Resistance to Oat Crown Rust in Diploid and Hexaploid *Avena*

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ABSTRACT

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The minimum number of *Pc* genes for resistance to oat crown rust (*Puccinia coronata* var. *avenae*) was determined from infection-type data based on the interactions of several oat lines and 47 isolates of crown rust from the Iowa State University collection. Infection-type data from seedlings of seven diploid oat accessions, a hexaploid chromosome addition line (X117), and its recurrent parent (C649), were evaluated in reference to 33 differentials to determine low or high infection type. At least 17 unique crown rust resistance genes can be detected in the hexaploid differentials with the Iowa State University crown rust collection. Four additional resistance genes can be detected among the diploid accessions. Among the diploid oat accessions, CI 2630, CI 3815, and CI 6954 (all *Avena strigosa*) were resistant to most isolates of crown rust, while CI 1994 (*A. wiestii*), CI 9009 (*A. nuda*), CI 3214 (*A. wiestii*), and CI 4748 (*A. strigosa*) were susceptible to most isolates. An evaluation of parents from two diploid mapping populations revealed 37 differential reactions that can be detected and mapped in the progeny from a cross between CI 2630 and CI 9009, and 40 from a cross between CI 3815 and CI 1994. The two crosses have 32 differential reactions in common.

Progress in plant breeding depends on successful detection and exploitation of genetic variability. In many cases, progress has been slowed by the lack of knowledge of important traits and of the influence of trait expression. Molecular markers have been proposed as a means of identifying chromosome segments or genes that have major effects on the expression of particular traits. Two types of molecular markers are used to develop genetic maps for this purpose: restriction fragment length polymorphisms (RFLP) and random amplified polymorphic DNA (RAPD). These markers can be used to follow chromosomal segments introduced from exotic germ plasms and backcrossed to a recurrent parent to incorporate new disease resistances (6,14). The availability of an RFLP or RAPD linkage map permits a plant-breeding program to simultaneously monitor many chromosome segments, measure their direct contribution to trait expression, and select genotypes with the most favorable genetic constitution.

Many traits important to oat breeding programs should be amenable to RFLP and RAPD analyses, particularly resistance to crown rust (caused by *Puccinia coronata* Corda var. *avenae* W. P. Fraser & Ledingham) (11-13). The pathogenic specialization of the cereal rusts is well documented (1), and Flor's gene-for-gene hypothesis (3) can be used to identify host-pathogen gene pairs among the cereals and their rusts. As a foundation for mapping genes for resistance to crown rust, we have evaluated several diploid oat accessions, using 47 isolates of *P. coronata* from the Iowa State University (ISU) collection. Seven diploid oat accessions and a hexaploid + diploid addition line were evaluated in reference to 33 standard differentials. Our objectives were to determine the minimum number of unique gene pairs that are detectable with the ISU crown rust collection, and to determine which of these gene pairs demonstrate differential reactions that could be useful in mapping projects for diploid and hexaploid oats.

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MATERIALS AND METHODS

Inoculum. Flats (30 × 60 cm) of the crown rust-susceptible oat cultivar Markton were inoculated with individual isolates of *P. coronata,* each of which possessed a different combination of avirulence and virulence genes. Urediniospores were suspended in Exxon Isopar M oil at a concentration of 5–6 × 10^6 urediniospores per milliliter. One-half milliliter of suspension was placed in an atomizer sprayer and used to inoculate 150–200 12-day-old Markton seedlings. The inoculated seedlings were placed in a dew chamber at 18–20 C for 24 hr, then moved to the greenhouse or growth chamber and kept at 18–21 C for 12–14 days to generate abundant fresh inoculum. Fresh urediniospores were collected from the leaves and inoculated as described above on 12-day-old seedlings of seven diploid accessions, 33 hexaploid differentials, one hexaploid addition line (X117), and its recurrent parent (C649) (Table 1). Two replications of five seed-

Table 1. Oat (*Avena*) lines inoculated, and *Pc* genes postulated in some of the lines

