

Virulence in Eastern North American Populations of *Puccinia sorghi* to *Rp* Resistance Genes in Corn

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ABSTRACT

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The effectiveness of 24 alleles from four *Rp* loci that condition race-specific resistance to common rust (*Puccinia sorghi*) in corn (*Zea mays*) was evaluated in field trials from 1987 to 1991 at many locations in eastern United States and one in central Mexico. In natural and/or inoculated epidemics, near-isogenic lines containing each gene were scored for the presence of susceptible-type uredinia. Only two genes (*Rp*₁^d and *Rp*₃^c) were totally effective, with no large uredinia observed in any trial. Also, an unnamed gene from M165sel was totally effective during the 3 yr it was tested in St. Paul, Minnesota. Four other genes—*Rp*₁^c, *Rp*₁^f, *Rp*₁^g, and *Rp*₁^k—showed no more than a trace of rust in a few trials. Lines containing any of the other 17 genes had light to heavy rust levels in most trials in which they were tested.

Common corn rust (*Puccinia sorghi* Schwein.) is a serious and chronic disease of processing sweet corn (*Zea mays* L.) in Wisconsin and Minnesota, where the hectareage of processing corn is the highest in the United States. In 1980, 52,611 ha of corn were harvested in Minnesota (14), and roughly equal amounts of corn are harvested in the two states each year. Contributing factors to the disease include relatively susceptible germ plasm (10), the need to plant and harvest very late in the season to maximize the use of processing facilities, and, more recently, increased production of winter corn in the southern Mississippi River valley. This probably provides a closer overwintering source and allows slightly earlier arrival of urediniospores in the Upper Midwest than in the past (5).

Many different genes for high level, race-specific resistance to common rust have been identified from diverse sources (7,8,12,13), and many of them were backcrossed into a common inbred background and maintained at the University of Illinois. One of these genes, *Rp*₁^d, has been incorporated by several seed companies into a number of previously important or new hybrids of processing sweet corn. No new races virulent to this gene have risen to prominence in central North America, although variants of the rust virulent on *Rp*₁^d are reported from time to time (3,4,8,9). Absence of the resistance gene in partially resistant dent

corn hybrids, which are thought to provide sufficient continuity and earliness to permit the rust to move north in the spring, may prevent or delay selection for virulence to *Rp*₁^d (6,10). Whether this will allow the *Rp* resistance in sweet corn to remain durable is uncertain. The *d* allele and several other alleles of the *Rp*₁ locus were quickly overcome when they were used on Oahu, Hawaii (2,4). Thus, some plant breeders may wish to begin incorporating other genes for rust resistance into sweet corn inbreds.

Recently, Hulbert et al (9) began to develop a collection of *P. sorghi* isolates from which a more complete picture of the distribution of virulences among isolates can be obtained. Such isolates can be immediately useful in identifying resistance alleles from new or known corn sources. Characterizing isolate virulence is laborious, and only a small number of isolates were included in their study (9). In contrast, the mass sampling of field populations through direct observation of disease severities on differential corn lines provides a complementary view of the prevalence of individual virulences in *P. sorghi*.

The objective of this work was to provide information on frequencies of *P. sorghi* virulence to the 24 genes, especially in the areas of Minnesota and Wisconsin where most processing sweet corn is grown. Data from other locations were included to identify potential sources of virulent races that could migrate into the Upper Midwest. Some information on virulence in Illinois to some or all of the genes has been published previously (8,10).

