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Full Length Research Article

Assessment of pathogenic variability in kabuli and desi Chickpea genotypes against Chickpea Blight (*Ascochyta rabiei*)

Junaid Iqbal, Syed Ali Zafar*, Awais Ashraf and Arbaz Hassan
Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan
Corresponding author: syedalizafar9@gmail.com

Abstract

Chickpea blight is one of the most destructive diseases of chickpea (*Cicer arietinum* L.) worldwide caused by Ascochyta rabiei (Pass.) Lab. The disease shows more devastating effects particularly in cold and humid ecological conditions. In epidemic condition it results in great damage by spreading at the entire crop in the deserted areas. To alleviate this setback, several interventions are practiced. However, breeding for resistance to the host is the most suitable and environmentally conducive strategy. The present study was conducted with three replications and three treatments (T_o with no spores, T_1 with approximately 8350 spores/ml and T_2 with approx. 16700 spores/ml) sprayed to screen the resistant source against chickpea blight in chickpea. Among total six genotypes, three kabuli and three desi genotypes were screened. Disease recorded at international rating scale 1-9. In kabuli genotypes, significant response was observed in treatment T_1 and T_2. When number of spores/ml increased from T_1-T_2 then kabuli genotype i.e. K-01248 move on rating scale from resistant to tolerant and K-01250 from tolerant to moderately susceptible. Desi chickpea genotypes showed more resistance against blight than Kabuli ones. The desi resistant and Kabuli tolerant genotypes can be utilized in further breeding program for development of resistant high yield genotypes.

Keywords: Chickpea, kabuli, desi, blight, *Ascochyta rabiei*

Introduction

Chickpea (*Cicer arietinum* L.) is the third most important pulse crop in all over the world (Hirich *et al.*, 2014; Sarwar *et al*., 2012; Shah *et al.*, 2015; Khan *et al.*, 2018) after soybean and peas (Malik *et al.*, 2011, Jabbar *et al*., 2014). Its cultivation ranges from the Mediterranean basin to the Indian sub-continent and south ward of Ethiopia and East African highlands. Every year in Rabi season, most of the rain-fed area of Pakistan remains under this crop (Iqtidar and Amanullah, 2002). Chickpea is prone to many biotic and abiotic stress factors which jeopardize its production (Pande *et al*., 2005). Among these, chickpea blight is the most important one. The causal organism of gram blight is Ascochyta rabiei (Pass.) Lab. Epidemics of chickpea blight may result 100% yield losses (Pande *et al*., 2005). Blight epidemics of 1980–1984 caused heavy yield losses in Pakistan (Bashir and Ilyas, 1986). While annually this disease is causing 20–25% yield losses in Pakistan (Jamil *et al*., 2010). In Pakistan, chickpea quantitatively takes as small portion and qualitatively as food supplement for the vegetarian diet (Jabbar *et al*., 2014). Area under cultivation in Pakistan is 978 thousand hectares and production is 340 thousand tons with an increase of 3% in production over last year (Agriculture Economic Survey 2017-2018). It has good quality protein, fix nitrogen (Sahi *et al.*, 2012) and can increase soil fertility when use in different cropping systems (Shah *et al.*, 2015). Among pulses, chickpea alone contributes 76% to total pulses grown in the Pakistan (Agriculture economic survey 2017-2018).

Currently, the management of chickpea blight is dependable to fungicides. Fungicides prove uneconomical, and augment input expenditures when fungicidal sprays are needed on vast area. Lethal effects of these fungicides on the environment are also making them unsuitable. Further, non-judicious use of these chemicals is causing resistance in *A. rabiei*, resulting in the production of new pathotypes or isotypes (Ilyas *et al*., 2007; Sarwar *et al*., 2012). Thus, the possible option remains left to control this disease is the development of chickpea resistant cultivars. Development of Resistant cultivars is the most effective and economical management tool to combat gram blight (Ilyas *et al*., 2007 and Benzohra *et al.*, 2013). But, available cultivars with desired agronomic characters are susceptible to chickpea blight disease, probably due to the appearance of new isotypes or pathotypes (Jamil *et al*., 2010). Hence, identification of durable resistant advanced lines is inevitable to find some good sources of resistance against this disease. Therefore, present study was designed to assess the pathogenic affect based genetic variability and to screen resistant genotypes against blight for future utilization under natural rain-fed environment.

Materials and Methods

Experiment location and germplasm:

Experiment was conducted in the University of Agriculture, Faisalabad (UAF) during 2017-18. Advance chickpea genotypes and varieties (3 Kabuli and 3 Desi) obtained from Pulses Research Institute (PRI), Ayub Agricultural Research Institute (AARI), Faisalabad. Genotypes consisted of kabuli (K-01250, K-01216 and K-01248) and desi (Punjab-2008, bittal-2016 and D-09027) shown in Table No. 1. Highly susceptible chickpea variety Punjab-1 (PB-1) was planted as a spreader to produce the disease pressure after every two lines. Experimental design was randomized complete block design (RCBD) with three replications and three treatments.

Fungal Material:

Isotypes of *Ascochyta rabiei* used in this experiment was obtained by isolation from samples of infected stems, sheath and chickpea pods. Sterilization was done in 5% sodium hypochlorite for 1-2 minutes. The samples were dried on sterilized filter paper and placed on Potato Dextrose Agar (PDA). Incubation was done at 20^{o}C±2 with 12 hours light/dark cycle for seven days to ensure optimum fungal growth. Developed colonies were sub-cultured on chickpea seed meal agar (CSMA) media. Streptomycin was used in petri dishes to grow free bacteria *A. rabiei* before pouring CSMA media (Sahi *et al*., 2012). Incubation on this media for 1-2 weeks was ensured. At the end colonies of fungus developed with pycnidia (Shah *et al.,* 2015).

