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Aller au sommaire du numéro

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Résumé de l'article

La mouche de Hesse est un important ravageur de blé (*Triticum spp.*) et le biotype L de cette mouche est reconnu comme le plus virulent des biotypes connus. L'héritabilité de la résistance au biotype L de la mouche de Hesse a été étudiée à l'aide de croisements entre, d'une part, une lignée résistante de *Triticum monococcum* et, d'autre part, deux lignées sensibles de T. monococcum et une lignée sensible de *T. boeoticum*, tous des blés diploïdes. Les familles de plante F2 ou issues de rétrocroisements ont été évaluées au stade de semis par leur réaction à la mouche de Hesse et les ratios de ségrégation génétique des familles résistantes ou ségréguées par rapport aux familles sensibles ont été analysés par des tests d'ajustement du chi-carré. Il a été découvert que l'héritabilité est simple et sous le contrôle d'un ou deux gènes. Ceci est la première mention de l'héritabilité de la résistance à la mouche de Hesse chez les blés diploïdes de génome A et son contrôle génétique simple suggère la possibilité de transférer ce caractère aux blés cultivés.

Genetics of resistance to Hessian fly (*Mayetiola destructor*) [Diptera : Cecidomyiidae] biotype L in diploid wheats

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Hessian fly (*Mayetiola destructor*) is a serious pest of wheat (*Triticum* spp.) and of the reported biotypes of Hessian fly, biotype L is described as the most virulent. Inheritance of resistance to Hessian fly biotype L was investigated in crosses of a resistant accession of *Triticum monococcum*, and two susceptible accessions of *T. monococcum* and one susceptible accession of *T. boeoticum*, all diploid wheats. F2 and testcross (backcross) families were classified for reaction to Hessian fly in the seedling stage and analysed by Chi-square goodness-of-fit tests for genetic segregation ratios of resistant or segregating families to susceptible families. Resistance was found to be simply inherited, controlled by one or two genes. This is the first report on the inheritance of resistance to Hessian fly in A-genome diploid wheats, and simple genetic control indicates possibility of transfer of this trait to cultivated wheats.

[Génétique de la résistance au biotype L de la mouche de Hesse (*Mayetiola destructor*) [Diptera : Cecidomyiidae] chez les blés diploïdes]

La mouche de Hesse est un important ravageur de blé (*Triticum* spp.) et le biotype L de cette mouche est reconnu comme le plus virulent des biotypes connus. L'héritabilité de la résistance au biotype L de la mouche de Hesse a été étudiée à l'aide de croisements entre, d'une part, une lignée résistante de *Triticum monococcum* et, d'autre part, deux lignées sensibles de *T. monococcum* et une lignée sensible de *T. boeoticum*, tous des blés diploïdes. Les familles de plante F2 ou issues de rétrocroisements ont été évaluées au stade de semis par leur réaction à la mouche de Hesse et les ratios de ségrégation génétique des familles résistantes ou ségréguées par rapport aux familles sensibles ont été analysés par des tests d'ajustement du chi-carré. Il a été découvert que l'héritabilité est simple et sous le contrôle d'un ou deux gènes. Ceci est la première mention de l'héritabilité de la résistance à la mouche de Hesse chez les blés diploïdes de génome A et son contrôle génétique simple suggère la possibilité de transférer ce caractère aux blés cultivés.

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INTRODUCTION

Hessian fly (*Mayetiola destructor* Say) [Diptera : Cecidomyiidae] is a serious pest of wheat (*Triticum* spp.). Damage to wheat by Hessian fly is most efficiently controlled by host plant resistance. Of the various biotypes (genotypes) of the fly identified, biotype L is the most virulent (Amri *et al.* 1990; Obanni *et al.* 1989; Sosa 1981). Genes that provide resistance to biotype L include H9, H10, H12, H13, H14, H16, H17, H18 and H19 (Maas *et al.* 1989; Patterson *et al.* 1988; Ratcliffe *et al.* 1994, 1996). Recently, resistance to biotype L has also been reported in rye (*Secale cereal* L.) and wheat-rye translocations (Hatchett *et al.* 1993).

