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**CEREAL RUSTS
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The leaf rust resistance genes most commonly found in the bread wheats being grown in different parts of the world are Lr2, Lr3, Lr10, Lr13, Lr14a, Lr17, Lr20, Lr23, and Lr26 (Saini and Gupta, 1979; Sharma et al., 1983; Saini, 1987). None of the named genes from Triticum aestivum is effective against the races prevalent in the Indian subcontinent (Saini et al., 1986). There is sufficient evidence to suggest that resistance to leaf rust in wheats being grown in many parts of the world is only due to adult plant resistance genes which are yet to be identified (Gupta and Saini, 1987; Gordon-Werner et al., 1989; Rajaram et al., 1988). The identification and designation of these adult plant resistance genes is difficult because of a poor understanding of their expression in different environmental conditions and backgrounds. The adult plant resistance genes Lr12 and Lr13 (temporary designations) have been reported to be present in a number of wheats (Dyck and Samborski, 1979; Dyck and Samborski, 1982; Shang et al., 1986; Claude et al., 1986). Dyck (1987) and Dyck et al. (1987) designated Lr12 and Lr13 in RL6058 and RL6057 derived from a Chinese line PI58548 as Lr34 and Lr33, respectively. The present report deals with expression and inheritance of these genes derived from lines PI58548, Terenzio and Lageadinho, backcrossed into the Thatcher background, against some Indian leaf rust races.

Multipathotype tests and inheritance studies were conducted on derivatives from the cultivars Terenzio, PI58548 and Lageadinho reported to carry the genes Lr12 and Lr13. The adult plant resistance gene Lr33(Lr13) designated from PI58548 derivative RL6057 was found to be different from the gene Lr13 present in lines 896 from Terenzio and 922 from Lageadinho. RL6058 and line 897 derived from PI58548 and Terenzio, respectively and reported to carry Lr34(Lr12) were found to possess additional resistance. Lr12 in line 920 from Lageadinho is different from the Lr12 reported from the other two lines.

ABSTRACT

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SHIWANI, R G SAINI AND A K GUPTA

ADDITIONAL RESISTANCE IN SOME DERIVATIVES WITH KNOWN ADULT PLANT LEAF RUST RESISTANCE GENES

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The infection type and disease severity recorded over the 11 lines/cultivars are given in Table 1. Against race 108 the seedlings of only RL 6059 gave ITs=1 whereas all other lines were susceptible. The infection types on adult plants of these lines to this race varied from 1 to X+ while Agra Local and Thatcher were susceptible. To race 77A only RL6057 and RL6059 were resistant at the seedling stage. The adult plants of RL6057, RL6058, RL6059, RL6050, lines 896, 897 and 922 were resistant to this race but the ITs on the remaining lines varied from 3C to 3+. Against race 77 all the lines except RL6059 were susceptible at the seedling stage. However, at the adult plant stage RL6057, RL6058 and RL6059 were resistant and the remaining lines were susceptible. During the year 1988-89 the disease severity over all the lines varied from 5MR to 20 MR/MS except for the susceptible checks. In the year 1989-90 RL6057 was moderately resistant with disease severity of 40S. The severity on RL6058, RL6059, RL6050 and

RESULTS AND DISCUSSION

RL6057, RL6058, RL6059, RL6050 and line 897 were crossed with cultivars Agra Local and Thatcher during the year 1987-88. Lines 922 and 896 were crossed to line 920 to study complementarity of genes for resistance to leaf rust. The F_2 populations obtained from all these crosses were grown under field conditions during the year 1989-90 in an epiphytotic of races 77A and 77-1. These populations were observed for susceptible (>50S) and resistant plants in terms of disease severity and appropriate genetic ratios were fitted using χ^2 test.

These lines were also subjected to multipathotype seedling and adult plant tests against races 108, 77 and 77A under controlled conditions at 20±1°C and 80% relative humidity. Race 77 is avirulent only on the gene Lr10 and race 108 is avirulent on Lr3 and Lr15 from T. aestivum. Biotypes 77A and 77-1 of race 77 are virulent over all the known Lr genes from T. aestivum. Seven day old seedlings and three flag leaves of adult plants of each line were inoculated with a uredospore-talc mixture of each race separately and kept in a glass-house under natural light. The infection types (ITs) were recorded 14 days after inoculation using the scale given by Stakman et al. (1962).

The present investigations were carried out using three derivatives from the Chinese line P158548, namely RL6057 (Lr33), RL6058(Lr34) and RL6059(Lr33+Lr34), three from cultivar Tereziio, namely line 896 (Lr13), line 897 (Lr12) and RL6050(Lr12+Lr13) and two derivatives from cultivar Lagadinho, namely line 920 (Lr12) and line 922 (Lr13). Three metre long paired rows of these lines were grown under field conditions during the years 1988-89 and 1989-90. Also two rows each of the cultivars Thatcher, Agra Local and ML711(Lr13) were grown around the experimental material as susceptible checks. During the year 1988-89 race 77A and during 1989-90 a mixture of races 77A and 77-1 was used to create an artificial epiphytotic. Terminal disease severity on these lines including the susceptible checks was recorded according to modified Cobb's scale in the first week of April.

