# Resistance to Wheat Stem Rust in Spring Spelts

D. V. McVEY and K. J. LEONARD, Cereal Rust Laboratory, United States Department of Agriculture, Agricultural Research Service, University of Minnesota, St. Paul, MN 55108

**ABSTRACT**

McVey, D. V., and Leonard, K. J. 1990. Resistance to wheat stem rust in spring spelts. Plant Dis. 74:966-969.

The minimum number of *Sr* genes for resistance to wheat stem rust (caused by *Puccinia graminis* f. sp. *tritici*) was determined from infection-type data of the interaction of spring habit spelts (*Triticum spelta*) and wheat stem rust. Infection-type data from seedlings infected with 35 isolates of *P. g.* f. sp. *tritici* were used to determine low or high infection-type of 578 spelt introductions of the USDA National Small Grain Collection. A "boxing" program based upon the gene-for-gene concept was used to identify corresponding gene pairs. Of the minimum 28 genes for resistance to stem rust present, 26 were new. More genes were probably present, and a few in combination could provide a useful level of resistance to stem rust.

Flor's (3) gene-for-gene concept led Loegering et al (5) to characterize host:pathogen associations. Infection type (IT) data have been used successfully to postulate genes for resistance in wheat (*Triticum* L. spp.) to wheat stem rust (caused by *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. & E. Henn. [4,10,11]) and wheat leaf rust (caused by *Puccinia recondita* Roberge ex Desmaz. f.sp. *tritici* [2,12,14]).

Loegering et al (7) developed a theoretical computerized model to derive hypothetical genotypes of host cultivars and cultures of *P. g.* f. sp. *tritici* based upon IT data which was later modified (6). Browder and Eversmeyer (1) also developed a system for sorting IT data that can be used in determining the minimum number of corresponding gene pairs that would explain the IT variation.

In a study of reactions of spring spelt (*Triticum spelta* L.) to stem rust, a number of *Sr* genes were identified (9). The IT data (9) indicated the presence of additional genes for resistance to stem rust beyond those identified. The objective of this study was to determine the minimum number of corresponding gene pairs present.

## MATERIALS AND METHODS

The 578 spelt accessions studied were part of the USDA National Small Grain Collection. Inoculation procedures and stem rust isolates used are described in a previous study (9). Each of the 35 isolates of *P. g.* f. sp. *tritici* used possessed a different combination of avirulence/virulence. The IT data, based upon the Stakman et al (13) scoring, were coded 1 for low IT (LIT) and 0 for high IT (HIT) for reaction of each of the 578 host entries. Isolates of *P. g.* f. sp. *tritici* headed columns and host entries rows. The 1s and 0s were transferred to a binary number data base file and sorted from lowest to highest binary number. The hosts were thus grouped according to similarities for LIT/HIT patterns. The isolates were originally arranged at random. However, if their order had been different, the arrangement of the sorted order would have been different but the groups would have been the same.

A smaller data base file was derived from the main file with a single representative of each LIT/HIT pattern. Next, each column was summed for the number of LITs and the columns were arranged with the least number(s) of LITs on the left to the most LITs on the right. These resulting data were sorted as ascending binary numbers so that the column with the LIT farthest down the data set became the left-hand column and the column with the uppermost LIT became the right-hand column. The other column LITs are ordered in upward steps from left to right. Thus, the first LIT of each column is the lowest binary number for the row in which it occurs.

Loegering and Burton's (6) method of identifying host entries with unique resistance genes in the smaller data base file was used with modifications. Their method is based on the assumption of the gene-for-gene interaction between genes for resistance in the host and genes for avirulence in the pathogen as illustrated in Figure 1. The hypothetical ITs in Figure 1 Pattern A indicate a gene for resistance is present in cultivar H2. Those in Figure 1 Pattern B indicate at least two distinct genes for resistance—one in H1 and one in H2. The ITs in

