*Lr3a*, *Lr13?*	*Sr9b*, *Sr11*
Bermet	Lutescence 1454-11/Erithrospermum1022/Lutscenece100/L 202-2	Kyrgyzstan	*Yr9*	*Lr26*, *Lr3bg*	*Sr31*
Erythrospermum 13	Red River 68/Bezostaya 1//Ae. Elongatum/3/Tom Pous	Kyrgyzstan	-	*Lr1*,*Lr2a*, *Lr3a*	*Sr5*, *Sr7b*, *Sr30*
Yuzhnaya 12	Krasnovodopadskaya-25/Besostaya-1//Erythrospermum-7020	Kazakhstan	*Yr1+*	*Lr3a*, *Lr13?*	*Sr8b*
Oktyabrina 70	Krasnovod.25/Khersonskaya 382//Krasnovod.210	Kazakhstan	*Yr1*	-	*Sr8b*
Karaspan	Krasnovodopadskaya 49/Bi-ma/Besostaya-1	Kazakhstan	*?*	-	-

[a] durum wheat cultivar
[b] * indicates heterogeneity
[c] undetermined

Table 3 Responses of differential wheat genotypes to eight Australian pathotypes of *Puccinia striiformis* f. sp. *tritici*.

Cultivar	Genotype	Pathotype [a]							
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Chinese 166	*Yr1*	0;[b]	0;	0;	0;	3^{+}	3^{+}	0;	0;
Lee	*Yr7*	$1^{=C}$	$;^{N}1^{-}$	$;^{C}1^{-}$	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Heines Kolben	*Yr6*, *Yr2*	$;;2^{CN}$	$;^{C}$,3	33^{+}	3^{+}	3	3^{+}	3	3^{+}
Vilmorin 23	*Yr3*	33^{+}	33^{+}	3^{+}	3^{+}	33^{+}	3^{+}	$;^{C}1^{=}$	33^{+}
Moro	*Yr10*	0;	0;	0;	0;	0;	0;	0;	0;
Strubes Dickkopf	*YrSD*	33^{+}	3	3^{+}	3^{+}	3^{+}	3^{+}	$;^{C}1^{=}$	33^{+}
Suwon 92/Omar	*YrSu*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	$;^{C}$	4
Clement	*Yr9*, *Yr2*,+	0;	;	0;	0;	0;	0;	23^{-}	3
T. spelta var. *album*	*Yr5*	0;	0;	0;	0;	0;	0;	0;	0;
Hybrid 46	*Yr4*	33^{-}	3^{-}	3^{-}	3^{-}	3^{C}	3	;	3
Reichersberg 42	*Yr7*,+	1-	$;^{CN}$	2^{-C}	3^{+}	3^{+}	3^{+}	$2^{+}3^{-}$	33^{+}
Heines Peko	*Yr6*,+	$;^{CN}$	;	3^{+}	3^{+}	33^{+}	3^{+}	3^{-C}	3^{+}
Nord Desprez	*YrND*	3^{+}	3^{+}	3^{+}	4	3^{+}	3^{+}	1^{C}	4
Compair	*Yr8*	0;	0;	0;	0;	0;	0;	3	0;
Carstens V	*Yr32*	$;^{C}1$	$;^{C}$	$;^{C}1^{-}$	$;^{C}1^{-}$	$;^{CN}1^{=}$	;	$;^{C}$	0;
Spaldings Prolific	*YrSP*	$;^{C}$	$;;^{C}$	$;^{C}1^{-}$	$;^{C}1^{-}$	$;^{C}$	;	0	$;^{C}1$
Heines VII	*Yr2*,+	33^{+}	3	3	3	3^{+}	3	1^{C}	3^{+}
Avocet 'R'	*YrA*	$3^{-}/1^{C}$	3^{+}	$3^{-}/2^{C}$	3^{+}	2^{+C}	2^{C}	3^{+}	3^{+}
Kalyansona	*Yr2*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	33^{+}	3^{+}
Trident	*Yr17*	$1^{=C}$	$;^{C}1$	1^{C}	1^{C}	1^{CN}	1^{C}	$1^{+}2^{C}$	1^{C}
Yr15/6*Avocet 'S'	*Yr15*	0;	0;	0	0	0	0	0;	0
Selkirk	*Yr27*	2^{-}	1^{+}	1^{+C}	1^{-}	1^{-}	33^{+}	2^{-}	1^{C}
Federation *4/Kavkaz	*Yr9*	0;	0;	0;	0;	0;	0;	3^{+}	3^{+}
Federation	-	3^{+}	3^{+}	3^{+}	$3^{+}4$	3^{+}	3^{+}	3^{+}	$3^{+}4$

[a] 1= 104 E137 A^{-}, 2= 104 E137 A^{+}, 3= 108 E141 A^{-}, 4= 110 E143 A^{+}, 5= 111 E143 A^{-}, 6= 111 E143 A^{-},*Yr27*$^{+}$, 7= 134 E16 A^{+}, 8= 238 E143 A^{+}

[b] Infection types: "0", no visible uredinia, ";", necrotic flecks, ";N", necrotic areas without sporulation, "1", necrotic and chlorotic areas with restricted sporulation, "2", moderate sporulation with necrosis and chlorosis, "3", sporulation with chlorosis, "4", abundant sporulation without chlorosis, C and N indicate more than normal chlorosis and necrosis, respectively, B indicates a characteristic browning associated with uredinia

Table 4 Responses of selected wheat cultivars and control differential genotypes to eight Australian pathotypes of *Puccinia striiformis* f. sp. *tritici*

Cultivar	Genotype	Pathotype[a]							
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Yr resistance group 2									
Krasnovodopadskaya 25	*Yr1*	0;[b]	0;	0;	0;	33^{+}	33^{+}	0;	0;
Oktyabrina 70	*Yr1*	0;	0	0;	0;	33^{+}	3^{+}	0;	0;
Vugar	*Yr1*+	0;,2[c]	0;,2P[d]3^{-}	0;,2P3^{-}	0;,3	3	2^{+}	;,3^{-}	0;,1P3
Melanopus 223	*Yr1*+	0;,3^{+}	0;,33^{+}	0;,3^{+}	0;,3^{+}	2^{+C},3^{+}	2^{+},3^{+}	0;,2^{-}	0;,3^{+}
Yuzhnaya 12	*Yr1*+	0;	0;	0;	0;	2^{+}	2^{+C}	0;	0;
Chinese 166[e]	*Yr1*	0;	0;	0;	0;	3^{+}	3^{+}	0;	0;
Yr resistance group 3									
Ekinchi	*Yr9*	;	;	0;;	;;^{C}	0;	;	3	33^{+}
Bermet	*Yr9*	;	;	;	;;^{C}	;	;$^{C}1^{-}$	33^{+}	3^{+}
Ani 435	*Yr9*+	0;;	0;	0;,2P33^{+}	0;	0;	0;	1^{+CN},1P33^{+}	0;,2P3
Ani 591	*Yr9*+	0;	0;	0;	0;	0;	0;	1^{+CN}	2^{+CN}
Lalvar	*Yr9*+	0;;	;^{CN}	0;	0;	0;	0;	1^{C}	3^{+}
Mtskhetskaya 1	*Yr9*+	0;;	0;;	0;	;	0;	0;;	1^{CN}	1^{CN},1P3
Nairi 131	*Yr9*+	0;	0;	0;	;;^{C}	0;;	0;	1^{-CN}	2^{-C}
Ani 352	*Yr9*, *Yr27*	0;,,^{N}	0;,,^{N}	0;, 2^{+N}	0;, 2P;^{CN}	0;	0;, 2P3	$2^{+}3^{-}$, 2P;^{N}	33^{+}, 2P;^{CN}
Clement	*Yr9*, *Yr2*,+	0;	;	0;	0;	0;	0;	23^{-}	3
Fed. /4*Kavkaz	*Yr9*	0;	0;	0;	0;	0;	0;	3^{+}	3^{+}
Selkirk	*Yr27*	2^{-}	1^{+}	1^{+C}	1^{-}	1^{-}	33^{+}	2^{-}	1^{C}
Federation	-	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Yr resistance group 4									
Mirabashir	*Yr3*, *Yr4?*	3	33^{+}	3-	33^{+}	3	3^{+}	1^{-}	3^{+}
BDME 9	*Yr3*, *Yr4?*	3	3	3	33^{+}	33^{+}	33^{+}	2^{-}	33^{+}
Vilmorin 23	*Yr3*	33^{+}	33^{+}	3^{+}	3^{+}	33^{+}	3^{+}	;$^{C}1^{=}$	33^{+}
Hybrid 46	*Yr4*	33^{-}	3^{-}	3-	3-	3^{c}	3	;	3
Yr resistance group 5									
Turkmenbashi	*Yr7,Yr9*	0;;,2P;^{N}	0;,,^{N}	0; ,1^{CN}	0;,33^{+}	0;,3^{+}	$3^{+}4$	33^{+}	3^{+}
Heines Kolben	*Yr6*	;;2^{CN}	;^{C}	33^{+}	3^{+}	3	3^{+}	3	3^{+}
Lee	*Yr7*	$1^{=C}$	;$^{N}1^{-}$	;$^{C}1^{-}$	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Fed.*4/Kavkaz	*Yr9*	0;	0;	0;	0;	0;	0;	3	3^{+}
Federation	-	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Yr resistance group 6									
Lori 292	*Yr27*	2^{+C}/2P;^{N}	;/1^{+C},3P1^{+}	2^{+C}/1P;	2	2^{NB}	33^{+}	1^{CN}	22^{+}
Selkirk	*Yr27*	2^{-}	1^{+}	1^{+C}	1^{-}	1^{-B}	33^{+}	2^{-}	1^{C}
Yr resistance group 7									
Tilek	?	;;^{N}	;,2P3^{+}	;;^{N},1P3	0;	0;,2P3^{+}	0;,1P3^{+}	;^{CN},1P3	;,2P3^{+}
Karaspan	?	33^{-}	23^{-}	23^{-}	$2^{+}3$	2	2^{+}	2^{-CN}	2^{+}

[a] 1= 104 E137 A^{-}, 2= 104 E137 A^{+}, 3= 108 E141 A^{-}, 4= 110 E143 A^{+}, 5= 111 E143 A^{-}, 6= 111 E143 A^{-},*Yr27*$^{+}$, 7= 134 E16 A^{+}, 8= 238 E143 A^{+}

[b] Infection types: "0", no visible uredinia, ";", necrotic flecks, ";N", necrotic areas without sporulation, "1", necrotic and chlorotic areas with restricted sporulation, "2", moderate sporulation with necrosis and chlorosis, "3", sporulation with chlorosis, "4", abundant sporulation without chlorosis, C and N indicate more than normal chlorosis and necrosis, respectively, B indicates a characteristic browning associated with uredinia

[c] heterogeneous response

[d] P denotes "plants" i.e. 2 plants

[e] cultivars in bold are Australian differential genotypes used to determine pathogenicity of *P. striiformis* f. sp *.tritici*

naya 12 in response to pathotypes avirulent for *Yr1*, and intermediate ITs of "$2^{+}3$" and "3" for virulent pathotypes, indicated that all cultivars likely possessed *Yr1* and additional resistance gene(s), the identity of which could not be determined using these pathotypes. The seed source of Vugar was evidently heterogeneous for *Yr1*. Plants lacking *Yr1* had IT of "2", "3^{-}" and "3" to pathotypes avirulent for this gene. Melanopus was heterogeneous for *Yr1* plus an unidentified resistance gene producing an IT of "2^{+}" to the two *Yr1* virulent pathotypes. Yuzhnaya 12 displayed a low IT of "0;" to all seven pathotypes avirulent for *Yr1* and ITs of "2^{+C}" to "2^{+}" with the two *Yr1* virulent pathotypes, revealing that it probably possesses *Yr1* in combination with an additional unidentified resistance gene(s).

