

Inheritance of Resistance to Powdery Mildew (*Erysiphe graminis* f. sp. *hordei*) in Barley

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ABSTRACT

Two barley (*Hordeum vulgare* L.) genotypes, Radical and Cwb, with good to moderate levels of resistance to powdery mildew were crossed with a highly susceptible cultivar (Afzal) to determine the genetics of resistance. The parents, F₁, F₂ and F₃ generations of each of the two crosses, were evaluated for powdery mildew resistance in the glasshouse and field at the College of Agriculture in Karaj during 2000. The χ^2 analysis of the segregating ratios in the F₃ generations indicated that the resistance was controlled by one gene at seedling stage and by two or three genes at adult plant stage in Cwb and Radical, respectively. Radical showed a higher level of resistance than the Cwb, therefore, it is a better source of resistance to powdery mildew.

Keywords: Barley, Genetics, Inheritance, Powdery mildew, Resistance,

INTRODUCTION

Powdery mildew caused by *Erysiphe graminis* f. sp. *hordei* is one of the most important diseases in barley particularly in northern parts of Iran. Based on the gene-for-gene hypothesis of Flohr (1955), which was confirmed for powdery mildew of barley by Moseman (1959), many race-specific powdery mildew resistance genes from different origins have been recognized in barley (Moseman, 1959; Wiberg, 1974; Gorge *et al.*, 1993; Giese *et al.*, 1993; Jorgensen 1994; Schonfeld *et al.*, 1996), but most of them have already been overcome by new virulent strains (Jahoor and Fischbeck, 1993). The most economical and environmentally safe method for controlling powdery mildew is by growing resistant cultivars. Resistant lines have infection types varying from complete to moderate resistance depending on which mildew culture is inoculated, indicating that the resistance genes involved has a race-specific character (Jensen *et al.*, 1982; Mastebrook *et al.*,

1995). Most studies reported that resistance is controlled by one or two dominant genes, depending on mildew culture (Jensen *et al.*, 1982; Jahoor and Fischbeck 1993). It is, therefore, important to collect more information on the genetics of resistance to this disease particularly using diverse germplasm. The present study was performed to determine the mode of inheritance of resistance to powdery mildew in two barley genotypes

MATERIAL AND METHODS

Two barley genotypes Radical and Cwb from Russia and England, respectively, were selected for their resistance to powdery mildew over several years and locations in the Seed and Plant Improvement Institute at Karaj, along with a susceptible cultivar from Iran, Afzal, which is very tolerant to salinity and drought stresses.

In order to test the mode of inheritance, two resistant genotypes were crossed to the susceptible cultivar and the F₂ and F₃ generations were produced for each cross. The

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F1 plants were harvested in bulk and their seeds were space planted in the College of Agricultural Experimental Station at Karaj during the 1999 season to produce F2 seeds. The F3 lines were obtained by harvesting approximately 90 single plants from each F2 population. This research was done in two separate experiments and each experiment was planted with five generations namely P1, P2, F1, P2 and F3 in glasshouse and field.

Experiment I

The P1, P2, F1, F2 and F3 generations of each cross were grown in a glasshouse and the seedlings were inoculated with conidiospores of a mildew culture, named Gorgan, by shaking sporulating plants above them when the first leaf was fully expanded. The powdery mildew employed isolate originated from a single spore culture and shows avirulence to Mla8, Mla6, Mla4, Mlp and mlo5 but virulence to Mla7, Mla9, Mla10, Mlk and Mlg resistance genes. During the periods of incubation a temperature of 18-20°C was maintained. Ten days after inoculation, each primary leaf was evaluated for its mildew reaction using the 0-9 scale of Mastebroek *et al.* (1995), where 0 and 9 were completely resistant and fully susceptible respectively. Plants with an infection type (IT) of more than 6 were regarded as susceptible, while those with lower than 6

were considered resistant.

Experiment II

The five generations were planted in a randomized complete block design with three replications and each replication consisted of one row of P1, P2 and F1, 10 rows of F2 and 30 rows of F3 generations. Field rows consisted of 1-metre rows seeded 15 cm apart with 50cm between rows. The powdery mildew epidemic was initiated by inoculating plants of Afzal, planted among each of the 10 rows at booting stage. The average disease severity was recorded according to a modified Cobb scale (Peterson *et al.* 1948), when the susceptible cultivar had reached 90 to 100 % disease severity.

RESULTS AND DISCUSSION

The two resistant genotypes, Radical and Cwb, showed a powdery mildew infection type of 0 to 1 and 4 to 5, and a disease severity of 1 and 10, respectively. In contrast, there were infection types and a disease severity of 9 and 100, respectively, for the susceptible cultivar Afzal, (Table 1).

The cross of Radical×Afzal, showed complete dominance resistance at seedling and adult plant stages, as the infection type and disease severity of the F1 plants were the same as resistant parent. The reaction of the

Table 1. Seedling infection type(IT) and disease severity assessment for barley genotypes and crosses(F1s) in glasshouse and field, respectively.

