Virulence and Epidemiology of *Puccinia recondita* f. sp. *tritici* in the United States in 1984

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ABSTRACT

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Puccinia recondita f. sp. *tritici* isolates 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 1984. Testing of 836 isolates for virulence to 12 single-gene differentially resistant tester lines showed 39 virulence/avirulence phenotypes, which were categorized into seven defined Unified Numeration races. No virulence was found to 12 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 and western regions consisted of several separate 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 most years over most of the U.S. wheat-growing areas. In 1984, estimated statewide wheat yield losses were as high as 5% in California and New York and averaged 1.4% on winter wheat and 0.6% on spring wheat in the United States (D. L. Long, *unpublished*). The objective of this study was to characterize the virulence on selected wheat tester stocks of the *P. recondita* population in the United States by areas and to present epidemiological implications. This information provides a data base to be used by epidemiologists, modelers, and wheat breeders. Results are presented in a form to provide useful historical continuity with a modified Unified Numeration (UN) designation and are a continuation of previous surveys of 1978–1983 (3).

MATERIALS AND METHODS

Leaf rust uredinial collections were made by cooperators throughout the United States and by personnel of the Cereal Rust Laboratory on annual field surveys. These surveys were conducted over a 24,000-km route covering the Gulf Coast and the Great Plains 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 each rusted field or nursery observed during 1984. 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 *Lr*1, 2a, 2c, 3, 3ka, 9, 10, 11, 17, 18, and 30 in a Thatcher genetic background (6) and the cultivar Agent, known to possess *Lr*24 (1), were inoculated as the differential host series used to evaluate these isolates. Observations were recorded 10–14 days later on a dichotomous high or low virulence basis, following the classes described by Levine et al (2) for host susceptibility and resistance.

Data were grouped by eight agroecological geographic source 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 winter wheats but appear to be 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, a mixture of wheat types but primarily hard red spring and durum; area 7, spring wheats planted in late fall; and area 8, a mixture of wheats but mostly soft white winter types.

A second sample of spores from each collection was bulked with those from other collections made in the same state at about the same time. A resistant series consisting of Thatcher isolines *Lr*19, 21, and 29 and of Anex, Aepoglom, Buck Manantiel, Clement, Coker 762, Columbus, Hahn 'S,' Lex, and CI 17907 (*Lr*9 and 24 [8]) was inoculated with these bulked collections.

After the initial identifications of isolates were made using the differential host series of 12 lines, 90 isolates possessing representative virulence combinations were saved. These were used to inoculate a supplemental differential host series of Thatcher isolines *Lr*2b, 3bg, 14a, 14b, 15, 16, 23, B, and ECH and of Kavkaz (*Lr*26), Arkan (*Lr*24 + additional resistance [4]), Klein

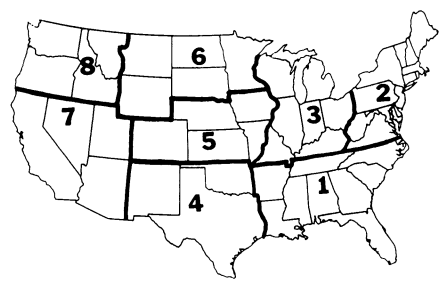

Fig. 1. Agroecological areas for *Puccinia recondita* f. sp. *tritici* in the United States: area 1, mainly southern-adapted soft red winter wheats; areas 2 and 3, mostly northern-adapted soft red winter and white winter wheats but appear to be partially separated epidemiologically by geographic features;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

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Sendero, Nelson, and Precoz Parena (possibly *Lr*1 and 9).

RESULTS AND DISCUSSION

The 39 virulence formulas describing the 836 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 *Lr*1, 2a, 2c, and 3, historical differential host materials (3). The sequence in Table 1 of the seven UN race categories places populations by apparent developmental or geographic relationships.

The most commonly identified phenotype (23%) (Table 1) was a UN 5 with a virulence formula (based on the series of 12 lines) of *p* 1,3,10 (*p* = virulence formula), which was found in quantity throughout the plains (areas 4, 5, and 6) and also in areas 3 and 1 to a lesser extent. This distribution was somewhat similar to that of a UN 17 phenotype (*p* 2a,2c,3,10), which at 17% also occurred widely on a national basis except for area 8. UN 5 was, however, isolated more frequently than UN 17 in areas 4 and 5 (Table 1). Over the previous 5 yr (3), UN 17 was frequently identified throughout the Great Plains. This wide distribution in areas 4, 5, and 6 of isolates of UN 17 and 5 of similar phenotype between areas suggests that these areas are a continuous south-north epidemiological unit. These two major phenotypes (40% of this survey) both possess virulence to *Lr*3 and 10. These two virulences are also common in other phenotypes (respectively, 100 and 88% in areas 4, 5, and 6 and 94 and 80% nationally) (Table 2). This continues the pattern of recent years (3) and is consistent with the wide use of these resistance genes in the central region (1,5,7). It further suggests that