***Yr-RG3*.** High ITs with pathotypes 7 and 8, both virulent for *Yr9*, and low ITs with pathotypes avirulent for *Yr9*, led to the postulation of *Yr*9 in eight cultivars, among which Ekinchi and Bermet appeared to carry *Yr9* alone (**Table 4**). Low ITs of "0;" and ";^{CN}" to all six pathotypes avirulent for *Yr9* and ITs ranging from "1^{-CN}" to "2^{+CN}" to the pathotypes virulent for *Yr9* (pts 7 and 8), indicated that cultivars Ani 435, Ani 591, Lalvar, Mtskhetskaya 1, and Nairio 131 likely carried *Yr9* in combination with additional unidentified resistance gene(s). Ani 352 showed heterogeneous IT responses to each of the eight pathotypes. Some plants produced a low IT "0;" with pathotypes avirulent for *Yr9* (pts. 1–6), which is typical for *Yr9*, and presumably these same plants produced IT "$2^{+}3^{-}$" to "33^{+}" to pathotypes virulent for *Yr9* (pts. 7 and 8). These plants were postulated to carry *Yr*9. The remaining plants produced low ITs ranging from ";^{N}" to "2^{+N}" to pathotypes avirulent for *Yr27* (pts. 1–5, 7, 8) and IT "3" to pt. 6, which is virulent for *Yr27*. It was concluded that Ani 352 was heterogeneous for *Yr9* and *Yr27*.

Yr-RG4. High ITs to all six pathotypes virulent for *Yr3* and *Yr4* and low ITs of "1^{-}" and "2^{-}" against the only pathotype avirulent for *Yr3* and *Yr4* (pt. 7), suggested the presence of *Yr3* and/ or *Yr4* in cultivars Mirabashir and BDME 9 (**Table 4**). The differential varieties Vilmorin 23 and Hybrid 46, carrying*Yr*3 and *Yr4* respectively, displayed ITs ";$^{C}1^{=}$" and ";" against *Pst* pt. 134 E16 A^{+} (Table 3), which was distinctly lower than the ITs observed on the test cultivars.

Yr-RG5. Turkmenbashi was the only member of this group, the seed source of which was evidently heterogeneous (**Table 4**). Plants displaying IT ";^{N}" to "1^{CN}" to pathotypes avirulent for *Yr7* (pts. 1–3) were assumed to be the same genotype as those giving IT "3^{+}" to pathotypes virulent for *Yr7* (pts. 4–8). Plants displaying IT "0;" to pts. 1–5 showed evidence of the typical low IT for *Yr9* and presumably these same plants showed the high ITs "33^{+}" to "3^{+}" to pathotypes virulent for *Yr9* (pts. 7 and 8). However, low ITs were not produced by pt. 6 (avirulent for *Yr9*) as expected, possibly due to sampling error. It was concluded that Turkmenbashi was heterogenous for both *Yr7* and *Yr9*.

Table 5 Responses of differential wheat genotypes to 11 Australian pathotypes of *Puccinia triticina*.

Cultivar	Genotype	Pathotype [a]										
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
Tarsa	*Lr1*	3^{+}[b]	3^{+}	3^{+}	3^{+}	3^{+}	0;$^{-}$	3^{+}	0;$^{-}$	3^{+}	3^{+}	0;$^{-}$
Webster	*Lr2a*	3^{+}	;1^{-C}	;12^{-}	;12^{-C}	;1^{-}	;12^{-C}	3^{+}	0;$^{-}$	;$1^{=}$	;12^{-C}	;12^{-C}
Mediterranean	*Lr2a, Lr3a*	3^{+}	;1^{-C}	;1^{-}	;12^{-}	;1^{-}	;12^{-C}	;	0;$^{-}$	;	;	;$^{-}$
Democrat	*Lr3a*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	;1^{-}	;	;$1^{=}$	;1^{-C}	;1^{+C}
Thew	*Lr20*	3^{+}	3^{+}	3^{+}	;1^{+N}	12^{N}	3^{+}	3^{+}	3^{+}	12^{CN}	3^{+}	;1^{N}
Gaza	*Lr23*	;1^{-C}, 3	$X^{++}3$	X^{+}	3^{+}	$X^{++}3$	;$^{N}1^{-}$	3^{+}	;12^{-C}	;$^{N}1^{-}$	;12^{-C}	;N1^{-}
Spica	*Lr14a*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	X^{++}	X^{++}	3^{+}	X^{+}
Kenya 1483	*Lr15*	3^{+}	;	;	;	;	;	3^{+}	;	;$^{N}1^{-}$	;	;
Klein Titan	*Lr3ka*	;12^{-}	;$1^{=}$	;$1^{=}$	;$1^{=}$	;$1^{=}$	3^{+}	;$^{N}1^{=}$	;$^{N}1^{=}$	;$^{N}1^{-}$	;$^{N}1^{-}$	;1^{-}
Gatcher	*Lr27+ Lr31*	$X^{++}3$	X^{+}	X^{+}	3^{+}	X^{++}	XX^{-}	$X^{=}$	X^{++}	X^{+}	;12^{-}	;$^{N}1^{-}$
Songlen	*Lr17a*	3^{+}	XX^{+}	XX^{+}	$X^{=}$	X^{+}	$X^{=}$	$X^{=}$	X^{-}	$X^{=}$	X^{-}	$X^{=}$
CS 2A/2M	*Lr28*	0;$^{-}$	0;$^{-}$	0;$^{-}$	0;$^{-}$	0;$^{-}$	0;$^{=}$	0;1$^{=}$	0;$^{-}$	0;	0;$^{-}$	0 , $^{=}$
Mildress	*Lr26*	0;$^{-}$	3^{+}	;$0^{=}$	3^{+}	0;$^{=}$	$2^{++}3$	;1^{+}	0;$^{=}$	0;$^{=}$	3	XX^{-}
Egret	*Lr13*	3^{+}	$X^{++}3^{C}$	$X^{---}3^{CN}$	X^{++C}	$X^{++}3^{C}$	3^{+}	;1^{-}	3^{+}	33^{+}	X^{---}	X^{-C}
Norka	*Lr1, Lr20*	3^{+}	3^{+}	3^{+}	12^{-N}	;1^{+N}	0;	3^{+}	0;	2^{++N}	3^{+}	0;
Mentana	*Lr3bg*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	;3^{+}	;	;	;	;	;
Sun 6B	*Lr1, Lr3a, Lr27+31*	$X^{++}3$	X^{+}	X^{+}	3^{+}	X^{+}	;$^{-}0;^{-}$	;	0;	;	;	;
Harrier	*Lr17b*	3^{+}	X^{++}	X^{++}	3^{+}	X^{++}	3^{+}	3^{+}	;$^{N}1^{-}$	;$^{N}1^{-}$	3^{+}	3^{+}
Kavkaz	*Lr26*	0;$^{-}$	3^{+}	0;$^{=}$	3^{+}	0;$^{=}$	-	;1^{-}	0;$^{=}$	0;$^{=}$	33^{+}	X^{-C}
Timson	*Lr17a*	3^{+}	X^{-}	X^{+}	;12^{-}	X^{+}	$X^{=}$	$X^{=}$	$X^{=}$	;12^{-}	$X^{-}X^{=}$	$X^{=}$
Exchange	*Lr16*	;1^{CN}	$2^{++}3^{CN}$	3^{-CN}	1^{+CN}	3^{CN}	1^{CN}	1^{+CN}	3^{+CN}	3^{CN}	12^{-CN}	1^{+CN}
Trident	*Lr37, Lr3a*	$X^{++}3$	X2^{-}	3^{+}	$X^{++}3^{C}$	X2^{+}	0; , X^{++}	X2^{-}	; , $X^{=}$	X2^{-}	X^{++}	0;
Sunlin	*Lr37, Lr3a*	XX^{-}	XX^{+}	3^{+}	X^{+}	X^{+}	0;	X^{+}	0;$^{-}$	X^{-}	X^{+}	0;$^{-}$, X^{-C}
Morocco	-	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}

[a] 1= 122-1,3,4,6,7,12; 2= 104-1,2,3,(6),(7),9,11; 3= 104-1,2,3,(6),(7),11+*Lr37*; 4= 104-2,3,6,9,12; 5= 104-2,3,(6),(7),11; 6= 76-1,3,5,10,12; 7= 10-1,2,3,4,12; 8= 53-1,(6),(7),10,11; 9= 64-(6),(7),(10),11; 10= 64-1,3,12; 11= 26-12

[b] Infection types, "0" no visible uredinia, ";" hypersensitive flecks, "1" small uredinia with necrosis, "2" small to medium sized uredinia with green islands and necrosis or chlorosis, "3" medium sized uredinia with or without chlorosis, "4" large uredinia without chlorosis, "X" heterogeneous ITs similarly distributed over the leaves. Variations in IT are indicated by the use of "-" (less than average for class) and "+" (more), as well as "C" and "N" to indicate more than usual chlorosis or necrosis, respectively.

Yr-RG6. Lori 292 had a high IT of "33^{+}" to the only pathotype virulent for *Yr27* (pt. 6) and low ITs to the remaining seven avirulent pathotypes, supporting the presence of *Yr27* (**Table 4**).

Yr-RG7. Two cultivars showed low to intermediate ITs to all pathotypes. Tilek produced a low IT of "0;" to ";^{N}" to all pathotypes, but was heterogeneous in its response in certain tests (**Table 4**). The absence of heterogeneity in response to pts. 1 and 4 may have been due to sampling error. Karaspan showed an intermediate IT to all eight pathotypes. The resistances in these two cultivars were phenotypically distinct, but their identities could not be postulated. Satheni 332 (Entry 5) was not included in stripe rust gene postulation tests due to insufficient seed.

Leaf rust

The ITs displayed by differential genotypes possessing known seedling resistance genes with the *Pt* pathotypes used in this study are listed in **Table 5**. Based on the similarity of IT patterns among the test lines with those of the differential varieties, eight *Lr*-resistance groups (*Lr*-RG) were identified.

Resistance Group 1 (*Lr-RG1*). This group included five cultivars (Tilek, Oktyabrina 70, Karaspan, Lutescens 72 and Satheni 332) that displayed a high IT of "33^{+}" to all 11 *Pt* pathotypes. This indicated an absence of resistance genes effective against these pathotypes.

Lr-RG2. Erythrospermum 13 was the only cultivar included in resistance group 2. Low ITs of ";;$^{-}$" and "0;$^{-}$" in response to pathotypes avirulent for *Lr1* only (pts. 6, 8, and 11) led to the postulation of *Lr1* in Erythrospermum. Intermediate ITs ranging from ";1^{-C}" to ";2^{+C}" to pathotypes virulent for *Lr1* indicated that this cultivar possesses additional resistance (**Table 6**). Despite the low ITs shown by all pathotypes, several contaminant pustules (IT of "3^{+}") were observed on Erythrospermum 13, and when subcultured, were subsequently identified as pathotype 122-1,2,3,5,7 (pt. 12), virulent for a range of genes including *Lr1*, *Lr2a, Lr3a*, and *Lr3ka*. This suggested that the gene in addition to *Lr1* was likely to be *Lr3ka* and/or *Lr2a* (Table 6). The pathotype array used in this study was unable to discriminate between these two genes.

Lr-RG3. Group 3 comprised nine cultivars (Sapaly, Krasnovodopadskaya 25, Steklovidnaya 24, Kyzyl Dan 27, Yuzhnaya 12, Melanopous 223, Bogarnaya 56, Zernokormonaya 50, and Mirabashir 128). Gene *Lr3a* was postulated in cultivar Sapaly based on an IT pattern identical to that of the control Democrat. Low ITs of "0;$^{-}$" to ";$1^{=}$" against pathotypes avirulent for *Lr3a* (pts. 7, 8, 9, 10 and 11) and high ITs of "33^{+}" and "3^{+}" to virulent pathotypes supported the presence of *Lr3a* (**Table 6**).

Melanopus 223 displayed low ITs of ";" and ";$1^{=}$" to pts. 7, 9, 10 and 11 (all avirulent for *Lr3a*), and high ITs of "X" to "3^{+}" to pts. 1, 2, 3, 4, 5 and 6 (all virulent for *Lr3a*). Therefore, it was postulated that Melanopus 223 carries *Lr3a*. This cultivar was heterogeneous in its responses to pts. 8 and 10 (both avirulent for *Lr3a* and virulent for *Lr13*) with some plants displaying a high IT of "3^{+}", consistent with the presence of *Lr13* alone in these plants or a lack of resistance genes. Cultivars Krasnovodopadskaya 25, Steklovidnaya 24, Kyzyl Dan 27, and Yuzhnaya 12 were similarly postulated to carry *Lr3a*.