**Table 1.** Infection type data[a] from a subset of spelt wheat plant introduction lines and isolates of *Puccinia graminis* f. sp. *tritici* indicating the presence of the first unique resistance gene of this subset in PI348687

| | Isolates | | | | | |
|---|---|---|---|---|---|---|
| PI | QCBS | NCCQ | BCBN | HNLQ | RKQS | MBCT |
| 348598 | 0 | 0 | 0 | 0 | 1 | 1 |
| 348448 | 0 | 0 | 1 | 1 | 0 | 0 |
| 348639 | 0 | 1 | 0 | 0 | 1 | 0 |
| 348581 | 0 | 1 | 0 | 0 | 0 | 1 |
| 355625 | 0 | 1 | 1 | 1 | 0 | 0 |
| 348687 | *1*[b] | 0 | 0 | 0 | 0 | 0 |

[a] 0 designates high infection type; 1 designates low infection type.
[b] Italicized number denotes unique resistance gene.

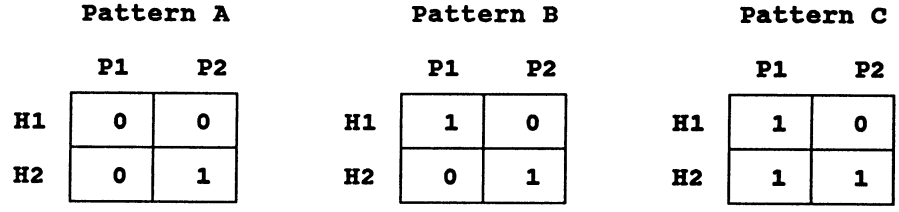


**Fig. 1.** Gene-for-gene interactions between two host cultivars (H1 and H2) and two pathogen isolates (P1 and P2) illustrating the patterns of infection types that indicate the presence of a gene for resistance in H2 that is absent in H1. **Pattern A** indicates a single resistance gene in H2, **pattern B** indicates different resistance genes in H1 and H2, and **pattern C** indicates a resistance gene in H1 and at least two in H2.

Joint contribution of the USDA-ARS and the Minnesota Agricultural Experiment Station.

Scientific Journal Series Paper 17193, Minnesota Agricultural Experiment Station, University of Minnesota, St. Paul.

Accepted for publication 13 April 1990.

Figure 1 Pattern C indicate a gene for resistance in H1 and at least one in H2 that is different from the gene in H1.

Once the data were sorted and arranged, the LITs that resulted from combinations of unique genes for resistance in host entries and genes for avirulence in the rust isolates were identified. The procedure followed is described below and illustrated in Tables 1–6.

**Step 1.** Start at the top of the first (left) column of ITs. Go down the column, mark the first LIT encountered to signify it was caused by the first unique gene for resistance for this set of host entries (Table 1). All other LITs in the same column or in the same row could be attributed to the same resistance/avirulence gene combination.

**Step 2.** Move to the next column to the right and begin at the top. If the first LIT encountered is in a row above any previously marked LIT, it will occur as illustrated in Figure 1, Pattern A. Mark it to signify that it is caused by a second unique gene for resistance (Table 2). If the first encountered LIT is in a row that already has a marked LIT, proceed down the column to the LIT in a row without a marked LIT. Draw a box(es) with that LIT and the previously marked LIT(s) at the opposite corners. If there are LITs at all four corners of any box, the newly encountered LIT cannot be established as resulting from a unique gene for resistance (Table 3). In that case, proceed down the column to the next LIT and repeat the process of drawing boxes with all previously marked LITs above the level of the newly encountered LITs. If there are no more LITs, proceed to the next column. Mark the first encountered LIT if it is in a row above any previously marked LIT (Table 4). If the newly encountered LIT is in a row below a previously encountered LIT, draw boxes with the newly encountered LIT and the previously encountered LITs at opposite corners (Table 5). If none of the boxes so drawn has LITs at all four corners, mark the newly encountered LIT to indicate the presence of another unique gene for resistance (Table 6). All of the boxes drawn with previously marked LITs should resemble either Pattern B or C in Figure 1.

**Step 3.** Repeat step 2 for each remaining column to the right of the last column read (sequential steps indicated in Tables 1–6).

**Step 4.** Count the number of marked LITs to obtain the minimum number of unique genes for resistance required to give the observed pattern of ITs with the isolates of *P. g.* f. sp. *tritici* used in the test. Host entries with marked LITs can be used as sources of the unique gene for resistance, although other host lines may also possess the same gene in combination with other genes.

