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Full Length Article

Evaluation of Chickpea Advance Genotypes against Blight and Wilt Diseases under Field Conditions

NIGHAT SARWAR[1], KHALID PERVAIZ AKHTAR, TARIQ MAHMUD SHAH AND BABAR MANZOOR ATTA
Nuclear Institute for Agriculture and Biology (NIAB), P.O. Box No. 128, Jhang road, Faisalabad, Pakistan
[1]Corresponding author's e-mail: nigsrw55@gmail.com

ABSTRACT

Blight and wilt diseases caused by *Ascochyta rabiei* (Pass.) Labrousse and *Fusarium oxysporum* Schlechtend emend. Snyd. and Hans. f. sp. *Ciceris* (Padwick) Synd. and Hans. (Foc), respectively is the major yield limiting factors to chickpea. Investigations were conducted for identification of resistance source against both diseases. Forty one advance genotypes of chickpea were screened against highly virulent isolate of *A. rabiei* (M-16) and *Fusarium* wilt. None of the tested genotypes was found to be highly resistant against *A. rabiei*. However, one genotype CH76/02 was found moderately resistant, while 27 were tolerant, 6 were moderately susceptible and 4 were susceptible against *A. rabiei*. Results of chickpea genotypes screened against wilt disease under sick field, indicated that 2 genotypes (CH32/02 & CH9/02) were highly resistant and 8 [Pb2008, CM2008, CH87/02(B8/02), CH7/02, CH31/02, CH34/03, CH4/02 & CH88/03] were resistant. These genotypes were found tolerant when tested against *Ascochyta* blight disease. Resistant genotypes that were identified in this study will be useful sources for developing blight and wilt resistant germplasm.

Key Words: Chickpea; Blight; *Ascochyta rabiei*; Wilt; *Fusarium oxysporum*

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is considered to be the third most important grain legume in the world after dry beans and pea, being widely grown in many subtropical and warm-temperate regions (Mansfeld, 2008). Chickpea is not only an important source of human food (Malik *et al*., 2011) and animal feed, but it also fixes nitrogen, which helps in the management of soil fertility, particularly in dry land areas (Sharma & Jodha, 1984; Islam *et al*., 2011).

In Pakistan it occupies more than one million hectares (1,022,100 ha) with an annual production of 749 thousand tones (Anonymous, 2010). Unfortunately this crop is badly affected by two important and yield limiting diseases *i.e*. chickpea blight and wilt caused by the fungi *Ascochyta rabiei* and *Fusarium oxysporum* f. sp. *ciceris* (Foc), respectively. It has been reported that both diseases can be controlled by the application of fungicides (Malik *et al*., 1991; Rauf *et al*., 1996). As chickpea is a rain fed crop and is grown under low input conditions, continuous seed treatment with fungicides are not possible (Chaudhry *et al*., 2006). Therefore importance of resistant cultivars is an established fact recognized by the researchers. Many sources of resistance to *Ascochyta* blight and Foc wilt have been reported mainly based either on field observations during natural epidemics or on artificial inoculation either in the field or green house. Host resistance, however does not persist as varieties presumed to be blight and wilt resistant failed, either as a result of genetic breakdown or a change in the virulence of the pathogen (Nene, 1987; Jamil *et al*., 2010). Since the host plant resistance provides the economical and the most practicable control of diseases, therefore, a reliable screening procedure is required for incorporating durable resistant in varieties. Conventional screening by using diseased plant debris or even spore suspension of a mixture of isolates is not as reliable as screening against individual, virulent isolates (Ilyas *et al*., 2007). In the present study, advance chickpea germplasm was evaluated against highly virulent isolate of *A. rabiei* and the same genotypes were also evaluated against *Fusarium* wilt in wilt sick field having heavy inoculum of Foc to identify resistance source.

MATERIALS AND METHODS

Forty-one chickpea genotypes originated from Plant Breeding and Genetics division of NIAB, Faisalabad were evaluated for disease resistance against *A. rabiei* and *Fusarium* wilt.