Zernokormonaya 50 also displayed low ITs of ";" to ";1^{-}" to pathotypes avirulent for *Lr3a* (pts. 7, 8, 9, 10 and 11). Based on the low IT pattern to pathotypes avirulent for *Lr3a* and high ITs of "33^{+}" to all six pathotypes virulent for this gene, it was hypothesised that this cultivar possessed *Lr3a*. While most plants of Zernokormonaya 50 showed the same IT pattern to pts. 6 and 1 (both avirulent for *Lr16* and virulent for *Lr3a*), several showed ITs ranging from "12^{+CN}" and "1^{+CN}", indicating that they have additional resistance, which on the basis of phenotype and specificity is likely to be *Lr16*.

Mirabashir 128 was also postulated to carry *Lr3a* but also produced low ITs of "12^{CN}" and "12^{+CN}" with pathotypes 6 and 1. In addition to *Lr3a*, the low ITs to pts. 6 and 1 suggested the additional presence of *Lr16*. However, a high IT of "3^{+}" to pt. 4, avirulent for *Lr16*, did not support this conclusion. Bogarnaya 56 produced low ITs of ";" to "0;" to pts. 7, 10 and 11 (all avirulent for *Lr3a* and *Lr13*), and 8 and 9 (both avirulent for *Lr3a* and virulent for *Lr13*), and 12^{-CN} to pt. 1 (virulent for *Lr3a* and *Lr13*). High ITs of

Table 6 Responses of selected wheat cultivars and control differential genotypes to 12 Australian *Puccinia triticina* pathotypes.

Cultivar	Genotype	Pathotype[a]											
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
Lr resistance group 2													
Erythrospermum 13	*Lr1, Lr2a, Lr3ka+*	;1^{-Cb}	;12^{-C}	;12^{-C}	;12^{-C}	;12^{-C}	0;$^{-}$	;;$^{-}$	0;;$^{-}$	;;$^{-}$	;;$^{-}$	0;$^{-}$	3^{-}
Tarsa[c]	*Lr1*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	0;$^{-}$	3^{+}	0;$^{-}$	3^{+}	3^{+}	0;$^{-}$	3^{+}
Webster	*Lr2a*	3^{+}	;1^{-C}	;12^{-}	;12^{-C}	;1^{-}	;12^{-C}	3^{-}	0;$^{-}$	;1^{-}	;12^{-C}	;12^{-C}	3^{+}
Democrat	*Lr3a*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	;1^{-}	;	;1^{-}	;1^{-C}	;1^{-C}	3^{+}
Klein Titan	*Lr3ka*	;12^{-}	;1^{-}	;1^{-}	;1^{-}	;1^{-}	3^{+}	;^{N}1^{-}	;^{N}1^{-}	;^{N}1^{-}	;^{N}1^{-}	;1^{-}	3^{+}
Lr resistance group 3													
Sapaly	*Lr3a*	3^{+}	33^{+}	9P[d]X^{++}3, 2P;1^{-}	33^{+}	33^{+}	3^{+}	;$^{-}$	0;$^{-}$	;$^{-}$	;;$^{-}$	;1$^{=}$	
Krasnovodopadskaya 25	*Lr3a, Lr13?*	3^{+}	3^{-CN}	X^{+C}	33^{+C}	X^{+C}	3^{+}	;$^{-}$	0;$^{-}$	;1$^{=}$	;	;	
Steklovidnaya 24	*Lr3a, Lr13?*	33^{+}	X^{++}3^{C}	X^{++}3^{C}	X^{++C}	33^{+}	3^{+}	;$^{-}$	0;;$^{-}$	;	;;$^{-}$	;1^{-}	
Kyzyl Dan 27	*Lr3a, Lr13?*	33^{+}	X^{++}3^{C}	X^{++}3^{C}	33^{+}	X^{+}3^{C}	3^{+}	;	0;;$^{-}$	;	;^{N}1^{-}	;1^{-}	
Yuzhnaya 12	*Lr3a, Lr13?*	3^{C}	X^{+C}	X^{+C}	33^{+C}	X^{++C}	3^{+}	;	0;;$^{-}$	;	;	;1$^{=}$	
Melanopus 223	*Lr3a, Lr13*[e]	33^{+}	X^{++C}	X^{++C}	X^{++C}	XX^{+C}	3^{+}	;	6P;$^{-}$, 3P3^{+}	;	4P;, 2P3^{+}	;1$^{=}$	
Bogarnaya 56	*Lr3a, Lr13**	12^{-CN}	7P3^{CN}, 3P3^{+}	2P3^{CN}, 5P3^{+}	5P3^{CN}, 1P3^{+}	6PX^{++}, 31P3^{+}	4P12^{+CN}, 1P3^{+}	;$^{-}$	0;$^{-}$	0;;$^{-}$	;$^{-}$	;	
Zernokormonaya 50	*Lr3a, Lr16**	3P3^{+}, 3P1^{+CN}	3^{+}	33^{+}	33^{+}	33^{+}	4P3^{+}, 3P12^{+CN}	;	0;-	;	;	;1-	
Mirabashir 128	*Lr3a, ?*	12^{+CN}	3^{+}	3^{+}	3^{+}	3^{+}	12^{CN}	5P;$^{-}$, 1P2^{CN}	0;$^{-}$	0;;$^{-}$	;1$^{=}$	;;$^{-}$	
Democrat	*Lr3a*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	;1^{-}	;	;1$^{=}$	;1^{-C}	;1^{+C}	
Egret	*Lr13*	3^{+}	X^{++}3^{C}	X^{---}3^{CN}	X^{++C}	X^{++}3^{C}	3^{+}	;1^{-}	3^{+}	33^{+}	X^{---}	X^{-C}	
Exchange	*Lr16*	;1^{CN}	2^{++}3^{CN}	3^{-CN}	1^{+CN}	3^{CN}	1^{CN}	1^{+CN}	3^{+CN}	3^{CN}	12^{-CN}	1^{+CN}	
Lr resistance group 4													
Zhetysu	*Lr13**	3^{+}	3^{+}	3^{+}	3^{+}	33^{+}	3^{+}	1P;-, 1P;, 5P3^{+}	3^{+}	3^{+}	X^{++}3^{C}	1P;, 1PX^{-C}, 6P3^{+}	
Ani 352	*Lr13, Lr16*	;1^{+CN}	1P1^{+}2$^{+C N}$, 4P3^{+}	1P3^{+}, 3P2^{CN}	3^{+}	5P33^{+}, 2P2^{+CN}	1^{-}2^{CN}	2P1^{+CN}, 4P33^{+}	33^{+}	X^{++}3	3P12^{CN}, 3P3^{+C}		
Lalvar	*Lr13, Lr26*	0;$^{-}$	3^{+}	0;$^{=}$	X^{++}3^{C}	0;1$^{=}$	X^{+CN}	;	0;$^{=}$	0;$^{=}$	X^{-C}	1^{-}	
Ekinchi	*Lr13, Lr26*	0;$^{-}$	X^{++}3^{C}	0;$^{=}$	X^{+C}	0;$^{=}$	X^{+CN}	0;$^{-}$	0;$^{=}$	0;$^{=}$	;;$^{-}$	;;$^{-}$	
Egret	*Lr13*	3^{+}	X^{++3C}	X^{---}3^{CN}	X^{++C}	X^{++}3^{C}	3^{+}	;1^{-}	3^{+}	33^{+}	X^{---}	X^{-C}	
Exchange	*Lr16*	;1^{CN}	2^{++}3^{CN}	3^{-CN}	1^{+CN}	3^{CN}	1^{CN}	1^{+CN}	3^{+CN}	3^{CN}	12^{-CN}	1^{+CN}	
Mildress	*Lr26*	0;$^{-}$	3^{+}	;0$^{=}$	3^{+}	0;$^{=}$	2^{++}3	;1^{+}	0;$^{=}$	0;$^{=}$	3	XX^{-}	
Kavkaz	*Lr26*	0;$^{-}$	3^{+}	0;$^{=}$	3^{+}	0;$^{=}$	$^{-}$	;1^{-}	0;$^{=}$	0;$^{=}$	33^{+}	X^{-C}	
Lr resistance group 5													
BDME 9	*Lr14a*	3^{+}	3^{+}	3^{+}	3^{+}	33^{+}	3^{+}/X^{++}3	33^{+}	X^{+}	X^{++}3/X^{+}	3^{+}	X^{++}	
Spica	*Lr14a*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	X^{++}	X^{++}	3^{+}	X^{+}	
Lr resistance group 6													
Karlygash	*Lr16*	12^{-CN}	3^{+}	3^{+}	22^{+CN}	3^{+}	1^{+CN}	12^{-CN}	3^{+}	3^{+}	12^{+CN}	2^{++CN}	
Naz	*Lr16*	12^{-CN}	3^{+}	3^{+}	2^{CN}	3^{+}	12^{+CN}	3^{-CN}	3^{+}	3^{CN}	12^{+CN}	12^{+CN}	
Exchange	*Lr16*	;1^{CN}	2^{++}3^{CN}	3^{-CN}	1^{+CN}	3^{CN}	1^{CN}	1^{+CN}	3^{+CN}	3^{CN}	12^{-CN}	1^{+CN}	
Lr resistance group 7													
Ani 591	*Lr26*	0;$^{-}$	3^{+}	0;$^{=}$	3^{+}	0;1$^{=}$	3^{C}	;1^{-}	0;$^{=}$	0;$^{=}$	3	X^{-C}	
Mtskhetskaya 1	*Lr26*	0;$^{-}$	3^{+}	0;$^{=}$	3^{+}	0;$^{=}$	X^{+}	;1^{-}	0;$^{=}$	0;$^{-}$	3	;1^{+}	
Nairi 131	*Lr26*	0;$^{=}$	3^{+}	0;$^{=}$	3^{+}	0;$^{=}$	12^{-CN}	;N	0;$^{-}$	0;$^{-}$	2^{+CN}	X^{-C}	
Ani 435	*Lr26**	3+	3+	2P0;$^{=}$, 3P3^{+}	3+	3P0;1$^{=}$, 4P3^{+}	3^{+}	2P;1^{-}, 5P3^{+}	3^{+}	3^{+}	3^{+}	3PX^{-C}, 4P3^{+}	
Lori 292	*Lr26**	7P0;$^{-}$ 1P3^{+}	3^{+}	0;$^{=}$	33^{+C}	6P0;$^{=}$1P 3^{+}	5PX^{-C}2P3^{+}	6P;1P3^{+}	5P0;$^{-}$ 2P3^{+}	6P0;$^{=}$2P 3^{+}	X^{-C}	;1^{-}	
Turkmenbashi	*Lr26, Lr3bg*	0;-	1P3^{+}, 6PX^{-CN}	0;$^{=}$	3P3^{+}, 4P;	1P;^{N}1^{-}, 4P;$^{N=}$	6PX^{CN}, 3P;^{N}1-	;	0;-	0;;-	;	;	
Bermet	*Lr26, Lr3bg*	0;$^{=}$	3^{+}	0;$^{=}$	33^{+}	0;$^{=}$	X^{+C}	0;$^{-}$	0;;$^{-}$	0;$^{=}$	;	;;$^{-}$	
Mildress	*Lr26*	0;$^{-}$	3^{+}	;0$^{=}$	3^{+}	0;$^{=}$	2^{++}3	;1^{+}	0;$^{=}$	0;$^{=}$	3	XX^{-}	
Kavkaz	*Lr26*	0;$^{-}$	3^{+}	0;$^{=}$	3^{+}	0;$^{=}$	$^{-}$	;1^{-}	0;$^{=}$	0;$^{=}$	33^{+}	X^{-C}	
Democrat	*Lr3a*	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	;1^{-}	;	;1$^{=}$	;1^{-C}	;1^{+C}	
Mentana	*Lr3bg*	3+	3+	3+	3+	3+	;3+	;	;	;	;	;	
Lr resistance group 8													
Mirabashir	?	;12^{+C}	3^{+}	3^{+}	3^{+}	3^{+}	33^{+}	3^{+}	3^{+C}	33^{+}	3^{+C}	3^{+}	
Vugar	?	X^{-}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+C}	3^{+}	3^{+C}	3^{+}	
Erythrospermum 350	heterogeneous	4P3^{+}, 1P1^{+CN}	5P^{X+}, 3P3^{+}	5P3^{+}, 3PX^{++C}	1P3^{+}, 6PX^{+C}	3P3^{+}, 5PX	2P12^{-CN}, 5P3^{+}	5P0;$^{-}$, 2P2^{CN}	3P3^{+}, 3P0;$^{-}$	3P;$^{-}$, 5P3^{+}	1P2^{CN}, 5P;;$^{-}$	5P;, 3P33^{+}	

[a] 1= 122-1,3,4,6,7,12; 2= 104-1,2,3,(6),(7),9,11; 3= 104-1,2,3,(6),(7),11+*Lr37*; 4= 104-2,3,6,9,12; 5= 104-2,3,(6),(7),11; 6= 76-1,3,5,10,12; 7= 10-1,2,3,4,12; 8= 53-1,(6),(7),10,11; 9= 64-(6),(7),(10),11; 10= 64-1,3; 11= 26-12

[b] Infection types, "0" no visible uredinia, ";" hypersensitive flecks, "1" small uredinia with necrosis, "2" small to medium sized uredinia with green islands and necrosis or chlorosis, "3" medium sized uredinia with or without chlorosis, "4" large uredinia without chlorosis, "X" heterogeneous ITs similarly distributed over the leaves. Variations in IT are indicated by the use of "-" (less than average for class) and "+" (more), as well as "C" and "N" to indicate more than usual chlorosis or necrosis, respectively.