MATERIALS AND METHODS

NE-124 disease and insect nursery. For several years, the USDA-ARS Cooperative Regional Research Project NE-124 (genetics and physiology of sweet corn quality, pest resistance, and yield) has coordinated a cooperative disease and insect nursery to monitor diseases and insects that are prevalent in areas where sweet corn is grown. From 1973 to 1986, the nursery included nine *sugary-1* hybrids that were grown in trials at more than 50 locations. In 1987, the NE-124 disease and insect nursery was modified to reflect the change in the sweet corn industry from *sugary-1* hybrids to *shrunk-2* and *sugary enhancer* hybrids. Since then, the nursery has consisted of eight hybrids (Table 1) that represent those grown currently and that also represent a range from resistant to susceptible reactions to common rust, Stewart's wilt, northern leaf blight, and common smut. Also, since 1987 the NE-124 nursery has included 23 lines of the dent corn inbred R168 into which *Rp* genes for resistance to *P. sorghi* were backcrossed (8). Only one source of each *Rp* gene was monitored in the NE-124 nursery (10), although more than one source of many of the *Rp* genes was backcrossed into R168 and B14 (8).

Table 1. Sweet corn hybrids evaluated in the NE-124 disease and insect nursery since 1987

Hybrid	Endosperm type	Seed source
Candy Bar ^a	<i>sh2</i> ^b	Ferry-Morse Seed Co.
Florida Staysweet	<i>sh2</i>	Illinois Foundation Seeds, Inc.
Honey n Frost	<i>su</i>	Seedway
Jubilee	<i>su</i>	Rogers NK Seed Co.
Miracle	<i>se</i>	Crookham
Phenomenal	<i>sh2</i>	Crookham
SsuperSweet 7710	<i>sh2</i>	Abbott and Cobb
Xtra Sweet 82	<i>sh2</i>	Illinois Foundation Seeds, Inc.

^aCandy Bar II was substituted for Candy Bar in 1990, and SsuperSweet 7710 was substituted for SsuperSweet 7200 in 1991.

^b*su* = *sugary-1*, *sh2* = *shrunk-2*, and *se* = *sugary enhancer*.

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Some of the R168 lines evaluated in the NE-124 nursery were heterozygous for *Rp* genes, and some may have lost the resistance genes they were thought to carry (9).

Eighteen cooperators (Table 2) have planted the NE-124 nursery at 21 locations since 1987. A total of 56 trials have been evaluated. Each cooperator planted one to three replicates of the hybrids and R168 lines on one or two dates that were most representative of sweet corn production in that area. Plant populations, widths and lengths of rows, and other production practices varied among locations according to each cooperator's standard practices. Incidence and severity of diseases were rated near harvest maturity on the eight hybrids, with each cooperator reporting the rating scales and/or standard diagrams that were used. Insect ratings were based on infestation and damage on Jubilee. Incidence, severity, and/or infection type were rated for rust on the R168 lines.

Virulence trials at St. Paul. Because NE-124 trials were so variable for amount of infection and method of recording data, we decided to subject the *Rp* series to more severe disease conditions, where even rare virulences would more likely be detected. In 1987, 1988, 1989, and 1991, all or most lines were planted in 3-m unreplicated rows at St. Paul, Minnesota. Planting was done very late, generally in mid-July, to ensure a severe rust epidemic because of high levels of inoculum and a late summer environment conducive to rust development. Plots were not inoculated but were infected by naturally occurring rust and rust from nearby plots that had been inoculated with mass collections of urediniospores obtained at St. Paul the previous season. About 3-4 wk after anthesis, all plants were examined and an average score recorded for level of infection, for presence of segregation for resistance (obvious susceptible segregants were excluded from the average score), and, if possible, for appearance of the resistant reaction. Five categories of severity were used: 1) no rust, where susceptible reactions were totally absent (indicating total effectiveness of the gene); 2) trace, with up to two or three large (fully susceptible reaction) uredinia per plant; 3) light, with several to many large uredinia per leaf but no aggregation of uredinia into bands; 4) medium, with many uredinia per leaf and some banding; and 5) heavy, with many uredinia per leaf and frequent banding. Selected plants of most lines were selfed to maintain the lines. In 1989, lines with obviously ineffective genes (based on data from the previous 2 yr) were not included.

