



Original Research Article

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Identification of novel chickpea genotypes for *Ascochyta* blight (*Ascochyta rabiei*) resistance under field conditions

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Article Info

Abstract

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Ascochyta blight (*Didymella rabiei*) is economical imperative foliar diseases limiting the yield and yield components that associated traits of (*Cicer arietinum* L.) worldwide. The purpose of the study is to evaluate the acquiesced chickpea genotypes from International Center for Agricultural Research in the Dry Areas (ICARDA) in Morocco. The experimental was designed as an optimized completed randomized block design during two consecutive growing seasons in 2018 to 2019 at Alem Tena and Dhera under natural conditions in hot spot area. The disease assessment was recorded on 1-9 based rating scale. The results revealed that a statistically significant difference ($P \leq 0.05$) on *Ascochyta* blight resistance due to the genotypes in two growing seasons except in 2019 at Alem Tena. From overall reflection due to genotypes and location seven genotypes were resistant. But there are no significant interaction effects by genotype by location in 2018 growing season. Thus, those genotypes are: FLIP-11-153C, FLIP-11-155C, Flip-10-369C, Flip-10-371 and FLIP-11-81C were durable sources of resistance and highly stable in 2018 and 2019 growing season over locations and years. This implies genotypes gets genotypic differences for their level of reactions and it suggested that clear evidences that ample of source of variability among the genotypes in the disease resistance. The genotypes which given a considerable level of resistance are suggested to be screened at reproductive stage to confirm resistance level. Therefore, the resistant source found in these findings can be utilized in chickpea improvement program for the parental materials to develop cultivar and their heritability will be determined.

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Introduction

Chickpea *Ascochyta* blight is caused by [*Didymella rabiei* (Kovachski) von Arx] is a global disease of in major chickpea producing areas where the growing conditions are is cool and humid weather season (Benzohra et al., 2014, Ibrahim et al., 2012). It has been

reported to hamper heavy yield losses about 100% under conducive climatic elements whereas the relative humidity is more than 60%, temperature varies from 10-20 °C and on susceptible host (Pande, 2005; Alwawi et al., 2009). In Ethiopia the pathogen is supposed to introduced, with seeds via Punjab7, C 217/3, C 410 cultivars (Bejiga, 1984). Recently, the disease is spread

in major chickpea growing areas of the country. Sally (2005), reported that the pathogen survives across consecutive season on diseased chickpea tissue and on the soil surface at temperatures of 10-35°C, relative humidity of 0-30%. *Ascochyta rabiei* loses its pathogenicity quickly at ranges of 65-100% relative humidity and under soil depths from 10 to 40 cm.

The rate of *Ascochyta* blight development is rather high in a maximum disease severity, it kills the host plants in four weeks, signifying a short duration epidemic nature (Shtienberg, 2010). Getaneh et al., (2021) found that genetically diverse *Ascochyta* blight pathogens in Ethiopia.

Through integrated management with the use of seed dressing of fungicides, foliar application of fungicides and crop rotation with non-host crops can be economical and efficient to minimize the primary inoculum and disease severity. Still, these methods are not practical applicable under field conditions (Malik et al., 2005).

Yet, only practical control of *Ascochyta* blight is using resistant cultivars is the most economical method to improve chickpea production (Chen & Muehlbauer, 2003). Host resistance is the most effective and environment friendly method to control the *A. rabiei* (Atta et al., 2006).

It has been reported that the resistance to *Ascochyta* blight is age related which tends to decrease, and with different stages of the host plant and the vegetative stage do not maintain resistance up to reproductive stage (Chongo and Gossen, 2001).

Previously from the introductions, *Ascochyta* blight resistant kabuli type chickpeas were obtained and released for large scale production. Currently, most of kabuli chickpea resistance source breakdown by *Ascochyta* blight disease and lack of stable sources of resistance in released popular chickpea varieties.