[c] cultivars in bold are Australian differential genotypes used to characterise isolates of *P. triticina*

[d] P denotes "plants" i.e. 9 plants

[e] * indicates heterogeneity

"3^{+}" to pts. 2, 3, 4, 5 and 6 (all virulent for *Lr3a* and *Lr13*) and a pattern of low ITs to pts. 1, 7, 8, 9, 10 and 11 were consistent with the presence of *Lr3a* and *Lr13* in this cultivar (**Table 6**).

Lr-RG4. This group comprised four cultivars. Cultivar Zhetysu produced low ITs to pts. 7, 10 and 11 (avirulent for *Lr13*) and high ITs of "3^{+}" to all other pathotypes virulent for *Lr13*, suggesting that it carries *Lr13*. Some plants in this cultivar produced high ITs of "3^{+}" with pathotypes 7 and 11 (avirulent for *Lr13*, *Lr16* and *Lr26*), indicating that they did not carry these genes (**Table 6**).

Ani 352 showed low ITs to pathotypes avirulent for *Lr13* and *Lr16*, and high ITs to pathotypes virulent for *Lr13* and *Lr16*, consistent with the presence of both genes in this cultivar. However, the high IT of "3^{+}" to pt. 4 (avirulent for *Lr16*) did not support this hypothesis. This cultivar was also heterogeneous in its response to pts. 2, 5, 7, and 10, with some plants displaying IT "3^{+}" to all pathotypes, indicating a lack of *Lr13* and *Lr16*. Based on the similarity of IT patterns of the test cultivars Lalvar and Ekinchi with the controls Egret (*Lr13*) and Mildress (*Lr26*), genes *Lr13* and *Lr26* were postulated for these cultivars. The presence of *Lr26* is consistent with the results from stripe rust resistance gene postulation of *Yr9* in both Lalvar and Ekinchi (**Table 4**).

Lr-RG5. The only member of this group was BDME 9, which displayed an IT pattern similar to that of the control cultivar Spica (*Lr14a*). Based on mesothetic ITs ("X^{+}" to "$X^{++}3/X^{++}$") to pathotypes avirulent for *Lr14a* (pts. 8, 9 and 11), and high ITs of "3^{+}" to all pathotypes virulent for *Lr14a*, this gene was postulated for BDME 9 (**Table 6**).

Lr-RG6. This group comprised the test cultivars Karlygash and Naz. The low and high IT patterns of both were very similar to that of the control Exchange (*Lr16*), and hence both were postulated to carry *Lr16* (**Table 6**).

Lr-RG7. This group included seven cultivars that were postulated to carry *Lr26* singly or in combination with additional unidentified *Lr* gene/s (**Table 6**). Low ITs of ";" to "12^{-CN}" to pathotypes avirulent for *Lr26* (pts. 1, 3, 6, 7, 8, 9 and 11) and a high IT of "3^{+}" to pathotypes virulent for *Lr26* (pts. 2, 4 and 10), implied the presence of *Lr26* in cultivars Ani 591, Mtskhetskaya 1, Nairi 131, and Lori 292. This conclusion was consistent with the postulated presence of the linked resistance gene *Yr9* in these cultivars (**Table 4**).

Ani 435 was heterogeneous for *Lr26*, and comprised two groups. One group showed low ITs of "$0;^{=}$" to "$;1^{-}$" to pathotypes avirulent for *Lr26* (pts. 3, 5 and 7) and high ITs to pathotypes virulent for *Lr26* (pts. 2 and 4), implying the presence of *Lr26*. Within this group, further heterogeneity was observed with a low frequency of plants displaying a high IT of "3^{+}" to pts. 3, 5 and 7 (all avirulent for *Lr26*), suggesting that *Lr26* was not present in them. The second group comprised plants with high ITs of "3^{+}" to all pathotypes, implying a lack of resistance effective to the pathotype array. In Lori 292, low and high ITs to pathotypes avirulent and virulent for *Lr26*, respectively, implied the presence of *Lr26*. Off-type plants within this cultivar produced high ITs of "3^{+}" to pathotypes avirulent for *Lr26*, indicating a lack of this gene in these individuals.

Turkmenbashi and Bermet displayed low ITs of ";" to "X^{CN}" to pts. 1, 3, 5, 6, 7, 8, 9 and 11 (all avirulent for *Lr26*), and high ITs of "3^{+}" to pathotypes virulent for this gene, suggesting the presence of *Lr26*. A low IT of ";" to pt. 10 (avirulent for *Lr3a* and *Lr3bg* and virulent for *Lr26*) and high IT to pts. 4 and 2 (both virulent for *Lr26, Lr3a* and *L3bg*) indicated the likely presence of *Lr3bg* and/ or *Lr3a*, and both were therefore postulated to carry *Lr26* and *Lr3a* and/or *Lr3bg*. The presence of *Lr26* in Ani 591, Metskhetskaya 1, Nairi 131, Ani 435, and Bermet, and Turkmenbashi was supported by the postulation of *Yr9* in these cultivars (**Table 4**).

Lr-RG8. Two cultivars, Mirbashir and Vugar, were susceptible (IT of "3^{+}") to all pathotypes except for pt. 122-1,3,4,6,7 (Table 6)**.** Unpublished data indicated that the control cultivar Brevit (*LrB*) had the same low IT to this pathotype (R.F. Park, unpublished). On this basis, it was concluded that *LrB* was present in these two cultivars.

The test cultivar Erythrospermum 350 was highly heterogeneous in its response and did not match any of the IT patterns generated by control genotypes.

Stem rust

Seedling infection types displayed by the stem rust differential genotypes infected with 10 *Pgt* pathotypes are presented in **Table 7**. Contrasting virulence/ avirulence among the 10 pathotypes to known *Sr*-genes allowed the postulation of nine *Sr*-genes in the test cultivars, which were classified into six resistance groups based on the similarity of IT patterns of each with those for the control genotypes with known *Sr*-genes.

Resistance Group 1 (*Sr-RG1*). Cultivar Karaspan produced high ITs of "3^{+}" to all 10 pathotypes of *Pgt*, indicating a lack of *Sr*-genes effective against these pathotypes.

Sr-RG2. The cultivar Sapaly showed a heterogeneous IT pattern that did not match any known resistance gene (data not shown).

Sr-RG3. This group included Steklovidnaya 24, Naz, Lutescens 72 and Erythrospermum 13. All pathotypes, with the exception of pt. 10, were virulent on Reliance (*Sr5*). Steklovidnaya 24 produced high ITs to the pathotypes virulent for *Sr5* (pts. 1–9), and a low IT of "2^{+CN}" to pt. 10 (avirulent for *Sr5*). Based on an IT pattern similar to the control genotype Reliance (*Sr5*), Steklovidnaya 24 was concluded to most likely possess *Sr5*. Naz showed high ITs to most of the pathotypes virulent for *Sr5* (pts. 4, 5, 7 and 8) and a low IT to pt. 10. Naz was also postulated to carry *Sr5* but low ITs to the *Sr5* virulent pathotypes 1 and 6 indicated that it carried additional resistance. Lutescens 72 displayed a high IT to pathotypes virulent for *Sr5* and *Sr7b* (pts. 4, 5, 6, 7, 8 and 9) and low ITs to pathotype 10 (avirulent for *Sr5* and *Sr7b*) and pts. 2 and 3 (avirulent for *Sr7b* and virulent for *Sr5*). Because the IT pattern of Lutescens 72 was similar to the combination of IT patterns of the control genotypes Reliance and Marquis, *Sr5* and *Sr7b* were postulated for this cultivar (**Table 8**).

Erythrospermum 13 displayed ITs of "2^{+}" to "33^{+C}" to pathotypes virulent for *Sr5*, *Sr7b* and *Sr30* (pts. 6 and 8, respectively), and low ITs of "12^{-}" to "$2^{-}2^{=}$" to pathotypes avirulent for at least one of these genes. On this basis, Erythrospermum 13 was postulated to carry *Sr5* in combination with *Sr7b* and *Sr30*.

Sr-RG4. Group 4 included eight cultivars. The IT patterns produced by cultivars Bogarnaya 56, Krasnovodopadskaya 25, Yuzhnaya 12, and Oktyabrina 70 were similar to that of the *Sr8b* control, Barleta Benvenuto, with high ITs of "33^{+}" to "3^{+}" to pathotypes virulent for *Sr8b* (pts. 4, 7 and 8) and low ITs of "$;1^{-}$" to "12^{+CN}" to pathotypes that were avirulent for *Sr8b*, indicating the likely presence of *Sr8b* in these cultivars. Tilek displayed an IT pattern similar to that of the control Barleta Benvenuto, except for a low IT of "12^{+CN}" with pathotype 4 (virulent for *Sr8b*), suggesting the presence of *Sr8b* and possibly additional resistance (**Table 8**). Similarly, Melanopus 223 was postulated to carry *Sr8b*, although some plants within this group produced low ITs of "$2^{-}2^{=}$" and "12^{-}" to pathotypes 4 and 7 and a low IT of "22^{+}" to pt. 10, indicating heterogeneity. The deviation from the IT pattern of *Sr8b* in these off-type plants was assumed to represent additional unknown resistance. Given the uniform high IT of "3^{+}" to pts 4, 7, and 8 (virulent for *Sr8b* and *Sr5*) and low ITs of "12^{+C}" to "3^{C}" to all other pathotypes avirulent for one or both genes, *Sr8b* and *Sr5* were postulated for cultivars Zhetysu and Erythrospermum 350 (**Table 8**).

Sr-RG5. Vugar displayed low ITs of ";" to "$12^{=}$" to all pathotypes avirulent on the differential varieties Emmer (*Sr9e*) and Entrelargo de Montijo (*SrEm*), and high ITs of "33^{+}" to the only pathotype virulent on Emmer and Entrelargo de Montijo (pt. 8) (**Table 8**). This implied the presence of *Sr9e* and/ or the uncharacterised resistance gene

Table 7 Responses of differential genotypes to 10 Australian pathotypes of *Puccinia graminis* f. sp. *tritici*.