RESULTS

Common rust was observed in 29 of the 56 NE-124 trials. Rust severity ranged

from 0 to 63% on the eight hybrids in the NE-124 nursery (Table 3). Severity was 15% or less in all trials on the hybrid Miracle with race-nonspecific partial resistance and ranged from 0 to 35% on the susceptible hybrid Florida Staysweet.

Rust incidence and severity in these

trials probably depended greatly on planting date and local weather conditions. For example, rust severity ranged from 5 to 30% for a trial planted 6 June 1990 and from 15 to 45% for a trial planted 21 June 1990 in Aurora, New York. Similarly, rust severity ranged

Table 2. Cooperators in the NE-124 sweet corn disease and insect nursery since 1986

Cooperator	Affiliation	Nursery location
J. E. Ayers	Pennsylvania State University	Landisville, PA Rock Springs, PA
J. L. Brewbaker	University of Hawaii	Waimanalo, HI
D. W. Davis	University of Minnesota	St. Paul, MN
D. E. Fisher	Del Monte Corp.	Rochelle, IL
S. L. Grier	Sunseeds	Farmington, MN
	Rogers NK Seed Co.	Stanton, MN
J. A. Hawk	University of Delaware	Newark, DE
D. R. Jeffers	Ferry-Morse Seed Co.	Caldwell, ID
S. K. Mohan	University of Idaho	Parma, ID
T. A. Natti	Harris Moran Seed Co.	Rochester, NY
J. I. Ortiz-Monasterio	ITESM	Querétaro, Mexico
J. K. Pataky	University of Illinois	Urbana, IL
P. Richter	Pillsbury/Green Giant	Le Sueur, MN
M. E. Smith	Cornell University	Aurora, NY
H. L. Warren	Purdue University	West Lafayette, IN
N. W. Widstrom	USDA-ARS	Tifton, GA
D. O. Wilson	University of Idaho	Parma, ID
E. A. Wolf	University of Florida	Belle Glade, FL
T. A. Zitter	Cornell University	Ithaca, NY

Table 3. Prevalence of common rust in the NE-124 sweet corn disease and insect nursery

Year	Location	Date planted	Rust ratings (%) ^a		
			Range ^b	Miracle ^c	Florida Staysweet ^d
1991	Aurora, NY	6 June	4-13	8	4
1990	Newark, DE	26 Apr.	0-5*	0.3*	5*
	Belle Glade, FL	28 Feb.	0.5-1.5*	0.5*	1.5*
	Urbana, IL	1 May	0-50	8	30
	Stanton, MN	26 May	1-10	1	10
		31 May	1-10	1	10
	Aurora, NY	6 June	5-30	5	20
		21 June	15-45	15	30
1989	Belle Glade, FL	21 Feb.	0.5-4*	0.5*	3*
		4 Apr.	0.5-4*	0.5*	2*
	Urbana, IL	18 May	5-22	5	18
	Farmington, MN	22 May	2-35	2	35
		5 June	2-18	2	15
	Aurora, NY	7 June	0-35	0	35
		19 June	0-23	0	23
	Ithaca, NY	26 June	0-30	0.5	9
		5 July	tr-30	tr	20
	Rock Springs, PA	19 June	1-12	1	12
1988	Tifton, GA	29 Apr.	4-13	3.5	10
	West Lafayette, IN	17 May	tr-1	1	1
		31 May	0-10	0	10
	Aurora, NY	12 May	0-7	0	1
		27 May	0-23	0	0
	Ithaca, NY	31 May	1-20	2.5	6
		15 June	0.5-25	1	15
	Rochester, NY	15 June	1-3*	1*	3*
1987	Belle Glade, FL	25 Feb.	5-50
	Urbana, IL	15 May	0-15
	Rochester, NY	21 May	0-63

^a Percent severity on a 0-100 scale unless noted by an asterisk (*), for which a 1-5 scale was used; tr = trace (less than 1%).