MATERIAL AND METHODS

line 897 varied from 55 to 105 whereas lines 896, 920 and 922 which were resistant during the previous year behaved as susceptible. The disease severity on susceptible checks varied from 605 to 90VS.

The F_2 populations obtained from the crosses of RL6057 with Agra Local and Thatcher segregated into 3 resistant (R) : 1 susceptible (S) ratio indicating presence of a single dominant gene conferring moderate resistance to RL 6057 (Table 2). The F_2 populations from the crosses of RL6058, RL6059 and line 897 with cultivars Agra Local and Thatcher segregated in a 15R : 1S ratio indicating the presence of two dominant independently inherited genes in each of these lines. The F_2 s from crosses RL6050/Agra Local, RL6050/Thatcher, RL6050/line 922 and RL6050/line 920 segregated in a 63R : 1S ratio indicating presence of three dominant independently inherited genes in RL6050. The cross, line 922/line 920 segregated in a 9R : 7S ratio indicating presence of a dominant complementary gene in each of these two lines. However, F_2 population from the cross line 896(LrT3 from Terezi) / line 920 (LrT2 from Lagadinho) did not contain resistant plants indicating that genes LrT2 from Lagadinho and LrT3 from Terezi do not complement with each other.

Dyck (1987) reported the presence of genes LrT2, and LrT3 from Terezi, PI58548 and Lagadinho. Gene LrT2 from PI58548 was reported to be present on chromosome 7D and designated as Lr34. Dyck et al. (1987) designated the gene LrT3 from PI58548 as Lr33. Accordingly, PI58548 derivatives RL6057, RL6058, and RL6059 have Lr33, Lr34 and Lr33+Lr34, respectively and Terezi derivatives line 896, line 897 and RL6050 should have Lr33, Lr34 and Lr33+Lr34, respectively. Likewise, Lagadinho derivatives lines 922 and 920 should have Lr33 and Lr34, respectively. However, the seedling and adult plant reactions of RL6057 (Lr33) against races 77 and 77A are different from those of other two lines expected to carry Lr33 (lines 896 and 922). Similar differences can be seen with respect to disease severity on these lines during the year 1989-90 when race 77-1 was used along with race 77A for field tests. Therefore, it appears that lines 896 and 922 may not carry Lr33. RL6058, lines 897 and 920, all expected to carry Lr34 also differ from each other with respect to their reactions on adult plants against the two races. The field scores of RL6058 and line 897 are comparable but an IT = 0; on the adult plants of RL6058 against race 77A in comparison to an IT=3 on line 897 confirms the presence of an additional resistance gene in RL6058. Similar conclusions can be drawn by comparing the infection types on the lines RL6058 and RL6050.

The segregation patterns for resistance in terms of disease severity on adult plants as observed in the F_2 suggest the presence of a single dominant gene in RL6057, two dominant independently inherited genes in RL6058, RL6059 and line 897 and three dominant independently inherited genes in RL6050. Since lines 922 and 920 are susceptible in field tests a 63R : 1S ratio in their crosses with RL6050 also confirms the presence of three dominant genes in RL6050. The F_2 generation obtained from the cross of lines 922 and 920 segregated in a 9R : 7S ratio suggesting the presence of a dominant complementary gene in each of these lines which has also been reported by Dyck and Samborski (1982). However, the gene in line 920 from Lagadinho did not

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complement with the gene in line 896 from Tereazio. Thus, it may be concluded from these observations that only RL6057 should be considered as a standard tester of the gene Lr33 while different gene/s are present in lines 896 and 922. The testers of Lr34, RL6058 and line 897 have additional resistance which needs to be characterised. It also appears that the genes Lr12 and Lr13 identified from different sources are different and detailed genetic studies are essential before the genes from these lines are given permanent designations.

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Table 1. Seedling and adult plant reactions of the derivatives carrying adult plant resistance

Line/Cultiver	Race		Field Score	
	SS	APS	SS	APS
108	77A	77	1988-89	1989-90
<hr/>				
PI58548 Derivatives				
RL6057	(Lr33)	33+	1+2-	X+
			2+3C	3-
				2+
RL6058	(Lr34)	33+	1+	3
				;1+
				33+
				0;
RL6059	(Lr33+Lr34)	;1	;1	0;
				;1=
				;1=
Terenzio Derivatives				
896	(LrT3)	3+	12-	3
				;1+
				3
897	(LrT2)	3+	12-	3+
				;1+
				3+
RL6050	(LrT2+LrT3)	33+	X+	3
				;1+
				33+
Lageadinho Derivatives				
922	(LrT3)	3+	2	3
				;1+
				33+
920	(LrT2)	33+	12-	3
				3C
				33+
				33+
Susceptible Checks				
Thatcher		3	3	3+
				3
				3+
Agra Local		3+	3+	3+
				3+
WL11	(Lr13)	3+	X-	3+
				3+