Studies have been conducted on the inheritance of resistance to Hessian fly in tetraploid wheat, hexaploid wheat and *Aegilops squarrosa* L. (Hatchett and Gill 1983; Maas *et al.* 1987; Obanni *et al.* 1989; Oellermann *et al.* 1983; Patterson and Gallun 1973; Stebbins *et al.* 1983). These studies showed that resistance to individual biotypes of Hessian fly is generally conditioned by a single dominant or partially dominant wheat gene. No such studies have been done on A-genome diploid wheats.

Diploid wheats, *T. monococcum* L. and *T. boeoticum* Boiss em. Schiem., are the A-genome progenitors of tetraploid and hexaploid wheats. The A genomes of the tetraploid and hexaploid wheats have been rich sources of genes for resistance to Hessian fly. Of the 27 genes that so far have been identified, 20 have been assigned to chromosomes in hexaploid and tetraploid wheats by monosomic and/or linkage studies. Of these 20, 12 (H3, H5, H6, H9, H10, H11, H12, H15, H16, H17, H25 and H27) have been found to be on A-genome chromosomes (Gallun and Patterson 1977; Ohm *et al.* 1995, 1997; Patterson and Gallun 1977; Roberts and Gallun 1984; Stebbins *et al.* 1980, 1983). The A genome of diploid wheats was thus considered worth searching for additional genes for resistance to Hessian fly. The potential value of a new source of resistance may be estimated from its reaction to the more virulent biotypes of Hessian fly and an analysis of the number of genes involved in resistance can be made at the diploid level.

Of the 38 accessions of diploid wheats evaluated for reaction to Hessian fly biotype L by Sharma *et al.* (1992), three accessions of *Triticum monococcum*, G1471, G1560 (PI 191146) and G3304 (PI 221415), were found resistant. The remaining were either susceptible or heterogeneous. The objective of the present study was to determine the number of genes for resistance to Hessian fly biotype L in the *T. monococcum* accession G1471.

MATERIALS AND METHODS

Resistant and susceptible accessions of diploid wheats were selected from those reported by Sharma *et al.* (1992). The resistant accession was G1471 of primitive diploid wheat *T. monococcum*. The susceptible accessions were G3312 and G863 of *T. monococcum*, and G2750 of wild diploid wheat *T. boeoticum*. These two taxa are considered to be one and the same species and produce self-fertile hybrids (Sharma and Waines 1994).

The resistant accession was crossed to the susceptible ones to obtain F1 hybrid seed in the three crosses. The resulting F1 plants were either allowed to self-pollinate to obtain F2 seed or were backcrossed to the susceptible parent to obtain testcross-1 (TC1) seed. F2 and TC1 families were obtained by self-pollination of F2 and TC1 plants, respectively. These families were tested against Hessian fly biotype L.

Seeds of F2 and TC1 families were grown and tested in standard greenhouse flats, all at the same time under the same conditions. Hexaploid wheat cv. Newton and germplasm line IN861A1-8-2 (H13H13) were used as susceptible and resistant checks, respectively, in each flat. The families were randomized within the flats. The checks were grown in the two center rows in each flat. The method of infestation and evaluation was similar to that of Cartwright and LaHue (1944) as used by

Sharma *et al.* (1992). Genotypes of individual F2 and TC1 plants were determined by reaction of 5-30 plants of each family to Hessian fly infestation, *i.e.* families were classified either as resistant, segregating or susceptible, and the ratio of segregating/resistant families to fully susceptible families was used to estimate the number of genes conditioning resistance from Chi-square tests (Steel and Torrie 1980).