^b Range of rust severity on eight hybrids in the nursery.

^c Partially resistant hybrid.

^d Susceptible hybrid.

from 0 to 50% (with 30% severity on Florida Staysweet) in a trial planted 1 May 1990 in Urbana, Illinois, but no rust was found in Urbana in 1991, a drought year. Thus, these data are useful because they indicate that common rust is frequently a problem in many areas where sweet corn is grown on large hectares (i.e., Minnesota, Illinois, New York, Florida). However, the data are of limited value for quantifying rust severity that may occur in a region because the numbers of planting dates at each location and locations are insufficient. The data do not reflect adequately the variation in rust severity over time at a location within a season and the variation between locations within an area that experience different weather conditions.

Severity of other diseases and pests also was measured in the NE-124 nurseries. As with common rust, the actual severities of these diseases and pests probably depend greatly on planting date, weather, etc. Therefore, actual severities probably are of less value than the qualitative observations that corn earworm, common rust, common smut,

European corn borer, northern leaf blight, and Stewart's wilt were prevalent in certain trials (Table 4).

Virulence of *P. sorghi* to some of the 22 genes occurred in 23 of the 29 trials, representing seven states and central Mexico (Table 4). Only gene *Rp1^d* was apparently 100% effective at all locations in all 4 yr. Plants with genes *Rp1^c* and *Rp3^c* were lightly rusted only at one and two locations, respectively. Five other genes—*Rp1^f*, *Rp1^g*, *Rp1ⁱ*, *Rp1^k*, and *Rp1^l*—were effective in more than half of the trials.

Inoculum loads were consistently heavy and the chance of detecting local rare virulent races was greater in trials at St. Paul (Table 5). Only two of the three effective genes tested in the NE-124 trials were disease-free all 4 yr at St. Paul. There were no susceptible uredinia on plants with genes *Rp1^d* or *Rp3^c* in the St. Paul trials, whereas plants with gene *Rp1^c* had a few large pustules on some leaves each year. In addition, an unnamed gene, *Rp_X* (called M165sel by Pataky [10]) was totally effective at St. Paul in the 3 yr that it was tested. *Rp5* was not tested at St. Paul.

Combined information from the NE-124 and St. Paul trials indicates that a few other genes may be useful, since virulence to them is rare. Plants with genes *Rp1^f*, *Rp1^g*, and *Rp1^k* were frequently rust-free but occasionally showed a few susceptible pustules. Plants with the gene *Rp1^a* were relatively rust-free at St. Paul, but virulence was observed in 16 of the 23 NE-124 trials. *Rp1ⁱ* was effective at St. Paul but not at several of the more eastern or southern locations. The resistant reaction of *Rp1ⁱ* was a distinct necrotic fleck, sometimes accompanied by very small uredinia. *Rp1ⁱ* was effective in 15 of 23 NE-124 trials but was not effective in any of the four St. Paul trials. Plants with the remaining 13 genes were rusted either consistently enough or heavily enough at several trials to be judged of little value if used singly in North American sweet corn production areas.

DISCUSSION

The common susceptible background of R168 and the high level of resistance that each gene confers to correspondingly avirulent races of rust suggest that

Table 4. Reactions of plants with *Rp* genes for resistance to *Puccinia sorghi* backcrossed into R168 and screened in the NE-124 disease and insect nursery

