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Inheritance of Russian wheat aphid resistance in Iranian bread wheat cultivar 'Azadi'

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ABSTRACT

The Russian wheat aphid (RWA), *Diuraphis noxia* (Mordvilko), is a major pest of cereal crops in many areas of the world, causing serious reduction in grain yield in wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.). Incorporating genetic resistance to *D. noxia* into wheat cultivars is paramount to effectively reduce damage inflicted by this pest. The availability of more resistance genes to RWA may provide additional protection from new virulent strains or biotypes of the insect. Genetic resistance to *D. noxia* has been identified in wheat, barley, and rye germplasm, and several resistance genes are available for use for cultivar improvement. In the United States of America and South Africa, only a few Russian wheat aphid (RWA) resistant winter wheat cultivars are currently available, and these cultivars contain only one of the six known RWA resistance genes. The objective of this study was to determine the inheritance of RWA resistance in an Iranian bread wheat cultivar 'Azadi', using a screening method based on differences in the leaf chlorosis of resistant and susceptible types following insect challenge. This Iranian bread wheat cultivar was selected for study, since it displayed high levels of resistance in a white-grained wheat background, the predominant wheat class produced in many countries of the world. Segregation analysis was conducted on an F_2 population developed by cross-hybridizing the susceptible soft white winter wheat cultivar 'Pishtaz' to the resistant cultivar 'Azadi'. Russian wheat aphid screening data from this population indicated that resistance in 'Azadi' is controlled by a single, dominant gene (χ^2= 2.601; $p \leq 0.102$).

Key words: *Diuraphis noxia*, inheritance, resistance, Russian wheat aphid, *Triticum aestivum*

Introduction

Russian wheat aphid (RWA), indigenous to Iran, Afghanistan, Southern Russia, and some Mediterranean countries, has now spread in many regions of the world. The aphid is a phloem feeder and reduces the photosynthetic capacity of plants by destruction of chloroplasts. Damage symptoms caused by RWA infestations involve loss of chlorophyll, leaf curling, and changes in the angle of the wheat tillers in relation to the rest of the wheat plant. A general symptom of infestation is leaves with white or yellowish colored streaks along the entire length of the leaf blade [6]. At low temperatures, the color of the streaking can change to purple, varying from dark red to purple-gray. The infested leaves curl longitudinally around the aphid colonies, with the outer margins of the leaves displaying a white or purple color [9]. These symptoms typically appear within seven days after the initial infestation, and can hinder the effectiveness of contact insecticides by sheltering the insect colonies. Du Toit [3] first reported genetic resistance to RWA in wheat (*Triticum aestivum*). Since then, resistance to RWA has been identified in several wheat lines [28,7,14,19,30,20,24,13]. Greenhouse tests indicated that different dominant genes, Dn1 and Dn2, control resistance in PI 137739 and PI 262660 (Du Toit, 1989). A recessive resistance gene, *dn3* [15], and a dominant resistance gene, *Dn4* [16], were found in *Triticum tauschii* (Coss.) and PI 372129, respectively. Marais & Du Toit [10] reported that PI 294994 carries a dominant gene (*Dn5*) different from other known genes. Elsidaig & Zwer [5] showed that there were two resistance genes in PI 294994, one dominant and one recessive. Saidi & Quick [22] found that two dominant genes controlled the resistance in PI

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294994. Finally, Zhang *et al.* [31] showed that different results obtained for the number of resistance genes in PI 294994 were due to the variation among resistant plants within this line. They concluded that there might be three resistance genes in PI 294994. Saidi & Quick [22] found the dominant resistance gene *Dn6* in wheat line PI 243781.

Russian wheat aphid resistant accessions typically are used in traditional breeding strategies to transfer the resistance gene from the donor to an adapted cultivar. Endosperm type, grain color and growth habit characteristics are used to distinguish among types of wheat for market purposes. Since soft white winter wheat is the predominant market class of wheat produced in many countries of the world, the best vehicle of transfer for incorporating a resistance gene into cultivated wheat for these countries would be a white winter wheat line. Many of the resistant accessions are hard red winter types. However, 'Azadi' an Iranian bread wheat cultivar displayed high levels of resistance to RWA [23,13,12], in a white-grained wheat background. The objective of this study was to determine the inheritance of RWA resistance in this bread wheat cultivar, using a screening method based on differences in the leaf chlorosis of resistant and susceptible types following insect challenge. This bread wheat cultivar will be used to develop adapted soft white, Russian wheat aphid resistant cultivars for production in these countries.