Preparation of *A. rabiei* culture and spore suspension: Boiled chickpea seeds were autoclaved in conical flasks and inoculated with spores of highly virulent isolate of *A. rabiei* (M-16) under aseptic conditions. These flasks were incubated at 20 ± 2°C for about ten days until all the grains were fully covered with fungal spores.

Fungus culture was shaken with 100 mL distilled

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sterilized water and filtered through muslin cloth. Spore concentration was adjusted to 10^6 spore/mL by using a Haemocytometer. A few drops of Tween 20 were mixed with spore suspension as a wetting agent before spraying on the plants.

Screening of chickpea genotypes against *Ascochyta* blight disease: Fifty seeds of each genotype were sown in a single row in four replicates with 30 cm and 15 cm inter row and intra row spacing, respectively following randomized completely block design. A row of a susceptible variety Aug-424 was planted after every two test lines as a spreader of disease. Plants were inoculated with spore suspension (10^6 spores/mL) of a highly virulent isolate at flowering stage and kept wet through spraying water to ensure good disease development. Disease data were recorded, when disease was fully developed on susceptible check, following a nine point (1–9) rating scale (Toker *et al.*, 1999), where 1 = no lesions (immune); and 9 = all plants dead (very highly susceptible). Individual symptomatic plant ratings for each genotype were added and divided by the number of infected plants to calculate the corresponding severity index (Akhtar *et al*., 2009).

Screening of chickpea genotypes against wilt disease: Same chickpea genotypes were also tested against wilt disease in the wilt sick plot, developed at NIAB. Twenty seeds of each entry were sown in a single row in four replicates with 30 cm row to row and 15 cm plant-to-plant distance, following randomized completely block design. After every 2 test rows, one row of Aug-424 were planted as susceptible check. Early and late wilt incidence was recorded during the last week of December and in first week of March, respectively. Reaction of all the chickpea test entries against wilt was determined by following the six point (1-6) disease rating scale based on plant mortality (Jamil, 2006) where; 1 = no mortality (immune); and 6 = 61 to 100% mortality (highly susceptible).

Statistical analysis: The data collected from all experiments was analyzed separately for each experiment and subjected to two ways Analysis of Variance (ANOVA) using STATICA computer preframe. The means were compared for significance using Fisher's LSD.

RESULTS AND DISCUSSION

Screening against *Ascochyta rabiei*: Use of resistant varieties is the most important aspect of integrated disease management strategy. The worldwide collection of cultivated chickpea germplasm has very low frequency of resistance to *A. rabiei* (Reddy & Singh, 1984). Forty-one promising chickpea genotypes tested against highly virulent isolate of *A. rabiei* showed a wide range of responses from moderately resistance to very highly susceptible reaction. The first disease symptom as few scattered lesions was observed on the susceptible spreader line Aug424 after 5 days of inoculation, which later progressed in to extensive lesions causing severe defoliation and drying of branches and ultimate death of all plants. Minimum severity index value of 4.5 was recorded in CH76/02 and maximum as 9.0 in Aug424. Disease severity index indicated that most of the test genotypes (27) exhibited tolerant response while genotype CH76/02 was moderately resistant, 6 were moderately susceptible, and 4 were susceptible (Table I). However, none of the tested genotype was found to be, resistant, highly resistant and immune. This may be due to high inoculum pressure (Akhtar *et al*., 2009). In this scenario chickpea lines showing moderately resistance or tolerance behavior against *Ascochyta* blight are good for using as commercial cultivars after testing their other agronomic characteristics or may be used in breeding program to develop resistant varieties. Present findings showed harmony with earlier studies of Shah *et al*. (2005) and Atta *et al*. (2006).