Host[a]	Iowa accession no.	CI or PI no.	Ploidy	Chromosome number	Genes[b]
Mapping lines					
strigosa	...	CI 2630	2*x*	14	*Pc*-18, *Pc*-29
nuda	...	CI 9009	2*x*	14	
strigosa	...	CI 3815	2*x*	14	*Pc*-19, *Pc*-30
weistii	...	CI 1994	2*x*	14	
weistii	...	CI 3214	2*x*	14	
strigosa	...	CI 4748	2*x*	14	
strigosa	...	CI 6954	2*x*	14	*Pc*-15, *Pc*-16, *Pc*-17
Addition lines					
sativa	X117	CI 9192	6*x* + 2	44	*Pc*-15
sativa	C649	CI 7555	6*x*	42	
Webster isolines					
sativa	D504	PI 501537	6*x*	42	*Pc*-14
sativa	D520	PI 501539	6*x*	42	
sativa	D486	PI 501535	6*x*	42	*Pc*-51
sativa	D535	PI 501541	6*x*	42	*Pc*-46
sativa	D634	PI 501542	6*x*	42	*Pc*-45
sativa	D526	PI 501540	6*x*	42	*Pc*-71 = *Pc*-*x*-2
sativa	D515	PI 501538	6*x*	42	*Pc*-36
sativa	D640	PI 501542	6*x*	42	*Pc*-57

[a] Mapping lines from Simons et al (13), addition lines from Frey et al (4), and Webster isolines from Frey et al (5).

[b] From K. Leonard and H. Rines, USDA-ARS, Cereal Rust Laboratory, St. Paul, Minnesota (*personal communication*), and Simons et al (12,13).

Table 2. Infection-type ratings for oat crown rust[a]

Infection type	Reaction
I	Immune: no macroscopic evidence of infection
0	Nearly immune: no uredinia, necrotic areas, or chlorotic flecks present
1	Highly resistant: a few small (0.1 mm wide × 0.4 mm long) uredinia, some necrotic areas without uredinia
2	Moderately resistant: plentiful small-to-medium (0.25 mm wide × 0.4–1.2 mm long) uredinia, necrotic areas seldom without uredinia
M	Mesothetic: a combination of two or more infection types in varying proportions, the most prevalent infection type listed first
3	Moderately susceptible: abundant medium-size uredinia in chlorotic areas, no necrosis
4	Completely susceptible: abundant large (≥0.25 mm wide × ≥1.2 mm long) uredinia without necrosis or chlorosis

[a]Adapted from Murphy (11).

lings of each line were inoculated with individual isolates. The test flats were incubated 24 hr in a dew chamber, then placed in a growth chamber at 18–21 C with a 14-hr photoperiod. Twelve to 14 days after inoculation, the seedlings were evaluated for reaction to *P. coronata* using the crown rust infection scale (Table 2) (11).

Data management. The stepwise method of McVey and Leonard (10) was used to identify host entries with unique resistance genes. This method is based on the assumption of gene-for-gene interactions between genes for resistance in the host and genes for avirulence in the pathogen (2,7,8). In this way, it is possible to derive the number of unique resistance genes that are detectable with a defined race collection. The detailed method of data management is covered by McVey and Leonard (10) and therefore will not be repeated here. Briefly, the infection-type data were converted to a binary code: 1 for low infection type (LIT), an infection-type rating of I, 0, 1, or 2; and 0 for high infection type (HIT), an infection-type rating of 3 or 4. Isolates of *P. coronata* headed columns, and the host lines tested were placed in rows.

The 1's and 0's within rows formed binary numbers so that the column with the LIT farthest down the database became the left-hand column and the column with the uppermost LIT became the right-hand column. The other LITs were ordered in upward steps from left to right based upon the number of LITs per column. Unique *Pc* genes were identified if a host accession-pathogen isolate interaction was different from that of any other gene identified by another host accession-pathogen isolate interaction. This does not imply that the gene does not exist in another accession of the same species or in a different species (9). Smaller database files were constructed to illustrate specific examples of isolates useful in the investigation of particular genes in the mapping populations.