Materials and Methods

Materials were obtained from an experiment conducted by Najafi Mirak *et al*. [11]. They screened 30 wheat, *Triticum* sp., genotypes including hexaploids and tetraploids from different parts of Iran for resistance to RWA. Genotypes were ranked according to plant resistance, leaf chlorosis and rolling indices [29]. A resistance hexaploid wheat cultivar, 'Azadi', and a susceptible one ('Pishtaz') were used in the present experiment. An Iranian winter wheat cultivars 'Azadi', previously identified as resistant to the Russian wheat aphid, were crossed with a susceptible cultivar 'Pishtaz'. The F_2 population was produced by selfing some of the F_1 plants. Backcross populations were produced by crossing F_1 plants with the resistant (BCR) and susceptible (BCS) parents. Parents, F_1, F_2, BCR, and BCS of each cross were planted in a greenhouse employing a 14 h photoperiod at 30/20° C day/night temperature. Each seed was planted in a small pot with 9 cm diameter. After emergence, seedlings of each populations (19 of 'Azadi'; 20 of 'Pishtaz'; 40 of F_1; 49 of BCR; 39 of BCS; 157 of F_2 and 12 each of 95 F_2-derived F_3 families) that were at the same growth stage (the one-leaf stage) were selected. The pots were placed close to each other (10 cm distance between two plants of each generation). The pots were uniformly irrigated throughout the experiment. Aphids were collected from volunteer common wheat in the province of Karaj, Iran. To obtain a colony of *D.noxia*, several aphids were reared on six-rowed, winter barley, 'Reyhan' separately under a light plastic cage with mesh top and mesh-covered ventilation holes on the side. After a month, a colony was obtained from each aphid. Only one of the aphid colonies was used in all experiments. Seedlings were infested with RWA one week after planting according to Nkongolo *et al.* [16] with some modifications. Individual plant at first- leaf seedling stage was infested with five late instar aphids using a moistened camel hairbrush. Plants and aphids were observed and controlled daily. Plants were evaluated for *D. noxia* feeding damage by measuring leaf chlorosis 21 days after infestation. Leaf chlorosis was measured using a 1-9 scale in which: 1, healthy plants; 2, prominent chlorosis spots; 3, less than 15% chlorosis; 4, 15-25% chlorosis; 5, 25-40% chlorosis; 6, 40-55% chlorosis; 7, 55-70% chlorosis; 8, 70-85% chlorosis and finally 9 represents dead plants [29]. Seedlings with scores 1-4 and those with scores 5-9 were considered as resistant and susceptible, respectively.

Counts of seedlings within the different damage classes were done when the susceptible parent showed severe chlorosis on the leaves. Data obtained from the F_2 populations (derived from crosses of resistant and susceptible parents) and BC populations were tested for goodness of the fit to different phenotypic segregation ratios. The Chi- square (X^2) test [27] with Yates correction was employed to test the goodness of fit of the F_2 and BC's observed segregation to expected phenotypic ratios.

Results:

The data of populations derived from cross 'Azadi' and 'Pishtaz' for leaf chlorosis were tested for goodness of fit to different phenotypic segregation ratios. The segregation ratios are presented in Table I for data that fit appreciates (X^2 were non-significant). 'Azadi' cultivar was found resistant based on leaf chlorosis; whereas, 'Pishtaz' showed severely streaked leaves. The F_1 and BCR plants from crossing 'Azadi' and 'Pishtaz' were all resistant, indicating that resistance in 'Azadi' is dominant. Segregation in BCS (1R: 1S) and in F_2 population (3R: 1S) indicated that the resistance to RWA in 'Azadi' is controlled by one dominant gene. The resistance level of F_1 and BCR plants of crossing 'Azadi' and 'Pishtaz' was similar to the level of their resistant parent 'Azadi', indicating that the resistance based on leaf chlorosis in 'Azadi' is dominate. The BCS and F_2 populations segregated in 1R: 1S and 3R: 1S ratio, respectively. This suggests that one dominant gene control the resistance based on leaf chlorosis in 'Azadi'.

Analysis of the number of homozygous RWA-resistance, homozygous susceptible, and segregating

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F_2-derived F_3 families was used to confirm the results obtained by analysis of the BCR, BCS and F_2 populations. Distributions of the 95 families fit the 1 resistance: 2 segregation: 1 susceptible ratio, indicating single dominant gene control of RWA resistance (Table I).

Table 1: Segregation for resistance (based on leaf chlorosis symptom) to the RWA among Parents, F_1, F_2, F_2-derived F_3 families, BCR (backcross to resistant parent) and BCS (backcross to susceptible parent) progenies of wheat cultivars in seedling screening tests

Parents and progenies	Reaction to Russian wheat aphid[1]			Ratio tested	χ^2	P
	Resistance	Segregating	Susceptible			
Azadi	19	0	0			
Pishtaz	0	0	20			
F_1	21	0	0			
BCR	49	0	0			
BCS	19	0	20	1:1	0.0	1.0
F_2	127	0	30	3:1	2.601	0.102
F_2-derived F_3 families	22	56	17	1:2:1	3.568	0.178

[1] Number of plants for 'Azadi', 'Pishtaz', F_1, BCR, BCS, and F_2; number of rows for F_2-derived F_3 families.

Discussion:

The soft white winter wheat cultivar 'Azadi' was selected for this study because visual observations of RWA feeding damage on it suggested that this source of resistance has a high level of resistance [23,13,12]. The results of this experiment indicate that resistance to RWA in the 'Azadi' cultivar is conditioned by one dominant gene. Five dominant resistance genes in hexaploid (AABBDD) and one recessive resistance gene in diploid (DD) wheat have now been identified [1]. Allelism testing is required to determine whether the dominant resistance gene in 'Azadi' cultivar is the same gene as one of those previously identified in other wheat accessions. If the resistance gene in 'Azadi' cultivar is unique, it may provide another useful genetic resource for developing RWA resistance cultivars. Identification of another RWA resistance gene would increase the number of genes available to plant breeders for pyramiding genes into a single cultivar.

Conclusion:

Although the presence of different new biotypes of RWA has been reported [18,2,25,8,21], it occurred upon development of resistant cultivars as it has for the green bug, *Shizaphis graminum* [17]. Production of new biotypes is likely to overcome monogenic resistance in wheat. Breeding strategies are necessary to minimize the development of aphides. The most important of these strategies is development of cultivars having a combination of different resistance genes.

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