Screening against *Fusarium* wilt: Fusarium wilt disease of chickpea is also equally important disease. Wilt caused about 10-50% losses on chickpea in the dry areas of Pakistan (Khan *et al*., 2002). Under the present study same chickpea lines as tested against blight disease were screened for their resistance potential against *Fusarium* wilt in wilt sick field. There was significant difference for both early and late season wilt incidence. The percentage of wilted plants ranged from 0 to 32.89% in the early season wilt and from 9.60 to 100% in the late season wilt. Data regarding early season wilt incidence exhibited that 12 genotypes namely 70022, CH85/02, CH20/02, CH87/02(B8/02), CH32/02, CM1529-3/03, CH1/02, CH4/02, CH 88/03, CH46/04, CH45/04 and CM2008 were immune, 23 were highly resistant, 3 were resistant, 2 were tolerant and 1 was susceptible. Late season wilt incidence data showed that 4 genotypes were highly resistant, 7 were resistant, 7 were tolerant, 10 were susceptible and 13 were highly susceptible but none was found to be immune. Data regarding total wilt percentage (early + late) showed that two genotypes (CH32/02 and CH9/02) were highly resistant, eight (Pb2008, CM2008, CH87/02[B8/02], CH7/02, CH31/02, CH34/03, CH4/02 & CH88/03) were resistant, 6 were tolerant, 11 were susceptible and 14 were highly susceptible. However, on the basis of total wilt incidence, none was immune (Table II). Our results are in line with the results of Iqbal *et al.* (2005), Ahmad *et al*. (2007), Neupane *et al*. (2007), Pande *et al*. (2007) and Shah *et al*. (2009) who found somewhat same results.

CONCLUSION

Chickpea blight and wilt are two important destructive diseases worldwide. Due to the introduction of new virulent strains there is continuous need to screen and develop new varieties using different breeding techniques against virulent strains to create variability to obtain sustainable yield. Under the present study new sources of resistance were observed against both diseases. These genotypes may be used directly as varieties in area having high incidence of these diseases

Table I: Response of chickpea genotypes against highly virulent isolate of *Ascochyta rabiei* tested in field conditions

Genotypes	Severity index	Disease response	Genotypes	Severity index	Disease response
70022	5.5 efg	Tolerant	CH88/03	5.0 fgh	Tolerant
CH24/00	6.0 de	Moderately susceptible	CH37/04	5.0 fgh	Tolerant
K850	8.5 a	Highly susceptible	CH38/04	5.0 fgh	Tolerant
CH85/02	6.5 cd	Moderately susceptible	CH39/04	5.0 fgh	Tolerant
CH20/02	6.0 de	Moderately susceptible	CH83/04	5.5 efg	Tolerant
CH87/02(B8/02)	5.0 fgh	Tolerant	CH85/04	5.0 fgh	Tolerant
CH38/00	5.0 fgh	Tolerant	CH119/04	5.0 fgh	Tolerant
CH76/02	4.5 h	Moderately resistant	CH120/04	5.0 fgh	Tolerant
CH7/02	5.0 fgh	Tolerant	CH73/02	5.0 fgh	Tolerant
CH31/02	5.5 efg	Tolerant	CH77/02	6.0 de	Moderately susceptible
CH32/02	5.5 efg	Tolerant	CH42/03	5.0 fgh	Tolerant
CH34/03	5.0 fgh	Tolerant	CH45/03	7.0 bc	Susceptible
CM1528-414/03	8.5 a	Highly susceptible	CH44/04	5.5 efg	Tolerant
CM1529-3/03	7.5 b	Susceptible	CH46/04	6.5 cd	Moderately susceptible
CH43/03	7.0 bc	Susceptible	CH47/04	5.5 efg	Tolerant
CH1/02	5.5 efg	Tolerant	CH50/04	5.5 efg	Tolerant
CH4/02	5.0 fgh	Tolerant	CH45/04	7.0 bc	Susceptible
CH12/02	5.5 efg	Tolerant	Pb 2008	5.5 efg	Tolerant
CH9/02	5.5 efg	Tolerant	CM2008	5.0 fgh	Tolerant
CH6/02	5.5 efg	Tolerant	Aug424	9.0 a	Very highly susceptible
CH21/02	6.0 de	Moderately susceptible			