Cultivar	Genotype	Pathotype[a]									
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Reliance	*Sr5*	$2^{++}3$[b]	2^{++}	22^{+}	22^{-C}	3	2^{++}	3^{+}	$2^{++}3$	33^{+}	0;
Marquis	*Sr7b*	22^{-}	22^{+}	22^{-}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Acme	*Sr9g , X*	3^{+}	$;1^{-C}$	$12^{=C}$	$;2^{=}$	3^{+}	3^{+}	3^{+}	33^{+}	3^{+}	2^{+C}
Emmer	*Sr9e*	$;2^{=}$	$;2^{=}$	$;12^{=}$	;	$;2^{=}$	$;2^{=}$	$;1^{-}$	3^{+}	$12^{=}$	$;1^{=}$
Einkorn	*Sr21*	$;1^{=}$	$;12^{=}$	$;12^{=}$	$;12^{=}$	;	;	;	;	12^{-C}	$;12^{=}$
Line S	*Sr13,Sr17*	2^{-}	2^{-}	2^{-}	2^{-}	2^{-}	$;1^{-}$	;	12^{-C}	$;1^{-}$	$;12^{-}$
McMurachy	*Sr6*	3^{+}	3^{+}	3^{+N}	3^{+N}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Yalta	*Sr11*	3^{+}	3^{+}	3^{+}	;	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
W2402	*Sr7b, Sr9b*	22^{-}	2^{-}	2^{-}	2^{-}	3^{+}	3^{+}	3^{+}	3^{+}	22^{-}	3^{+}
TD	*Sr36*	$;^{N}1^{-N}$	3^{+}	$;1^{-N}$	33^{+}	3^{+}	;1	3^{+}	3^{+}	$;1^{-}$	X^{-N}
Renown Seln	*Sr7b,Sr17*	2^{-}	2^{-}	2^{-}	3	3^{+}	-	3^{+}	3^{+}	$X^{=N}$	X
Mentana	*Sr8a*	3^{+}	3^{+}	3^{+}	3	3^{+}	3^{+}	3^{+}	3^{+}	2^{-}	2^{-}
Norka	*Sr15*	X^{-N}	X^{-N}	X^{-N}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Festiguay	*Sr30*	2^{-}	$2^{-}2^{=}$	3^{+}	$2^{-}2^{=}$	2^{-}	3^{+}	2^{-}	3^{+}	2^{-}	3^{+}
TAF 2	*SrAgi*	12^{-}	$12^{=}$	3^{+}	$12^{=}$	12^{-}	3^{+}	$12^{=}$	3^{+}	12^{-}	3^{+}
Ent. De Montijo	*SrEm*	2^{-}	2^{-}	2^{-}	$2^{=}$	2^{-}	2^{-}	$2^{-}2^{=}$	3^{C}	2^{-}	2^{-}
Barleta Benvenuto	*Sr8b*	X^{-N}	$;12^{=}$	$X^{=N}$	3^{+}	X^{-}	X^{-N}	3^{+}	3^{+}	X^{-N}	X^{-}
Coorong	*Sr27*	$;1^{+C}$	$;12^{=}$	$;12^{=}$	;	;	$;1^{-}$	;	;	$;1^{-}$	$;1^{C}$
Sr Nin	*SrNin*	$;12^{-C}$	$;2^{=}$	$;2^{=C}$	$;^{-}$	;	;	;	0;	$;12^{=C}$	$;2^{=C}$
Agent	*Sr24*	$2^{-}2^{=}$	$2^{-}2^{=}$	$2^{-}2^{=}$	$2^{-}2^{=}$	2^{-}	2^{-}	$2^{-}2^{=}$	$2^{-}2^{=}$	2^{-}	2^{-C}
Mildress	*Sr31*	$2^{-}2^{=}$	$2^{-}2^{=}$	$2^{-}2^{=}$	$12^{=}$	2^{-}	2^{-}	$2^{-}2^{=}$	$2^{-}2^{=}$	2^{-}	2^{-C}
Mokoan	*Sr9b*	3^{+}	3^{+}	3^{+}	12^{-CN}	3^{+}	3^{+}	3^{+}	3^{+}	22^{-}	3^{+}
Trident	*Sr38*	X^{-N}	X^{-N}	X^{-N}	;	X^{-N}	X^{-N}	$X^{=N}$	$X^{=N}$	3	X^{-N}
Morocco	-	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$	$3^{+}4$

[a] 1= 98-1,2,3,5,6, 2= 343-1,2,3,4,5,6, 3= 343-1,2,3,5,6,(8),9, 4= 126-1,4,5,6,7,11, 5= 34-1,2,3,4,5,6,7, 6= 34-1,2,3,6,7,8,9, 7= 34-1,2,3,4,5,6,7,11, 8= 40-1,2,3,4,5,6,7,8,9,10,11, 9= 34-1,2,7+*Sr38*, 10= 21-2,3,7,8,9

[b] Infection types, "0" no visible uredinia, ";" hypersensitive flecks, "1" small uredinia with necrosis, "2" small to medium sized uredinia with green islands and necrosis or chlorosis, "3" medium sized uredinia with or without chlorosis, "4" large uredinia without chlorosis, "X" heterogeneous ITs similarly distributed over the leaves. Variations in IT are indicated by the use of "-" (less than average for class) and "+" (more), as well as "C" and "N" to indicate more than usual chlorosis or necrosis, respectively.

SrEm in this cultivar. The differential Entrelargo de Montijo is a durum wheat with two *Sr* genes that confer IT "2" and "X", respectively (Luig 1983). Given that Vugar is a tetraploid wheat, it may carry the same genes present in the Emmer tetraploid differential. However, further work is needed to confirm this hypothesis.

Sr-RG6. Mirabashir and Mirabashir 128 showed IT patterns that mirrored those of the *Sr9b* and *Sr11* control genotypes W2402 and Yalta, respectively. High ITs of "33^{+}" and "3^{+}" were displayed to pts 1, 2, 3, 5, 6, 8 and 10 (all virulent on *Sr11*) and low ITs of "12^{-C}" and ";12^{-C}" were displayed to pts 4 (avirulent for *Sr9b* and *Sr11*) and 9 (virulent for *Sr9b* and avirulent for *Sr11*). According to this IT pattern, *Sr9b* and *Sr11* were postulated in Mirabashir and Mirabashir 128 (**Table 8**). Kyzyl Dan 27 also displayed high ITs to pathotypes virulent for *Sr9b* and *Sr11* (pts. 1– 3, 5–8, and 10) and low ITS of "12^{+C}" to pts. 4 and 9, consistent with the presence of *Sr9b* and *Sr11*. Because some plants within Kyzyl Dan 27 showed a high IT of "3^{+}" to pt. 4 and a low IT of ";" to pts. 6 and 9, it was not possible to postulate any *Sr* gene (**Table 8**). A low IT of "12^{-CN}" displayed by Karlygash to the only pathotype avirulent for *Sr11* (pt. 4), and a high IT of "3^{+}" to pathotypes virulent for this gene, supported the presence of *Sr11* in this cultivar.

Sr-RG7. The only member of this group, BDME 9, displayed a low IT of "0;" to pts 4 (avirulent for *Sr11* and virulent for *Sr7b* and *Sr17*), 6 and 9 and an IT of "$2^{++}3$" to pathotype 10 (avirulent for *Sr17* and virulent for *Sr7b* and *Sr11*) and high ITs of "3^{+}" to the other pathotypes (**Table 8**). Based on this IT pattern, BDME 9 was postulated to carry *Sr17* and *Sr11*.

Sr-RG8. The IT patterns of the nine cultivars in this group to the 10 *Pgt* pathotypes are listed in **Table 8**. Mtskhetskaya 1, Ekinchi, Nairi 131, Bermet, and Ani 591 had the same low IT pattern as Mildress (*Sr31*), suggesting the presence of *Sr31* in these cultivars. Turkmenbashi and Lalvar showed ITs lower than the control Mildress with some pathotypes, indicating the possible presence of an additional resistance gene(s). The ITs of the cultivars Ani 435 and Lori 292 were heterogeneous, indicating a lack of *Sr31* in some plants.

Due to the lack of recombination between *Yr9*, *Lr26*, and *Sr31* in wheat, the presence of any of these genes supports the postulation of the other two genes. Accordingly, the postulation of *Yr9* (**Table 4**) and *Lr26* (**Table 6**) for all cultivars in stem rust resistance group 7 (**Table 8**), supported the postulation of *Sr31* for these cultivars.

DISCUSSION

Stripe rust

In the present study, evidence was obtained for the presence of six known genes conferring seedling resistance to stripe rust either singly or in combination in the 32 wheat genotypes examined. One genotype was not tested with *Pst* due to insufficient seed, and the identity of stripe rust resistance in two genotypes remained uncharacterised.

Yr1 was postulated singly in two cultivars, and in combination with unknown resistance in three other cultivars. Of the three cultivars postulated to carry *Yr1* plus additional unknown gene/s, two (Vugar and Melanopus 223) were durum wheats. This is the first report of the possible presence of *Yr1* in tetraploid wheat, and it should be tested more critically using other *Pst* pathotypes virulent for *Yr1* and genetic analysis. Virulence for *Yr1* was reported in East Asia (Stubbs 1985) and more recently in CAC countries (Yahyaoui *et al.* 2002; Yahyaoui 2005) from where Chinese 166, the differential genotype carrying *Yr1*, probably originated (McIntosh *et al.* 1995).

Two cultivars were postulated to carry either *Yr3* or *Yr4* singly, or in combination. The only pathotype that was avirulent for these genes, pt. 7, was unable to differentiate between them. Although virulence for these genes is very common in Europe (Bayles and Priestley 1983) and in Australia (Wellings and McIntosh 1990), these genes are very effective in CAC regions (Yahyaoui 2005). Following an epidemic of stripe rust in Iran in 1992 (Torabi *et al.* 1995), Euro-

Table 8 Responses of selected wheat cultivars and control differential genotypes to 10 Australian pathotypes of *Puccinia graminis* f. sp. *tritici*.

