Virulence of *Puccinia recondita* f. sp. *tritici* in the United States in 1986

D. L. LONG, Plant Pathologist, and J. F. SCHAFER and A. P. ROELFS, Research Plant Pathologists, Cereal Rust Laboratory, USDA-ARS, Department of Plant Pathology, University of Minnesota, St. Paul 55108, and J. J. ROBERTS, Research Plant Pathologist, USDA-ARS, Georgia Agricultural Experiment Station, Experiment 30212

ABSTRACT

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Isolates of *Puccinia recondita* f. sp. *tritici* were obtained from wheat leaf collections made by cooperators throughout the United States and from cereal rust field surveys of the Great Plains and Gulf Coast states in 1986. Testing of 972 isolates for virulence to 14 single-gene differentially resistant test lines showed 44 virulence/avirulence phenotypes, which were categorized into 11 Unified Numeration (UN) races. An increased frequency of virulence to *Lr*24 over recent years was found, and combined virulence to *Lr*24 and 26 was observed for the first time. No virulence was found to 11 of 21 additional entries in a resistant test series. Regional race distribution patterns again suggested that the central United States was a single epidemiological unit.

Additional key words: plant disease monitoring, rust epidemiology, wheat leaf rust

Wheat leaf rust, caused by *Puccinia recondita* Rob ex. Desm. f. sp. *tritici*, occurs in varying amounts annually over most wheat-growing areas of the United States. Leaf rust was severe in 1986; estimated statewide wheat yield losses ranged up to 8% in Kansas, with an average of 4.9% on winter wheat and 1.1% on spring wheat in the United States (D. L. Long, *unpublished*). The pathogen population varies in specific virulence (1–3). The objective of this study was to characterize the virulence of the *P. recondita* population in the United States in 1986 on selected wheat test stocks.

MATERIALS AND METHODS

Leaf rust uredinial collections were made from wheat over a 22,000-km route that included the Gulf Coast and Great Plains states and by cooperators throughout the United States. The surveys followed predetermined routes through selected areas where small grain cereals are important. Stops were made at commercial fields 32 km apart or at the first field thereafter. Additional stops were made at nurseries and trap plots along the route. Rust collections were made in at least one rusted field per county or nursery per county observed during 1986. Collections were also made from *Aegilops cylindrica* Host (goatgrass) growing near wheat fields in the southern Great Plains. A collection consisted of a varying number of leaves, bearing uredinia, from a single plant or cultivar.

Urediniospores from each collection were used to inoculate 7-day-old seedlings of wheat (*Triticum aestivum* L. 'Thatcher,' CI 10003) treated at emergence with maleic hydrazide (1 g "practical"/3 L H_2O) to enhance spore production. Plants were sprayed with spores suspended in a lightweight mineral oil, then placed in a dew chamber overnight at 18 C. The plants were then placed in a greenhouse in which temperatures varied between 18 and 28 C during the diurnal cycle. After 12–15 days, up to three leaves, each bearing a single uredinium or pruned to a single uredinium, were saved per collection. Six to nine days later, urediniospores were collected separately from one or two such uredinia per collection and directly inoculated onto a differential host series consisting of wheat single-gene isolines known to possess resistance genes *Lr*1, 2a, 2c, 3, 3ka, 9, 10, 11, 16, 17, 18, 24, 26, and 30 in a cv. Thatcher genetic background (4). Observations were recorded 10–14 days later as a dichotomous high or low infection type as in previous surveys (3).

Data were grouped by eight agroecological geographic areas (Fig. 1) on the basis of the source of the collections: area 1, mainly southern-adapted soft red winter wheats; areas 2 and 3, mostly northern-adapted soft red and white winter wheats but apparently partially separated epidemiologically by geographic features; area 4, mixed wheat types but primarily hard red winter; area 5, hard red winter wheat; area 6, mixed wheat types but primarily hard red spring and durum; area 7, spring wheats planted in late fall; and area 8, mixed wheat types but primarily soft white winter (3). Results are presented in a form to provide historical continuity with a modified Unified Numeration (UN) race designation and are a continuation of previous surveys (1–3).