SS = Seedling Stage, APS = Adult Plant Stage

Table 2. Segregation for disease severity on adult plants in different F₂ populations

Cross	Number of plants	Resistant Susceptible	Ratio	X ₂
Resistant x Susceptible				
RL6057/Agra Local	63	16	3:1	0.95
RL6057/Thatcher	67	19	3:1	0.38
RL6058/Agra Local	98	9	15:1	0.85
RL6058/Thatcher	71	2	15:1	1.53
RL6059/Agra Local	75	7	15:1	0.73
RL6059/Thatcher	80	0	-	-
RL6050/Agra Local	72	1	63:1	0.03
RL6050/Thatcher	57	1	63:1	0.01
Line 897/Agra Local	95	2	15:1	2.90
Line 922/RL6050	74	1	63:1	0.02
RL6050/Line 920	78	1	63:1	0.04
Susceptible x Susceptible				
Line 922/Line 920	57	22	9:7	8.11*
Line 896/Line 920	0	71	All susceptible	

* Significant at 10% level

Through the courtesy of the Laboratory of Plant Immunology, Shenyong Agricultural University, 127 isolates from 70 collections (Table 1) of *Puccinia graminis* f. sp. *tritici* collected from 16 provinces (Fig. 1) were obtained. Uredinal collections were inoculated onto 7 day old seedlings of susceptible host cultivars, McNair 701 or Ming-sian 169, for spore increase using rubbing inoculation techniques (Browder, 1971). After incubation, plants were covered with a glass tube (9 cm diam., 20 cm long) to minimize contamination between cultures. The spores were collected after pustules were fully developed using a

MATERIALS AND METHODS

Wheat stem rust is one of the important diseases worldwide. It has caused severe damage in China historically, e.g. in 1923, 1948, 1956, 1958, 1960 and 1964 (Hu and Roelfs, 1985). For the past 20 years, stem rust has been controlled through the use of resistant cultivars. However, resistant cultivars may not be effective when new pathogen virulences appear. Thus, the continual monitoring of changes in pathogen virulence has been an important strategy to avoid crop losses through the support of effective programmes for breeding for rust resistance. The emphasis in virulences studied has shifted since the 1960's from the use of cultivars to single gene resistances as differential hosts. In China, this is the first attempt to determine virulence frequencies in the pathogen population using such a system.

INTRODUCTION

Virulence of *Puccinia graminis* f. sp. *tritici* was studied by testing 40 near-isogenic lines for stem rust resistance. Race HKR (21C3) was the most common virulence combination, making up 33.1% of the 127 isolates from 70 collections. The second most common race was RKR (34C2), which made up 24.4% of the isolates. No virulence was found on wheat lines with genes Sr9e, 11, Tt-3, Tt-2, Tmp and Gt. The virulence frequency to Sr13, 22, 24, 25, 26, 27, 29, 30 and 37 was low, all below 10% and none were verified in subsequent tests. The virulence frequency to Sr6, 7b, 8a, 9a, 9d, 9f, 9g, 10, 12, 14, 15, 16, 18, 20, 23, 28, dp-2 and H was high, all above or near 90%. Both the virulence combinations and virulence frequencies of *Puccinia graminis* f. sp. *tritici* are different between China and North America.

ABSTRACT

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VIRULENCE OF *Puccinia graminis* f. sp. *tritici* IN CHINA IN 1987.

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small test tube and were kept in a refrigerator for further use. The single gene lines tested include Sr5, 6, 7a, 7b, 8a, 9a, 9b, 9c, 9f, 9g, 10, 11, 12, 13, 14, 15, 17, 18, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 36, 37, Mid-1 and Gt (Roelfs and McVey, 1979). Additionally, some isolates were evaluated to Sr16, 34, Tt-3, Tmp, dp-2 and H.

The differential hosts were planted in a 36 x 25 x 10 cm plastic box. Seven days after planting, when the first leaf was fully extended, the plants were inoculated and placed into a metal tube for incubation for approximately 24 hours at 18°C. The plants were then moved to a greenhouse at 20°C. After 14 days infection types were recorded. The race nomenclature used was from the system by Roelfs (Table 2). Selected cultures virulent to Sr13, 22, 24, 25, 26, 27, 37 and Mid-1 were re-evaluated under standard conditions (Roelfs and Martens, 1988).

RESULTS AND DISCUSSION

Based on the reaction of 127 Chinese isolates to 12 isogenic lines (Sr5, 6, 7b, 8a, 9a, 9b, 9c, 9e, 10, 11, 13 and 36), races of Puccinia graminis f. sp. tritici were divided into two race clusters (Table 3) that differed in virulence to Reliance Sr5 and Sr21. Sr5 is the important gene in Reliance and Sr21 in Einkorn of the Stakman differentials (Stakman et al, 1962). The most common race, HKR, made up 33.1% of all isolates. Other races in the 21C3 Chinese race cluster were HKM (14.9%), HFM (4.7%) and HFR (4.7%). The second most common race, RKR, was in the 34C2 cluster and made up 24.4% of the isolates. The other races in this cluster were RKM (7.1%), RFM (1.6%) and QKR (1.6%). Another ten races were only identified once each. Races of Puccinia graminis f. sp. tritici identified in China were quite different to those identified in the U.S. The dominant race in the U.S. was 15-TNM, which comprised over 90% of the population (Roelfs et al, 1989).