RESULTS AND DISCUSSION

The primary reason for performing these analyses was to determine the minimum number of different resistance genes

Table 3. High/low infection-type data from *Avena* sp.: *Puccinia coronata* var. *avenae* interaction tests arranged in ascending binary number for low infection type, identifying unique *Pc* genes for resistant to crown rust[a]

	Isolates																						
Host	Pc49	345	262	258	298	276	264A	290	263	264B	203	325A	Pc54	Pc51	Pc46	456	Pc63	Pc56	Pc55	Pc47	321	Pc50	Pc57
Markton	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Appler	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bond	0	0	0	...	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthony	0	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Landhofer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Santa Fe	0	0	0	0	...	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bondvic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ukraine	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trispernia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Victoria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*1*	1	1	1
D504	0	0	0	0	0	0	0	0	0	0	0	0	*1*	1	1	1	1	1	1	0	0	0	0
D520	0	0	0	0	0	0	0	0	0	0	0	*1*	0	1	1	1	1	1	1	1	0	1	1
Ascencao	0	0	0	0	0	0	0	0	*1*	1	1	0	1	1	1	1	1	1	1	1	1	0	1
D486	0	0	0	0	0	0	0	*1*	0	1	1	0	1	1	1	1	1	1	1	0	1	1	1
SD 800287	0	0	0	0	0	0	*1*	1	1	0	1	0	1	0	1	1	0	0	1	0	1	0	1
D535	0	0	0	0	0	*1*	0	1	1	0	1	1	0	1	0	1	1	1	1	1	1	1	1
Centennial	0	0	0	0	0	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
D515	0	0	0	*1*	1	0	1	1	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1
P76178RD1	0	0	*1*	0	1	0	1	1	1	1	1	0	1	0	1	1	1	0	1	0	1	0	1
D634	0	*1*	1	0	0	1	0	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1
ND 8205590	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
WI X4361-9	0	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1
D526	*1*	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
H561	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
IA X421	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0
H547	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Coker 234	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
D640	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Tam-O-301	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
Steele	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
H617-751	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
IL-82-1657	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Amagalon	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CI 2630	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1
CI 9009	0	0	0	0	0	0	0	0	0	0	*1*	0	0	0	1	0	0	0	0	0	0	0	0
CI 3815	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1
CI 1994	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CI 3214	0	0	0	0	0	0	0	0	0	*1*	0	0	0	0	0	0	0	0	0	0	0	0	0
CI 4748	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	*1*	0	0	0	0
CI 6954	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
X117	0	0	0	0	0	0	1	1	1	1	1	0	1	1	1	0	0	1	0	0	0	1	1
C649	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0

(*continued on next page*)

[a]0 = high infection type, 1 = low infection type, and *1* = unique *Pc* gene. Unique *Pc* genes were identified using the method of McVey and Leonard (10) after Loegering and Burton (7).

that could be detected with the ISU crown rust collection. Recently, efforts were begun to develop genetic maps of diploid and hexaploid oats based on morphological, RFLP, and RAPD markers. The usefulness of the RFLP maps will be enhanced by mapping genes for resistance to crown rust, one of the most important fungal pathogens of oats. Among diploid oats, populations have been developed that allow the simultaneous mapping of several genes for crown rust resistance in reference to RFLP-based markers (P. J. Rayapati, M. Lee, J. W. Gregory, and R. P. Wise, *unpublished*). One population is from a cross between CI 2630 of *Avena strigosa* Schreb., representing the A genome of cultivated hexaploid oats, and CI 9009 of *A. nuda* L. (= *A. nudibrevis* Vavilov). A second population is from a cross between CI 3815 of *A. strigosa* and CI 1994 of *A. wiestii* Steud. CI 2630 and CI 3815 are resistant to nearly all races of crown rust, whereas CI 9009 and CI 1994 are susceptible to most races. Therefore, these two populations should provide the maximum number of differential reactions for crown rust resistance.