Cultivar	Genotype	Pathotype[a]									
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Sr resistance group 3											
Steklovidnaya 24	*Sr5*	$2^{+}3^{CNb}$	33^{+}	3^{C}	33^{+CN}	33^{+}	3^{+}	3^{+}	3^{+}	$3^{C}/3^{+c}$	0;
Naz	*Sr5*+	X^{-C}	$2^{+C}/3^{+}$	$22^{+}/3$	33^{+CN}	3^{+}	12^{+C}	3^{+}	3^{+}	-	0;
Lutescens 72	*Sr5*,*Sr7b*	22^{-C}	22^{-C}	22^{+}	3^{+}	$1P3^{+}$	3^{+}	3^{+}	3^{+}	3^{+}	0;
Erythrospermum 13	*Sr5*, *Sr7b*, *Sr30*	12+	2-2=	12C, 2+C/3[d]	12=CN	12-	33+C	12+	2+	12-C	0;
Reliance[e]	*Sr5*	$2^{++}3$	2^{++}	22^{+}	22^{-C}	3	$2^{++}3$	3^{+}	$2^{++}3$	33^{+}	0;
Marquis	*Sr7b*	22^{-}	22^{+}	22^{-}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Festiguay	*Sr30*	2^{-}	$2^{-}2^{=}$	3^{+}	$2^{-}2^{=}$	2^{-}	3^{+}	2^{-}	3	2-	3^{+}
Sr resistance group 4											
Bogarnaya 56	*Sr8b*	$12^{=}C,3^{+}$	$12^{-C}/3^{+}$	$12^{-C},3^{+}$	3^{+CN}	$;1^{-}$	$;12^{-}$	3^{+}	3^{+}	12^{+C}, 3^{+}	$12^{=C}$ 3^{+},
Krasnovodopadskaya 25	*Sr8b*	$2^{CN}/3^{+}$	2^{CN}/3C	2^{CN}	33^{+}	$;12^{+CN}$	$;12^{-C}$	3^{+}	3^{+}	12^{+C}	$2^{CN}/3^{+}$
Yuzhnaya 12	*Sr8b*	$12^{+CN}/3$	$12^{+C}/3$	$12^{+C}/3$	33^{+}	$X^{+C}/3$	$12^{+}C$	3^{+}	3^{+}	$X^{-CN}/3^{+}$	$12^{+CN}/3$
Oktyabrina 70	*Sr8b*	12^{+CN}	12^{CN}	12^{CN}	33^{+}	12^{+CN}	$;12^{-C}$	3^{+}	3^{+}	$X^{-CN}/3^{+}$	12^{+CN}
Tilek	*Sr8b*+	X^{-C}	$;12^{-C}$	12^{-C}	12^{+CN}	12^{-CN}	12^{-C}	3^{+}	3^{+}	$X^{-C}/33^{+}$	X^{-C}
Melanopus 223	*Sr8b?*	$22^{+}/2$	$2^{+C}/3$	$22^{-}/2^{++}$	$3^{+},2^{-}2^{=}$	$12^{+},3^{+}$	22^{-}	$3^{+},12^{-}$	3^{+}	$3^{C}/3^{+}$	$22^{+}/2$
Zhetysu	*Sr8b*,*Sr5*	$2^{+C}/3$	$2^{+}/3^{C}$	22^{-C}	3^{+}	$2^{+C}/3$	$22^{-C}/33^{+}$	3^{+}	3^{+}	3^{C}	0;
Erythrospermum 350	*Sr8b*,*Sr5*	$2^{+C},12^{=}$	22^{-C}	12^{+C}	3^{+}	12^{+C}	12^{+C}	3^{+}	3^{+}	12^{+C}	0;
Barleta Benvenuto	*Sr8b*	X^{-N}	$;12^{=}$	$X^{=N}$	3^{+}	X^{-}	X^{-N}	3^{+}	3^{+}	X^{-N}	X^{-}
Reliance	*Sr5*	$2^{++}3$	2^{++}	22^{+}	22^{-C}	3	2^{++}	3^{+}	$2^{++}3$	33^{+}	0;
Sr resistance group 5											
Vugar	*Sr9e*, *SrEm*?	$12^{=}$	$12^{=}$	$;12^{=}$	0;	$;1^{-C}$	$;1^{-}$	;	33^{+}	$12^{=}$	$12^{=}$
Emmer	*Sr9e*	$;2^{=}$	$;2^{=}$	$;12^{=}$	;	$;2^{=}$	$;2^{=}$	$;1^{-}$	3^{+}	$12^{=}$	$;1^{=}$
Ent. de Montijo	*SrEm*	2^{-}	2^{-}	2^{-}	$2^{=}$	2^{-}	2^{-}	$2^{-}2^{=}$	3^{C}	2^{-}	2^{-}
Sr resistance group 6											
Mirabashir	*Sr9b*, *Sr11*	3^{+}	33^{+}	33^{+}	12^{-C}	3^{+}	3^{+}	3^{+}	3^{+}	$;12^{-CN}$	3^{+}
Mirabashir 128	*Sr9b*, *Sr11*	33^{+}	33^{+}	33^{+}	12^{+CN}	3^{+C}	33^{+C}	3^{+}	3^{+}	12^{-}	33^{+}
Kyzyl Dan 27	*Sr9b*, *Sr11*	3^{C}	33^{+}	3^{+}	12^{+C}, 3^{+}	3^{+}	3^{+}, $;^{-}$	3^{+}	3^{+}	12^{+C}, ;	3^{C}
Karlygash	*Sr11*	3^{+}	3^{+}	3^{+}	12^{-CN}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Yalta	*Sr11*	3^{+}	3^{+}	3^{+}	;	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
W2402	*Sr7b*, *Sr9b*	22^{-}	2^{-}	2^{-}	2^{-}	3^{+}	3^{+}	3^{+}	3^{+}	22^{-}	3^{+}
Marquis	*Sr7b*	22^{-}	22^{+}	22^{-}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Sr resistance group 7											
BDME 9	*Sr17*, *Sr11*	$2^{++}3$	3^{+}	3^{+}	0;	3^{+}	0;	33^{+}	3^{+}	0;	$2^{++}3$
Marquis	*Sr7b*	22^{-}	22^{+}	22^{-}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Yalta	*Sr11*	3^{+}	3^{+}	3^{+}	;	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}	3^{+}
Renown Seln	*Sr7b*, *Sr17*	2^{-}	2^{-}	2^{-}	3	3^{+}	-	3^{+}	3^{+}	$X^{=N}$	X
Sr resistance group 8											
Mtskhetskaya 1	*Sr31*	2^{-C}	$2^{-}2^{=}$	$2^{-}2^{=}$	$2^{-}2^{=}$	2^{-}	2^{-}	$2^{-}2^{=}$	$12^{=}$	$12^{=}$	2^{-C}
Ekinchi	*Sr31*	$2^{-}2^{=C}$	$2^{-}2^{=}$	$2^{-}2^{=}$	$12^{=}$	$12^{=}$	12^{-}	$12^{=}$	$;12^{=}$	2^{-}	$2^{-}2^{=C}$
Nairi 131	*Sr31*	$;12^{=}$	$12^{=}$	$2^{-}2^{=}$	$12^{=}$	12^{-}	12^{-}	12^{-}	$;12^{=}$	2^{-}	$;12^{=}$
Bermet	*Sr31*	2^{-C}	$2^{-}2^{=}$	$2^{-}2^{=}$	$12^{=}$	12^{-}	12^{-}	$12^{=}$	$;12^{-}$	$;12^{-}$	2^{-C}
Ani 591	*Sr31*	12^{-}	$22^{=}$	$2^{-}2^{=}$	$12^{=}$	12^{-}	12^{-}	$12^{=}$	$12^{=}$, 3^{+}	12^{-C}	12^{-C}
Ani 352	*Sr31*+	12^{-CN}	$;12^{-C}$	$12,^{-}3^{+}$	$12^{-C},2^{+C}$	12^{-}	12^{-}	$12,^{=}3^{+}$	$12^{+},3^{+}$	2^{-}	12^{-CN}
Turkmenbashi	*Sr31*+	$2^{+C},;12^{=}$	$2^{-}2^{=}$	$2^{-}2^{=}$	$;^{CN}$	2^{-}	$;1^{-}$	12^{-}	$;12^{=}$	0;	$2^{+C},;12^{=}$
Lalvar	*Sr31*+	$;^{+C}$	$;^{-}$	$;^{+C}$	$;12^{=}$	$;12^{=}$	$;^{+C}$	12^{-C}	$;12^{-}$	;1	$;^{+C}$
Ani 435	*Sr31**[d]	$2^{-},3^{+}$	$2^{-}2^{=},3^{+}$	12^{+CN}	$2^{-}2^{=},3^{+}$	3^{+}	$2^{-},3^{+}$	$3^{+},2^{-}2^{=}$	$3^{+},12^{-}$	33^{+}	$3^{+},2^{-}$
Lori 292	*Sr31**	$3^{+},;1^{=}$	$3^{+},;$	;	$2^{-}2^{=}$	$;1^{-}$	;	$12^{-},3^{+}$	$;12^{-}$	;	$3^{+},;1^{=}$
Mildress	*Sr31*	$2^{-}2^{=}$	$2^{-}2^{=}$	$2^{-}2^{=}$	$12^{=}$	2^{-}	2^{-}	$2^{-}2^{=}$	$2^{-}2^{=}$	2^{-}	2^{-C}

[a] 1= 98-1,2,3,5,6, 2= 343-1,2,3,4,5,6, 3= 343-1,2,3,5,6,(8),9, 4= 126-1,4,5,6,7,11, 5= 34-1,2,3,4,5,6,7, 6= 34-1,2,3,6,7,8,9, 7= 34-1,2,3,4,5,6,7,11, 8= 40-1,2,3,4,5,6,7,8,9,10,11, 9= 34- 1,2,7+*Sr38*, 10= 21-2,3,7,8,9

[b] Infection types, "0" no visible uredinia, ";" hypersensitive flecks, "1" small uredinia with necrosis, "2" small to medium sized uredinia with green islands and necrosis or chlorosis, "3" medium sized uredinia with or without chlorosis, "4" large uredinia without chlorosis, "X" heterogeneous ITs similarly distributed over the leaves. Variations in IT are indicated by the use of "-" (less than average for class) and "+" (more), as well as "C" and "N" to indicate more than usual chlorosis or necrosis, respectively.

[c] "/" separates infection types on the primary and secondary leaves, where differences were seen

[d] comma and * indicate heterogenous response

[e] cultivars in bold are Australian differential genotypes used to characterise isolates of *P. graminis* f. sp. *tritici*

pean wheat cultivars with *Yr3* and *Yr4* were used extensively in national breeding programs because of a lack of virulence for both genes. Given the common occurrence of virulence for *Yr3* and *Yr4* in Australia, it is expected that virulence will develop rapidly if cultivars carrying these genes are released and grown widely in the Middle East.

Genotypes in *Yr*-RG 3 were postulated to carry *Yr9* either singly or in combination with unknown resistance gene/s. This gene originated from *Secale cereal*e and is completely linked with *Lr26* and *Sr31* in the 1BL/1RS translocation (McIntosh *et al.* 1993). Tests with *Pt* and *Pgt* provided additional evidence for *Yr9* in these genotypes by demonstrating the likely presence of *Lr26* and *Sr31*, respectively. Virulence for *Yr9* has been detected in many wheat-growing areas, especially in countries where CIMMYT nurseries have been used for cultivar selection. For example, Veery was selected and released under different names in Ethiopia (cv. Dashen; Badebo and Bayu 1992), Syria (cv. Mexipak; Mamluk and El-Naimi 1992), Turkey (Seri 82; Dusunceli *et al.* 1996), Iran (cv. Falat; Torabi *et al.* 1995), Pakistan (cv. Pak 82; Ahmed *et al*. 1991), and in CAC countries (Yahyaoui 2005). Several epidemics of stripe rust in West Asia and North Africa (WANA) were attributed to virulence for *Yr9* and the widespread cultivation of wheats carrying this gene, and pathotypes with virulence for *Yr9* still predominate in these regions. Despite the stripe rust susceptibility of genotypes with the 1BL/1RS translocation, many have had a great impact on wheat production

in developing countries because of their widespread adaptability and high yield. There is clearly a need to improve the rust resistance of these genotypes for the CAC region. A combination of *Yr7* and *Yr9* was postulated in Turkmenbashi. Gene *Yr7* has been deployed in wheat cultivars in Europe, Australia and New Zealand (Wellings 1986; Wellings and McIntosh 1990) and virulence for it is common in many wheat growing areas (McIntosh *et al*. 1995). Gene *Yr7* is closely linked with *Sr9g* (McIntosh *et al*. 1981) and is allelic or closely linked with *Yr5* (McIntosh *et al*. 1995). One genotype was postulated to carry *Yr27*. This gene originated from the wheat cultivar Selkirk. Again, this gene is present in many CIMMYT genotypes (Wellings 1992). Virulence for *Yr27* was found in New Zealand (Wellings and Burdon 1992), India, Pakistan, Tajikistan, Kyrgyzstan, (Singh *et al*. 2004) and Iran (Nazari and Torabi 2000; Afshari 2004).

Leaf rust

Multi-pathotype tests revealed a lack of detectable leaf rust resistance genes in five cultivars. It is possible that these cultivars may carry *Lr10*, because an *Lr10*-avirulent culture was not used. Among the cultivars, evidence was obtained for the presence of nine designated genes, either singly or in combination. *Lr26* was the most commonly postulated gene, likely present in five genotypes singly or in combination with *Lr3bg* and/ or *Lr3a* (two cultivars) and *Lr13* (two cultivars). The postulated presence of *Lr26* in cultivars Lalvar, Ekinchi, Ani 591, Mtskhetskaya 1, Nairi 131, Ani 435, Lori 292, Turkmenbashi and Bermet was in agreement with the postulation of *Yr9* in these cultivars. Virulence for *Lr26* has been reported in many wheat growing areas including Europe (Bartos *et al*. 1984), Australia (Park *et al.* 2000), Iran (Torabi *et al*. 2001), USA (Kolmer *et al*. 2004), the WANA region (Yahyaoui *et al*. 2000) and CAC countries (Kolmer 2004, pers. com.).