Year	Location	<i>Rp1</i>														<i>Rp3</i>						<i>Rp4</i>		<i>Rp5</i>	Other pests ^a
		a	b	c	d	e	f	g	h	i	j	k	l	m	n	a	b	c	d	e	f	a	b		
1991	Tifton, GA ^b	A ^c	A	V	A	A	A	A	V	A	V	A	A	V	V	A	V	A	V	V	V	V	V	V	CEW,CS
	Le Sueur, MN	V	V	V	A	A	A	A	V	A	V	A	I	I	I	V	V	A	V	V	V	I	V	V	...
	Aurora, NY	V	V	V	A	A	A	A	A	V	A	A	A	A	A	V	V	A	V	V	V	A	V	V	CS,ECB,SW
1990	Newark, DE	A	V	I	A	A	A	A	A	V	...	I	I	V	I	A	V	V	V	I	V	I	CS,ECB,NLB
	Urbana, IL	V	V	V	A	A	A	A	V	A	V	A	V	V	V	V	V	A	V	V	V	V	V	V	SW
	Stanton, MN	V	...	V	A	A	I	A	V	I	V	...	V	V	I	...	V	V	...	V	...	V	CS,ECB
	Aurora, NY	A	...	A	A	A	A	A	V	A	A	...	A	V	V	...	V	V	...	A	...	A	ECB,SW
1989	Newark, DE	A	V	V	A	A	A	A	V	I	V	A	A	V	V	V	V	A	A	V	V	V	V	A	CS,ECB,SW
	Belle Glade, FL	V	V	V	A	A	A	A	A	V	A	V	A	A	V	A	V	A	A	V	...	V	A	A	NLB
	Tifton, GA ^b	A	V	V	V	A	A	V	V	A	V	V	A	V	V	V	V	A	V	V	V	V	V	A	CS
	Urbana, IL	V	V	V	A	A	A	A	V	V	V	A	A	V	V	V	V	A	V	V	V	V	V	V	SW
	Farmington, MN	V	V	V	A	A	I	A	V	A	V	A	A	V	V	V	V	A	V	A	V	V	V	V	CS,ECB
	Aurora, NY	A	V	A	A	A	A	A	V	V	V	A	A	A	V	A	V	A	A	V	V	A	V	A	NLB,SW
	Ithaca, NY	V	V	A	A	A	A	A	A	A	A	A	V	A	V	A	V	A	A	V	V	A	A	A	CS
	Rock Springs, PA	V	V	V	A	A	A	A	V	V	V	A	A	V	V	V	V	A	V	V	V	I	V	A	CEW,ECB
1988	Tifton, GA ^b	I	I	V	A	A	A	I	V	V	V	I	A	A	V	V	V	I	I	V	V	I	V	I	CS,NLB
	Urbana, IL	I	I	V	A	A	A	A	V	A	V	I	V	V	V	V	A	V	V	V	V	V	V	V	CEW,NLB
	Aurora, NY	I	I	I	A	A	A	A	I	I	I	A	A	V	V	V	V	A	I	V	V	I	V	A	CS,ECB
	Ithaca, NY	I	I	A	A	V	A	CS
	Rochester, NY	V	V	V	A	A	A	A	V	V	A	A	A	A	I	V	V	A	V	V	V	A	I	A	CS
1987	Urbana, IL	V	V	V	A	A	A	A	V	A	V	V	V	V	V	V	V	A	V	V	V	V	V	V	CS
	St. Paul, MN	A	V	V	A	I	A	I	V	A	V	A	V	V	V	V	V	A	V	V	V	V	V	A	...
	Querétaro, Mexico	V	V	V	A	A	I	V	V	A	V	A	V	V	V	V	V	I	V	V	V	V	V	V	...
Total sites	with some rust	16	20	19	0	1	3	4	18	10	16	6	8	15	21	16	22	2	16	20	19	17	19	12	

^aCEW = corn earworm, CS = common smut, ECB = European corn borer, NLB = northern leaf blight, PBS = Physoderma brown spot, SW = Stewart's wilt. Additional locations reporting other diseases: 1991—Urbana, IL, CS, SW; Rock Springs, PA, CS, ECB, SW. 1990—Belle Glade, FL, NLB; Parma, ID, CEW. 1988—Newark, DE, CEW, CS, SW; Waimanalo, HI, CEW, PBS; Caldwell, ID, CEW; Parma, ID, CEW; Landisville, PA, CS. 1987—Newark, DE, SW; Belle Glade, FL, CS, NLB; Tifton, GA, CS; Rochester, NY, CS.

