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Evaluation of population of Hessian fly *Mayetiola destructor* (Say) in the South-West of Spain

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SUMMARY – The aim of the present study was to determine the biotype of Hessian fly which is prevalent in the SW of Spain, and to study its response to different resistance genes *H*. The four differential cultivars 'Monon', 'Abe', 'Caldwel' and 'Seneca' were resistant at both field and greenhouse conditions, although some variability in infestation level was detected across years. These results suggest that the prevalent biotype at the SW of Spain is 'GP'. However, we cannot discard the presence of other biotypes. Cultivars of the "Uniform Hessian fly Nursery" (UHFN) were evaluated at the same conditions. Cultivars with *H3*, *H5*, *H6*, *H11*, *H13, H21* or *H24* gene were resistant, while those with *H9, H10* or *H12* were moderately resistant to this population. Our results are in agreement with studies of Hessian fly populations from North Africa.

Introduction

Hessian fly (Hf), *Mayetiola destructor* (Say), is a major pest of wheat worldwide. It is also an endemic pest in the SW of Spain, and two generations per year occur in infested fields in this area (Delibes *et al.*, 1997). The most practical control method for Hessian fly is the use of resistant cultivars. A gene-for-gene relationship has been demonstrated for host resistance and avirulence in the insect (Hatchett and Gallum, 1970). Resistance in wheat to *M. destructor* attack is conditioned mostly by dominant alleles at single loci (*H* genes). Virulence against each resistance wheat allele is determined by recessive alleles at a single locus in *M. destructor* (vH^v genes). To date, 33 resistance genes have been identified (*H1-H32* and *Hdic*) (Liu *et al.*, 2005). Sixteen possible biotypes of *M. destructor* have been identified by their response (virulence or avirulence) to four common wheat cultivars carrying *H3, H5, H6* or *H7H8* resistance genes, biotypes were designated Great Plains 'GP' and A-O (Gallum, 1977).

Insect biotypes occur in nature as results of selection from the population in response to exposure to resistant cultivars. However, Hessian fly virulence has been confirmed to some resistance genes that have not been deployed in wheat cultivars in USA (Ratcliffe *et al.*, 1994, 2000). Therefore, it is necessary to test the available genes against as many biotypes and current populations of Hessian fly as possible. This would prevent the release of wheat cultivars with ineffective sources of resistance.

The main objective of the research was to determine the biotype of Hessian fly prevalent in the south-west of Spain, and to test the effectiveness of wheat cultivars carrying different *H* genes (*H3*, *H5* to *H15, H18*, *H21 and H24*) from UHFN collection against this population.

Material and methods

In order to determine the biotype of Hessian fly, the four differential cultivars: 'Monon' *H3*, 'Abe' *H5*, 'Caldwell' *H6*, and 'Seneca' *H7H8*, were evaluated for resistance (4 consecutive years) at Azuaga (Badajoz) (38°15'N; 5°40'W) and, t he last season, also at La Granjuela (Córdoba) (38°22'N; 5°21'W) locations. In addition, they were evaluated for two years in greenhouse with controlled conditions. Besides, we have screened at the same conditions a series of wheat cultivars carrying *H* genes from the "Uniform Hessian fly Nursery" (UHFN). This collection was supplied by Dr. H.E. Bockelman and F. Maas from the National Small Grains Collection of USDA-ARS. Wheat cultivars 'Newton' and 'Astral' were used as susceptible controls.

Each experiment was completely randomized with three replications and thirty seed were planted per cultivar and test. In greenhouse, plants were infested with a fly population collected on susceptible cultivar 'Astral' during previous season at Azuaga, and stored in the flaxseed stage at 5ºC. The infestation was carried out according to Cartwright and LaHue (1944). Plants were examined for presence of puparia as described by Martín-Sánchez *et al.* (2003). Data for each cultivar were calculated as average of number of puparia per tiller.

Results and discussion

The four differential cultivars 'Monon' *H3*, 'Abe' *H5*, 'Caldwell' *H6*, and 'Seneca' *H7H8,* were resistant to Hessian fly population from the SW of Spain at all the conditions evaluated (Fig. 1). Differences in field tests observed across years could be due to environmental fluctuations, such as temperature, rainfall and humidity, insect population density or, if biotypic variation exists, to changes in their frequencies. These results suggest that biotype 'GP', no virulent to any of these resistance genes, could be the prevalent biotype at the SW of Spain. However we do not discard the presence of other biotypes. In the Washington State of USA, were Hessian fly resistance genes are not yet deployed, biotype 'GP' is also the prevalent, but it coexists with another biotypes (Ratcliffe *et al*., 2000). Thereby, populations of flies are heterogeneous in biotype composition, but a single virulent biotype is usually prevalent, and corresponds with the predominant resistance genes deployed in the region (Ratcliffe *et al*., 1996, 2000; Naber *et al.*, 2003; Bouktila *et al.*, 2005).