Of the three alleles at the *Lr3* locus (*Lr3a*, *Lr3bg*, and *Lr3ka*), *Lr3a* is the most common (McIntosh *et al*. 1995). It was postulated singly in one cultivar (Sapaly) and in combination with *Lr13* in six cultivars (Krasnovodopadskaya 25, Steklovidnaya 24, Kyzyl Dan 27, Yuzhnaya 12, Melanopus 223, Bogarnaya 56) and was also considered present in combination with *Lr16* (two cultivars). *Lr3a* is one of the most common leaf rust resistance genes and matching virulence is very common throughout the world (McIntosh *et al*. 1995). Virulence for *Lr3a* was detected in Azerbaijan, Georgia, Kazakhstan, Kyrgyzstan, Uzbekistan, and Tajikistan (Kolmer 2004, pers. comm.). The pathotype arrays used in the present study led to the postulation of *Lr1*, *Lr2a* and one of the alleles of *Lr3*, most likely *Lr3ka*, in cultivar Erythrospermum 13. With the exception of Georgia and Uzbekistan, virulence for this gene combination was common in the CAC region (Kolmer 2004, pers. comm.; Yahyaoui 2005).

Lr13 was postulated singly in one cultivar, in combination with *Lr16* (one cultivar), and in combination with *Lr26* (two cultivars). *Lr13* is regarded as the most widely distributed leaf rust resistance gene in world wheat growing areas, and is considered to have originated from the wheat cultivars Frontana, Frondoso and Fronteria (McIntosh *et al*. 1995). Although virulence for *Lr13* has been detected in many regions, it is still considered effective when used in combination with certain seedling resistance genes. Virulence for *Lr13* was reported in Iran and Syria (Torabi *et al*. 2001; Yahyaoui 2005) using disease trap nurseries, but in pathotype surveys in countries of the CAC region virulence for *Lr13* was not detected (Kolmer 2004; pers. comm.). Kolmer (1992) demonstrated that this gene shows enhanced interaction when present in combination with other leaf rust resistance genes.

The genotype BDME 9 was postulated to carry *Lr14a* alone. It was released recently in Uzbekistan as the cultivar Dostyk (A. Morgounov pers. comm.). *Lr14a* is ineffective in many parts of the world (McIntosh *et al*. 1995). It is genetically linked to powdery mildew and stem rust resistance genes *Pm5* and *Sr17*, respectively (McIntosh *et al.* 1967, 1995). The presence of *Lr14a* in BDME 9 was supported by the additional postulation of *Sr17* in this genotype in the present study. Because of the high frequency of virulence for *Lr14a* in the CAC region (Torabi *et al*. 2001; Kolmer 2004, pers. comm.), it cannot be recommended as an effective resistance source.

Lr16 was postulated to be present singly in the genotypes Karlygash and Naz, and in combination with *Lr3a* in two genotypes (Zernokormonaya 50 and Mirabashir 128) and with *Lr13* in Ani 352. Although the frequency of virulence for this gene was reported to be relatively low (Huerta-Espino 1992; McIntosh *et al*. 1995), more recent studies showed that virulence for *Lr16* is present in some of the wheat growing areas in CAC and WANA (Kolmer 2004, pers. comm..; Yahyaoui 2005). However, this gene could still be of value if combined with effective seedling and adult-plant resistance genes in countries where matching virulence is low or has not been detected.

Two of the test lines were postulated to carry a resistance gene similar to the resistance of Brevit, the identity of which could not be determined with the pathotypes used. Brevit was reported by Dyck and Samborski (1968) to carry *LrB*. This gene can not be detected with Australian pathotypes of *Pt*. Further work is needed to characterise the resistance in these two lines.

Stem rust

Multi-pathotype tests of the wheat genotypes with 11 *Pgt* pathotypes produced evidence for the presence of the seedling resistance genes *Sr5*, *Sr7b*, *Sr8b*, *Sr9e*, *Sr9b*, *Sr11*, *Sr30*, and *Sr31*, either singly or in combination.

Among these genes, *Sr5* was postulated in genotype Steklovidnaya 24, in Lutescens 72 in combination with *Sr7b* and in Erythrospermum 13 with *Sr7b* and *Sr30*. Bezostaya 1, a wheat cultivar from the former USSR, is present in the pedigree of Erythrospermum 13 (**Table 2**). This cultivar was postulated to carry *Sr5* plus an additional resistance gene (Luig 1983), consistent with the present postulation of *Sr5* in Erythrospermum 13. *Sr5* is present in the Stakman *et al*. (1962) differential Reliance C.I. 7370, having been inherited from Kanred (Luig 1983; McIntosh *et al*. 1995), and is present in Thatcher and several other well-known cultivars from North America that were used extensively in generating CIMMYT germplasm (Luig 1983). Virulence for *Sr5* was reported as common in many geographical areas by Huerta-Espino (1992) and Luig (1983). Genes *Sr7b* and *Sr30* are present in the differentials Marquis and Webster, respectively (Stakman *et al*. 1962). In the present study, Festiguay was used as the differential genotype for *Sr30* (McIntosh *et al*. 1986). Although *Sr7b* was effective in many geographical areas in an international survey of virulence in *Pgt* (Luig 1983), it has not been selected consciously as a source of stem rust resistance. Caution is needed in replacing current cultivars with new genotypes in CAC regions. The wheat cultivar Webster, introduced to the USA from the former USSR, is regarded to be the origin of *Sr30* (Zeven and Zeven-Hissink 1976). Gene *Sr30* is present in several Australian cultivars including Festiguay, and in Mexican wheats (McIntosh *et al*. 1995). Virulence for *Sr30* was not common in many wheat growing areas in the survey conducted by Luig (1983), but virulence for this gene has been detected in Australia on several occasions (Park and Wellings 1992). Therefore, the deployment of *Sr30* alone has a high risk of an increase in frequency of the matching virulence.

Sr8b was postulated singly in four genotypes and in combination with *Sr5* in the genotypes Zhetysu and Erythrospermum 350. The genotypes Tilek and Melanopus 223 were postulated to possess *Sr8b* and an additional uncharacterised seedling resistance gene. Although *Sr8b* was considered to be a rare gene by McIntosh *et al*. (1995), in the early 1970s virulence for *Sr8b* was reported in several geographical areas including North and South America, Europe

and Africa (Luig 1983). High levels of virulence were also found in western Asia and Eastern Europe, Northern Africa and Western Europe and South America by Huerta-Espino (1992). In contrast to the allele *Sr8a*, *Sr8b* can provide a high level of resistance in field plots (Singh and McIntosh 1986). Bezostaya 1 was reported to carry *Sr5* and additional uncharacterised resistance gene (Luig 1983), and its presence in the pedigree of Erythrospermum 350 supports the postulation of *Sr5* in combination of *Sr8b* in this genotype.

Sr9e, derived from Vernal emmer wheat (*Triticum turgidum*), was postulated in the durum genotype Vugar in the present study. Virulence for *Sr9e* has been detected at a high frequency in North America and at relatively low frequencies in other geographical areas (Luig 1983; Huerta-Espino 1992). *Sr9b* was postulated in combination with *Sr11* in Mirabashir 128 and Kyzyl Dan 27, and in the durum wheat Mirabashir. High frequencies of virulence on *Sr9b* are common in most geographical areas (Huerta-Espino 1992). This gene is linked with *Lr13* (McIntosh *et al*. 1995). Although Singrün *et al.* (2004) postulated *Lr3* for Mirabashir 128 and Kyzyl Dan 27, in the present study the combination of *Lr3a* and *Lr13* in both genotypes was postulated, supporting the presence of *Sr9b*. *Sr11* originated from the durum wheat cultivar Gaza and was also postulated singly in Karlygash. Virulence for *Sr11* is common in most wheat growing areas (McIntosh *et al*. 1995).

Sr17, the only recessive gene detected in present study, was postulated in the line BDME 9 along with an additional uncharacterised seedling resistance gene. *Sr17* is genetically linked to *Pm5* and *Lr14a* (McIntosh *et al.* 1967). BDME 9 was postulated to possess *Lr14a* in the present study, but it was postulated to possess *Lr23* by Singrün *et al* (2004). The presence of *Lr14a* in this genotype is consistent with the additional postulation of *Sr17*. *Sr17* is present in a wide range of wheat genotypes (Roelfs and McVey 1979; McIntosh *et al*. 1995), particularly those with *Lr14a* and *Pm5*. It has been suggested that *Sr17* is a significant component of the durable stem rust resistance found in a wide range of Australian, Mexican, American, Canadian and Indian cultivars (McIntosh *et al*. 1995).

Sr31 was the most common stem rust resistance gene postulated, present in 10 lines. Gene *Sr31* has been used extensively worldwide, and is present in many European wheat cultivars, in some Chinese wheats and USA wheats and it has been widely used in wheat breeding programs at CIMMYT (McIntosh *et al*. 1995). Despite the widespread use of *Sr31*, virulence for this gene was not reported until 1999 when pathotype *Ug99* was detected in Uganda (Pretorius *et al*. 2000). This pathotype poses a major threat to wheat production in many regions (Anonymous 2005). It is avirulent for *Sr13*, *Sr22*, *Sr26*, *Sr29*, *Sr36* and *SrR* and these may have some immediate value in crop protection, although combinations involving adult-plant resistance genes such as *Sr2* will be expected to prolong their use. PCR-based molecular markers have already been developed for stem rust resistance genes *Sr2* (Spielmeyer *et al*. 2003; Hayden *et al*. 2004), *SrR* (Mago *et al*. 2004) and *Sr24* and *Sr26* (Mago *et al*. 2005). These markers should accelerate pyramiding these resistance genes in order to enhance their longevity.

ACKNOWLEDGEMENTS

Financial support from the University of Sydney through the International Postgraduate Research Scholarship (IPRS) and International Postgraduate Award (IPA) schemes is greatly acknowledged. The authors thank Mr. Keshab Kandel for his technical help. Seeds of the CAC cultivars were provided kindly by Dr. A. Morgounov, CIMMYT, Ankara, Turkey.

REFERENCES

Absattarova AS, Baboyev S, Bulatova K, Karabayev M, Koishibayev M, Kokhmetrova A, Kuklacheva V, Morgunov A, Rsaliev S, Sarbayev A, Urazaliev RA, Yessimbekova M, Wellings CR (2002) Improvement of wheat yellow rust in Kazakhstan and Uzbekistan through sub-regional co-operation. In: Johnson R, Yahyaoui A, Wellings CR, Saidi A, Ketata H (Eds) *Meeting the Challenge of Yellow Rust in Cereal Crops,* International Centre for Agricultural Research in the Dry Areas (ICARDA), Aleppo, pp 34-41

Afshari F (2004) Challenge of new race of *Puccinia striiformis* f. sp. *tritici* in Iran. In: *Second Regional Yellow Rust Conference for Central and West Asia and North Africa*, 22-26 March, 2004, ICARDA: Islamabad, pp 16 (Abstract)

Ahmed S, Rodriguez A, Farid GBS, Khan R, Panah M (1991) Economic losses of wheat crops infested with yellow rust in highland Balochistan. In: *MART/AZR Project Research*, Report 67, ICARDA Quetta. 15 pp

Anonymous (2005) Sounding the Alarm on Global Stem Rust: An assessment of race Ug99 in Kenya and Ethiopia and the potential for impact in neighbouring regions and beyond. (International Maize and Wheat Improvement Centre (CIMMYT), Mexico City. Available online: http://www.cimmyt.org/English/wps/news/2005/aug/pdf/Epert_Panel_Report.pdf

Badebo A, Bayu W (1992) The importance of stripe rust in the major bread wheat-producing region of Ethiopia 1988-90. In: Tanner DG, Mwangi W (Eds) *Proceedings of the 7th Regional Wheat Workshop for Eastern, Central and Southern Africa*, Nakuru, Kenya, pp 196-202

Badebo A, Stubbs RW, van Ginkel M, Gebeyehu G (1990) Identification of resistance genes to *Puccinia striiformis* in seedling of Ethiopian CIMMYT bread wheat varieties and lines. *Netherlands Journal of Plant Pathology* **96**, 199-210

Bartos P, Stuchlikova E, Kubova R (1984) Wheat leaf rust epidemics in Czechoslovakia in 1983. *Cereal Rusts Bulletin* **12**, 40-41

Bayles RA, Priestely RH (1983) Yellow rust of wheat. United Kingdom Cereal Pathogen Virulence Survey. *Annual Report, National Institute Agricultural Botany*, pp 27-36