RESULTS AND DISCUSSION

The checks reacted as expected : 99.6% of the 'Newton' plants were susceptible and 99.2% of the 'IN861A1-8-2' plants were resistant. Eighty F2 families, 1515 plants total, were classified for reaction to biotype L in the cross G3312 x G1471 (Table 1). The segregation of F2 families fitted a 3:1 ratio of resistant and segregating families to susceptible families as expected for resistance controlled by a single dominant or partially dominant gene. In the cross of G2750 x G1471, 78 F2 families, 1776 plants total, segregated with a satisfactory fit to a 3:1 ratio of resistant and segregating families to susceptible families indicating a single dominant or partially dominant gene for resistance. In the testcross, (G863 x G1471) x G863, 67 TC1 families, 1705 plants total, fitted a 3:1 ratio indicating that two genes condition resistance to biotype L of Hessian fly (Table 1).

As far as we are aware, this is the first report on the inheritance of resistance to Hessian fly in A-genome diploid wheats. The three crosses studied involved the same resistant accession and three susceptible accessions. The resistance was controlled by a single gene or two genes. The difference could be due to some lack of genetic uniformity within the genotypes used. As another possibility, since to produce the backcross from G863 x G1471 F1 hybrid, the hybrid was used as male, the gamete carrying resistance from G1471 might have been more competitive because of genetic reasons, or because of chromosome structural advantage. Either situation might explain an excess of resistant plants in the backcross, even though only one factor for resistance might actually be involved. All the three crosses qualified segregation ratios (13:3 in F2 and 3:1 in TC1) for two gene control, one dominant and the other additive (Table 1). However, considering the genotype of G1471 as R1R1r2r2, where R1 is dominant and r2 additive, it has to be assumed that in the first two

Table 1. Reaction of F2 families, and TC1 families to Hessian fly biotype L

Checks or crosses	Generation	Reaction to Hessian fly[a]		Ratio tested	Chi-square	
		R or H (No. of families)	S (No. of families)		Value	Probability
Checks :						
Newton	-	2	506	-	-	-
IN861A1-8-2	-	597	5	-	-	-
Crosses :						
G3312 x G1471	F2 families	66	14	15:1	25.81	< 0.01
				3:1	2.40	0.10-0.20
				13:3	0.08	0.70-0.80
G2750 x G1471	F2 families	65	13	15:1	14.44	< 0.01
				3:1	2.89	0.05-0.10
				13:3	0.22	0.50-0.70
(G863 x G1471) x G863	TC1 families	52	15	3:1	0.24	0.50-0.70
				1:1	20.44	< 0.01

[a] R : resistant; H : segregating; S : susceptible.

crosses genotype --r2- was susceptible, while in the third cross it was resistant. Whether this difference was due to different insect pressure is hard to say when the testing was done at the same time under the same conditions. Furthermore, genotypes containing R1R1 should have behaved homozygous regardless whether they were heterozygous or not for r2 but the number of homozygous resistant families was very low (2, 2, 0, respectively, in the three crosses). Although, these explanations are speculative, the study has satisfactorily shown that the genetics of resistance in *T. monococcum* is simple.

Resistant genes from *T. monococcum* will have to be transferred to tetraploid or hexaploid wheats in order to determine if the genes from diploid wheat are different from known genes for resistance to Hessian fly. If these genes are new, it should be determined whether there is adequate gene expression for their use in commercial wheat cultivars. Provided there is adequate gene expression in the tetraploid (AABB) or hexaploid (AABBDD) background, the gene or genes identified here are simple elements that would be easy to add to the collection of genes useful against the Hessian fly of wheat, since they belong to A genome. This being the first study on the genetic control of resistance to Hessian fly in *T. monococcum*, further confirmation of the results by molecular methods would be the next step. Linkages to DNA markers may also be helpful in determining if the genes for resistance from the diploid wheat are unique from known genes in tetraploid or hexaploid wheats. Finally, improved methods must be devised for the transfer and expression of genes from diploid wheats to hexaploid wheats (Dyck and Kerber 1985; Sharma 1995; Sharma and Gill 1983).

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