Relations of Races and Virulences of *Puccinia recondita* f. sp. *tritici* to Wheat Cultivars and Areas

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ABSTRACT

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Comparisons of the isolates of *Puccinia recondita* f. sp. *tritici* obtained in 1986 by means of source cultivar, UN race, virulence phenotype, specific virulence character, and source area and state showed seven relationship patterns. Several populations of UN 14 were closely associated with the northeastern United States and with the eastern white winter wheat cultivars. UN 14 (p 1,2c,10,11,18) showed a special affinity for Coker 983. UN 2 (p 3,11) showed a special affinity for derivatives of Purdue 4946. Virulence to *Lr*1 was required to parasitize Tyler. Virulences to *Lr*24 and 26 were associated with, but not limited to, cultivars known to possess those resistance genes. Combined virulence to *Lr*1 and 16 was associated with ProBrand 812. Combined virulence to *Lr*2a and 9 was associated with Coker 762 and Coker 93-23.

Additional key words: host-parasite/cultivar-race (virulence) relations, wheat leaf rust

Surveys monitoring cereal rust virulence may provide useful information of various sorts in addition to the occurrence and combinations of specific virulence. The objective of this study was to ascertain if there were any aberrations from uniformity in the relations of specific virulence or virulence combinations to particular cultivars or groups of cultivars and source areas in the 1986 virulence survey of *Puccinia recondita* Rob. ex Desm. f. sp. *tritici* in the United States (7). Such occurrences indicate specialized epidemiological patterns with respect to cultivars or geographic areas. Applications of this knowledge should increase the efficiency of breeding for leaf rust resistance.

MATERIALS AND METHODS

The collections of *P. r.* f. sp. *tritici* studied by Long et al (7) often indicated, in addition to other information, the location and wheat cultivar from which they were collected and whether they came from a commercial field or an experimental nursery. The data on isolates were successively sorted by cultivar from which collected, UN race as defined by Long et al (4), virulence phenotype determined (7), and area and state where collected. Comparative observations of these data showed several specialized relationships.

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RESULTS AND DISCUSSION

UN 14 relationships. UN 14 (4) was much more prevalent in 1986 than in recent years (7). It was identified from three general localities: 1) New York, Michigan, and Ohio (essentially the white wheat area on the northern edge of areas 2 and 3 as defined by Long et al [7]), 2) Texas, Mississippi, Alabama, Florida, Georgia, and South Carolina (the Deep South portion of areas 1 and 4 [7]), and 3) California (area 7 [7]), two of only five isolates collected (Table 1).

The UN 14 population was diverse, comprising seven virulence phenotypes on the basis of other differentially resistant test lines (Table 1). In addition to being virulent to *Lr*1 and 2c and avirulent to *Lr*2a and 3, UN 14 collected in 1986 varied in virulence to *Lr*10, 11, 17, 18, and 30 and was avirulent to other tested isolines (Table 1). These variations apparently occur readily with four of the seven phenotypes collected from New York and nearby areas, two from the South, and one from California (Table 1). With the exception of two isolates, one each from Florida and New York, the specific UN 14 phenotypes from the three areas are distinct from each other (Table 1). The difference in specific phenotypes among areas and the lack of isolates of UN 14 from the wide intervening regions suggest that these three areas represent independent UN 14 populations, at least two of which vary internally.

UN 14 relation to northeastern white wheats. UN 14 accounted for 59% of the isolates from the three listed northern states; 94% of the UN 14 from these three states was collected on four white wheat cultivars (Augusta, Frankenmuth, Geneva, and Houser); and UN 14 comprised 73% of the isolates from these cultivars. When two isolates from an Ohio unknown commercial wheat field are excluded, these figures for New York and Michigan only become 66, 100, and 73%, respectively. We may conclude that UN 14 is the predominant UN race in the eastern white winter wheat area (66%), is the predominant race parasitic on eastern white wheats (73%), and was isolated almost totally from known white wheats (94%) (Table 2). Because these UN 14 phenotypes are unique to the area, they probably overwintered on these white wheats in New York and Michigan. Because UN 14 is avirulent to *Lr*3 (4), this occurrence provides evidence that the eastern white wheats do not possess *Lr*3, apparently now common in other U.S. wheats and ineffective to most other elements of the current North American populations of *P. recondita*.

