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FORUM

Proposed System of Nomenclature for Biotypes of Hessian Fly (Diptera: Cecidomyiidae) in North America

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ABSTRACT Twenty genes in wheat, *Triticum spp.*, for resistance to Hessian fly, *Mayetiola destructor* (Say), have been previously designated *H1* to *H20*. The location on wheat chromosomes of some of the genes is known, but several have not yet been assigned to specific chromosomes. Four wheat differential cultivars have been used to identify 16 possible biotypes of Hessian fly; biotypes were designated GP and A–O. If an additional differential host genotype were added, it is apparent that there are not enough letters in the alphabet to designate all of the biotypes. Therefore, a new system of biotype designation is proposed. Three differential cultivars or lines are assigned to a set. Sets are designated A, B, C, and so on. There are eight combinations of resistant and susceptible reactions within a set. These are coded 1 to 8 for each set. Three sets are proposed to begin biotype designation. A biotype avirulent to all differentials in three sets is coded 111. If set C were not used, a zero (untested) replaces the digit. In the above case, the biotype is designated 110. The biotype designation system provides flexibility for the addition of new sets as new genes are identified and for the deletion of sets no longer deemed useful.

KEY WORDS Insecta, *Mayetiola destructor*, host plant resistance, wheat

DAMAGE TO WHEAT by the Hessian fly, *Mayetiola destructor* (Say), may be controlled by breeding resistant cultivars. The Hessian fly population has been able to overcome single genes that condition resistance in wheat in ≈8–10 yr in Indiana (Patterson et al. 1990). Current strategies are to monitor and predict Hessian fly biotype changes, to develop and maintain pure biotypes for research, to locate new genes for resistance from common wheat, *Triticum aestivum* L.; durum wheat, *T. durum* Desfontaines; wild wheats, *Triticum* spp.; and other grass species, and to deploy effective genes for resistance in new cultivars.

The four purposes of this article are (1) to summarize the current status of Hessian fly biotypes and known wheat genes for resistance, (2) to propose a new system of naming biotypes, (3) to select three sets of wheat differentials for identifying biotypes in North America, and (4) to compare the proposed and previous designations for current biotypes.

Genes for Resistance. Twenty genes in wheat that condition resistance to Hessian fly have previously been designated *H1* to *H20* (Table 1). All show dominance or partial dominance for resistance except for one, which is recessive for resistance and is designated *h4*. Four genes have been assigned to linkage blocks on wheat chromosomes by cytogenetic methods. Using monosomic analyses, *H6* was assigned to chromosome 5A (Gallun & Patterson 1977), and *H5* was assigned to chromosome 1A (Roberts & Gallun 1984). *H13* was assigned to chromosome 6DL, 35 ± 8 recombination units from the centromere, using telosomic analysis by Gill et al. (1987). *H20* was assigned to chromosome 2B by aneuploid analysis using 'Langdon' durum wheat D-genome disomic substitution lines (Amri et al. 1990).

Most known genes for resistance to Hessian fly are believed to be located on the A or B genomes based on durum wheat source or durum wheat parentage. Some genes have been assigned to linkage blocks on chromosomes by genetic linkage tests. *H3* is linked to *H6* at 9 recombination units (Patterson & Gallun 1977) and *H3* with H9 at 15.5 ± 4.8 recombination units (Stebbins et al. 1980), with the probable gene order of *H3 H6 H9* on chromosome 5A (Stebbins et al. 1982). *H10* appeared to be on the same chromosome as *H9*, with 36 recombination units between the two, in

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Table 1. Wheat genes conditioning resistance to Hessian fly in the United States

Gene	Source	Reference
H1	Dawson, CI 3342[a]	Cartwright & Wiebe (1936) Noble & Suneson (1943)
H2	Dawson, CI 3342[a]	Cartwright & Wiebe (1936) Noble & Suneson (1943)
H3	Ill, No. 1, W-38 sel., CI 12061[a]	Caldwell et al. (1946)
h4	Java, CI 10051[a]	Suneson & Noble (1950)
H5	Ribeiro, PI 56206-8[a]	Shands & Cartwright (1953)
H6	PI 94587[b]	Caldwell et al. (1946) Allan et al. (1959)
H7	Seneca, CI 12529[a]	Patterson & Gallun (1973) Cebert et al. (1988)
H8	Seneca, CI 12529[a]	Patterson & Gallun (1973) Cebert et al. (1988)
H9	Elva, CI 17714[b]	Carlson et al. (1978) Stebbins et al. (1980)
H10	Elva, CI 17714[b]	Carlson et al. (1978) Stebbins et al. (1980)
H11	PI 94587[b]	Stebbins et al. (1983)
H12	Luso, Port. 3478[a]	Oellermann et al. (1983)
H13	*Triticum tauschii* via HU 2076	Hatchett et al. (1981) Hatchett & Gill (1983) Gill et al. (1987)
H14	ELS 6404-160, CI 1764[b]	Maas et al. (1989)
H15	ELS 6404-160, CI 17647[b]	Maas et al. (1989)
H16	PI 94587[b]	Patterson et al. (1988)
H17	PI 428435[b]	Obanni et al. (1988)
H18	Marquillo, CI 6887[a]	Maas et al. (1987) Obanni et al. (1988)
H19	PI 422297[b]	Obanni et al. (1989)
H20	Jori[b]	Amri et al. (1990