The virulence frequency of the 127 Chinese isolates of Puccinia graminis f. sp. tritici to 40 single gene lines is shown in Table 4. A comparison of virulence frequencies to some important Sr genes for China, the U.S. and Canada is shown in Table 5. The results indicate that the virulence frequencies of Puccinia graminis f. sp. tritici in North America. No virulence was observed to Sr22, 24, 25, 26, 27, 29, 30, 37 and Gt in the U.S. (Roelfs et al, 1989). Virulence to Sr22, 24, 27, 29, 30 and 37 were low in China, and were not verified in a controlled environment. No virulence was found to Sr9e, 11, 38, Tmp and Gt in China. However, virulence frequencies to Sr9e, 11 and Tmp were all 99% in the U.S. In China, virulence frequencies to Sr6, 7b, 8a, 9a, 9d, 9f, 9g, 10, 14, 15, 18, 20, 23, 28, 34, dp-2 and H were high, (above 90%). However, the virulence frequencies to Sr6, 9a and 15 were low in the U.S., 3, 2 and 5%, respectively.

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Table 1. Source of the wheat stem rust collections made in China in 1987

Province ^a	Number of	
	Collections ^b	Isolates ^c
Nei Mongol	5	14
Shanxi	3	6
Liaoning	12	31
Jilin	1	1
Heilongjiang	3	5
Jiangsu	11	13
Fujian	1	1
Shandong	2	3
Guangdong	1	1
Hubei	11	28
Hunan	1	1
Henan	2	3
Sichuan	3	4
Yunnan	6	7
Guizhou	4	5
Gansu	4	4
Total	70	127

^a See Fig. 1
^b A series of rust infected leaves from a field or cultivar
^c The culture established in the greenhouse from a collection

Table 2. A key defining the cereal rust laboratory races of *Puccinia graminis* f. sp. *tritici*.^a

Code ^b	Response of host with Sr genes ^c
-------------------	---

Set 1:	Set 2:	Set 3:
5	11	36
9d	6	9b
9e	8a	13
7b	9a	10

^a From Roelfs et al, 1989.
^b A combination of host responses from set 1 determines the first letter of code, set 2 the second and set 3 the third.
^c R = hoar not susceptible, S = host susceptible

Table 4. Number of isolates of *Puccinia graminis* f. sp. tritici virulent on 40 single gene lines for resistance to stem rust in China in 1987

Sr	No. of virulent isolates		Sr	No. of virulent isolates	
	Percent	virulent isolates		Percent	virulent isolates
5	48	37.8	20	87	95.6
6	102	86.3	21	48	40.7
7a	103	84.4	22a	5	4.3
7b	122	96.1	23	103	98.1
8a	124	97.6	24a	0	0.0
9a	127	100.0	25a	0	0.0
9b	87	68.5	26a	0	0.0
9d	127	100.0	27a	0	0.0
9e	0	0.0	28	67	95.7
9f	120	98.4	29	3	2.9
9g	120	98.4	30	3	2.5
10	125	98.4	34	16	84.2
11	0	0.0	36	117	92.1
12	117	93.6	37a	0	0.0
13a	0	0.0	Tt-3	0	0.0
14	116	98.3	Gt	0	0.0
15	108	93.9	dp-2	32	88.9
16	27	100.0	H	35	94.6
17	92	75.4	Imp	0	0.0
18	75	93.8	W1d-1a	0	0.0

^a Virulences identified in initial testing but not verified in subsequent testing under standard environmental conditions.

Table 5. Virulence frequency of *Puccinia graminis* f. sp. *tritici* in China, the United States and Canada in 1987

St gene	Frequency of virulence (%)		
	China	U.S. ^a	Canada ^b
5	38	100	99
6	80	1	0
7b	96	100	90
8a	98	100	92
9a	100	1	7
9b	69	1	1
9d	100	100	98
9e	0	99	90
10	98	99	99
11	0	99	90
15	94	1	10
16	100	100	-- ^c
17	75	100	99
36	92	100	90
Imp	0	99	--

^a From Roelfs et al, 1989.
^b From Martens and Dunsmore, 1988.
^c -- not tested.

Table 3. Summary of the identified races of *Fusarium graminearum* f. sp. *tritici* in China in 1987

Race	Number of isolates	Percent of isolates
21C3-HKR	42	33.1
-HKM	19	14.9
-HFM	6	4.7
-HFR	6	4.7
34C2-RKR	31	24.4
-RKM	9	7.1
-RFM	2	1.6
-OKR	2	1.6
2a	10	7.9
Total	127	100.0

^a Each race was isolated once.