A second sample of spores from each collection was bulked with those from other collections made in the same state about the same time. A broadly resistant series of wheat lines consisting of Thatcher isolines *Lr*19, 21, 25, and 29 (4) and of Aepoglom, Alondra, Anex, Buck Manantiel, Chasqui INTA, CI 17907 (*Lr*9 and 24) (9), Columbus (*Lr*13 and 16) (5), Granka, Hahn S, Lex, PI 436414 (Chile), RL 6059 (*Lr*33 and 34) (5), Siouxland (*Lr*24 and 26) (7), Stoa, Veery S, and two AZ-male sterile selected lines (8) was inoculated with 57 such bulked collections. Clement, Coker 762, and Exchange were no longer included because virulence was detected in 1985 (3).

After the initial identifications of isolates were made using the differential host series of 14 lines, 32 isolates possessing representative virulence combinations were saved. These were used to inoculate a cultivar series of Agassiz, Amigo, Arkan, Benito, Brule, Caldwell, Centurk 78, Coker 762, Coker 983, Collin, Fla 302, Hawk, Len, Magnum, Marshall, Newton, Pike, ProBrand 812, Stephens, TAM 105, TAM 108, Vic, Vona, and Wheaton.

RESULTS AND DISCUSSION

The 44 virulence formulas describing the 972 isolates obtained, based on the 14

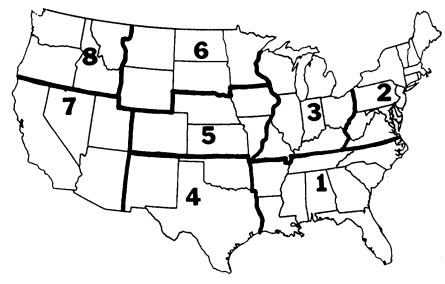

Fig. 1. Agroecological areas for *Puccinia recondita* f. sp. *tritici* in the United States. Area 1, mainly southern-adapted soft red winter wheats; areas 2 and 3, mostly northern-adapted soft red and white winter wheats; area 4, mixed wheat types but primarily hard red winter; area 5, hard red winter wheat; area 6, mixed wheat types but primarily hard red spring and durum; area 7, spring wheats planted in late fall; and area 8, mixed wheat types but primarily soft white winter.

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differential host lines each possessing a known single gene for resistance, are summarized by area from which collected in Table 1. Results are presented as percentages of isolates within areas. Virulence formulas are arranged in Table 1 by modified UN race numbers, which are based on the reactions of *Lr*1, 2a, 2c, and 3, historical differential hosts (1).

Over 45% of the total isolates identified in 1986 were in the UN 5 race category. The most commonly identified phenotype (19%) was UN 5 with a virulence formula of p 1,3,10 (p = virulence), which was found throughout the Great Plains (areas 4, 5, and 6) and to a lesser extent in areas 1, 2, and 3 (Table 1). This is similar to the distribution in

Table 1. Virulence formulas of *Puccinia recondita* f. sp. *tritici* isolates from collections made in the United States in 1986 as determined by the reactions of 14 wheat lines containing single genes for resistance and categorized by modified Unified Numeration (UN) races

