A Nomenclature for *Rhynchosporium secalis* Pathotypes

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ABSTRACT

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A "standard" nomenclature based on octal numbers was developed for naming pathotypes of the barley scald fungus, *Rhynchosporium secalis*. Twenty-four barley differential cultivars were included in this nomenclature. These cultivars were chosen for nomenclatural purposes because they have been the most commonly used in previous studies, and because jointly they carry all of the known genes for scald resistance. The octal nomenclature allows a unique appellation to be generated for each possible combination of pathogenicities in the fungus; and, because only eight different patterns must be learned, this system can be quickly and easily applied by those not familiar with it. Cultivars with related resistance genes were grouped, so far as possible, in the same octal digits because this simplifies genetic interpretation of the names obtained. In this way, the results from studies by different investigators who do not use the same differentials can be compared easily. Use of the octal nomenclature developed in this study mitigates the barriers to comparisons among studies caused by previous nomenclatures.

The nomenclatures used to designate pathotypes of *Rhynchosporium secalis* (Oud.) Davis, the causal organism of the barley scald disease, have varied widely. Each of the studies published thus far has been based on a different set of barley differential cultivars, and on a different nomenclature for naming the pathotypes identified in the study. In general, pathotypes have been arranged in either increasing or decreasing order according to the number of cultivars they can infect, and then they have been numbered consecutively, with or without a prefix indicating the geographical area from which each pathotype was derived. As examples, United States pathotypes were originally named U.S.-1 to U.S.-7 by Schein (32,33); U.S.-8 and U.S.-9 were added later by Dyck and Schaller (12). Similar methods have been used to designate pathotypes from Argentina (32), California (21), Australia (4,8), and Italy (10). Four main difficulties arise from this type of nomenclature: 1) Names used in different parts of the world bear little or no relationship to each other, e.g., pathotype 1 in Australia is not at all similar to pathotype 1 in California, U.S.-1, or RC-1 in Italy. This seriously impedes the ability to compare the results of studies conducted by different investigators in different geographical areas. 2) New pathotypes identified using identical sets of differentials cannot be accommodated into the previously existing nomenclature, e.g., pathotype 1 of Jackson and Webster (21) is pathogenic to none of the differentials (except the universal suscept), whereas pathotype 75 infects them all. Naming a previously unknown pathotype of intermediate pathogenicity becomes troublesome because the numbers 2 through 74 have already been assigned. 3) The existing methods of nomenclature provide no information regarding the pattern of pathogenicities on each of the differential cultivars. We know that pathotype 10 of Jackson and Webster (21) attacks relatively few of the differentials, but not the specific differentials it infects; this information can only be obtained by consulting the original source. 4) Genetic relationships among the resistance genes in the differential cultivars are not reflected in the nomenclature. Some of the cultivars used to differentiate *R. secalis* pathotypes have more than one resistance gene, and some resistance genes may be shared among two or more cultivars (16). Cultivars having shared resistance genes should be grouped together for easy comparison, yet in previous nomenclatures differential cultivars have been listed alphabetically, without regard for the resistance genes they contain.

A new nomenclature is needed to circumvent these problems; and to be effective, it should fulfill the following requirements: 1) A standard set of differentials comprising all of the important *R. secalis* resistance genes should be used in a fixed linear order. 2) The system should assign a unique name to each potential combination of pathogenicities; the set of possible names will thus be known in advance. 3) Each pathotype name should convey as much information as possible concerning the pattern of pathogenicities produced by an isolate on the differential cultivars; and, given the name of the pathotype, it should be possible to determine easily which differentials are susceptible, and which are resistant. 4) Differentials should be listed in such a way as to facilitate genetic interpretation; thus, differentials possessing related resistance genes should be grouped accordingly.

In this paper, we propose a standard set of barley differential cultivars which encompasses all of the known genes for resistance to barley leaf scald, and an octal nomenclature for naming the resultant pathotypes. It is hoped that this nomenclature will lessen the previously existing barriers to comparisons among studies conducted by investigators in different geographical areas and/or at different times.