Table 1. Virulence formulas of isolates of *Puccinia recondita* f. sp. *tritici* from collections made in the United States in 1984 as determined by the reactions of 12 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		
UN race and virulence formula[a]	Southern (area 1)[c]	North-eastern (area 2)	North central (area 3)	Southern (area 4)	Central (area 5)	Northern (area 6)	Southern (area 7)	Northern (area 8)	United States total
UN 2									
3	...	6	23	2	7	1	25	...	5
3,10	8	11	2	2	5	2	16	2	4
3,11	8	...	2	10	...	2	4	...	5
3,24	...	...	...	...	...	1	...	...	*[d]
3,10,11	...	...	2	...	3	*	4	...	1
3,10,24	...	...	...	1	...	*	...	...	*
UN 5									
1,3,10	8	3	12	31	47	27	4	...	23
1,3,10,11	3	3	2	20	1	*	...	...	7
1,3,10,17	4	6	...	1	...	*	...	...	1
1,3,10,24	1	...	...	2	...	3	...	...	2
1,3,10,17,18	...	6	...	...	...	1	...	...	*
UN 17									
2a,2c,3,10	8	11	12	15	31	27	2	...	17
2a,2c,3,10,30	...	...	...	...	...	...	14	...	1
UN 13									
1,2a,2c,3,10	...	3	...	11	1	14	...	...	7
1,2a,2c,3,11	...	...	...	2	...	...	...	...	*
1,2a,2c,3,10,11	...	...	2	2	...	...	...	...	1
1,2a,2c,3,10,18	...	...	...	...	...	2	...	...	*
1,2a,2c,3,11,18	11	...	...	...	...	...	...	...	1
1,2a,2c,3,3ka,10,18	...	...	...	...	...	3	...	...	1
1,2a,2c,3,10,17,18	...	3	2	2	...	3	5	...	2
1,2a,2c,3,10,11,17,18,30	1	...	...	*	...	5	...	...	1
UN 3									
2c,3,11	...	...	...	...	...	1	...	...	*
2c,3,3ka,9,11	...	...	5	...	...	...	...	...	*
2c,3,3ka,18,30	7	6	7	...	1	...	...	...	2
2c,3,3ka,9,18,30	12	3	2	...	...	1	...	...	2
2c,3,3ka,9,11,18,30	3	6	...	...	...	2	...	...	1
2c,3,3ka,10,17,18,30	...	6	...	...	...	...	...	...	*
UN 6									
1,2c,3,10	...	11	2	*	3	1	...	5	1
1,2c,3,10,11	3	...	16	...	...	...	...	...	2
1,2c,3,3ka,9	2	3	...	...	...	...	...	...	*
1,2c,3,10,11,17	1	8	4	...	...	...	...	...	1
1,2c,3,10,17,18	...	6	...	...	1	*	2	...	1
1,2c,3,3ka,9,18,30	18	...	...	...	...	...	...	...	2
1,2c,3,3ka,10,17,30	...	...	...	...	...	*	14	5	1
UN 14									
1,2c,10	...	...	...	...	...	...	...	20	1
1,2c,10,11	...	...	4	...	...	...	...	...	*
1,2c,10,17	...	...	...	...	...	...	7	...	*
1,2c,10,18	2	3	4	...	...	...	4	62	4
1,2c,10,17,18	...	...	...	...	...	...	...	5	*
Number of collections									
	55	27	41	159	46	140	32	21	521
Number of isolates									
	92	36	57	269	75	211	56	40	836

[a] The *Lr* single-gene differentials tested = 1,2a,2c,3,3ka,9,10,11,17,18,24,30.
[b] Column total 100% (±4%).
[c] Areas are based on host types and geographic isolation (Fig. 1).
[d] Less than 0.6%.

virulence to them readily remains in the pathogen population (3).

The third most common virulence phenotype was UN 13, which is *p* 1,2a,2c,3,10. Like UN 17 and 5, it was common in areas 4 and 6 but, in contrast, conspicuously lacking in area 5 as were all of the other UN 13 phenotypes. This suggests that it moved north from area 4 but was timely or competitive farther north (only in area 6). This major detection of UN 13 in area 6 was new in 1984 (3).

