

Virulence and Epidemiology of *Puccinia recondita* f. sp. *tritici* in the United States in 1985

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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 in 1985. Testing of 1,148 isolates for virulence to 12 single-gene differentially resistant tester lines showed 40 virulence/avirulence phenotypes, which were categorized into nine defined Unified Numeration races. An increased frequency of virulence to *Lr16* (11%) was found after 7 yr of near absence. A combination of virulence, attacking both *Lr2a* and 9, was identified for the first time. No virulence was found to nine of 18 additional entries in a resistant tester series. Regional race distribution patterns indicated that the central United States was a single epidemiological unit, whereas the eastern region consisted of three partially distinct epidemiological areas.

Additional key words: plant disease monitoring, wheat leaf rust

Wheat leaf rust, caused by *Puccinia recondita* Rob. ex Desm. f. sp. *tritici*, occurs in varying amounts annually over most of the U.S. wheat-growing areas. Leaf rust was severe in 1985, with estimated statewide wheat yield losses ranging up to 28% in Texas and an average of 7.4% on winter wheat and 0.1% on spring wheat in the United States (D. L. Long, unpublished). This appears to be the largest loss ever reported for leaf rust on wheat in the United States (3,7). The objectives of this study were to characterize the virulence on selected wheat tester stocks of the *P. recondita* population in the United States and to present epidemiological implications. This information provides a data base for use by epidemiologists, modelers, and wheat breeders. 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 of 1978-1984 (4,5).

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MATERIALS AND METHODS

Leaf rust uredinial collections were made by cooperators throughout the United States and by personnel of the Cereal Rust Laboratory on field surveys. These surveys were conducted over a 22,000-km route covering the Gulf Coast and the Great Plains states of 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 or nursery per county observed during 1985. 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 with maleic hydrazide to enhance spore production. Plants were sprayed with spores suspended in lightweight mineral oil, then placed in a dew chamber overnight at 18 C. They 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 9 days later, urediniospores were collected separately from up to two such uredinia per collection to provide isolates to inoculate a differential host series.

Wheat single-gene isolines known to possess resistance genes *Lr1*, 2a, 2c, 3,

3ka, 9, 10, 11, 16, 17, 18, and 24 in a Thatcher genetic background (8) were inoculated as the differential host series used to evaluate these isolates. Observations were recorded 10-14 days later as a dichotomous high or low infection type, following the classes described by Levine et al (2) for host susceptibility and resistance.

Data were grouped by eight agroecological geographic areas (Fig. 1) on the basis of the locations of collections: area 1, mainly southern-adapted soft red winter wheats; areas 2 and 3, mostly northern-adapted soft red winter and white wheats but apparently partially separated epidemiologically by geographic features; area 4, a mixture of 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 types (4).

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 resistant series consisting of Thatcher isolines *Lr19*, 21, 29, and of Aepoglom, Anex, Buck Manantiel, Chasqui, Clement, Coker 762, Cowbird 'S,' Exchange, Granka, Hahn 'S,' PI 436414 (Chile), RL 6059 (10), Siouxland (11), Transec (*Lr25*), and Veery 'S' was inoculated with 55 bulked collections.

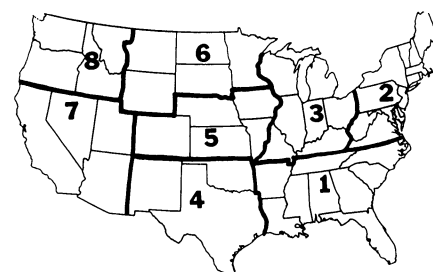


Fig. 1. Agroecological areas for *Puccinia recondita* f. sp. *tritici* in the United States: area 1, mainly southern-adapted soft red winter wheats; areas 2 and 3, mostly northern-adapted soft red winter wheats; area 4, a mixture of wheat types but primarily hard red winter; area 5, hard red winter wheat;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

After the initial identifications of isolates were made using the differential host series of 12 lines, 114 isolates possessing representative virulence combinations were saved. These were used to inoculate a supplemental differential host series of Thatcher isolines *LrB*, 2b, 14a, 14b, 15, 23, 28, 30, and *ECH* and of Thew (*Lr20*), Kavkaz (*Lr26⁺*), Timvera (*Lr31*), Alondra, Centurk, Klein Sendero, Marshall, Mit, Pro Brand 812, Precoz Parena, TAM 105, Vona, and Wheaton.