MATERIALS AND METHODS

The goals set in choosing differentials to be included in the standard nomenclature were to maintain continuity with previous studies and to include all of the known genes for scald resistance. Table 1 summarizes the results from 18 studies on pathotype identification in *R. secalis*. Cultivars frequently included in these studies which consistently received ratings of R (uniformly resistant) or D (able to differentiate the isolates) were retained in the standard set. Cultivars which were uniformly susceptible were dropped from further consideration. A rating of X in Table 1 implies that the expression of resistance in a cultivar may be particularly sensitive to environmental influence. Such

cultivars were not eliminated from the standard set; however, when such cultivars are used as differentials, the X designation implies that careful control of the environmental conditions under which pathogenicity is assessed may be necessary.

The *R. secalis* resistance genes thought to be present in 32 widely tested cultivars are summarized in Table 2. The largest number of genes reported in a cultivar was taken to be correct unless convincing contradictory evidence was presented in other studies. The relationships among the resistance genes in the differential cultivars were also deduced from Table 2. When the relationships among the genes were not clear, the order in which the cultivars were presented in the differential series was based on the results of Goodwin (16). That study summarized the reactions of 14 differential cultivars to 269 *R. secalis* isolates from California (21), Idaho, and Oregon, representing over 100 different pathotypes (16).

Among the most commonly used nomenclatures (reviewed in 30), an octal nomenclature was chosen for naming *R. secalis* pathotypes. This nomenclature was chosen for its precision and flexibility. It allows the maximum amount of information to be presented in a concise form. An additional advantage is that the differentials can be grouped to provide meaningful genetic information from each octal digit.

RESULTS

Among the 41 potential differential cultivars listed in Tables 1 and 2, 24 were chosen for inclusion in the standard set, including a "universal suscept." These 24 cultivars were arranged in a fixed linear order from right to left, making eight octal digits with three cultivars per digit. This is a departure from most other nomenclatures in which the cultivars are listed from left to right and was necessary to make sense of the octal numbers. With this system, the names range from 00000001 for the pathotype that infects only the universal suscept, to 77777777 for the pathotype that infects all 24 cultivars. The composition of each digit, probable number of resistance genes in each cultivar, and geographical areas in which each has been studied are indicated in Table 3. The cultivars as listed from top to bottom in Table 3 correspond to their order from right to left in the standard nomenclature. Cultivars sharing genes, or with related resistance genes, were grouped as much as possible into the same digits. Among the three cultivars comprising each digit, those with the fewest resistance genes were placed to the right (toward the top of Table 3), and those with the most resistance genes toward the left. When the cultivars comprising a digit had the same number of resistance genes, those which were found to be the most resistant in previous studies were placed in the leftmost positions (toward the bottom of Table 3) within the digits. Although these cultivars together contain all of the known genes for scald resistance, gene designations are not given in Table 3 because there are no internationally accepted designations for these genes.

Digits 1 and 2 contain the cultivars which have been the most commonly used historically (Table 1); the inclusion of these cultivars in the first two digits ensures continuity with previous studies. Digit 1 (Table 3) contains the universal suscept, which can be any cultivar lacking resistance genes; thus the specific composition of digit 1 may vary from study to study. Atlas 46 and La Mesita probably have unrelated resistance genes (Table 2). Atlas 46 is placed in the leftmost position within digit 1 (closer to the bottom of Table 3), due to the smaller number of pathotypes

TABLE 1. Previous use of differential cultivars in studies on pathotype identification in *Rhynchosporium secalis*