Most of the UN 17 found in area 7 differed from the more nationally distributed phenotype of UN 17 in its virulence to *Lr*30. Otherwise, this UN race is more uniform in virulence than other UN races (Table 1) as previously observed (3). A large portion of the UN 5 in area 4 differed from the more common UN 5 phenotype in virulence to *Lr*11. Virulence to *Lr*11 was concentrated in areas 1, 3, and 4 (Table 2). *Lr*11 is believed to be present in Hart (5) and in the parentages of various Purdue/ARS and Coker cultivars widely grown in these areas. The occurrence of virulence to *Lr*17, 18, and 30 also varied among regions (Table 2). However, these resistance genes are not known to have been used in cultivar development. As in the previous 6 yr, all of the *Lr*24 virulence occurred in UN 2 and 5. The incidence of this virulence character (Table 2) continued to be low (2%) and was found mainly in areas 4 and 6, which is the same pattern observed in 1978–1983 (3).

UN 3 and 6 occurred primarily in the eastern soft wheat region (areas 1, 2, and 3) and UN 6 to a lesser degree in the western region (areas 7 and 8) and are conspicuously sparse in the Great Plains (areas 4, 5, and 6). All of the *Lr*9 virulence (6%) occurred in UN 3 and 6 (Table 2) and was always in combination with virulence to *Lr*3ka (10%) in 1984. In the last 2 yr, *Lr*9 virulence has decreased overall and particularly in areas 2 and 3 (3). This appears to parallel a reduction in the prevalence of cultivars possessing *Lr*9 resistance in the eastern region.

The preponderance of a different virulence phenotype of UN 6 in each of areas 1, 2, and 3 (Table 1) suggests that these areas were largely separate epidemiological areas in 1984. In area 1, phenotype *p* 1,2c,3,3ka,9,18,30 made up 18% of the isolates and was not found in any other area. In area 2, phenotype *p* 1,2c,3,10 made up 11% of the isolates but did not occur in area 1 and rarely elsewhere. In area 3, phenotype *p* 1,2c,3,10,11 made up 16% of the isolates but did not occur in area 2 and rarely elsewhere. 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). Epidemiological independence implies overwintering and oversummering within each such area.

The UN 13 phenotype *p* 1,2a,2c,3,11,18 was found only in area 1. This population consisted of 10 isolates, nine of which were from northern Florida, suggesting that small area was nearly separate epidemiologically from the rest of area 1 in 1984. These nine are among 16 total Florida isolates; the others are UN 2, 6, and 13 but not any of the nationally common UN 5 and 17 races.

The only major occurrence of isolates avirulent to *Lr*3 (UN 14) was in the west, primarily area 8 (Tables 1 and 2), which appears to be a distinctly separate epidemiological area with its nearly unique UN 14 population and absence of nationally common races.

Although a few uredinia were observed on entries in the resistant series, after bulked collection inoculation, no subsequent cultures were obtained from these uredinia that were virulent on any of these entries. Localized physiological variation within resistant leaf tissue occasionally occurs, possibly because of environmental effects, that permits uredinia of avirulent races to develop. *Lr*19 was placed in this resistant series in 1984 because no virulence to it was obtained during 1978–1983 (3).

The supplemental differentially resistant series provided three general groups of susceptible/resistant patterns. Group 1 consisted of the Thatcher isolines *Lr*3bg, 14a, 14b, 15, 23, and B, which were susceptible to most of the cultures tested. Group 2 consisted of Tc *Lr*16, Kavkaz (*Lr*26), Arkan, Klein Sendero, and Precoz Parena, which were resistant to all but a few isolates. Group 3 consisted of Thatcher isolines *Lr*2b and ECH and Nelson, each of which was more evenly divided between susceptibility and resistance to the selected isolates.

Arkan was susceptible only to isolates also virulent to Agent, thus indicating the presence of *Lr*24 (4). *Lr*2b generally showed the resistance pattern of *Lr*2a, as expected. Other relationships of the supplemental differental series were not apparent.

Table 2. Percentage of isolates of *Puccinia recondita* f. sp. *tritici* virulent to the single-gene differential lines used in 1984 survey

Area[a]	Isolates virulent to *Lr* genes (%)												Number of isolates
	1	2a	2c	3	3ka	9	10	11	17	18	24	30	
1	55	20	68	98	42	36	39	29	7	54	1	40	92
2	53	17	67	97	22	11	78	17	33	33	0	19	36
3	46	16	58	93	14	7	61	35	5	14	0	9	57
4	71	32	32	100	0	0	87	33	3	3	3	0	269
5	53	32	37	100	1	0	92	4	1	3	0	1	75
6	62	54	61	100	7	4	90	11	10	18	5	9	211
7	36	21	48	89	14	0	71	7	32	11	0	29	56
8	98	0	98	13	5	0	100	0	10	68	0	5	40
USA 1984	62	32	51	94	10	6	80	21	9	18	2	11	836
USA 1978–1983[b]	34	25	53	95	26	25	73	···[c]	11	10	4	···	1,928

[a] Area description in text and Figure 1.
[b] Long et al (3).
[c] Not used in 1978–1983 survey.

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