To provide a foundation for detecting specific genes for resistance to crown rust, 47 isolates of rust were screened on the diploid parents and on 33 hexaploid differentials (Table 3). At least 17 unique resistance genes were detected in the hexaploid differentials, and four in the diploid accessions, with the ISU crown rust collection. An evaluation of parents used in two diploid mapping populations revealed that 37 differential reactions can be detected and mapped in F_3 families from a CI 2630 × CI 9009 cross, and 40 can be similarly analyzed from a CI 3815 × CI 1994 cross. The two crosses have 32 of the differential reactions in common.

Table 4 shows differential reactions among a subset of crown rust infection-

Table 4. Infection-type data from eight Webster hexaploid isolines with unique genes for resistance, and isolates of *P. coronata*: The boxed areas show the unique resistance genes that can be detected in D515 with isolate 264A, in D486 with isolate 203, and in D504 with isolate Pc55[a]

	Isolates									
Cultivar	**264A**	**258**	**345**	**262**	**276**	**203**	**325A**	**290**	**Pc57**	**Pc55**
D504	0	0	0	0	0	0	0	0	0	*1*
D520	0	0	0	0	0	0	*1*	0	1	1
D486	0	0	0	0	0	*1*	0	1	1	1
D535	0	0	0	0	*1*	1	1	1	1	1
D634	0	0	*1*	1	1	1	1	1	1	1
D526	0	0	1	1	1	1	1	1	1	1
D515	*1*	1	0	0	0	1	1	1	1	1
D640	1	1	1	1	1	1	1	1	1	1

[a] 0 = high infection type, 1 = low infection type, and *1* = unique *Pc* gene.

Table 3. (*continued from preceding page*)

	Isolates																							
Host	**427**	**Pc59**	**322**	**Pc62**	**264BA**	**Pc43**	**Pc38**	**294**	**326**	**Pc52**	**Pc58**	**Pc60**	**Pc37**	**Pc40**	**295**	**Pc61**	**Pc45**	**216**	**213A**	**202**	**241**	**205**	**280**	**Pc48**
Markton	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Appler	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bond	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthony	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	...	0	0	0	0	0	0	*1*	1
Landhofer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*1*	1	1	1	1	1	0
Santa Fe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*1*	1	1	1	1	1	1	0
Bondvic	0	0	0	0	0	0	0	*1*	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0
Ukraine	0	0	0	0	*1*	1	1	0	0	0	1	1	1	1	1	1	1	0	0	0	0	1	0	0
Trispernia	0	0	*1*	1	1	0	0	0	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0
Victoria	1	1	0	0	0	0	1	0	0	1	0	1	0	0	0	1	1	0	0	1	1	1	0	1
D504	1	1	0	1	1	0	1	1	0	0	0	1	1	1	...	1	1	1	0	1	1	1	1	1
D520	1	1	1	1	1	1	0	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0
Ascencao	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1
D486	1	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	0	1	1	1	1	1
SD 800287	1	1	1	1	1	1	1	0	1	1	0	1	0	0	1	1	1	1	1	1	1	1	1	1
D535	0	1	1	0	1	1	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Centennial	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
D515	1	1	1	1	1	1	1	1	1	1	0	1	0	0	0	1	1	1	1	1	1	1	0	1
P76178RD1	1	1	1	1	1	1	1	...	1	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
D634	1	1	1	0	1	1	1	0	0	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1
ND 8205590	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
WI X4361-9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
D526	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
H561	1	1	1	1	1	1	1	1	1	1	1	1	1	1	...	1	1	1	1	1	1	1	1	1
IA X421	1	1	1	1	1	1	1	1	1	1	1	1	1	1	...	1	1	1	1	1	1	1	1	1
H547	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1
Coker 234	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
D640	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Tam-O-301	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Steele	1	1	1	1	1	1	1	1	1	1	1	1	1	1	...	1	1	1	1	1	1	1	1	1
H617-751	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
IL-82-1657	1	1	1	1	1	1	1	1	...	1	1	1	1	1	...	1	1	1	1	1	1	1	1	1
Amagalon	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CI 2630	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
CI 9009	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
CI 3815	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	1	0	1	1	1
CI 1994	0	0	0	0	0	0	0	0	0	0	0	0	*1*	0	0	0	0	0	0	0	0	0	0	0
CI 3214	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
CI 4748	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CI 6954	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
X117	1	1	1	1	1	1	0	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1
C649	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	1	1	1	1	0	1	0