	Reference																	
Cultivar	(31)	(20)	(28)	(33)	(12)	(24)	(27)	(36)	(19)	(3)	(26)	(4)	(21)	(10)	(14)	(5)	(23)	(8)
Abyssinian C.I. 668[a]									R			D			D	R		R
Algerian C.I 1179					D					X	S				D			
Atlas C.I. 4118	R[b]	D	R		S			X	D	D	S	D		R	D			D
Atlas 46 C.I. 7323		D	R	D	D	R	D	D	D	R	R	R	R	R	D	R		R
Brier C.I. 7157			R	D	D	D	S	D	D	D	R	D	D	D	D	D		D
Cambrinus								S	S	X								
C.I. 2376													D	D				
C.I. 3515				R								D						R
C.I. 4364												D				R		R
C.I. 5831													D					
C.I. 8618				D								D						
Clipper C.I. 14844												S						S
Dea C.I. 11759								D	D	R								
Gospeck C.I. 9094												D			D			
Hudson C.I. 8067				D	D	D		D	R	R	R	D	D	D	D	D		R
Jet C.I. 967	R		R												D	R		
Kitchin C.I. 1296									R				D	D		R		
La Mesita C.I. 7565		D		D	R	X	R	R	D	D	R	D	D	D	R	R	D	R
Modoc C.I. 7566				D	R		D	X	D	D	X	D	D	D	D	R		R
Nigrinudum C.I. 2222									R			D		D	D	R		R
Nigrum C.I. 2338[c]	D		D			D	D			X								
Osiris C.I. 1622	R	D			R			R	R	R	D	D	D	R	R	R	R	R
Pioneer C.I. 9508							D	D	D	X						D		
Prefect C.I. 9509							D	D	D	X						S		
Psaknon 6305	R									R		D			R			
Sakigake C.I. 7388						D				X		D						
Steudelli C.I. 2266									R			D	D	D	D			D
Sultan C.I. 5577										R		D						
Trebi C.I. 936	R	D			R			R	D	R	D		D	D				
Turk C.I. 5611-2[c]	R	D	R		R			D	R	R	R	D	D	D	D	D		R
West China C.I. 7556	D		D			D	D	X		X		D			D			
WW × G[d] C.I. 8162	D		R	D	D	D	D	D	D		D	D	D		D	D		R
Wong C.I. 6728				S	S	D			D	X	S		S		D			

[a] Cereal Inventory number, Agricultural Research Service, U.S. Department of Agriculture.
[b] For each study in which it was used, a cultivar was rated as uniformly susceptible to all isolates tested (S), uniformly resistant (R), able to differentiate the isolates (D), or gave results that were inconclusive, ambiguous, or difficult to score (X).
[c] More than one C.I. number has been assigned to this cultivar.
[d] Wisconsin Winter × Glabron.

TABLE 2. Genes reported to condition resistance to *Rhynchosporium secalis* in barley cultivars[a]