RESULTS AND DISCUSSION

The 40 virulence formulas describing the 1,148 isolates obtained, based on the 12 differential host lines each possessing a known single gene for resistance, are shown by area in Table 1. Results are presented as percentages within areas. Virulence formulas are arranged in Table 1 by modified UN race numbers, which in turn are based on the reactions of *Lr1*, 2a, 2c, and 3, historical differential hosts (4). The sequence in Table 1 of the nine UN race categories places populations by

apparent developmental or geographic relationships.

The most commonly identified phenotype (39%) was UN 17, with a virulence formula (based on the series of 12 lines) of p 2a,2c,3,10 (p = virulence), which was found in quantity throughout areas 4, 5, and 6 (Great Plains) and to a lesser extent in areas 1, 2, 3, and 7 (Table 1). The uniformity in virulence within a widely found UN race is unique to UN 17, which has varied only on *Lr30* in past virulence surveys (5). This phenotype appears well

Table 1. Virulence formulas of *Puccinia recondita* f. sp. *tritici* isolates from collections made in the United States in 1985 as determined by the reactions of 12 wheat lines containing single genes for resistance and categorized by modified Unified Numeration (UN) races

UN race and virulence formula ^a	Percent isolates per area ^b								United States total
	Eastern soft wheat region			Great Plains region			Western region		
	Southern (area 1) ^c	Northeastern (area 2)	North central (area 3)	Southern (area 4)	Central (area 5)	Northern (area 6)	Southern (area 7)	Northern (area 8)	
UN 1									
18	...	1	*d
UN 11									
1,17	1	3	*
1,10,18	*	5	*
1,17,18	...	1	*
UN 2									
3	...	1	...	1	*
3,11	7	...	9	2	1	...	20	...	3
3,10	1	3	...	1	10	...	1
3,24	*	*
3,10,11	1	*	*
3,10,24	1	*
UN 5									
1,3,10	27	10	...	14	13	6	20	...	14
1,3,10,17	...	3	...	1	1	1
1,3,10,16	3	...	5	16	11	2	8
1,3,10,24	1	1	1	4	1
1,3,10,11,17	1	1	*	1
1,3,10,17,18	...	5	*
1,3,10,16,18	4	*	1
UN 17									
2a,2c,3,10	6	5	18	42	59	66	20	...	39
UN 13									
1,2a,2c,3	2	1	1
1,2a,2c,3,10	1	1	...	4	3	10	4
1,2a,2c,3,18	1	*
1,2a,2c,3,11,18	3	3	1
1,2a,2c,3,10,16	5	3	3	1	2
1,2a,2c,3,10,18	1	*
1,2a,2c,3,10,11,18	1	*
1,2a,2c,3,10,17,18	1	1	9	4	...	5	3
1,2a,2c,3,9,11,18	8	1	2
UN 3									
2c,3,3ka,18	1	*	*	*
2c,3,3ka,9,18	3	3	9	1	...	*	1
2c,3,9,10,3ka	1	1	*
UN 6									
1,2c,3,10	*	*	*
1,2c,3,10,17	1	24	9	...	1	*	20	50	2
1,2c,3,3ka,18	7	8	5	...	3	3
1,2c,3,3ka,10,17	2	1
1,2c,3,10,11,17	...	10	27	...	1	*	1
1,2c,3,3ka,9	1	*
1,2c,3,3ka,9,18	16	12	5	1	...	1	5
UN 14									
1,2c,10	10	...	*
1,2c,10,18	1	50	*
1,2c,10,11,18	4	1	1
				Number of collections					
	166	48	14	241	131	143	5	1	749
				Number of isolates					
	261	78	22	328	196	251	10	2	1,148

^aThe *Lr* single-gene differentials tested = 1, 2a, 2c, 3, 3ka, 9, 10, 11, 16, 17, 18, and 24.