## RESULTS AND DISCUSSION

Ordering the LITs in upward steps from left to right based upon the number of LITs per column and converting HIT (0) and LIT (1) to binary numbers determined the host entries selected regardless of the order of either host or isolate of *P. g.* f. sp. *tritici*. The host entries selected have the lowest binary number for host:pathogen isolate interaction and are not random selections.

The maximum number of corresponding gene pairs that can be identified is limited by the number of isolates of

**Table 2.** Infection type data[a] from a subset of spelt wheat plant introduction lines and isolates of *Puccinia graminis* f. sp. *tritici* indicating the second and third unique resistance genes in PI348639 and PI348448

| | Isolates | | | | | |
|---|---|---|---|---|---|---|
| PI | QCBS | NCCQ | BCBN | HNLQ | RKQS | MBCT |
| 348598 | 0 | 0 | 0 | 0 | 1 | 1 |
| 348448 | 0 | 0 | *1*[b] | 1 | 0 | 0 |
| 348639 | 0 | *1* | 0 | 0 | 1 | 0 |
| 348581 | 0 | 1 | 0 | 0 | 0 | 1 |
| 355625 | 0 | 1 | 1 | 1 | 0 | 0 |
| 348687 | *1* | 0 | 0 | 0 | 0 | 0 |

[a] 0 designates high infection type; 1 designates low infection type.
[b] Italicized numbers denote unique resistance genes.

**Table 3.** Infection type data[a] from a subset of spelt wheat plant introduction lines and isolates of *Puccinia graminis* f. sp. *tritici*

| | Isolates | | | | | |
|---|---|---|---|---|---|---|
| PI | QCBS | NCCQ | BCBN | HNLQ | RKQS | MBCT |
| 348598 | 0 | 0 | 0 | 0 | 1 | 1 |
| 348448 | 0 | 0 | *1*[b] | 1[c] | 0 | 0 |
| 348639 | 0 | 1 | 0 | 0 | 1 | 0 |
| 348581 | 0 | 1 | 0 | 0 | 0 | 1 |
| 355625 | 0 | *1* | 1 | 1[c] | 0 | 0 |
| 348687 | *1* | 0 | 0 | 0 | 0 | 0 |

[a] 0 designates high infection type; 1 designates low infection type.
[b] Italicized numbers denote unique resistance genes.
[c] The low infection type of PI348448 with isolate HNLQ may be attributed to the same gene that confers resistance to isolate BCBN. The low infection type of PI355625 with isolate HNLQ could be accounted for by the resistance gene in PI348448 which may be shared by PI355625.

**Table 4.** Infection type data[a] from a subset of spelt wheat plant introduction lines and isolates of *Puccinia graminis* f. sp. *tritici* indicating a fourth unique resistance gene in PI348598

| | Isolates | | | | | |
|---|---|---|---|---|---|---|
| PI | QCBS | NCCQ | BCBN | HNLQ | RKQS | MBCT |
| 348598 | 0 | 0 | 0 | 0 | *1*[b] | 1 |
| 348448 | 0 | 0 | *1* | 1 | 0 | 0 |
| 348639 | 0 | *1* | 0 | 0 | 1 | 0 |
| 348581 | 0 | 1 | 0 | 0 | 0 | 1 |
| 355625 | 0 | 1 | 1 | 1 | 0 | 0 |
| 348687 | *1* | 0 | 0 | 0 | 0 | 0 |

[a] 0 designates high infection type; 1 designates low infection type.
[b] Italicized numbers denote unique resistance genes.