Cultivar	Resistance gene(s)	Reference
36 Ab 1991 C.A.N. 136[b]	One dominant gene, identical or closely linked to that in Turk.	(35)
Abyssinian C.I. 668[c]	Rh9.	(6)
Atlas C.I. 4118	Rh2.	(12)
	Rh2.	(34)
	One dominant gene, probably the same as Rh2.	(25)
	One gene which may also occur in C.I. 5831.	(16)[d]
Atlas 46 C.I. 7323	Rh2 and Rh3.	(12)
	Rh.	(18)
	Two dominant genes, Rh2 and one at Rh-Rh3-Rh4 complex.	(34)
	Two dominant genes, one probably the same, allelic, or closely linked to that in Turk.	(1)
	One dominant gene, probably Rh3.	(25)
	One gene.	(16)
Atlas 57	Two dominant genes, one probably the same, allelic, or closely linked to that in Turk.	(1)
	Two dominant genes, probably Rh2 and Rh3.	(25)
Atrada × Atlas C.I. 7189	Two dominant genes, one the same as in Osiris.	(13)
Bey C.I. 5581	One dominant gene, the same or closely linked to that in Turk.	(35)
Brier C.I. 7157	Rh.	(9)
	Rh.	(12)
	Rh and rh6.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
	One dominant gene.	(25)
	One gene, probably the same as one of those in Hudson.	(16)
C.I. 2376	Two dominant linked genes.	(25)
	Two genes, one may be Rh9, the other may be shared with Osiris and C.I. 5831.	(16)
C.I. 3515	One dominant gene, the same or closely linked to that in Turk.	(35)
	Rh^4 and Rh10.	(18)
	Two dominant genes, one at Rh-Rh3-Rh4 complex, the other one not linked to Rh2.	(34)
C.I. 4364	rh11.	(18)
C.I. 4368	rh11.	(18)
C.I. 5831	Two dominant linked genes.	(25)
	Three genes, one may be Rh2, another may be shared with Osiris and C.I. 2376.	(16)
C.I. 8256	One dominant gene, the same or closely linked to that in Turk.	(35)
	Rh^4 and Rh10.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
C.I. 8618	One dominant gene, not allelic to Rh-Rh3-Rh4 or Rh2.	(34)
Dea Cb 1092[e]	Rh.	(18)
Gembloux 14 C.I. 8286	Rh^4 and Rh10.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
Hudson C.I. 8067	Rh.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
	Two dominant genes, one probably the same, allelic, or closely linked to that in Turk.	(1)
	Two genes, one may be the same as in Brier and Turk.	(16)
Jet C.I. 967	Two complementary recessive genes, rh6 and rh7.	(6)
	rh^5 and rh6.	(18)
	Two recessive genes on chromosomes 3 and 4.	(7)
Kitchin C.I. 1296	Rh9.	(6)
	One dominant gene on chromosome 4.	(7)
	One gene, which may also occur in C.I. 2376 and C.I. 5831.	(16)
La Mesita C.I. 7565	One dominant gene.	(29)
	Rh4.	(12)
	Rh^4 and Rh10.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
	Two dominant genes.	(2)
	One dominant gene, the same one as in Osiris.	(25)
	One gene.	(16)
Modoc C.I. 7566 (= California 1311)	Two genes, one dominant (the same as in La Mesita) and one recessive.	(29)
	$Rh4^2$.	(12)
	Rh^2 and rh6.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
	One dominant gene, different from the one in Trebi, Osiris, and La Mesita.	(25)
	One gene.	(16)
Nigrinudum C.I. 2222	One recessive gene (rh8), unlinked to that in Turk.	(35)
	rh8.	(18)
Osiris C.I. 1622	Rh4.	(12)
	One dominant gene, the same or closely linked to that in Turk.	(35)
	One dominant gene, the same as in Psaknon.	(13)
	Rh^4, rh6, and Rh10.	(18)
	Two dominant genes, one probably the same as Rh4.	(25)
	Two genes, one of which may be common to C.I. 2376 and C.I. 5831.	(16)
Psaknon C.I. 6305	One dominant gene, the same as in Osiris.	(13)
	Three dominant genes, one probably the same, allelic, or closely linked to that in Turk.	(1)
Rivale C.A.N. 258	One dominant gene, the same or closely linked to that in Turk.	(35)
Sakigake C.I. 7388	One dominant gene.	(2)
Steudelli C.I. 2266	Two complementary recessive genes, rh6 and rh7.	(6)
	One gene.	(16)
Trebi C.I. 936	Two genes, one dominant (the same as in La Mesita), one recessive.	(29)
	Rh4.	(12)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
	One gene.	(16)
Turk C.I. 5611-2	Two or more genes, one probably the same as in La Mesita, Trebi, and Modoc.	(29)
	Rh3 and Rh5.	(12)
	One dominant gene.	(35)
	One dominant gene.	(6)
	Rh and rh6.	(18)
	One dominant gene at Rh-Rh3-Rh4 complex.	(34)
	One dominant gene, probably the same as Rh3 or Rh.	(1)
	One dominant gene.	(25)
	One gene, probably identical to that in Turk.	(16)
West China C.I. 7556 WW × G[f] C.I. 8162	Two dominant genes.	(2)
	Rh^3.	(18)
	One gene.	(16)

[a] Gene designations are those given in the original sources; no attempt was made at standardization. Therefore, the same gene can be designated as part of an allelic series, or closely linked to other genes depending on the original source.
[b] Canadian accession number.
[c] Cereal inventory number, Agricultural Research Service, U.S. Department of Agriculture.
[d] This study was based on computer-aided analysis of host-pathogen interaction data, not on crossing data.
[e] Accession number of Arable Crop Breeding Department, Welsh Plant Breeding Station, Aberystwyth, Wales.
[f] Wisconsin Winter × Glabron.

able to attack it relative to La Mesita (16), and in deference to previous studies in which two resistance genes were reported in this cultivar.

Among the three cultivars comprising digit 2 (Table 3), Hudson, with two resistance genes (Table 2), is placed at the leftmost position, next to Brier, which probably carries one of the resistance genes in Hudson. Pathogenicity to Wisconsin Winter × Glabron is highly correlated with that of Hudson and Brier (Q. Zhang, *personal communication*); consequently, it was placed at the rightmost position within digit 2 (closer to the top of Table 3).