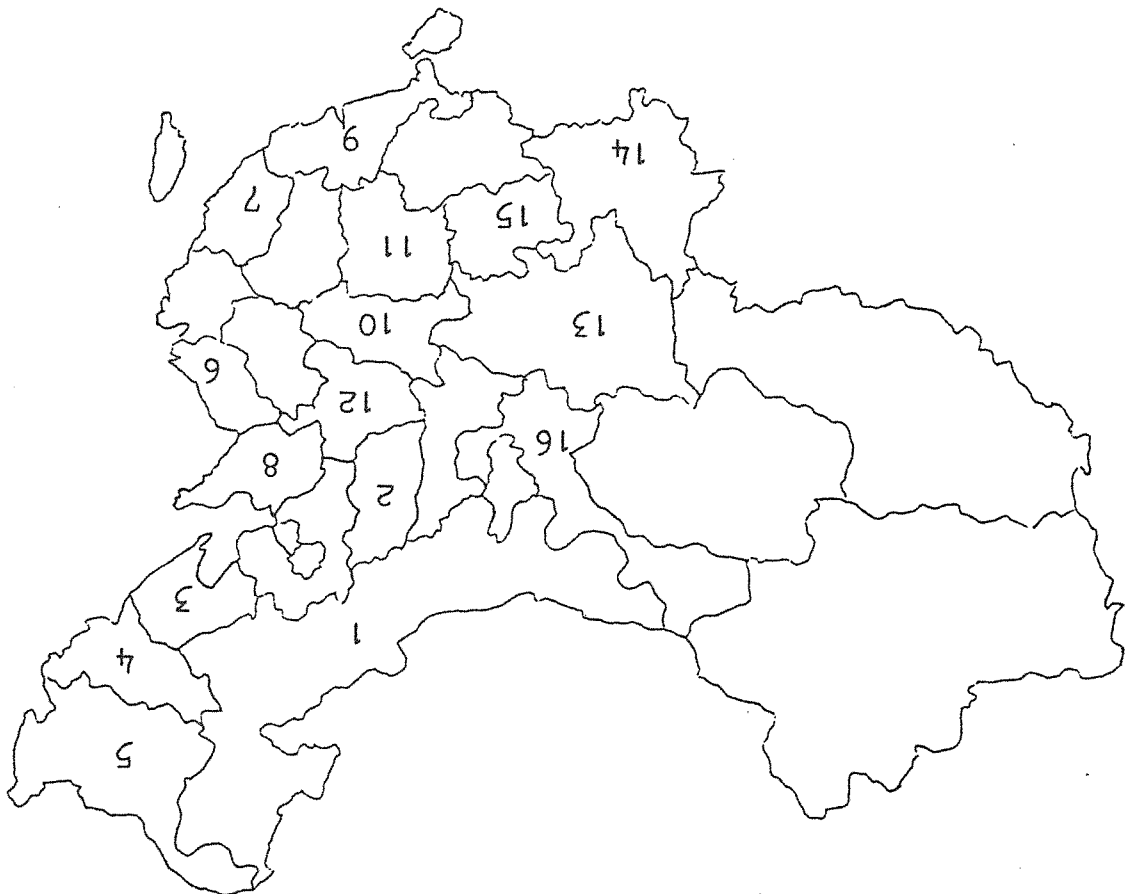


Fig. 1. Provinces in which collections were made are included. Provincial names are given by Hanyu Pinyin system, older transliterations in parenthesis. 1. Nei Mongol (Inner Mongolia), 2. Shanxi (Shansi), 3. Liaoning (Liaoning), 4. Jilin (Jilin), 5. Heilongjiang (Heilungkiang), 6. Jiangsu (Kiangsu), 7. Fujian (Fukien), 8. Shandong (Shantung), 9. Guangdong (Kwangtung), 10. Hubei (Hupai), 11. Hunan (Hunan), 12. Henan (Honan), 13. Sichuan (Szechwan), 14. Yunnan (Yunnan), 15. Guizhou (Kweichow), 16. Gansu (Kansu).

UNDERSTANDING AND INTERPRETING ISOZYME UNIFORMITY IN THE RUSTS AND
POWDERY MILDWEES

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Surveys of variability in isozyme patterns have been used to analyse the genetics of many populations of higher organisms and several populations of fungi (Newton, 1987). The technique has also been used in taxonomic studies where the emphasis has been on inter-specific, inter-forma specialis or inter-variety rather than population variation (Frankel, 1973; Snider, 1973; Shipton and Fleischmann, 1969; Burdon and Marshall, 1981; Nygaard et al., 1989). However, a wide range in the degree of variability has been found between different studies and much less variability was found than may have been expected from the pathogenic variability in some populations, particularly in the rusts and powdery mildews (Newton et al., 1985; Clarke et al., 1989).

Considering the data from the various studies of plant pathogenic fungi a general relationship between increased isozyme variability and diversity in mode of nutrition is apparent, albeit with exceptions (Table 1 and Newton, 1987). Powell (1971) argued that environmental heterogeneity was a major factor maintaining polymorphisms in populations. However, other factors such as the presence of an active sexual recombination system may modify the distribution of variability (Burdon and Roelfs, 1985). Conversely, a low level of isozyme polymorphism may be a reflection of the uniformity of substrate and host environment associated with, for example, the obligate and highly specialised biotrophic cereal rusts (Newton et al., 1985; Newton, 1987). In this paper I wish to suggest that it may be not only the substrate itself but also the obligate nature of the pathogen which determines the degree of isozyme polymorphism rather than any secondary attributes of a biotrophic lifecycle.