^bColumn total 100% (±4%).

^cAreas are based on host types and geographic isolation (Fig. 1).

^dLess than 0.6%.

adapted to the favorable environment that occurred in 1985 for rust development in the Great Plains region.

The second most common phenotype (14%) was a UN 5 with a virulence formula of p 1,3,10, whereas all UN 5 phenotypes made up 26% of the total (Table 1). In 1984, UN 5 was the most common UN race found (32%) (5), thus a reversal in 1985 of the relative prevalence with UN 17. The wide distribution of the same phenotypes of UN 5 and 17 through areas 4, 5, and 6 again suggests that these areas are a continuous south-north epidemiological unit as previously proposed (5). However, the proportion of UN 5 decreased from south to north, whereas that of UN 17 increased (Table 1). All isolates representing these two UN races (65% of total) possess virulence overcoming *Lr3* and 10. Virulences overcoming these two genes are also common in other phenotypes (98 and 83% of the total, respectively) (Table 2). This follows the pattern of recent years (4,5) and is consistent with the wide use of these genes in the central region (1,6,12). It further suggests that virulence overcoming them, once attained, remains in the pathogen population (4,5).

Two phenotypes of UN 5 possessed virulence overcoming *Lr16* (p 1,3,10,16; p 1,3,10,16,18), as did one phenotype of UN 13 (p 1,2a,2c,3,10,16). These phenotypes were common in areas 4 and 5 (Table 1) and collectively constituted 11% of the survey (Table 2). Leaf rust was severe in 1985 on the cultivar Pro Brand 812, widely planted in Texas in 1984 (14) and 1985, and collections from Pro Brand 812 had a 74% frequency of virulence overcoming *Lr16* (and *Lr1*). A major portion of the large leaf rust loss estimated for Texas (D. L. Long, unpublished) may be attributed to the occurrence of this virulence. Virulence overcoming *Lr16* was common in the northern plains and Canada during the late 1960s and early 1970s, when Selkirk was grown, but was not found during 1977–1983 (4,9) and infrequently in the United States in 1984 (5,13). This suggests a fast buildup of *Lr16* virulence over a 2-yr period.

As in the previous 7 yr (4,5), all of the *Lr24* virulence occurred in UN 5 and 2 (Table 1). Eighty percent of the isolates possessing *Lr24* virulence were collected from cultivars with known *Lr24* resistance (e.g., Agent [1] and Siouxland [11]). The incidence of virulence overcoming *Lr24* (Table 2) continued low (2%) and was found mainly in the Great Plains (areas 4, 5, and 6) and from known cultivars in nurseries, which is the same pattern observed in 1978–1984 (4,5).

UN 13 included nine virulence phenotypes (Table 1), which was more than any other UN race and in great contrast to the more prevalent but uniform UN 17. Two previously undetected UN 13 phenotypes were of

Table 2. Percentage of isolates of *Puccinia recondita* f. sp. *tritici* virulent to the single-gene differential lines used in the 1985 survey

Area ^a	Isolates virulent to <i>Lr</i> genes (%)											Number of isolates	
	1	2a	2c	3	3ka	9	10	11	16	17	18		24
1	80	22	57	94	30	30	51	26	3	14	46	1	261
2	88	10	69	88	23	15	69	17	0	49	40	0	78
3	64	32	86	100	18	14	73	36	9	45	27	0	22
4	51	54	59	100	5	2	94	15	22	7	11	1	328
5	39	68	72	100	3	0	94	2	15	2	4	2	196
6	31	83	85	100	1	2	98	2	4	6	7	4	251
7	50	20	50	90	0	0	80	20	0	20	0	0	10
8	100	0	100	50	0	0	100	0	0	50	50	0	2
USA 1985	54	52	68	98	11	9	83	9	11	9	19	2	1,148
USA 1984 ^b	62	32	51	94	10	6	80	21	... ^c	9	18	2	836
USA 1978–1983 ^d	34	25	53	95	26	25	73	... ^c	0	11	10	4	1,928

^a Area description in text and Figure 1.