Turk occupies the leftmost position within digit 3 (Table 3), due to the small number of pathotypes able to attack it in the western United States (16); another consideration was that this cultivar has been reported to have more than one gene for resistance in some inheritance studies (12,29). Trebi and Modoc are included in the same digit because, although possessing different genes for resistance, pathogenicity to them is highly correlated with pathogenicity to Turk in California (Q. Zhang, *personal communication*).

The three cultivars included in digit 4 (Table 3) apparently possess completely independent resistance genes (Table 2). Osiris, with 2 genes, occupies the leftmost position, followed by Steudelli, due to the slightly smaller number of pathotypes able to attack it relative to Atlas (16). The two complementary recessive genes in Steudelli (Table 2) function as a single gene for the purposes of pathotype identification. The cultivar Jet has the same two genes (6), and thus may be used interchangeably with Steudelli.

The cultivars in digit 5 have not been used as widely as those included in the previous four digits. Cultivar C.I. 5831 probably has 3 resistance genes. Because it is resistant to more pathotypes than any other cultivar in the western United States (16), it is placed at the leftmost position within digit 5 (Table 3). Cultivar C.I. 2376 has two genes for resistance, one of which may be common to C.I. 5831; consequently, it is placed in the middle, next to Kitchin, which has a single resistance gene. The resistance gene in Kitchin may be identical to one of those found in each of C.I. 5831 and C.I. 2376 (16). Baker and Larter (6) found the same resistance gene in the cultivars Abyssinian and Kitchin: in Australia, Abyssinian has been used as the source of this resistance instead of Kitchin. For the purposes of this study, resistance in the two cultivars has been assumed to be identical. Although this may not be a valid assumption (21), the currently available data do not permit the hypothesis of different resistance genes in these two cultivars to be tested rigorously. Thus, Abyssinian and Kitchin may be used interchangeably.

Digits 6, 7, and 8 apply primarily to the results of Ali et al (4), although some of the individual cultivars have been used in other studies. The inclusion of these three digits accounts for all of the previously designated resistance genes not accounted for in digits 1–5. Too little information is available concerning the resistance genes present in these cultivars to firmly establish relationships among them; consequently, they were grouped primarily according to the numbers of resistance genes reported in the literature and the relative frequency with which pathogenicity to each of these cultivars was reported by Ali et al (4): cultivars which resisted the largest numbers of pathotypes and had the most resistance genes were placed in the leftmost position within each digit.

For those not familiar with octal numbers, the conversion between binary and octal as used in this study is illustrated in Table 4. When applying this system to pathogenicity data, any digit in which one or more differentials is missing is indicated by the use of an underscore character. Examples of conversions from binary into the octal nomenclature using data from previous studies are given in Table 5. A computer program for converting pathogenicity data into the standard nomenclature for digits 1–5 is available from Stephen B. Goodwin.

TABLE 3. The standard nomenclature for *Rhynchosporium secalis* pathotypes[a]

Digit	Cultivars	Probable number of resistance genes	Where studied
1	Universal Suscept	none	worldwide
	La Mesita C.I. 7565	one dom.[c]	worldwide
	Atlas 46 C.I. 7323	one dom.	worldwide
2	WW × G[b] C.I. 8162	one dom.	worldwide
	Brier C.I. 7157	one dom.	worldwide
	Hudson C.I. 8067	two dom.	worldwide
3	Modoc C.I. 7566	one dom.	worldwide
	Trebi C.I. 936	one dom.	worldwide
	Turk C.I. 5611-2	one dom.	worldwide
4	Atlas C.I. 4118	one dom.	worldwide
	Steudelli C.I. 2266	two rec.[d]	Australia; Calif.; Italy
	Osiris C.I. 1622	two dom.	worldwide
5	Kitchin C.I. 1296	one dom.	Calif.; Italy; Sweden
	C.I. 2376	two dom.	California; Italy
	C.I. 5831	three[e]	California
6	C.I. 4364	one rec.	Australia; Sweden
	C.I. 8618	one dom.	Australia; Pennsylvania
	C.I. 3515	two dom.	Australia; Pennsylvania
7	Nigrinudum C.I. 2222	one rec.	Australia; Italy; Sweden
	West China C.I. 7556	two dom.	worldwide
	Psaknon C.I. 6305	three dom.	Australia
8	Gospeck C.I. 9094	n.c.[f]	Australia
	Sakigake C.I. 7388	one dom.	Australia; Japan
	Sultan C.I. 5577	not studied	Australia

[a] The cultivars in the standard nomenclature are listed from right to left, which corresponds to their order from top to bottom in this table.
[b] Wisconsin Winter × Glabron.
[c] Dominant = dom.
[d] Recessive = rec.
[e] At least two are dominant; the third has not been characterized.
[f] Not characterized = n.c.