^bBecause substantial amounts of rust (probably caused by *Puccinia polysora*) were observed on all plants, reactions of *Rp* genes were based on comparisons to *Rp1^d*, which was assumed to be resistant.

^cA = avirulent population, no large uredinia (type 0); I = intermediate, few pustules (type 1); V = virulent, high severity (types 2, 3, and 4).

^dNo plants to evaluate.

relative rust severity on a given line of R168 reflects the frequency of races in the population with virulence corresponding to the resistance gene in that line. By our scale at St. Paul, rust severity that is light, moderate, or heavy indicates an unacceptably high frequency of races virulent to a gene. By this criterion, most of the 23 genes were ineffective at most locations. Combined data from many locations (Table 4) do not agree totally with data from St. Paul (Table 5). Most notably, Rp_1^c was effective at all locations in the large survey, whereas a small fraction of the population at St. Paul was virulent on the gene each year. Some of this virulence probably would not have been detected in less severe rust epidemics. Virulence to Rp_1^c from North American single-uredinium isolates was observed by Hagan and Hooker (7) (eight of 10 isolates) and by Hulbert et al (9) (three of eight isolates).

The earliest published survey of virulence to many of these genes was by Hagan and Hooker in 1965 in Urbana, Illinois (7). In this and a subsequent study by Wilkinson and Hooker in 1968 (13), selected isolates from maize differentials were used in seedling inoculations to represent the rust population, thus establishing that there was diversity for virulence in *P. sorghi* in North America. In a later paper (8), Hooker used severity readings on mature plants to characterize effectiveness of each gene when exposed to natural populations of the pathogen. In this way, he identified the genes Rp_1^d , Rp_1^g , Rp_1^i , and Rp_1^k as being most effective; all showed only a trace of rust (several biotypes of rust were introduced into the plot, and some may have been exotic). Lines containing all other genes were at least 5% rusted, while plants with genes Rp_1^b and Rp_1^f expressed only 5%. Aside from the trace of rust on Rp_1^d , the only notable discrepancies in comparing Hooker's results from 1966 with ours are that: 1) Rp_1^b can no longer be considered effective because lines containing it were notably rusted at most locations and 2) the line with Rp_3^c was reported to have 20% leaf area infection in 1966 but no infection in recent trials. This gene confers an incomplete resistance in later stages of growth. When inoculum loads were heavy, many small pustules can occur, and these could have been interpreted as infection by a virulent race.

In Urbana in 1984 and 1986, Pataky (10) planted the same inbred lines as were used in the St. Paul trials from 1987 to 1991. Rust inoculum was applied that was increased from collections from many locations in Illinois. The genes Rp_1^d , Rp_1^c , Rp_1^f , Rp_1^g , Rp_1^i , and Rp_3^c as well as Rp_X were totally effective in both years. This differs from our results (Tables 4 and 5) in that we report some virulence to all of these except genes Rp_1^d , Rp_3^c , and Rp_X . Virulence to Rp_1^k

was rare in more severe trials in St. Paul, so this allele could be included in the short list of potentially useful genes.

The present results are a more extensive geographic survey of virulence diversity in common rust populations than have been reported previously. They extend our knowledge of the usefulness of most race-specific, single dominant genes for rust resistance currently available to plant breeders. Data from Illinois and Minnesota are especially useful in that these locations bracket areas where much of the processing sweet corn industry is located. Data from all locations presented no convincing evidence that *P. sorghi* populations in distant locations of eastern United States contain more virulent races. Variation in assessing disease levels or in interpreting reactions among the many cooperators in the NE-124 nursery require that any apparent differences between regions would have to be confirmed by more precise trials. For example, the New York-Pennsylvania rust populations appeared to express more virulence to Rp_1^i (five of seven locations or years) than did the midwestern populations (two of eight locations or years).