	Percent isolates per area[b]							
	Eastern soft wheat region			Great Plains region			Western region	United States total
UN race and virulence formula[a]	Southern (area 1)[c]	Northeastern (area 2)	North central (area 3)	Southern (area 4)	Central (area 5)	Northern (area 6)	Southern (area 7)	
UN 1	...	3	3	...	...	...	...	*[d]
UN 11								
1,17	...	3	...	...	...	...	...	*
UN 9								
1,2a,2c,17	...	...	...	*	1	1	...	*
UN 2								
3	...	...	3	*	...	...	...	*
3,10	*	...	...	*	...	...	...	*
3,11	8	4	6	4	...	1	...	4
3,17	1	...	...	*	...	...	...	*
3,24	*	...	...	*	...	...	...	*
3,3ka,10	...	...	9	...	...	...	...	*
UN 5								
1,3	...	...	...	...	...	...	40	*
1,3,10	10	3	3	17	37	26	...	19
1,3,10,11	2	...	6	...	...	1	...	1
1,3,10,16	1	1	6	27	14	7	...	14
1,3,10,11,16	...	...	...	2	...	...	...	1
1,3,10,24	11	1	...	11	7	6	...	8
1,3,10,24,26	...	...	...	1	...	2	...	1
1,3,11,18,30	...	...	...	2	...	...	...	1
UN 17								
2a,2c,3,10	5	...	6	19	26	20	...	16
2a,2c,3,10,24	...	...	...	3	1	...	...	1
UN 13								
1,2a,2c,3	1	...	...	1	...	1	...	1
1,2a,2c,3,10	4	1	9	5	13	22	...	9
1,2a,2c,3,11	2	...	...	...	1	...	...	*
1,2a,2c,3,10,16	...	...	...	4	...	4	...	2
1,2a,2c,3,17,26	...	...	...	*	1	...	...	*
1,2a,2c,3,10,17,18	8	...	...	*	...	10	...	3
1,2a,2c,3,9,11,18	9	...	11	1	...	...	...	3
1,2a,2c,3,9,11,18,30	7	...	...	*	...	...	...	1
UN 10								
2c,18	...	7	...	...	...	...	...	*
UN 14								
1,2c	...	8	6	...	...	...	...	1
1,2c,10	*	13	...	...	...	...	...	1
1,2c,10,11	4	...	...	...	...	...	...	1
1,2c,10,17	...	...	...	...	...	...	40	*
1,2c,10,18	...	6	11	...	...	...	...	1
1,2c,10,11,18	8	1	...	2	...	...	...	2
1,2c,10,11,18,30	...	13	...	...	...	...	...	1
UN 3								
2c,3,3ka,11,30	*	...	6	...	...	...	...	*
UN 6								
1,2c,3,3ka	1	11	...	...	...	...	...	1
1,2c,3,10	*	3	...	...	...	...	20	*
1,2c,3,10,11	*	7	...	...	...	...	...	1
1,2c,3,11,17	1	...	6	...	...	...	...	*
1,2c,3,10,11,17	...	7	...	...	...	...	...	*
1,2c,3,3ka,9	3	3	6	...	...	...	...	1
1,2c,3,3ka,9,30	10	6	3	*	...	...	...	2
1,2c,3,3ka,10,11,18	...	...	*	...	...	...	...	*
	Number of collections							
	124	68	28	250	114	147	4	735
	Number of isolates							
	185	72	35	353	142	180	5	972

[a] The *Lr* single-gene differentials tested = 1, 2a, 2c, 3, 3ka, 9, 10, 11, 16, 17, 18, 24, 26, and 30. The virulence formula indicates differentials that are susceptible. The UN race designation is based on the reactions of *Lr*1, 2a, 2c, and 3 (1).
[b] Column total 100% (±4%).
[c] Areas are based on host types and geographic isolation (Fig. 1).
[d] Less than 0.6%.

Table 2. Percentage of isolates of *Puccinia recondita* f. sp. *tritici* virulent to the single-gene differential lines used in the 1986 survey

Area[a]	Isolates virulent to *Lr* genes (%)														No. of isolates
	1	2a	2c	3	3ka	9	10	11	16	17	18	24	26	30	
1	84	35	64	88	15	29	55	43	1	10	32	11	0	34	185
2	86	1	85	47	25	8	50	38	1	7	21	4	0	18	72
3	69	26	60	74	37	20	40	49	6	6	14	6	6	9	35
4	73	35	36	98	*[b]	2	91	8	35	2	4	14	1	1	353
5	73	42	42	99	0	0	98	1	14	1	0	8	1	0	142
6	79	58	58	98	0	0	97	2	11	11	10	8	2	0	180
7	100	0	60	60	0	0	60	0	0	40	0	0	0	0	5
USA 1986	77	37	51	91	6	7	81	16	17	6	12	10	1	5	972
USA 1985[c]	54	52	68	98	11	9	83	9	11	9	19	2	...[d]	...	1,148
USA 1984[e]	62	32	51	94	10	6	80	21	...	9	18	2	...	11	836
USA 1978–1983[f]	34	25	53	95	26	25	73	...	0	11	10	4	...	...	1,928

[a] Area description in text and Figure 1.
[b] Less than 0.6%.
[c] Long et al (3).
[d] Not used in this survey.
[e] Long et al (2).
[f] Long et al (1).