DISCUSSION

Many systems of nomenclature are currently in use for naming fungal pathotypes. One commonly used system names each isolate according to the host differentials (or resistance genes, if sufficiently characterized) which it can overcome; an isolate pathogenic to differentials 1, 3, and 8 would be named pathotype 1,3,8. This method provides the maximum amount of information pertaining to the pathogenicity of an isolate, and the method can be used to advantage when the number of differentials is small. However, this system becomes cumbersome when large numbers of pathogenicity genes are involved, as is the case with *R. secalis*. Another disadvantage of this method is that it is not flexible enough to accommodate missing differentials, e.g., designating a pathotype 1,3,8 as above gives no information respecting differentials 2, 4, 5, 6, and 7, and there is no way of indicating whether any differentials were omitted during testing. This clearly presents problems in comparing results from studies in which different sets of differential cultivars were used.

TABLE 4. Conversions between binary and octal notation

Binary	Octal
000	0
001	1
010	2
011	3
100	4
101	5
110	6
111	7

In the nomenclature proposed by Habgood (17), the differentials are listed in a fixed linear order and each is assigned the value 2^{n-1}, where n is the number of the corresponding differential in the series. A name is determined by summing the values for the differentials susceptible to a particular isolate. The Habgood name for pathotype 1,3,8 above would thus be $2^0 + 2^2 + 2^7 = 133$. This nomenclature has several advantages (17,22): a unique number is assigned to each pathotype; new differentials are easily added on if needed; and the name provides the essential information about the pathogenicity of the isolate in question. However, reproducing the pattern of pathogenicities from the name is time consuming, and no allowance can be made for missing differentials. Comparisons among different studies are, therefore, not facilitated by this system.

An octal nomenclature has been adopted in this study to circumvent the inherent problems associated with other methods. This method, first proposed by Gilmour (15), has subsequently been used to name *R. secalis* pathotypes in Great Britain (23). With the octal nomenclature, the differentials are placed in a fixed linear order from right to left, and scores for a particular isolate on each of the differential cultivars are denoted by a series of binary digits (bits); one is used to indicate a susceptible reaction, zero for resistance. The complete pattern of zeros and ones for each isolate is then broken down into groups of three, and each group of three bits comprises one octal digit. With this method, a unique number is assigned to each pathotype; thus, for any given set of differentials, all possible names are known in advance. The total number of digits required to describe completely each isolate on a particular set of differential cultivars is one-third the number of differentials used: five digits are required to describe completely the pathotypes obtained with 15 differentials, eight digits for 24 differentials.

One advantage of this system is that it is very flexible. Additional differentials can be accommodated easily by adding them to the left of those currently used; missing differentials can be denoted by underscoring any digits in which they occur. With octal numbers, only 8 patterns must be learned (Table 4) and, if necessary, are easily generated with binary arithmetic, obviating the need for memorization. If the number of digits becomes too large, this method can be converted to a hexadecimal (base 16) system to reduce the total number of digits used. However, this doubles the number of patterns which must be learned, and the resulting combination of letters and numbers is likely to add confusion; the octal system has, therefore, been retained for use with *R. secalis* pathotypes.

To maximize the effectiveness of the octal nomenclature, attention must be given to the order in which the differentials are listed. The relationships among the resistance genes in the differential cultivars should be considered; those with one or more genes in common should be grouped in the same digit, if possible, to facilitate genetic interpretation of the results. In general, complex differentials (those possessing two or more resistance genes) should be placed in the leftmost (most significant) position among the three cultivars comprising a digit. Because the frequencies of pathogenicity to complex differentials should be lower than those for simple ones, the occurrence of even numbers will be minimized for the reason that those cultivars in the most significant locations of each digit will be attacked less frequently than those in the less significant positions; if attacked, and a one- or two-gene differential having shared genes occurs in the same digit, any pathotype attacking the most complex differential should also infect those of lower complexity which incorporate shared resistance genes. For example, if the three cultivars of a digit have resistance genes ABC,AB,A (this may be the case for digit 5), the only octal numbers that can result will be 0, 1, 3, or 7 (see Table 4); values of 2, 4, 5, or 6 indicate a potential problem with the data. This provides an effective method of screening for pathotypes which do not conform to the expected configuration. Another advantage of this type of grouping is that in many cases single-gene differentials can be substituted for complex