**Table 5.** Infection type data[a] from a subset of spelt wheat plant introduction lines and isolates of *Puccinia graminis* f. sp. *tritici* illustrating the presence of a fifth unique resistance gene in PI348581[b]

| | Isolates | | | | | |
|---|---|---|---|---|---|---|
| PI | QCBS | NCCQ | BCBN | HNLQ | RKQS | MBCT |
| 348598 | 0 | 0 | 0 | 0 | *1*[c] | 1 |
| 348448 | 0 | 0 | *1* | 1 | 0 | 0 |
| 348639 | 0 | *1* | 0 | 0 | 1 | 0 |
| 348581 | 0 | 1 | 0 | 0 | 0 | 1 |
| 355625 | 0 | 1 | 1 | 1 | 0 | 0 |
| 348687 | *1* | 0 | 0 | 0 | 0 | 0 |

[a] 0 designates high infection type; 1 designates low infection type.
[b] Boxes drawn with the low infection type of PI348581 with isolate MBCT at one corner and a low infection type previously associated with a unique resistance gene at the diagonally opposite corner have a high infection type in at least one other corner, which indicates that the low infection type of PI348581 with isolate MBCT is caused by a unique resistance gene.
[c] Italicized numbers denote unique resistance genes.

*P. g.* f. sp. *tritici* used. Isolate TMRT was virulent on all host entries and thus excluded from Table 7. Therefore, the maximum number of corresponding gene pairs identifiable was 34 (Table 7). There were 28 unique *Sr* genes identified, although others may be present but cannot be identified from among the 222 LIT/HIT patterns of the 578 entries. With isolates QCCQ and HNLQ, no unique *Sr* gene was identified. Only a single *Sr* gene can be postulated with isolates QSHS, RSHS, GLCN, and GDCN, though the possibility exists that each isolate was identifying a different gene. Of the 28 *Sr* genes identified, only *Sr*9f in PI347914 with isolate LBBL, and *Sr*LC postulated in PI348453 with isolate QCCN were the same as those identified previously (no segregation from 85 and 264 $F_2$ plants, respectively, from test crosses [9]). Therefore, a minimum of 26 new *Sr* genes were identified within these spring spelts. None of the designated *Sr* genes (*Sr*9e, *Sr*9f, *Sr*18, *Sr*LC, and *Sr*McN) previously postulated (9) as possibly being present were among the 26 new *Sr* genes present in Table 7.

Some of the PIs may possess only two or three *Sr* genes identifiable with the set of isolates used. For example, PI355564, PI355664, PI355692, PI348687, PI355585, PI348453, and PI355611 each possess a different *Sr* gene and probably a gene in common as indicated by the LIT with isolate LBBL (Table 7). On the other hand, PI348464, PI348673, and PI348742 possess genes for resistance against most of the isolates of *P. g.* f. sp. *tritici* used in this test. These entries could have few highly effective genes in common, or they could each possess several different genes. This may be determined only by crossing these lines to a susceptible line and making a progeny test. Among the designated *Sr* genes proved to be present and postulated to be present, *Sr*9e can occur only in PI348464 and PI348673.

The spelts are a rich source of *Sr* genes. Among 222 LIT/HIT patterns, a minimum of 26 new *Sr* genes were identified, and several more were probably present. Although many of the genes lack sufficient resistance for use singly, in combination some of these genes may provide new useful sources of resistance.

**Table 6.** Infection type data[a] from a subset of spelt wheat plant introduction lines and isolates of *Puccinia graminis* f. sp. *tritici* illustrating all five of the unique resistance genes that can be detected from these infection types with this subset of lines and isolates

| | Isolates | | | | | |
|---|---|---|---|---|---|---|
| PI | QCBS | NCCQ | BCBN | HNLQ | RKQS | MBCT |
| 348598 | 0 | 0 | 0 | 0 | *1*[b] | 1 |
| 348448 | 0 | 0 | *1* | 1 | 0 | 0 |
| 348639 | 0 | *1* | 0 | 0 | 1 | 0 |
| 348581 | 0 | 1 | 0 | 0 | 0 | *1* |
| 355625 | 0 | 1 | 1 | 1 | 0 | 0 |
| 348687 | *1* | 0 | 0 | 0 | 0 | 0 |

[a] 0 designates high infection type; 1 designates low infection type.
[b] Italicized numbers denote unique resistance genes.