[a] Common wheat.
[b] Durum wheat.

an analysis following transfer of *H9 H9 H10 H10* from the tetraploid to hexaploid wheat (Carlson et al. 1978). *H9* and *H10* were found to be independently inherited in an analysis at the tetraploid level (Stebbins et al. 1982). *H15* was found to be closely associated with *H9* (Maas et al. 1989). *H11* was reported to be linked with *H5* on chromosome 1A with 4.4 ± 1.8% recombination between the two genes (Stebbins et al. 1983). Obanni et al. (1988) reported that *H17* may be located on chromosome 5A because *H17* did not segregate independently from *H9H10* of 'Elva'. Linkages of *H7, H8, H12, H14, H16, H18,* or *H19* with genes in linkage blocks on chromosomes 1A or 5A have not been reported, but all have not been tested. None of the genes discussed above has been reported as having been tested for linkage with *H13* or *H20* on chromosomes 6D and 2B.

Biotypes of Hessian Fly. Biotypes (formerly called races) of Hessian fly in the United States that can arise from mutation or genetic recombination in the Hessian fly (Gallun et al. 1961, Gallun & Patterson 1981) have been designated by capital letters based on their virulence or avirulence on specific host wheat plants. The interaction between the insect and the host wheat plant is very specific. A gene-for-gene relationship between resistance in the wheat plant and avirulence in the Hessian fly has been described (Hatchett & Gallun 1970). This allows biotypes to be defined specifically by their virulence or avirulence on wheat cultivars or lines with specific genes for resistance. Gallun (1977) noted that using four differential cultivars, 16 biotypes (2^4) could be differentiated. Eleven of the biotypes have been identified in the field (Painter 1930, Gallun et al. 1961, Hatchett 1969, Sosa 1981, unpublished data). They designated the biotypes GP and A–O. Twenty genes that condition resistance to Hessian fly have been identified and named. The traditional use of alphabetical letters is inadequate to designate the potential biotypes that may be identified as additional wheat genes for resistance are identified.

Materials and Methods

Proposed Biotype Nomenclature. A system of using host plant sets composed of three differentials is proposed with a digit to indicate the reactions of each host plant set. In concept, this is similar to that proposed for identifying races of *Puccinia recondita* f. sp. *tritici* Roberge ex. Desmazieres (Long & Kolmer 1989). Eight host set

Table 2. Codes for host set reactions to Hessian fly using three differential wheat hosts

Host set reaction code	Host differential[a]		
	First	Second	Third
1	R	R	R
2	R	R	S
3	R	S	R
4	R	S	S
5	S	R	R
6	S	R	S
7	S	S	R
8	S	S	S

[a]Host reaction; R, resistant; S, susceptible.

reactions can occur using a host set of three wheat cultivars or lines (Table 2). Host set reactions are coded from 1 to 8 with 0 (zero) reserved to indicate that the Hessian fly biotype was untested to this set. Sets are designated as set A, set B, etc. With three sets based on available wheat differential genotypes, there would be a three-digit code. A biotype to which all differential host genotypes in the three sets are resistant is designated biotype 111. If the biotype is untested to set C in the above case, the biotype is described as 110. After a number of years, testing certain sets may be meaningless. In such a case, testing to set A may be omitted and the biotype described as 011. This system allows for the addition of sets and for the omission of sets as practicality dictates.

If an incomplete set is used, the set code is replaced by the host plant reactions of the one or two hosts used. The unused host reaction is designated as a dash (–). Thus if only the first two differentials are used in set C of the above example for three sets, the code is written 11(RR–).

Choosing Differential Hosts. The differential host cultivars or lines should ideally have a single resistant gene pair, but there are exceptions. 'Knox 62' has been used as a differential host for gene pair *H6H6*, but 'Knox 62' must have additional resistance gene(s). 'Knox 62' and 'Caldwell' both have gene pair *H6H6*, but 'Knox 62' is resistant to biotype E and 'Caldwell' is not (Hatchett 1969, Patterson et al. 1982). Cultivar 'Seneca' (*H7H7H8H8*) was used as a differential genotype. Because the resistance of *H7H7* or *H8H8* singly is not strongly expressed (Cebert et al. 1988), 'Seneca' is still the best choice for the differential cultivar representing *H7* and *H8*. There are some important reasons for continuing to use some historical cultivar as differentials based on previous biotype designation to relate the old and new systems of biotype designations.

The differential cultivars should represent the resistant wheat genes previously deployed, those genes currently deployed, those genes expected to be deployed soon, and the additional genes recently identified. We suggest they be assigned to sets in the above order. The genes may be used in differential host lines in either winter or spring types for the identification of biotypes from seedling responses. If the sets are also to be used for biotype analyses with adult plants as in the Uniform Hessian Fly Nursery, coordinated by personnel of the USDA–ARS Small Grain Insect Control project at Purdue University, then the differential cultivars or lines should be of suitable growth habit and hardiness.