Genotype and Cross	Seedling IT ^a	Disease severity ^b
Radical	0 to 1	1
Cwb	4 to 5	10
Afzal	9	100
Radical×Afzal (F1)	0 to 1	2
Cwb×Afzal(F1)	7 to 8	10

^a ITs are based on a 0 to 9 Mastebroek (1995) where: 0= no symptoms visible;1= distinct necrosis without visible mycelium; 4= distinct necrosis with moderate sporulation; 5=moderate necrosis with moderate sporulation;7=weak necrosis and/or moderate chlorosis with heavy sporulation; 8=weak chlorosis with heavy sporulation; and 9=no resistance reactions, abundant sporulation.

^bDisease severities are based on the modified Cobb scale(19).

Table 2. The χ^2 values for the segregation ratio of F3 lines from crosses between the susceptible genotype, Afzal, and the two resistant genotypes, Radical and Cwb, in glasshouse and field.

Cross	Number of F3 lines			Expecte ratio	X ²
	HR ^a	Seg ^b	HS ^c		
Glasshouse:					
Radical×Afzal	22	44	24	1:2:1	0.13 ^{ns}
Cwb×Afzal	19	48	23	1:2:1	0.48 ^{ns}
Field					
Radical×Afzal	83	5	2	59:4:1	0.081 ^{ns}
Cwb×Afzal	56	28	6	10:5:1	0.026 ^{ns}

^a Homozygous resistant,^b Segregation for resistance^c Homozygous susceptible

ns: Not significant

F1 plants from Cwb×Afzal cross indicated moderate susceptibility at seedling stage, as the infection level was closer to the susceptible parent than to resistant one, whereas it showed moderate resistance at adult plant stage (Table 1).

The F3 data were used to estimate the number of loci controlling resistance, since it provided a better estimate than the F2 data. Tests of F3 plants at seedling stage for each cross showed a good fit of ratio 1 resistance: 2 segregating: 1 susceptible, indicating that resistance in both crosses was controlled by a single dominant gene. However, at adult stage and taking into consideration either homozygous or segregating as resistance (Singh *et al.*, 1995), the F3 lines from Radical×Afzal fitted a 63:1 ratio and these of Cwb×Afzal cross fitted a 15:1 ratio. These results indicated that resistance at adult plant stage in Radical was controlled by three dominant genes and in Cwb by two dominant genes. Thus, Radical should have a greater potential than Cwb in improving powdery mildew resistance in cultivated barley.

The results of this study are in agreement with the findings of Jensen *et al.* (1982); Jahoor and Fischbeck (1993); and Mastebroek and Balkema-boomstra (1995), for the number for resistance genes to powdery mildew in populations of wild barley (*Hordeum spontaneum*) from different origins. In a

previous study, Schonfeld *et al.* (1996) reported a recessive and semi-dominant mode of inheritance in segregating F2 populations of barley lines derived from crosses with wild barley.

Jahoor and Fischbeck (1993) suggested increasing the efficiency in breeding for disease resistance by increasing different resistant genes in the same breeding cycle. However, the identification of the genes which are present in a new breeding line or cultivar is difficult using the traditional method based upon differentiation of reaction spectra according to Flor's gene-for-gene hypothesis (Jeger and Viljanen-Rollinson, 2001). This difficulty may be overcome if closely-linked molecular markers become available. In recent years, a number of gene loci for powdery mildew resistance in barley have been mapped using molecular markers (Schuller *et al.*, 1992; Schonfeld *et al.*, 1996; Buschges *et al.*, 1997; Lahaye *et al.*, 1998; Schwarz *et al.*, 1999; Wei *et al.*, 1999; Kurth *et al.*, 2001).

The two resistance genotypes, Radical and Cwb, are suitable sources of powdery mildew resistance for localization of resistance genes at seedling and adult plant stages by molecular markers and can be used for the pyramiding of different resistance genes in future barley breeding.

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توراث مقاومت به سفیدک سطحی در جو

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چکیده

به منظور تعیین ژنتیک مقاومت به سفیدک سطحی در جو، دو ژنوتیپ مقاوم با یک وارسته حساس (افضل) تلاقی داده شدند. واکنش والدین و نسلهای F1, F2, F3 حاصل از دو تلاقی نسبت به ایزوله سفیدک سطحی در شرایط گلخانه و مزرعه دانشکده کشاورزی کرج در سال ۱۳۷۹ مورد ارزیابی قرار گرفتند. تجزیه کای اسکور برای نسبتهای تفرق یافته در نسل F3 ی هر دو تلاقی مشخص نمود که مقاومت در مرحله گیاهچه با یک ژن کنترل می شود. در صورتیکه در مرحله گیاه بالغ، مقاومت در ژنوتیپ Cwb با دو ژن در ژنوتیپ Radical با سه ژن کنترل می گردد. از آنجایی که ژنوتیپ Radical علاوه بر داشتن ژنهای مقاوم بیشتر (در مرحله گیاه بالغ) دارای سطح مقاومت زیادتری نیز در مرحله گیاهچه می باشد، از این رو میتوان از آن به عنوان منبع بهتری از مقاومت به سفیدک سطحی در برنامه های اصلاحی در آینده استفاده نمود.