Therefore, germplasm will be introduced from international chickpea improvement centers and discovery extra stable chickpea genotypes under Ethiopian condition.

Objective(s)

To evaluate of chickpea genotype for their resistance to *A. rabiei*.

Materials and methods

Trial materials and design

The trial was executed for two consecutive years during the post-rainy season of 2018 to 2019 in a field where a disease is hot spot area at Alem Tena and Dhera which are the sub stations of Debre Zeit and Kulumsa Agricultural Research Center. The genotype was composed of 39 Kabuli type of chickpea and 1 genotype highly susceptible check ILC-263 for disease spread and its distribution in the field was used in 2018 growing season which is the acquired from ICARDA.

In 2019 growing season the 20 genotypes were selected from 2018 entries and 1 released resistant kabuli chickpea cultivar was included. The trial experiment was arranged as an optimized randomized complete block design (RCBD) with two replications that about 40 seeds for each genotype were sown in 4 m length size and seed were planted in 40 cm between row spacing and 10 cm between seeds (DZARC, 2017).

Ascochyta blight severity

Ascochyta blight severity assessment was started immediately after disease onset was visible as lesion on upper leaf and wilting of leaf tips was observed. Severity was recorded on plot base and assessed four times after every ten days' breaks using 1–9-point disease scores scale (Pande et al., 2011) the last score data was used for analysis since it is disease severity that is progress from seedling to podding stage.

The disease severity scoring scale (1-9) description (Pande et al., 2011)

As follow: 1=no visible symptoms; 2=minute lesions prominent on the apical stem; 3=lesions up to 5 mm in size and slight drooping of apical stem; 4=lesions obvious on all plant parts and clear drooping of apical stem; 5=lesions on all plants parts, defoliation initiated, breaking and drying of branches slight to moderate; 6=lesions as in 5, defoliation, broken, dry branches common, some plants died; 7=lesions as in 5, defoliation, broken, dry branches very common, up to 25% of plants died; 8= symptoms as in 7 but up to 50% of the plants died and 9= symptoms as in 7 but up to 100% of the plants died. Scored genotypes were further categorized for their reaction to AB infection on the basis of Gowen et al., (1989) scale, according to this

scale; 1-<2= Highly resistant (HR); 2<4= resistant (R); 4-<6=moderately resistant (MR); 6<7= moderately susceptible (MS); 7-<9= susceptible (S); and 9-10=highly susceptible (HS).

Ascochyta blight severity analysis

Ascochyta blight severity data on were subjected R package software using anova model. Mean separation was done at LSD (5%) probability level. In both 2018 or 2019 growing season since the disease severity over locations and years were tested using combination testing method that the ratio of larger error mean square to lower mean square values less 5 acceptable and homogenous, the results were analyzed in combined way.

Results and discussion

The results of the present studies showed a distinct variation for Ascochyta blight resistance had highly a significant difference among chickpea genotypes ($P<0.05$) both at Alem Tena and Dhera in 2018 and in 2019 growing seasons at Dhera testing location (Table 1 and Table 3) respectively. In 2018 growing season it was recorded that 16 genotypes found resistant, 19 genotypes moderately resistant, 3 showed moderately susceptible, 1 was found susceptible and 1 highly susceptible at Alem Tena. Whereas, at Dhera only 5 genotypes resistant, 30 genotypes found moderately resistant, 2 found susceptible and 2 scored highly susceptible in 2018 growing season. In 2018 growing season chickpea genotypes viz (FLIP-10-356C, FLIP-10-359C, FLIP-10-363C, FLIP-10-369C, FLIP-10-371C, FLIP-10-372C, FLIP-10-373C, FLIP-10-378C, FLIP-11-113C, FLIP-11-114C, FLIP-11-148C, FLIP-11-154C, FLIP-11-17C, FLIP-11-203C, FLIP-11-228C and FLIP-11-234C were resistant at Alem Tena.