LITERATURE CITED

1. Browder, L. E., and Eversmeyer, M. G. 1980. Sorting of *Puccinia recondita:Triticum* infection-type data sets toward the gene-for-gene model. Phytopathology 70:666-670.
2. Dyck, P. L., Samborski, D. J., and Martens, J. W. 1985. Inheritance to leaf rust and stem rust in the wheat cultivar Glenlea. Can. J. Plant Pathol. 7:351-354.
3. Flor, H. H. 1955. Host-parasite interaction in flax rust—Its genetics and other implications.


**Table 7.** High/low infection-type[a] data from *Triticum spelta:Puccinia graminis* f. sp. *tritici* interaction trials arranged in ascending binary number for low infection-type, identifying unique *Sr* genes[b] for resistance to stem rust in hosts using the Loegering and Burton (6) "boxing" method

| | Isolates | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Spelt PI number | DKCS | TMMT | TNMK | TNMH | NMLQ | TMDH | QCBS | NCCQ | QFBS | FCCS | FBBQ | QCCN | BCBN | HNLQ | RTQQ | RKQS | MBCT | PPQQ | HRCS | CCQS | TTQS | BBCS | DBLQ | CBCS | CCCS | BSSS | SSHS | RBHS | SSCN | DLCN | JCCS | BBCS | BBNL |
| 367200 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 347914 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* |
| 348518 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 1 |
| 355611 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 1 |
| 348740 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 348551 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 |
| 348534 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 |
| 355618 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| 348465 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 |
| 348582 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 |
| 348580 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 |
| 348588 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 1 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 348587 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 |
| 348598 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 |
| 348683 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 348448 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| 348453 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 355585 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 349040 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 0 | 1 |
| 348771 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 |
| 348639 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 348581 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 355625 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 348687 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 1 |
| 355692 | 0 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 355664 | 0 | 0 | 0 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 348464 | 0 | 0 | 0 | *1* | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 348673 | 0 | 0 | *1* | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 355564 | 0 | *1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| 348742 | *1* | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

[a] 0 = High infection type; 1 = low infection type.
[b] Italics = unique *Sr* gene.

Phytopathology 45:680-685.
4. Loegering, W. Q. 1968. A second gene for resistance to *Puccinia graminis* f. sp. *tritici* in the Red Egyptian 2D wheat substitution line. Phytopathology 58:584-586.
5. Loegering, W. Q. 1971. Specificity in plant disease. Pages 29-31 in: Biology of Rust Resistance in Forest Trees. R. T. Bingham, R. J. Hoff, and G. I. McDonald, eds. Proc. NATO-IUFRO Adv. Study Inst. U. S. Dep. Agric. For. Serv. Misc. Publ. 1221.
6. Loegering, W. Q., and Burton, C. H. 1974. Computer-generated hypothetical genotypes for reaction and pathogenicity of wheat cultivars and cultures of *Puccinia graminis tritici*. Phytopathology 64:1380-1384.
7. Loegering, W. Q., McIntosh, R. A., and Burton, C. H. 1971. Computer analysis of disease data to derive hypothetical genotypes for reaction of host varieties to pathogens. Can. J. Genet. Cytol. 13:472-478.
8. McVey, D. V. 1989. Verification of infection-type data for identification of genes for resistance to leaf rust in some hard red spring wheat. Crop Sci. 29:304-307.
9. McVey, D. V. 1990. Reaction of 578 spring spelt wheat accessions to 35 races of wheat stem rust. Crop Sci. 30:In press.
10. McVey, D. V., and Hamilton, K. 1985. Stem rust resistance gene from Triumph 64 identified in four other winter wheats. Plant Dis. 69:217-218.
11. McVey, D. V., and Roelfs, A. P. 1975. Postulation of genes for stem rust resistance in the entries of the Fourth International Winter Wheat Performance Nursery. Crop Sci. 15:335-337.
12. Modawi, R. S., Browder, L. E., and Heyene, E. G. 1985. Use of infection-type data to identify genes of low reaction to *Puccinia recondita* in several winter wheats. Crop Sci. 25:9-13.
13. Stakman, E. C., Stewart, D. M., and Loegering, W. Q. 1962. Identification of physiological races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS Bull. E.617. 53 pp.
14. Statler, G. D. 1984. Probable genes for leaf rust resistance in several hard red spring wheats. Crop Sci. 24:883-886.