Browder LE, Eversmeyer MG (1980) Sorting of *Puccinia recondita*: *Triticum* infection-type data sets toward the gene-for-gene model. *Phytopathology* **70**, 666-670

Dubin HJ, Johnson R, Stubbs RW (1989) Postulated genes for resistance to stripe rust in selected CIMMYT and related wheats. *Plant Disease* **73**, 472-475

Dusunceli F, Getin L, Albustan S, Beniwal SPS (1996) Occurrence and impact of wheat stripe rust (*Puccinia striiformis*) in Turkey in 1994/95-crop season. In: Kema GHJ, Niks RE, Daamen RA (Eds) *Proceedings of the 9th European and Mediterranean Cereal Rusts and Powdery Mildews Conference*, Lunteren, The Netherlands, p 309

Dyck PL, Samborski DJ (1968) Genetics of resistance to leaf rust in the common wheat varieties Webster, Loros, Brevit, Carina, Malakof and Centenario. *Canadian Journal of Genetics and Cytology* **10**, 7-17

Flor HH (1956) The complementary genetic system in flax and flax rust. *Advances in Genetics* **8**, 29-54

Hayden MJ, Kuchel H, Chalmers KJ (2004) Sequence tagged microsatellites for the *Xgwm*533 locus provide new diagnostic markers to select for the presence of stem rust resistance gene *Sr2* in bread wheat (*Triticum aestivum* L.). *Theoretical and Applied Genetics* **109**, 1641-1647

Huerta-Espino J (1992) Analysis of wheat leaf and stem rust virulence on a worldwide basis. PhD thesis, University of Minnesota, 472 pp

Johnson R (1988) Durable resistance to yellow (stripe) rust in wheat and its implications in plant breeding. In: Simmonds NW, Rajaram S (Eds) *Breeding Strategies for Resistance to the Rusts of Wheat*, CIMMYT, Mexico, pp 63-75

Johnson R, Stubbs RW, Fuchs E, Chamberlain NH (1972) Nomenclature for physiologic races of *Puccinia striiformis* infecting wheat. *Transaction of the British Mycological Society* **58**, 475-480

Johnston CO, Browder LE (1966) Seventh revision of the international register of physiologic races of *Puccinia recondita* f. sp. *tritici*. *Plant Disease Reporter* **50**, 756-760

Kolmer JA (1992) Enhanced leaf rust resistance in wheat conditioned by resistance gene pairs with *Lr13*. *Euphytica* **61**, 123-130

Kolmer JA (1996) Physiologic specialization of *Puccinia recondita* f. sp. *tritici* in Canada, Winnipeg, Manitoba. *Canadian Journal of Plant Pathology* **18**, 300-302

Kolmer JA, Long DL, Hughes ME (2004) Physiologic specialization of *Puccinia triticina* on wheat in the United States in 2002. *Plant Disease* **88**, 1079-1084

Loegering WQ (1985) Genetics of the pathogen-host association. In: Bushnell WR, Roelfs AP (Eds) *The Cereal Rusts*, Academic Press, New York, pp 165-192

Luig NH (1983) A survey of virulence genes in wheat stem rust, *Puccinia graminis* f. sp. *tritici*. In: *Advances in Plant Breeding*, Supplement 11 to *Journal of Plant Breeding*, Paul Parey, Berlin and Hamburg, 199 pp

Mago R, Bariana HS, Dundas IS, Spielmeyer W, Lawrence GJ, Pryor AJ, Ellis JG (2005) Development of PCR markers for the selection of wheat stem rust resistance genes *Sr24* and *Sr26* in diverse wheat germplasm. *Theoretical and Applied Genetics* **111**, 496-504

Mago R, Spielmeyer W, Lawrence GJ, Ellis JG, Pryor AJ (2004) Resistance genes for rye stem rust (*SrR*) and barley powdery mildew (*MIa*) are located in syntenic regions on short arm of chromosome 1. *Genome* **47**, 112-121

Mamluk OF, El-Naimi M (1992) Occurrence and virulence of wheat yellow

rust in Syria. In: Zeller FJ, Fischbeck G (Eds) *Proceedings of the 8th European and Mediterranean Cereal Rusts and Mildews Conference,* Weihenstephan, Germany, pp 115-117

McIntosh RA (1988) The role of specific genes in breeding for durable stem rust resistance in wheat and triticale. In: Simmonds NW, Rajaram S (Eds) *Breeding Strategies for Resistance to the Rusts of Wheat*, CIMMYT, Mexico, pp 1-9

McIntosh RA, Luig LH, Baker EP (1967) Genetics and cytogenetics studies of stem rust, leaf rust and powdery mildew resistance in Hope and related wheat cultivars. *Australian Journal of Biological Sciences* **20**, 1181-1192

McIntosh RA, Hart G, Gale M (1993) Catalogue of gene symbols for wheat. In: Li ZS, Zin ZY (Eds) *Proceedings of 8th International Wheat Genetic Symposium*, Beijing, China, pp 1133-1500

McIntosh RA, Luig NH, Johnson R, Hare RA (1981) Cytogenetical studies in wheat XI. *Sr9g* for reaction to *Puccinia graminis tritici*. *Zeitchrift für Pflanzenzüchtung* **87**, 274-289

McIntosh RA, Wellings CR, Park RF (1995) *Wheat Rusts: An Atlas of Resistance Genes*, CSIRO Publications: Victoria, Australia, 200 pp

McVey DV, Roelfs AR (1975) Postulation of stem rust resistance in the entries of Fourth International Wheat Performance Nursery. *Crop Science* **15**, 335-337

Nazari K, Torabi M (2000) Distribution of yellow rust (*Yr*) resistance genes in Iran. *Acta Phytopathologica et Entomologica Hungarica* **35**, 121-131

Oelke LM, Kolmer JA (2004) Characterization of leaf rust resistance in hard red spring wheat cultivars. *Plant Disease* **88**, 1127-1133

Park RF (1996) Pathogenic specialisation of *Puccinia graminis* on winter cereals and grasses in Australia in 1990 and 1991. *Australasian Plant Pathology* **25**, 135-140

Park RF, Burdon JJ, McIntosh RA (1995) Studies on the origin, spread, and evolution of an important group of *Puccinia recondita* f. sp. *tritici* pathotypes in Australasia. *European Journal of Plant Pathology* **101**, 613-622

Park RF, Jahoor A, Felsenstein FG (2000) Population structure of *Puccinia recondita* in Western Europe during 1995, as assessed by variability in pathogenicity and molecular markers. *Journal of Phytopathology* **148**, 169-179

Park RF, Wellings CR (1992) Pathogenic specialisation of wheat rusts in Australia and New Zealand in 1988 and 1989. *Australasian Plant Pathology* **21**, 61-69

Person C, Samborski DJ, Rohringer R (1962) The gene-for-gene concept. *Nature* **194**, 561-562

Pretorius ZA, Singh RP, Wagoire WW, Payne TS (2000) Detection of virulence to wheat stem rust resistance gene *Sr31* in *Puccinia graminis* f. sp. *tritici* in Uganda. *Plant Disease* **84**, 203

Rajaram S, Singh RP, Torres E (1988) The strategy of rust resistance breeding. In: Simmonds NW, Rajaram S (Eds) *Breeding Strategies for Resistance to Rusts of Wheat*, CIMMYT, Mexico, pp 101-118

Roelfs AP, McVey DV (1979) Low infection types produced by *Puccinia graminis* f. sp. *tritici* and wheat lines with designated genes for resistance. *Phytopathology* **69**, 722-730

Sharma S, Louwers JM, Karki CB, Snijders CHA (1995) Postulation of resistance genes to yellow rust in wild emmer wheat derivatives and advanced lines from Nepal. *Euphytica* **81**, 271-277

Singh D, Park RF, McIntosh RA (2001) Postulation of leaf (brown) rust resistance genes in 70 wheat cultivars grown in the United Kingdom. *Euphytica* **120**, 205-218

Singh RP, Huerta-Espino J, William HM (2005) Genetics and breeding for durable resistance to leaf and stripe rusts in wheat. *Turkish Journal of Agriculture and Forestry* **29**, 121-127

Singh RP, McIntosh RA (1986) Cytogenetical studies in wheat XIV. *Sr8b* for resistance to *Puccinia graminis tritici*. *Canadian Journal of Genetics and Cytology* **28**, 189-197

Singh RP, Rajaram S (1991) Resistance to *Puccinia recondita* f. sp. *tritici* in 50 Mexican bread wheat cultivars. *Crop Science* **31**, 1472-1479

Singh RP, William HM, Huerta-Espino J, Rosewarne G (2004) Wheat rust in Asia: meeting the challenges with old and new technologies. In: *Proceedings of the 4th International Crop Science Conference*, 26 September – 1 October, 2004, Brisbane, Australia

Singrün C, Rauch P, Morgounov A, Hsam S, Zeller F (2004) Identification of powdery mildew and leaf rust resistance genes in common wheat (*Triticum aestivum* L.). Wheat varieties from the Caucasus, Central and Inner Asia. *Genetic Resources and Crop Evolution* **51**, 355-370

Spielmeyer W, Sharp PJ, Lagudah ES (2003) Identification and validation of markers linked to broad-spectrum stem rust resistance gene *Sr2* in wheat (*Triticum aestivum* L.). *Crop Science* **43**, 333-336

Stakman EC, Stewart DM, Loegering WQ (1962) Identification of physiologic races of *Puccinia graminis* var. *tritici*. Agricultural Research Service E 617, USDA, Washington DC, 54 pp

Stubbs RW (1985) Stripe rust. In: Roelfs AP, Bushnell WR (Eds) *The Cereal Rusts, Vol II, Diseases, Distribution, Epidemiology, and Control*, Academic Press, Orlando, USA, pp 61-101

Torabi M, Mardoukhi V, Nazari K, Afshari F, Forootan AR, Ramai MA, Golzar H, Kashani AS (1995) Effectiveness of wheat yellow rust resistance genes in different parts of Iran. *Cereal Rusts and Powdery Mildew Bulletin* **23**, 9-12

Torabi M, Nazari K, Afshari F (2001) Genetics of pathogenicity of *Puccinia recondita* f. sp. *tritici*, the causal agent of leaf rust of wheat. *Iranian Journal of Agricultural Sciences* **32**, 625-635

Wellings CR (1986) Host-pathogen studies of wheat stripe rust in Australia. PhD thesis, University of Sydney, 237 pp

Wellings CR (1992) Resistance to stripe (yellow) rust in selected spring wheats. *Vorträge för Pflanzenzüchtung* **24**, 273-275

Wellings CR, Burdon JJ (1992) Variability in *Puccinia striiformis* f. sp. *tritici* in Australasia. *Vorträge för Pflanzenzüchtung* **24**, 114

Wellings CR, McIntosh RA (1990) *Puccinia striiformis* f. sp. *tritici* in Australasia: pathogenic changes during the first 10 years. *Plant Pathology* **39**, 316-325

Wellings CR, McIntosh RA, Hussain M (1988) A new source of resistance to *Puccinia striiformis* f. sp. *tritici* in spring wheats (*Triticum aestivum* L.). *Plant Breeding* **100**, 88-96

Yahyaoui A (2005) Cereal rust monitoring in Central, West Asia and North Africa: current status and future challenges. In: *Global Landsacpes in Cereal Rust Control*, 20-21 September, 2005, Katoomba, Australia, p 40 (Abstract)

Yahyaoui A, Hakim MS, Nazari K, Torabi M, Wellings CR (2002) Yellow (stripe) rust (*Puccinia striiformis* f. sp. *tritici*) in Central and Western Asia. In: Johnson R, Yahyaoui A, Wellings CR, Saidi A, Ketata H (Eds) *Meeting the Challenge of Yellow Rust in Cereal Crops*, International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, pp 69-77

Yahyaoui A, Hakim S, Al-Naimi M, Nachit MM (2000) Multiple disease resistance in durum wheat (*Triticum turgidum* L. var. *durum*). *Options Mediterraneennes. Serie A, Seminaires Mediterraneens* **40**, 387-392

Zeven AC, Zeven-Hissink NC (1976) *Genealogies of 14000 Wheat Varieties*, Institute of Plant Breeding, Agricultural University, Wageningen: The Netherlands, 121 pp