Both *Ustilago maydis* and other biotrophic pathogens such as *Phytophthora infestans* (Tooley et al., 1985), may survive in a quiescent state on debris, volunteer crop plants or plant propagules, and show high levels of isozyme variability unlike some other biotrophic pathogens such as the *Puccinia* rusts, (Burdon and Roelfs, 1985), indicating that saprophytic and quiescent rather than biotrophic ability may be the crucial factor governing the degree of isozyme variability.

An association of isozyme variability with saprophytic growth in a facultative pathogen may enable the fungus to exploit variable substrates more efficiently, whereas during the pathogenic phase the host tissue will provide a high degree of uniformity across a wide range of environments. Thus only pathogens which are exclusively

biotrophic, i.e. the obligate pathogens, can afford to lose isozyme variability. However, the converse is not necessarily true, that uniformity is advantageous to exploit a uniform substrate. Presumably there are optimum isozymes for a given substrate under a given set of environmental conditions, but this may not be the prime reason for the selection of uniformity.

From the above evidence a hypothesis can be set up which suggests that diversity is selected for saprotrophic habit and uniformity for biotrophy. While optimal isozymes may be selected, particularly if they are involved in substrate utilization, where they are not, a greater degree of diversity would be expected even in biotrophs. However, in *P. striiformis* isozyme uniformity is found for all enzymes except acid phosphatase and catalase which differentiate *P. striiformis* f.sp. tritici and *P. striiformis* f.sp. hordei.

There are two main explanations for such similarity and difference between the two *forma* specialis. Firstly, they may be due to genetic divergence followed by seasonal population bottlenecks. Secondly, they may be due to selection by their respective hosts. If the latter is true then such isozymes are far from being selectively neutral, indeed they must be strongly selected by their hosts. If the former were the case as is generally favoured by pathologists, then several large populations of isozyme phenotypes would be expected, each associated with a geographic location or a seasonal bottleneck. This is apparently not the case with *P. striiformis* and thus the latter theory is at least as valid. Similarly *Phytophthora megasperma*, ecologically an obligate biotroph, has highly uniform isozyme phenotypes within *forma* specialis but differences between them, confirming the view that they should really be classified at a higher taxon than *forma* specialis (Hansen et al., 1986).

The selection imposed on isozymes in populations of obligate pathogens may not only be for substrate utilization, but also to the effects of pathogen metabolites on induction of general (or even specific) resistance. Some cellular products, for example cell wall glucans, are capable of enhancing or inducing resistance to mildew and other pathogens in barley and various other hosts, while other extracts derived from microorganisms do not elicit any response (Steiner et al., 1988; Schonbeck et al., 1980; Schonbeck et al., 1982; Unpublished data). Thus there is likely to be pressure for pathogens to select metabolites and isozymes which do not stimulate resistance mechanisms even at a low level.

An example of the above may be found in *P. striiformis*. Isolates of *forma* specialis tritici having virulence towards the resistance expressed by the wheat cultivar Chinese 166 achieve a full level of infection on Chinese 166 while those isolates of f.sp. hordei which are virulent, achieve only partial infection (Newton et al., 1986). The isozymes of acid phosphatase and catalase in f.sp. hordei isolates which are different from f.sp. tritici isolates (Newton et al., 1985) could be involved in the production of metabolic products responsible for inducing resistance in f.sp. tritici but not in f.sp. hordei. Other rusts such as *Puccinia graminis* f.sp. tritici which exhibit slightly more variation in isozymes (Burdon and Roelofs, 1985),

presumably only tolerate variants which do not induce resistance. This would explain why certain enzymes are always invariant in some obligate pathogens on their host, while obligate pathogens on other hosts are invariant for other isozymes.

The substrates of saprophytes are so variable that a range of selective pressures are exerted and the resulting isozyme variability will reveal no discernible pattern associated with any particular substrate selection pressure. In practice such characteristics may therefore be used as independent markers. Facultative pathogens are generally intermediate between saprophytes and obligate pathogens in both the degree of isozyme variability (Table 1) and the selective pressures imposed which result in the observed level of variability. The biological nature of the pathogen is therefore of crucial importance when interpreting isozyme data. Clearly more specific factors need to be identified to explain all the differences between isozyme variability in different fungal species. However, it can be concluded that these factors are likely to be predominantly related to substrate and possibly to resistance induction mediated selection pressures.