Preparation of inoculum and experimental conditions:

Two inoculums were prepared by adding fungal spores in sterilized water. Spores were counted by Haemocytometer. Treatment (T_o) used as check with no inoculum spray, treatment (T_1) was inoculated with approximately 8350 spores/ml and treatment (T_2) was inoculated with approx. 16700 spores/ml. Fresh prepared inoculums were used for spray until blight symptoms appeared. The process of spraying of inoculum continued until susceptible spreader (Pb-1) showed the symptoms to severe conditions i.e. death of spreader line. The inoculums were sprayed at mid pod stage of chickpea. During experiment all agronomical practices were followed to raise the crop. During experiment 80-90% humidity was maintained by tap water spraying in the morning and evening. Polythene sheet was used for the isolation of Treatment (T_1) and (T_2).

Rating Scale:

Disease was estimated when pods of susceptible variety$_{(s)}$ was completely infected. Infection was classified as follow (Manjunatha and Saifulla, 2013).

Results

Results based on susceptibility and resistance of genotypes is summarized in table-3. Susceptible PB-1 showed severe symptoms of disease at mid pod stage. Experiment showed more resistance in desi as compared to Kabuli genotypes. In control condition (T_o), all lines are healthy and showed no blight symptoms. In treatment (T_1) with approx. 8350 spores/ml, Kabuli chickpea genotypes K-01248 showed resistant, K-01250 proved as tolerant and K-01216 was recorded as moderately susceptible; desi chickpeas genotypes showed no sign of lesions (table-3). In treatment (T_2) with approx. 16700 spores/ml, Kabuli chickpea genotypes K-01248 observed as tolerant, K-01250 as moderately susceptible and K-01216 as moderately susceptible to susceptible whereas desi chickpea showed again no lesions (table-3).

Discussion

Most of the researchers identified resistant genotypes by evaluation of germplasm against blight in field conditions (Bashir *et al.,* 2006; Iqbal *et al.,* 2010 and Sarwar *et al.,* 2012). The most important aspect of integrated disease management strategy is the use of resistant cultivar. Very low frequency of resistance to *A. rabiei* has been found and very rare in global chickpea germplasm (Sarwar *et al.,* 2012). Use of fungicide to control the disease is not a feasible and economical approach for farmers. Highly resistant chickpea genotypes were found against blight and due to the presence of high disease pressure in the environment (Akhtar *et al.,* 2009). When new physiological races appear than lose in resistance of resistant cultivars is observed (Jabbar *et al.,* 2014). In present study, resistance in the desi chickpea genotypes was observed based on the rating scale. But in case of Kabuli genotypes, K-01248 showed tolerance in T_2. Present study also explained the significant response of the Kabuli genotypes against the conditions which are favorable for disease spread at pod stage. In Punjab-1 variety maximum number of lesions was observed when inoculated with the *A. rabiei* spores (Sahi *et al.,* 2012). Our study supported that Punjab-1 showed the severe symptoms of blight upon inoculation. Desi chickpea proved more resistance as compared to Kabuli ones (Shah *et al.,* 2015). The results showed that desi chickpea genotypes have more resistance as compared to Kabuli chickpea genotypes. Desi chickpea germplasm i.e. Punjab-2008, bittal-2016 and D-09027 have no infection (0%) of disease. The genotype D-09027 can be used in breeding for the development of resistant genotypes of chickpea against blight.

Conclusion;

Chickpea blight is one of the most destructive disease of chickpea which decreases the crop yield

up to a great extent. Use of fungicides is not a useful method to control disease. Present study explained significant variation among genotypes according to the above mentioned scale of resistance. That can be used as direct source of hybridization for the transfer of resistant gene into high yield susceptible genotypes. The results depicted that desi chickpea genotypes had more resistance against blight disease as compared to Kabuli genotypes.

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Author contribution

All authors in this research have equally contributed.

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Table. 1: List of germplasm used in research work

Sr. No.	Genotypes (Kabuli)	Genotypes (Desi)
1	K-01250	Punjab-2008
2	K-01216	Bittal-2016
3	K-01248	D-09027

Table. 2: Criteria for the classification of infected genotypes

Sr. No.	Scale	Percentage	Infection
1	1	0	No infection
2	2	1-5	Highly resistant
3	3	6-10	Resistant
4	4	11-15	Moderately resistant
5	5	16-40	Tolerant
6	6	41-50	Moderately susceptible
7	7	51-75	Moderately susceptible to susceptible
8	8	76-100	Susceptible
9	9	Up to 100	Highly susceptible

Table. 3: Susceptibility and resistibility of studied genotypes

Sr. No.	T_0 (control)		T_1 (Approx. 8350 spores/ml)		T_2 (Approx. 16700 spores/ml)	
	Scale	**Genotypes**	**Scale**	**Genotypes**	**Scale**	**Genotypes**
1	No infection (0%)	Kabuli (K-01250, K-01216, K-01248)	Resistant (6-10%)	Kabuli (K-01248	Tolerant (16-40%)	Kabuli (K-01248
2			Tolerant (16-40%)	K-01250	Moderately susceptible (41-50%)	K-01250
3		Desi (Punjab-2008, bittal-2016, 09027)	Moderately susceptible (41-50%)	K-01216)	Moderately susceptible to susceptible (51-75%)	K-01216)
4			No infection (0%)	Desi (Punjab-2008, bittal-2016, D-09027)	No infection (0%)	Desi (Punjab-2008, bittal-2016, D-09027)