UN 14 (p 1,2c,10,11,18) relation to Coker 983. In contrast, UN 14 accounted for only 7% of the isolates from the southern states listed, with 55% of the isolates of the southern UN 14 collected from one cultivar, Coker 983. UN 14 comprised 76% of the isolates collected from Coker 983. This race is widely dispersed in this southern area, which is characterized by diverse races, but is not

Table 1. Phenotypes and source areas of isolates of UN 14 of *Puccinia recondita* f. sp. *tritici* in the United States in 1986[a]

Virulence phenotype[b]	States[c] and no. of isolates: NY, MI, OH	TX, MS, AL, FL, GA, SC	CA	Total
1,2c	8	...	...	8
1,2c,10	9	1	...	10
1,2c,10,18	8	...	...	8
1,2c,10,11,18,30	9	...	...	9
1,2c,10,11	...	7	...	7
1,2c,10,11,18	1	21	...	22
1,2c,10,17	...	...	2	2
Total	35	29	2	66

[a] Data from Long et al (7).
[b] *Lr* single-gene differential lines tested = 1, 2a, 2c, 3, 3ka, 9, 10, 11, 16, 17, 18, 24, 26, and 30.
[c] New York, Michigan, Ohio, Texas, Mississippi, Alabama, Florida, Georgia, South Carolina, and California.

common except on this one cultivar. This occurrence suggests that Coker 983 possesses resistance characteristics for which a southern UN 14 population possesses nearly unique specific virulence. Of 29 UN 14 isolates collected in the South, 21 were phenotype p 1,2c,10,11,18 (p = virulence) (Table 1), 14 (67%) of which were from Coker 983; eight were phenotype p 1,2c,10,11, or 1,2c,10 (Table 1), only two (25%) of which were from Coker 983. Of the 16 isolates of UN 14 from Coker 983, 14 (88%) were virulent to *Lr*18. Of the 13 UN 14 isolates collected from other cultivars in the South, only seven (54%) were virulent to *Lr*18. Of the 50 isolates of UN 14 collected nationally on other cultivars, 25 (50%) were virulent to *Lr*18. This indicates that virulence to *Lr*18 occurs at random in the generally collected UN 14 population but at a much higher rate in isolates from Coker 983. This virulence or some associated character appears related to pathogenicity to Coker 983. Of the five non-UN 14 isolates collected on Coker 983, three were UN 13 isolates virulent to *Lr*18. However, virulence to *Lr*18 is probably not the only factor for pathogenicity to Coker 983, as there were 79 non-UN 14 isolates virulent to *Lr*18 in the survey (mostly in UN 13) (7), with only these three obtained from Coker 983. We may thus conclude that the southern population of UN 14 possessing *Lr*18 virulence, phenotype p 1,2c,10,11,18, has a specific affinity for parasitizing Coker 983, lacking in any other portion of the *P. recondita* population (Table 2). If it were not for the presence of Coker 983, this phenotype conceivably might not reach a detectable level in this area. Cultures of UN 14 (p 1,2c,10,11,18) would be valuable for testing breeding progenies derived from Coker 983 for the addition of other sources of resistance. We may also conclude that Coker 983 does not possess *Lr*3, a widely used resistance gene.