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Table 1. Isozyme variability in populations of fungi

Species	% ^a variable	Enzyme systems	Sample size	Obligate pathogen	PS ^b	Sexual cycle	Reference
<u>Neurospora intermedia</u>	100	2	145	-	-	+	Speith (1975)
<u>Aspergillus nidulans</u>	75	8	59	-	-	+	Moorhouse (1977)
<u>Gaeumannomyces graminis</u>	100	2	23	-	-	+	Abbott & Holland (1975)
<u>Pyricularia oryzae</u>	100	2	132	-	+	+	Matsuyama & Kozaka (1971)
<u>Uromyces appendiculatus</u>	87	15	27	+	+	+	Linde et al. (1990)
<u>Sclerotinia sclerotiorum</u>	80	5	21	-	-	+	Wong & Willets (1975)
<u>Phytophthora infestans</u>	76	17	97	(+)	+	+	Tooley et al. (1985)
<u>Phytophthora cinnamomi</u>	69	13	183	(+)	-	+	Old et al. (1984)
<u>Rhynchosporium secalis</u>	67	3	288	-	+	-	Newman (1985)
<u>Puccinia graminis f.sp. tritici</u>	47	17	54	+	+	+	Burdon & Roelfs (1985)
<u>Ustilago maydis</u>	40	10	22	-	(+)	+	Newton (1991)
<u>Phytophthora megasperma f.sp. medicaginis</u>	18	11	56	(+)	-	+	Nygaard et al. (1989)
<u>Septoria nodorum</u>	11	18	64	-	-	+	Newton (1991)
<u>Puccinia recondita f.sp. tritici</u>	9	11	44	+	+	+	Burdon & Roelfs (1985)
<u>Erysiphe graminis f.sp. hordei</u>	0	10	280	+	+	+	Koch & Kohler (1990)
<u>Erysiphe graminis spp.</u>	5 ^d	10	50	+	+	+	Koch & Kohler (1990)
<u>Phytophthora megasperma f.sp. glycinea</u>	0	11	209	(+)	-	+	Nygaard et al. (1989)
<u>Puccinia striiformis f.sp. tritici</u>	0	5	38	+	+	-	Newton et al. (1985)

^a = Percentage of enzyme systems found to be variable

^b = Physiologic specialization

^c = f.sps. avenae, secalis and tritici

^d = percent of total isozyme bands

DIVERSITY FOR LEAF RUST RESISTANCE IN SPECIES RELATED TO WHEAT

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SUMMARY

Different collections of six species of *Aegilops*, viz, *Aegilops speltoides*, *Ae. squarrosa*, *Ae. ovata*, *Ae. triaristata*, *Ae. trinuncialis*, *Ae. cylindrica* and two wild wheat species *Triticum dicoccoides* and *T. araraticum* were tested for seedling reaction to three Indian cultures of leaf rust of wheat (*Puccinia recondita* f.sp. *tritici*). The three cultures of leaf rust are diverse with respect to their pathogenecity and are important in India. The pattern of reactions to the three leaf rust cultures varied among different germplasm accessions of the same species. This indicated diversity for resistance to leaf rust within each of the eight species tested in this experiment. These observations are important with respect to their use as sources of resistance in breeding for resistance to leaf rust in cultivated wheats.

INTRODUCTION

The wild relatives of wheat, both closely as well as distantly related, have served as a good source of resistance to wheat diseases (Sharma and Gill, 1983). Resistance to all the three rusts, including leaf rust caused by *Puccinia recondita* f.sp. *tritici* has been transferred to wheat from *Aegilops* and wild *Triticum* species (Knot and Dvorak, 1976; Knot, 1989). Since resistance to rusts is overcome by evolution of new virulent strains of the pathogen, it is necessary to identify and transfer other resistance gene(s) from related species. In this article we report our observations on seedling reactions of different accessions of *Aegilops* and *Triticum* species to three cultures of leaf rust.

MATERIALS AND METHODS

Four to six accessions of each of six *Aegilops* species (Table 1) and two wild tetraploid *Triticum* species from the wheat germplasm collection at the Punjab Agricultural University, Ludhiana, India were evaluated. These accessions were tested for seedling reaction to three Indian cultures of leaf rust, viz, 77-2, 77-1 and 104-1. These three virulences have recently become important in India due to increase in their frequency. The leaf rust cultures were obtained from the Indian Agricultural Research Institute, Regional Research Station, Simla.

1 IARI Regional Station, Flowerdale, Simla-171002, India.

Seven standard differential lines (Table 2) were also tested along with these materials to confirm purity of rust cultures. The seedling reactions of these materials were studied by following standard procedures for inoculation of seedlings. Seedling reactions were recorded according to the key developed by Mains and Jackson (1926). In Tables 1 and 2, the range of infection types produced on different plants of an accession/line by a given leaf rust culture is presented as the extremes observed without spaces or dashes between them.

RESULTS AND DISCUSSION

The seedling reactions of the seven standard differential lines to the three leaf rust cultures (Table 2) show that the three cultures are diverse with respect to their pathogenicity.