For use singly, the two or three genes for which no virulence was seen (Rp_1^d , Rp_3^c , and Rp_X) are the obvious first choices. Since Rp_1^d apparently has been used widely in recently released sweet corn hybrids, incorporation of Rp_3^c into elite inbreds seems prudent. Likewise, resistance from sources such as M165sel (e.g., PI 190081 and PI 193427) needs to be characterized genetically.

Those genes for which virulence is consistently rare (Rp_1^c , Rp_1^f , Rp_1^g , and Rp_1^h) may prove to be useful as single genes in sweet corn as well, but they might better be used in pairwise combinations. Single-gene tests like those reported here can tell nothing definite about the co-occurrence of virulences in individual races. Other species of rust fungi for which extensive data on virulence combinations are available, such as the wheat stem rust pathogen (*P. graminis* f. sp. *tritici*), indicate that virulence is generally not randomly distributed among isolates, even when the population has frequent sexual recombination (1). If virulences were strongly associated, the frequency in the population of races with combined virulence could be nearly as high as the frequency of the rarer of the two individual virulences. In the absence of data on virulence associations in the common corn rust pathogen, however, this should not be considered a likely expectation; the frequency of doubly virulent races is more likely to be much lower than the frequency of either virulence singly, particularly if both virulences are rare. Extensive sampling of the pathogen through characterization of the virulence spectra of many isolates is the most direct way to determine virulence associations. Whether such race identification will be as useful with *P. sorghi* as it has been with some of the cereal rusts remains to be seen, since it depends on the stability of race identities. The usefulness of race surveys based on isolate characterization is greatest with pathogens that have

Table 5. Severity of common rust on backcrossed lines of inbred R168 containing 23 different *Rp* alleles in field plots at St. Paul, MN

<i>Rp</i> allele	Incompatible reactions	Rust severity ^a				Number of years with virulence
		1987	1988	1989	1991	
1 ^a	Necrotic fleck	0	0	T	L	2
1 ^b	Chlorotic fleck	M	L	M	M	4
1 ^c	Chlorotic fleck	M	M	...	M	3
1 ^d	Chlorotic fleck	0	0	0	0	0
1 ^e	Chlorotic fleck	T	T	T	T	4
1 ^f	Necrotic fleck	0	L	T	0	2
1 ^g	Chlorotic fleck, small pustule	T	T	0	T	3
1 ^h	None	H	H	H	H	4
1 ⁱ	Necrotic fleck	0	T	T	T	3
1 ^j	Chlorotic fleck	M	L	...	L	3
1 ^k	Chlorotic fleck	0	T	0	0	1
1 ^l	Chlorotic fleck	M	L	M	L	4
1 ^m	None	H	M	...	M	3
1 ⁿ	None	H	H	...	H	3
3 ^a	None	H	M	M	H	4
3 ^b	None	M	M	M	H	4
3 ^c	Chlorotic fleck, small pustule	0	0	0	0	0
3 ^d	None	L	M	...	M	3
3 ^e	None	M	M	...	H	3
3 ^f	None	H	M	...	M	3
4 ^a	Chlorotic fleck	M	L	M	...	3
4 ^b	None	H	H	...	M	3
X	Chlorotic fleck	0	0	...	0	0

^a0 = No uredinia, T = trace (a few large uredinia only), L = light rust (at least several uredinia per leaf), M = moderate rust (many uredinia per leaf and occasional crowded bands of uredinia), H = heavy rust (frequent banding).

^bAllele not included.

limited variability and highly stable races, such as *P. g. tritici* in the North American Great Plains (11). The greater the pathogenic variability (number of races detected) or plasticity (rapid temporal change in race identities), the less useful becomes race identification to plant pathologists and plant breeders. Neither the racial variability nor the plasticity of *P. sorghi* in the eastern United States is understood at this time.

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