^b Long et al (5).

^c Not used in 1984 survey.

^d Long et al (4).

^e Not used in 1978–1983 surveys.

special interest. One possessed virulence overcoming *Lr16* and was noted previously with the similar *Lr16*-virulent UN 5 phenotypes. The other was p 1,2a,2c,3,9,11,18, identified largely from collections from Coker 762 in the southern soft red winter wheat region (area 1). This previously undetected combination of virulence overcoming both *Lr2a* and 9 caused disease on the previously resistant Coker 762.

UN 6 again predominated in the eastern soft winter wheat region (areas 1, 2, and 3) and was again conspicuously sparse in the Great Plains (areas 4, 5, and 6) (Table 1). *Lr9* virulence, previously found primarily in UN 6 and 3 (4,5) again predominated in UN 6 but now also occurred, as noted, in UN 13. Two years ago, the predominant UN race with *Lr9* virulence was UN 3, but in the last 2 yr, UN 6 with a combination of *Lr1* and *Lr9* virulence has been more common. *Lr9* virulence increased slightly over 1984 (Table 2) after decreasing for several years, particularly in areas 2 and 3 (4,5).

The preponderance of a different virulence phenotype of UN 6 in each of areas 1, 2, and 3 (Table 1), as also noted in 1984 (5), suggests that these areas were to some extent separated epidemiologically in 1985. However, the distinctions among these areas were not as sharp as in 1984. The most common phenotype in area 1 was p 1,2c,3,3ka,9,18 (16%); in area 2, p 1,2c,3,10,17 (24%), and in area 3, p 1,2c,3,10,11,17 (27%). The common area 1 phenotype was the same as in 1984. In both areas 2 and 3, the most common phenotype differed from 1984 by the addition of p 17. Although specifically differing from each other, these three areas have a general similarity in occurrence of UN races that suggests they are more closely related to each other epidemiologically over time than to the central United States (areas 4, 5, and 6).

Virulence overcoming each *Lr3ka*, 9, 17, and 18 was concentrated in areas 1, 2,

and 3 (Table 2), with that overcoming *Lr11* occurring most heavily in areas 1 and 3. Isolates avirulent to the *Lr3* isoline (UN 1, 11, and 14) were found only in areas 1, 2, 7, and 8 (Table 1). These are areas of greater epidemiological separation and apparently without the great selection pressure of *Lr3* found in the Great Plains, where *Lr3* virulence is common.

The rare virulence phenotypes identified (Table 1) were more often obtained from nurseries with their genetically diverse host lines than from field collections.

Among the supplemental differentially resistant host series, the Thatcher isolines *LrB*, 14a, 14b, 15, 23, and 28 and cultivars Thew, TAM W-105, and Vona were susceptible to most of the isolates tested. The Thatcher isolines *Lr2b*, 30, and ECH, and Timvera, Centurk, Marshall, Mit, Pro Brand 812, Precoz Parena, and Wheaton, were more evenly divided between susceptible and resistant responses. Klein Sendero, Alondra, and Kavkaz (*Lr26*⁺) were resistant to all but a few isolates.

No virulence was found to nine resistant series entries: Aepoglom, Anex, Buck Manantiel, Cowbird 'S,' PI 436414 (Chile), RL 6059, Siouxland, and Thatcher isolines 19 and 29. Virulence was found to the other nine entries in this series.

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