1984 (2).

The second most common phenotype (16%) was UN 17 with a virulence formula of p 2a,2c,3,10, as it was in 1984 (2). In 1985, this was the most common phenotype and UN 17 was the most common UN race found, at 39% (3). The wide distribution of the same phenotypes of UN 5 and 17 throughout areas 4, 5, and 6 in 1986 again suggests that these areas are a continuous south-north epidemiological unit as previously proposed (2,3). Most isolates representing these two UN races (61% of total) possess virulence to *Lr*3 and 10. Virulence overcoming either of these two genes is also common in other phenotypes (91 and 81% of the total, respectively) (Table 2). This follows the pattern of recent years (1–3).

UN 13 was the second most frequent UN race category, surpassing UN 17, and was quite diverse in the number of virulence phenotypes (Table 1), with no one phenotype over 10%.

UN 14 was the most prevalent of the recently uncommon *Lr*3-avirulent races (Table 1). It was much more prevalent than in recent years, accounting for nearly 7% of the isolates. This increase may be related to the fivefold increase in number of collections received from New York in 1986, as New York isolates accounted for nearly 50% of the UN 14 races reported. Like most other *Lr*3-avirulent races, UN 14 was conspicuously absent from the main wheat areas of the central region.

UN 9, another rare *Lr*3-avirulent race, was identified from three wheat collections made in three different areas in the central United States (Table 1). Two UN 9 phenotypes with virulence formulas of p 1,2a,2c and p 1,2a,2c,17 were also identified from eight *A. cylindrica* collections made in Texas and Kansas. Although UN 9 was the only UN race obtained from *Aegilops*, it was very rare from wheat.

UN 6 was again found in the eastern soft winter wheat region (areas 1, 2, and 3) and was again conspicuously absent in the Great Plains (areas 4, 5, and 6) (Table 1).

UN 11 was very rare, with only two isolates in 1986, from central Pennsylvania (Table 1). This supports previous data indicating this race to be primarily a local population in Pennsylvania, implying oversummering and overwintering in that locality (6).

There was an increase in 1986 in prevalence of *Lr*24 virulence, which was found in 10% of the total population. This may represent the selective advantage to these isolates of an increase in cultivars that have *Lr*24 as their leaf rust resistance. As in the previous 8 yr (1–3), *Lr*24 virulence occurred in UN 2 and 5, but in 1986 it also was identified for the first time in UN 17, which previously had been unusually uniform in virulence (3).

Combined virulence to *Lr*24 and 26 was also found for the first time, with six such isolates occurring in the common UN 5 race category (Table 1). Siouxland has both *Lr*24 and 26 (7) and is now grown from southern Texas to North Dakota. This cultivar provides selective host advantage for this virulence combination in the pathogen population. Even this very infrequent occurrence indicates the potential for leaf rust development on this cultivar.

Virulence to *Lr*16 occurred in two phenotypes of UN 5 (p 1,3,10,16 and p 1,3,10,11,16) and one phenotype of UN 13 (p 1,2a,2c,3,10,16). These *Lr*16-virulent phenotypes were common in areas 4 and 5 and collectively constituted 17% of the survey (Table 2). In 1986, *Lr*16 virulence was identified from collections made from many different cultivars, whereas in 1985 most were from ProBrand 812 (3). There has been a considerable buildup of *Lr*16 virulence over the past 3 yr (Table 2).

*Lr*9 virulence was found only in UN 6 and 13. As recently as 1983 (1), the predominant UN race possessing *Lr*9 virulence was UN 3, but in the last 3 yr, UN 6 with virulence to both *Lr*1 and 9 has largely replaced it. Two phenotypes of UN 13 virulent to *Lr*9 were isolated that possess combined virulence to *Lr*2a and 9, first found in 1985 (3).

No virulence was found on 11 of the resistant series entries: Aepoglom, Anex, Buck Manantiel, CI 17907 (9), Lex, RL 6059 (5), Stoa, two AZ-male sterile germ plasm selections (8), and Thatcher isolines *Lr*19 and 29 (4).

Each of the entries in the cultivar series was susceptible to at least one of the isolates representing the most common virulence phenotypes found in 1986 in the United States.

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