The pattern of reaction of different germplasm accessions of the six Aegilops species as well as the two Triticum species to the three leaf rust cultures was variable within each species. Accession Nos. 3737 and 3767 of Aegilops squarrosa gave susceptible (3- to 3+) reaction to 77-2 but gave varied reactions to 77-1 and 104-1. Similarly, the reactions of accession Nos. 3508 and 3515 of Aegilops speltoides were different to the leaf rust culture 77-1. Similar variations in Triticum species. Even where the reactions of two accessions of a species could be classified as resistant to all the three cultures, there was variation in reaction pattern. For example, accession Nos. 3622 and 3669 of Aegilops triuncialis differed in their reactions to the three cultures.

These observations suggest that there is considerable variability for resistance to leaf rust within each species. The amount of variation observed in a small sample of different collections of these species tested with only three diverse cultures of leaf rust indicates that there is great scope to find variability for resistance to leaf rust in the germplasm of wheat. The diversity within species suggests that genetic analysis for rust resistance should be conducted within donor species to plan strategies for transfer of resistance into cultivated wheats. As the matching technique is not useful to catalogue variability for rust resistance in alien species, the accessions, within each donor species, giving different pattern of reaction, should be crossed among themselves for genetic analysis. Crosses among resistant accessions should also be made to identify diverse sources of resistance.

In the present study, Aegilops triuncialis appeared to be a good source of resistance to leaf rust. However, it will be easier to transfer resistance from Ae. speltoides and Ae. squarrosa into cultivated wheats than from Ae. triuncialis, Ae. ovata or Ae. triaristata, as the genomes of the latter are not closely related to those of wheat. Resistance from T. aestivum can be transferred to susceptible durum lines as well as T. aestivum as there is sufficient homology between their A's and the B and G genomes.

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Table 1. Seeding reaction of different germplasm accessions of six *Aegilops* species and two *Triticum* species to three cultures of *Puccinia recondita* f. sp. *tritici*.

Species and genome Accession No. Reaction to culture
 77-2 77-1 104-1

Species and genome	Accession No.	77-2	77-1	104-1	
<i>Aegilops speltoides</i> (S)	3508	X+3+	XZ*	3-3+	
	3515	X+3+	0;2	33+	
	3573	0;	0	-	
	3574	0	0	0;1	
	3577	0	0	0	
	3737	3+	2	X	
	3738	3+/0**	3-3	3-	
	3748	0;	0;	0;	
	3749	0;	0;	0;	
	3767	33+	X	2+3-	
<i>Ae. ovata</i> (UM*)	3547	0;1	0;	2	
	3548	0;X	0;	2+	
	3561	3+	33+	-	
	3562	33+	0;1	-	
	3565	0;1	0;1	22+	
	3709	33+/0;1	0;1/X	3-3/0;1	
	<i>Ae. triaristata</i> (UM†)	3492	3+	0;2	-
		3494	X	0;2	-
		3530	X+	X+	3-3
		3545	0;	0	0
3549		0;	0;	0	
3621		0;	0;	2+	
3622		0;	0;1	0;2	
3662		X	-	2	
3669		0;2	0;	0;	
3653		0	3+	3-3	
<i>Ae. cylindrica</i> (CD)	3695	3+	3+	3-3+	
	3717	3+	3+	33+	
	3724	0;2	0;	0;	
	4627	0;2/X	0;	X+	
	4637	0;	0;	0;	
	4654	0/33+	0;2	33+	
	4657	0;2/X+	0;2/33+	X+3+	
	4665	3+	X-X+	3+	
	4679	33+	33-	33+	
	4747	2+	0;	0;	
<i>Triticum dicoccoides</i> (AB)	4627	0;2/X	0;	X+	
	4637	0;	0;	0;	
	4654	0/33+	0;2	33+	
	4657	0;2/X+	0;2/33+	X+3+	
	4665	3+	X-X+	3+	
	4679	33+	33-	33+	
	4747	2+	0;	0;	
	4749	X+	-	X	
	4756	X+/X+3+/X	-	X	
	Local Agra Check (<i>Triticum aestivum</i>)				

* Mesothetic reaction of typical Z type
 ** Segregating for reaction, the commonest infection type is placed first.

Table 2. Seeding reaction of seven standard differential lines to three cultures of leaf rust (*Puccinia recondita* f. sp. *tritici*).

Differential line/Lr* line	77-2	77-1	104-1
Malakof (Lr 1)	3+	3+	3+
Lr 10	X+3+	3+	X
Lr 15	3+	X+	0;1
Thew (Lr 20)	3+	3+	3+
Benno (Lr 26)	0;	3+	0;
IWP 94	3+	0;	3+
Jayaraj (<i>Triticum durum</i>)	0;	0;	X+3
Agra local (Susceptible check)	3+	3+	3+

*Lr = leaf rust resistance gene.

PREPARATION OF PAPERS FOR PUBLICATION IN THE CEREAL RUSTS AND POWDERY MILDEWS BULLETIN

1) All types of papers on cereal rusts and powdery mildews are acceptable, including variability of the pathogens, genetical and physiological studies and breeding for resistance. Papers may be of standard form or as letters and short notes on any relevant subject including the occurrence of epidemics and evolution of new races.

2) Papers should be typed double-spaced on A4 (the same size as the Bulletin) or similar sized sheets and have a 3 cm margin at the top, bottom and both sides.

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