TABLE 5. Examples of conversions between previous nomenclatures and the standard nomenclature

Old name	New name	Type of data	Digit 8	7	6	5	4	3	2	1
Aust. 2	33117031[a]	binary	011	011	001	--1	111	0-0	011	001
		octal	3	3	1	1	7	0	3	1
Aust. 33	10002001[a]	binary	001	000	000	--0	010	0-0	000	001
		octal	1	0	0	0	2	0	0	1
II	0001001[a]	binary	---	--0	0-0	--0	001	0-0	000	001
		octal	_	0	0	0	1	0	0	1
U.S.-9	1075	binary	---	---	---	---	0-1	000	111	101
		octal	_	_	_	_	1	0	7	5
U.S.-2	131	binary	---	---	---	---	---	--1	011	001
		octal	_	_	_	_	_	1	3	1
Race 10	11001	binary	---	---	---	001	001	000	000	001
		octal	_	_	_	1	1	0	0	1
Race 61	36317	binary	---	---	---	011	110	011	001	111
		octal	_	_	_	3	6	3	1	7
RC-3	1 32723	binary	---	--1	---	-11	010	111	01-	011
		octal	_	1	_	3	2	7	2	3

[a] In these studies, Abyssinian was used as the source of the Rh9 resistance instead of Kitchin.

differentials without changing the pathotype names. If the digit with the resistance genes ABC,AB,A above is reduced to the three single-gene differentials having genes C,B,A, all pathotypes with octal numbers 3 and 7 will remain the same. Among the four additional pathotypes that can be differentiated, those with octal numbers 2, 4, and 6 will have been subsumed under the old octal digit 0, while those with new number 5 would have been mixed in with old number 1. This type of substitution would cause changes to all of the names with most other systems of nomenclature.

Differentials should also be grouped according to their historical usage; those common to the largest number of previous studies should be grouped together to maintain continuity and to facilitate comparisons. Differentials commonly used in a particular geographical area, but not used in other areas, should be grouped; some digits may only be relevant to specific areas.

All of the above qualities have been incorporated into the naming scheme developed in this study. This nomenclature incorporates all of the designated genes for resistance to *R. secalis* in barley and reflects, as much as possible, the relationships among these genes. To facilitate comparisons among studies, pathotypes from Schein (32), Dyck and Schaller (12), Ali et al (4), Jackson and Webster (21), Ceoloni (10), Aström (5), and Brown (8) have been renamed according to this nomenclature (Table 6). Corresponding digits are aligned in the same column, and missing differentials are indicated by an underscore character. This nomenclature will be particularly useful in areas of low pathogenic diversity, such as parts of Australia, Britain, and the northeastern United States. Even in areas with high pathogenic diversity, a list of pathotypes is still the most efficient means of summarizing the data. Furthermore, because the nature of this nomenclature facilitates determining the particular differentials that are sus-

TABLE 6. Previously identified *Rhynchosporium secalis* pathotypes renamed according to the standard nomenclature