UN 2 (p 3,11) relation to Purdue 4946 derivatives. The UN 2 phenotype, virulent only to *Lr*3 and 11, was a relatively limited part of the survey, with 37 isolates (7), 30 of which were from Texas, Oklahoma, Mississippi, Alabama, and Georgia. Of these 37 isolates, 19 (51%) were collected on five cultivars believed to have a Purdue 4946 selection as a parent. Stacy (2) and Coker 68-15 trace directly to Purdue 4946. Saluda (13), Pioneer 2550, and probably Milburn in turn are Coker 68-15 derivatives. All except two of the 21 isolates collected from these five cultivars (90%) were UN 2 (p 3,11). The 1984 survey (5) provided similar data, with 43% of 42 isolates of UN 2 (p 3,11) being from Coker 68-15 and Southern Belle (another Coker 68-15 derivative) and with 65% of the 26 isolates from Coker 68-15 being UN 2 (p 3,11). These occurrences suggest that this group of cultivars possesses a resistance characteristic for which this UN 2 phenotype possesses uniquely specific virulence (Table 2). This resistance probably includes *Lr*3 and 11 but is probably more complex, as 78 other isolates representing 11 virulence phenotypes in four other UN races also are virulent to *Lr*3 and 11 (7). The extreme example of this affinity of this phenotype to these cultivars is that only two isolates were obtained from Coker 68-15 in Minnesota, in a nursery far from the area where this cultivar is normally grown, and both were UN 2 (p 3,11). No other isolates of UN 2 phenotype p 3,11 were obtained from Minnesota. In contrast to the strong evidence for a geographic relation of races and phenotypes present in many of our data, leading to conclusions on overwintering and oversummering (5–7), this occurrence suggests that large numbers of spores may travel great distances but lead to detectable disease only when there is a particular host selective advantage.

Cultures of UN 2 (p 3,11) would be of primary use in testing breeding progenies derived from this group of cultivars for the addition of other sources of resistance. Coker 983 also traces in part to the same parental source as these other six cultivars but must possess a different resistance combination that is specifically parasitized by a different element of the *P. r.* f. sp. *tritici* population, as previously noted.

These occurrences of certain races being isolated primarily from certain cultivars are similar to that reported in 1946 by Johnson and Newton (3), who found newly identified Standard Race 128 accounting for 66% of the isolates from Regent and other Hope derivatives, which previously had shown an adult plant resistance.

***Lr*1 virulence relation to Tyler.** The 34 isolates collected from Tyler represented 10 virulence phenotypes in four UN races and were collected in seven states. Thus, no specific phenotype parasitized Tyler, but all 34 isolates possessed virulence to *Lr*1 (Table 2), suggesting that Tyler, in turn, might possess *Lr*1. One of the parents of Tyler is Blueboy (12), known to possess *Lr*1 (1). As 77% of the 1986 isolates were virulent to *Lr*1 (7), Tyler was generally susceptible in 1986.

***Lr*24 and 26 virulence relationships.** Ninety-four isolates in 1986 (10% of the total) were virulent to *Lr*24 (7). This group of isolates consisted of four phenotypes: p 1,3,10,24—UN 5 (76 isolates), p 1,3,10,24,26—UN 5 (six isolates), p 2a,2c,3,10,24—UN 17 (10 isolates), and p 3,24—UN 2 (two isolates). Forty-three (46%) of these 94 isolates were collected from cultivars with a known *Lr*24 parentage (Agent [1], Arkan [5], Payne [11], Pony, Sage [1], and Siouxland [10]), 25% were from unknown fields or nursery lines, and 29% were from miscellaneous other cultivars. The *Lr*24-virulent isolates from cultivars possessing *Lr*24 made up 74% of the isolates from those cultivars, showing a significant affinity (Table 2). However, their presence on other cultivars indicates they are not limited to this group. The occurrence of most of these isolates within the widespread UN races, 5 and 17, suggests they might not be limited in their broader parasitic capacity. Twenty-four of the *Lr*24-virulent isolates were obtained from Siouxland, known to possess both *Lr*24 and 26 (10). Six of these 24 were virulent to both *Lr*24 and 26 (Table 2). Three other isolates attacked *Lr*26 but not 24. Virulence to *Lr*26 was reported in trace amounts in North America in 1984 and 1985 (5,6,9). *Lr*26 has been tested in Canada since 1983 (8,9) and in the United States since 1984 (5,6). Cultures with combined virulence to *Lr*24 and 26 would be useful in testing breeding progenies derived from Siouxland for the addition of other sources of resistance.