Results and Discussion

Proposed Differential Sets. Nine cultivars or lines with specific genes for resistance were assigned to three differential sets (Table 3). Set A contains three of the four cultivars used previously in identifying biotypes. Set B contains 'Abe' (*H5H5*), also a differential cultivar used previously, and two new differential genotypes possessing genes expected to be deployed soon in new cultivars. Set C contains 'Marquillo', with gene *H18* previously deployed in the hard red winter wheat region of USA, and two durum lines with gene *H14* or *H16*. The latter genes are being used in the wheat breeding program at Purdue University. Additional genes for resistance can be represented in future differential sets as their deployment is anticipated in new cultivars. The need for new sets, appropriate differential cultivars, and the deletion of old sets might best be decided in working group meetings of personnel involved with biotype determination or deployment of genes for resistance in cultivars, or both. The discontinuation of certain sets may be decided also by the specific objectives of a researcher. Seed stocks with single genes for resistance should be developed and increased to sufficient amounts to serve as differential lines.

Seedlings of the three differential genotypes in a set and a universal susceptible cultivar can be

Table 3. Proposed sets for identifying biotypes of Hessian fly

Set	Differential cultivar or line[a]		
	First	Second	Third
A	Seneca (*H7H7H8H8*)	Monon (*H3H3*)	Caldwell (*H6H6*)
B	Abe (*H5H5*)	Ella (*H9H9*)	IN85141 (*H13H13*)
C	Marquillo (*H18H18*)	IN80601 (*H14H14*)	IN80164 (*H16H16*)

[a]Spring durum lines: IN80601 and IN80164, Purdue University; IN85141 common winter wheat line, Purdue University.

Table 4. Comparison of proposed and former methods of Hessian fly biotype designations[a]

Biotype, proposed designation	Set A			Set B			Set C			Biotype, former designation
	H7H7H8H8 Seneca	*H3H3* Monon	*H6H6* Caldwell	*H5H5* Abe	*H9H9* Ella	*H13H13* IN85141	*H18H18* Mq1	*H14H14* IN80601	*H16H16* IN80164	
1(R--)(R--)	R	R	R	R	—	—	R	—	—	GP
5(R--)(R--)	S	R	R	R	—	—	R	—	—	A
711	S	S	R	R	R	R	R	R	R	B
631	S	R	S	R	S	R	R	R	R	C
811	S	S	S	R	R	R	R	R	R	D
311	R	S	R	R	R	R	R	R	R	E
2(R--)0	R	R	S	R	—	—	—	—	—	F
4(R--)0	R	S	S	R	—	—	—	—	—	G
1(S--)0	R	R	R	S	—	—	—	—	—	H
5(S--)0	S	R	R	S	—	—	—	—	—	I
7(S--)0	S	S	R	S	—	—	—	—	—	J
6(S--)0	S	R	S	S	—	—	—	—	—	K
851	S	S	S	S	R	R	R	R	R	L
3(S--)0	R	S	R	S	—	—	—	—	—	M
2(S--)0	R	R	S	S	—	—	—	—	—	N
4(S--)0	R	S	S	S	—	—	—	—	—	O

[a] Differential cultivar reactions to former biotype designations are from Gallun (1977). Only the biotypes that are maintained in our laboratory have been tested to all three sets, A, B, and C. Host reaction: R, resistant; S, susceptible.

grown in a small plastic pot containing soil and tested in a greenhouse (Gallun et al. 1961). The common wheat cultivars Turkey, Blueboy, and Newton, and the durum germplasm line D6647 have been used as susceptible checks. Genetic and cytogenetic analyses help assure that a resistance type is not duplicated in differential cultivars or lines.

Biotype Designation Comparisons. The former and proposed biotype comparisons can be made using pure biotypes maintained in the greenhouse and growth chambers at Purdue University (Table 4). Biotypes B, C, D, E, and L were available for making comparisons of the two methods of biotype designation. Biotype A, used earlier, is no longer maintained. Biotype J has been identified, but a pure biotype has not been developed yet. As shown in Table 4, previously described biotypes B, C, D, E and L (right column) have been tested by us to all differential genotypes of the proposed three new sets and can be assigned complete new three digit codes (column 1). Former biotypes GP and A have been tested previously to set A and the first differential in each of sets B and C and so have the first digit code and incomplete designations for sets B and C. The remaining former biotypes (F, G, H, I, J, K, M, N, O) have been tested to set A differentials and the first differential in set B but are untested to set C. They are designated with set A code, incomplete set B code, and untested set C code. For example, the code for previously designated biotype F is designated 2(R--)0 in the proposed new system.

Advantages of using digits rather than alphabetical letters for designating biotypes are that the use of digits avoids confusion with the past system of designation that used letters. Single digits will suffice if sets are limited to three differential genotypes, and workers will be able to associate a digit with a set reaction type readily. The proposed system allows for the addition of sets, the deletion of sets, and the use of incomplete sets. Biotype designations from incomplete sets are of less value than those from complete sets, but some data from incomplete sets now exist and are of value. For example, reactions of 'Abe' in set B and 'Marquillo' in set C have been published for several biotypes.

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