New name[a]	Previous name	Reference	New name	Previous name	Reference	New name	Previous name	Reference
0000471	Pathotype 1	(5)	0 32723	RC-7	(10)	57003	Race 35	(21)
0000001	Pathotype 2		1 10763	RC-8		17103	Race 36	
			1 10723	RC-9		30147	Race 37	
31113531	Aust.-1	(4)	0 12361	RC-10		36203	Race 38	
33117031	Aust.-2		1 12121	RC-11		11475	Race 39	
33713041	Aust.-3		0 12121	RC-12		03475	Race 40	
17117003	Aust.-4		1 12021	RC-13		55113	Race 41	
33113111	Aust.-5		0 12021	RC-14		57013	Race 42	
33112451	Aust.-6		1 02021	RC-15		17231	Race 43	
13112471	Aust.-7		0 02021	RC-16		73111	Race 44	
32112471	Aust.-8		0 00023	RC-17		33113	Race 45	
33013051	Aust.-9					04357	Race 46	
34013431	Aust.-10		1001	U.S.-8	(12)	12475	Race 47	
11112451	Aust.-11		1075	U.S.-9		74303	Race 48	
11117003	Aust.-12		0001	U.S.-1		36303	Race 49	
31117001	Aust.-13		0001	U.S.-7		13475	Race 50	
31103111	Aust.-14					11575	Race 51	
15113001	Aust.-15		00001	Race 1	(21)	37213	Race 52	
51113001	Aust.-16		01001	Race 2		33513	Race 53	
11117001	Aust.-17		00003	Race 3		17313	Race 54	
31113001	Aust.-18		00011	Race 4		53313	Race 55	
13113001	Aust.-19		02001	Race 5		10757	Race 56	
34012411	Aust.-20		01011	Race 6		13575	Race 57	
11113101	Aust.-21		05001	Race 7		37313	Race 58	
13110401	Aust.-22		41001	Race 8		57313	Race 59	
33003001	Aust.-23		03001	Race 9		76313	Race 60	
32003003	Aust.-24		11001	Race 10		36317	Race 61	
11007003	Aust.-25		41003	Race 11		37317	Race 62	
31003011	Aust.-26		03003	Race 12		77117	Race 63	
11113001	Aust.-27		43001	Race 13		32767	Race 64	
11112001	Aust.-28		03011	Race 14		34757	Race 65	
30203001	Aust.-29		07001	Race 15		14777	Race 66	
11012001	Aust.-30		11003	Race 16		77317	Race 67	
30002001	Aust.-31		13001	Race 17		16777	Race 68	
10003001	Aust.-32		02031	Race 18		36757	Race 69	
10002001	Aust.-33		12003	Race 19		34777	Race 70	
00003001	Aust.-34		14003	Race 20		74777	Race 71	
10000001	Aust.-35		43011	Race 21		36777	Race 72	
			51021	Race 22		76777	Race 73	
0000001	I	(8)	53001	Race 23		37777	Race 74	
0001001	II		13021	Race 24		77777	Race 75	
0002001	III		17001	Race 25				
0000021	IV		13003	Race 26		0 101	U.S.-1	(33)
0002021	V		13011	Race 27		0 031	U.S.-2	
			01055	Race 28		0 011	U.S.-3	
1 32763	RC-1	(10)	17003	Race 29		0 175	U.S.-4	
1 32363	RC-2		13013	Race 30		0 171	U.S.-5	
1 32723	RC-3		63011	Race 31		0 113	U.S.-6	
1 30763	RC-4		01455	Race 32		0 111	U.S.-7	
1 12703	RC-5		17013	Race 33				
1 32323	RC-6		57011	Race 34		0001	U.K.1	(36)
						0475	U.K.2	

[a] Missing differentials are indicated by an underscore character. Missing digits (i.e., when all three differentials comprising a digit were not tested) can be dropped when they occur to the left-hand side of a name only.

ceptible to a pathotype, it allows groups of similar pathotypes to be identified easily through visual inspection.

Another useful naming system which also accounts for a large number of differentials has recently been applied to *R. secalis* pathotypes by Crandall (11). In this system, a modification of the nomenclature used to describe cereal rust pathotypes (30), the differentials are arranged in a fixed linear order into three groups of four and one group of three. This is essentially a combination of a hexadecimal and an octal system, except that each digit is designated by a letter rather than a number. Drawbacks to this system are that 20 different patterns must be memorized, and that the use of letters precludes easy regeneration of the conversion table. Still another problem is that the cultivars are listed in order of decreasing susceptibility to California isolates of *R. secalis*. Although this order is meaningful within California, it becomes less effective when applied to populations of the fungus from different geographical areas. Thus far, no two studies have found similar relative frequencies of pathogenicity to particular differentials; nor would this be expected, considering the varying selection regimes likely to be imposed on populations of the fungus in different temporal and spacial environments. The octal nomenclature developed in this study has many advantages over previous nomenclatures applied to *R. secalis* pathotypes. This system provides information about pathogenicity to all of the currently known *R. secalis* resistance genes and eliminates the barriers to comparisons among studies caused by the plethora of present nomenclatures.

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