Table II: Response of chickpea genotypes against *Fusarium* wilt in wilt sick field

Genotype	Early wilt (%)	Late wilt (%)	Total wilt (%)	Disease response	Genotype	Early wilt (%)	Late wilt (%)	Total wilt (%)	Disease response
70022	0.00 e	20.02 klmno	20.02	Tolerant	CH88/03	0.00	11.8 mno	11.08	Resistant
CH23/00	2.62 de	42.11 ghij	44.73	Susceptible	CH37/04	30.56 a	69.44 cd	100.00	Highly susceptible
K850	3.12 de	45.77 fghi	48.89	Susceptible	CH38/04	17.89 bc	82.11 abc	100.00	Highly susceptible
CH84/02	1.24 e	30.03 ijkl	30.03	Tolerant	CH39/04	24.06 ab	75.94 abcd	100.00	Highly susceptible
CH20/02	0.00 e	59.21 defg	59.21	Susceptible	CH83/04	2.94 de	88.7 ab	91.66	Highly susceptible
CH87/02(B8/02)	0.00 e	15.75lmno	15.75	Resistant	CH85/04	5.26 de	81.57 abc	86.84	Highly susceptible
CH38/00	6.25 de	40.62 hij	46.87	Susceptible	CH19/04	2.63 de	80.84 abc	83.47	Highly susceptible
CH76/02	3.84 de	37.08 hijk	40.93	Susceptible	CH20/04	2.50 de	89.44 ab	91.94	Highly susceptible
CH7/02	10.00cde	3.33 o	13.33	Resistant	CH73/02	11.45 cd	62.07def	73.53	Highly susceptible
CH31/02	4.16 de	12.50lmno	16.66	Resistant	CH77/02	11.69 cd	88.31 ab	100.00	Highly susceptible
CH32/02	0.00 e	9.60 no	9.60	Highly resistant	CH42/03	7.14 de	27.38 ijklmn	34.52	Susceptible
CH34/03	5.00 de	10.62 mno	15.62	Resistant	CH45/03	3.84 de	42.31 fghij	46.15	Susceptible
CM1528-14/03	5.28 de	23.61 jklmn	28.89	Tolerant	CH44/04	2.78 de	28.75 ijklm	31.53	Susceptible
CM1529-3/03	0.00 e	50.00 efgh	50.00	Susceptible	CH46/04	0.00 e	35.12 hijk	35.12	Susceptible
CH43/03	4.54 de	24.74 jklmn	29.29	Tolerant	CH47/04	2.78 de	25.00 jklmn	27.78	Tolerant
CH1/02	0.00e	25.33 jklmn	25.33	Tolerant	CH50/04	8.18 cde	75.58 bcd	83.77	Highly susceptible
CH4/02	0.00 e	15.44 lmno	15.44	Resistant	CH45/04	0.00 e	40.28 hij	40.28	Susceptible
CH12/02	6.25 de	60.41defg	66.66	Highly susceptible	Pb 2008	5.55 de	13.45 lmno	19.0	Resistant
CH9/02	2.94 de	2.94 0	5.88	Highly resistant	CM2008	0.00 e	15.79 lmno	15.79	Resistant
CH6/02	9.37cde	84.37abc	93.75	Highly susceptible	Aug424 (check)	32.8 a	67.10 cde	100.00	Highly susceptible
CH21/02	2.78 de	94.28 a	97.06	Highly susceptible					

after evaluating them for high yield and other suitable agronomic characteristics. In addition to these genotypes, seventeen other genotypes showing susceptibility to wilt were also found to be tolerant to moderately resistant against *Ascochyta* blight. These genotypes could be used to develop blight resistant varieties. Two genotypes showing susceptibility to blight were also found to be tolerant against wilt and could be used directly in the areas, where wilt is the sole problem.

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