Virulence to ProBrand 812. Of 42 isolates obtained from ProBrand 812, 35

Table 2. Summary of associations of UN races, pathogenicity phenotypes, or specific pathogenicity of *Puccinia recondita* f. sp. *tritici* with groups of wheat cultivars, particular cultivars, or geographic areas

UN race	Pathogenicity phenotype	Specific pathogenicity to:	Association
14	p 1,2c		Eastern white winter wheats, New York and Michigan area
	p 1,2c,10		
	p 1,2c,10,18		
	p 1,2c,10,11,18,30		
14	p 1,2c,10,11,18		Coker 983
2	p 3,11		Purdue 4946 derivative cultivars[a]
Several	Several	*Lr*1	Tyler
Several	Several	*Lr*24	*Lr*24 derivative cultivars[b]
5	p 1,3,10,24,26	*Lr*24 and 26	Siouxland
5	p 1,3,10,16	*Lr*1 and 16	ProBrand 812
13	p 1,2a,2c,3,9,11,18	*Lr*2a and 9	Coker 762
	p 1,2a,2c,3,9,11,18,30		Coker 93-23

[a] A group of cultivars known to have Purdue 4946 in their parentage.
[b] A group of cultivars believed to have derived *Lr*24 from a parent cultivar in their breeding.

(83%) were virulent to *Lr*1 and 16. Thirty-four of these were UN 5 (p 1,3,10,16) (Table 2) and one was UN 13 (p 1,2a,2c,3,10,16). One hundred thirty-six isolates of phenotype p 1,3,10,16 and 21 of p 1,2a,2c,3,10,16 were obtained, so they were not limited to ProBrand 812. However, phenotype p 1,3,10,16 (UN 5) was concentrated in Texas, as is ProBrand 812 (6), with 29 isolates from ProBrand 812, 30 from unknown sources, and 30 from miscellaneous other sources, with no more than four from any other single cultivar in Texas. Phenotype p 1,2a,2c,3,10,16 (UN 13) was obtained solely from diverse winter wheats, largely in Texas and North Dakota. These large numbers of isolates virulent to *Lr*16 follow the initial report in 1985 (6). Our data suggest that at least phenotype p 1,3,10,16 may have been initially selected and increased on ProBrand 812 (Table 2) and has now become established as a major element of the *P. recondita* population, primarily in Texas, Oklahoma, and Kansas. Either of these two virulence phenotypes would be of primary use in testing breeding progenies derived from ProBrand 812 for the addition of other sources of resistance.

Virulence to Coker 762 and Coker 93-23. Eleven of 13 isolates obtained from Coker 762 (85%) were of two phenotypes of UN 13 virulent to *Lr*9 (p 1,2a,2c,3,9,11,18 and p 1,2a,2c,3,9,11,18,30). Six of seven isolates obtained from Coker 93-23 (86%), a derivative of Coker 762, were of these same two virulence phenotypes. Forty-one isolates of these two phenotypes were obtained, so they were not limited to Coker 762 germ plasm. However, 17 of the 41 isolates (42%) came from these two cultivars (Table 2), 12 (29%) from unknown sources, and 12 (29%) from diverse other cultivars, including five from McNair 701, known to possess *Lr*9. Phenotype p 1,2a,2c,3,9,11,18 was first detected in 1985, largely from Coker 762 (6), and caused disease on this previously resistant cultivar. This was the first report of combined virulence to *Lr*2a and 9 in North America. The 1986 survey shows a repetition of this occurrence, continuing at an increased but relatively low frequency. Either of these two virulence phenotypes would be of primary use in testing breeding progenies derived from these Coker lines for the addition of other sources of resistance.

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