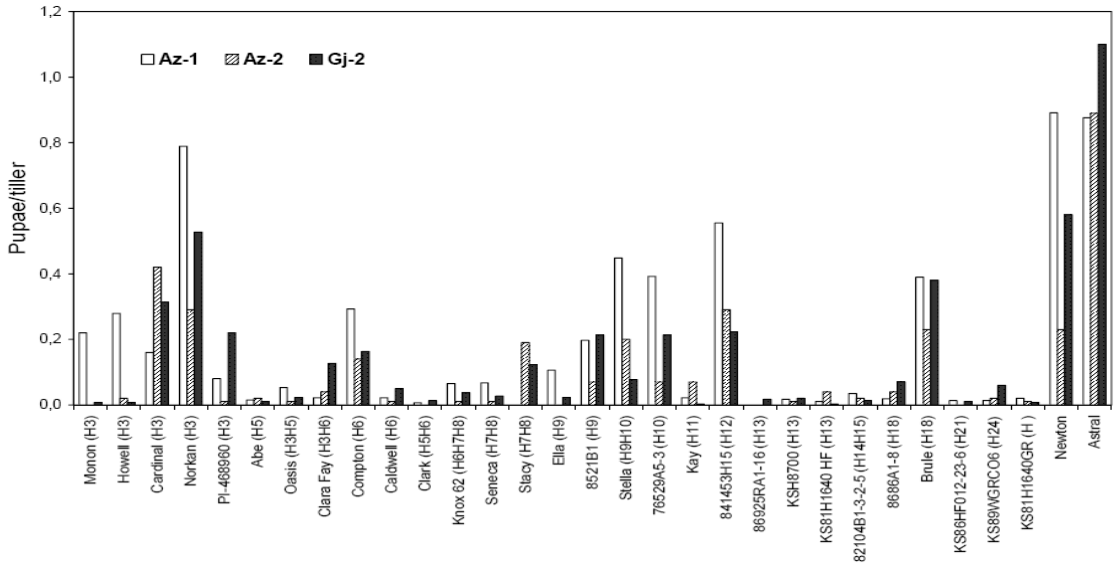

Fig. 1. Response of wheat lines and cultivars from the UHFN collection to Hessian fly population from SW of Spain. *T. aestivum cv* 'Astral' was used as susceptible control. Each bar represents the average of a minimum 100 tillers per stock. Data from two years, 1 and 2. Az: Azuaga and Gj: La Granjuela locations.

The level of virulence to *H5, H11, H13, H21* and *H24* genes was low at all conditions. *H3, H6*, *H7H8* and *H18* genes showed different levels of resistance against Hessian fly population, depending on the genetic background in which they were expressed as previously reported Amri *et al.* (1992) and El Bouhssini *et al.* (1992a, 1999). Most of the wheat carrying *H9, H10* or *H12* genes showed higher levels of infestation. Both *H14* and *H15* genes are found in the same line (82104B1-3-2-5); hence, in the reported conditions it was not possible to determine whether one or both of them were conferring the observed resistance against Hessian fly. Cultivar response was similar in both greenhouse and field conditions, but at the former the infestation level were higher, especially cultivars carrying *H9* and *H10* resistance gene (data not shown). The Spearman rank correlation analysis indicated a 0.88 significant correlation between results obtained from field and greenhouse test. In field conditions, the widely grown cultivar 'Astral' showed the highest infestation level as

reported Amri *et al.* (1992). In greenhouse conditions, no differences were observed between susceptible checks.

Most of these genes (*H9* to *H24*) have been tested previously against biotypes A, B, C, D, E, L and GP in greenhouse conditions. All of them are effective except *H9, H10 and H12* genes, which present susceptibility or weak resistance to biotype C; *H12* gene also presents weak resistance to biotype E; and *H11* and *H15* genes to biotype L. Several of them are also affected by high temperatures (Amri *et al.*, 1992; El Bouhssini *et al.*, 1999). Besides, they are tested against different Hessian fly populations throughout main areas where flies are a pest. Our results are according to studies of Hessian fly populations in North Africa. Cultivars with *H5, H7H8, H11* and *H14H15 genes* and genes from relatives of wheat (*S. cereale* and *T. tauschii*) were effective against Hessian fly populations, and cultivars with *H9*, *H10* and *H12* genes were only moderately resistant (Amri *et al.*, 1992; El Bouhssini *et al.*, 1992a,b, 1996; Naber *et al.*, 2003; Bouktila *et al*., 2005). In populations from USA, the *H9, H10* and *H12* genes also showed weak resistance to fly populations in which biotype C are not present (Ratcliffe *et al*., 1996).

In this study, the importance of wheat genetic background in the expression of Hessian fly resistance genes has been reflected, and thereby the necessity of no separate Hessian fly gene resistance from wheat genetic background. Virulence to *H3, H6, H9, H10* and *H12 g*enes was present in Hessian fly population from Azuaga and so the use of these resistance genes in wheat cultivars adapted to this region may be limited. Resistant genes from wild relatives are effective but, because of potential rapid change in Hessian fly populations, it is important to continue studying virulence in the field. This would help develop appropriate gene deployment strategies for Hessian fly in Spain.

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