Table 5. Infection-type data from four diploid accessions used as parents for restriction fragment length polymorphism (RFLP) mapping populations, and isolates of *P. coronata*: Isolate 264A is useful for detecting a differential reaction in populations derived from a CI 2630 × CI 9009 cross as well as from a CI 3815 × CI 1994 cross; isolates Pc55 and 203 are useful for detecting differential reactions in a population derived from a CI 3815 × CI 1994 cross but not from a CI 2630 × CI 9009 cross[a]

	Isolates									
Cultivar	**Pc55**	**264A**	**258**	**345**	**262**	**276**	**325A**	**290**	**Pc57**	**203**
CI 1994	0	0	0	0	0	0	0	0	0	0
CI 9009	0	0	0	0	0	0	0	0	0	*1*
CI 2630	0	*1*	1	1	1	1	1	1	1	1
CI 3815	*1*	1	1	1	0	1	1	1	1	1

[a]0 = high infection type, 1 = low infection type, and *1* = unique *Pc* gene.

Table 6. Infection-type data from a chromosome addition line (X117) and its recurrent parent (C649), and isolates of *P. coronata*: Isolate 264A is useful for detecting a differential reaction between X117 and C649, whereas race Pc55 and race 203 are not[a]

	Isolates									
Cultivar	**Pc55**	**264A**	**258**	**345**	**262**	**276**	**325A**	**290**	**Pc57**	**203**
X117	0	1	0	0	0	0	0	1	1	1
C649	0	0	0	0	0	0	0	0	0	1

[a]0 = high infection type, 1 = low infection type.

type data on eight hexaploid, nearly-isogenic lines. For illustration, the boxed areas show the unique resistance genes that can be detected in D515 with isolate 264A, in D486 with isolate 203, and in D504 with isolate Pc55. Table 5 shows differential reactions among a subset of crown rust infection-type data on four diploid mapping parents. The boxed areas demonstrate that, although isolates Pc55, 264A, and 203 can detect unique resistance genes, these isolates are useful for mapping these genes only in appropriate host lines. For example, isolate 264A is useful for detecting differential reactions among populations derived from both the CI 2630 × CI 9009 and the CI 3815 × CI 1994 crosses. In contrast, isolate Pc55 is only useful in a population derived from the CI 3815 × CI 1994 cross, because Pc55 is virulent on both CI 2630 and CI 9009 and cannot detect differential reactions in progeny from a cross between them. Isolate 203 can be used to detect differential reactions in a population derived from the cross between CI 3815 and CI 1994. However, since isolate 203 is avirulent on both CI 2630 and CI 9009, it would be difficult to detect differential reactions in progeny from crosses between these two lines. Race 203 may be of limited use for this cross if each line has a different resistance gene that matches different avirulence genes in our isolate of 203. In this situation, and if the two resistance genes are unlinked, the $F_{2:3}$ progeny might segregate in a 15:1 ratio. Table 6 shows differential crown rust reactions between a hexaploid chromosome addition line (X117) and its recurrent parent (C649). Isolate 264A can be used to detect a differential reaction between the X117 and C649, whereas Pc55 and 203 cannot, because Pc55 is virulent and 203 is avirulent on these two lines.

The A genome of cultivated hexaploid oats is represented in part by the diploid oat lines evaluated in this paper. Diploid genomes provide a useful and convenient way to analyze a portion of the more complex hexaploid genome. Diploid oats have been shown to be a rich source of genes for resistance to *P. coronata* (12). This report provides a database for genetic and molecular analysis of many of these genes, helping to further the research on this important disease of oats.

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