Furthermore, at Dhera these were: FLIP-10-369C, FLIP-10-371C, FLIP-11-130C, FLIP-11-153C and FLIP-11-81C were resistant. But, two genotypes FLIP-10-369C and FLIP-10-371C stable and consistently durable source of resistant over locations to Ascochyta blight disease. The result exhibited that all genotypes had great genetic differences among genotypes with different reactions to Ascochyta blight in this growing season. There was non-significant difference at ($P<0.05$) due to genotype by location interactions

among the genotypes and Ascochyta blight severity was revealed that highly significant at ($P<0.05$) due genotypes and locations. Out of the tested genotypes combined over location where 10 genotypes resistant, 25 genotypes exhibited moderately resistant, 4 showed susceptible and 1 genotype found highly susceptible in in 2018 growing season (Table 2).

In compression, among advanced 20 genotypes in 2019 growing season 8 genotypes were showed resistant, followed by 12 genotypes were moderately resistant to Ascochyta blight at Alem Tena. Similarly, at Dhera 5 genotypes were found resistant, 6 genotypes were moderately, followed by 7 genotypes moderately susceptible and 2 genotypes found susceptible.

These resistant lines are: FLIP-10-361C, FLIP-10-363C, FLIP-10-371C, FLIP-10-377C, FLIP-11-153C, FLIP-11-154C, FLIP-11-155C and FLIP-11-81C at Alem Tena and followed by Dhera site resistant genotypes: FLIP-11-130C, FLIP-11-153C, FLIP-11-155C, FLIP-11-20C and FLIP-11-81C (Table 3).

In 2019 growing season three genotypes such as FLIP-11-153C, FLIP-11-155C and FLIP-11-81C were durable resistance and highly stable in each location (Table 3). This implies this diseases pressure at Dhera is higher that of Alem Tena that most of the genotype moderately resistant in 2018 become moderately susceptible to susceptible reaction (Table 3). On the other hand, there was no significant effects at ($P\leq 0.05$) difference on severity due genotype by location interaction over location in 2019 growing season (Table 4).

The differential reaction of these genotypes in Dhera indicates the presences of an aggressive pathotype of *A. rabiei* in that testing location. There was a varied difference among genotypes for response to disease. Toker & Canci, (2003) reported that the resistance response of 41 genotypes from ICARDA against *Ascochyta rabiei* under natural screening in Antalya-Turkey and seven found were resistant while all the remaining genotypes were exhibited moderate resistance to highly susceptible response which in agreement with our findings of present studies. The results of resistance to *Ascochyta rabiei* suggested clear evidence that there was tolerable genetic diversity in genotypes for this attribute.

Table 1. Mean severity for *Ascochyta* blight on chickpea genotypes in 2018 growing season in Alem Tena and Dhera.

Genotype	Pedigree	Alem Tena Mean±SD	Reaction	Dhera Mean±SD	Reaction
FLIP-10-317C	X04TH13/X03TH-13XFLIP96-154	6.50±0.70	MS	8.00±1.41	S
FLIP-10-320C	X04TH86/X03TH-154XS01116	4.50±0.70	MR	5.50±0.70	MR
FLIP-10-335C	X04TH57/X03TH-57XFLIP97-116	4.00±0.00	MR	5.00±0.00	MR
FLIP-10-336C	X04TH63/X03TH-131XFLIP99-34	4.00±0.00	MR	5.50±0.70	MR
FLIP-10-356C	X04TH131/FLIP95-68XFLIP97-83	3.00±0.00	R	4.50±0.70	MR
FLIP-10-359C	X04TH138/FLIP98-22XFLIP95-51	3.50±0.70	R	4.50±0.70	MR
FLIP-10-361C	X04TH151/S01020XFLIP95-68	4.00±0.00	MR	4.50±0.70	MR
FLIP-10-363C	X04TH152/S01069XFLIP97-90	3.50±0.70	R	4.00±0.00	MR
FLIP-10-369C	X04TH172/ICCV-2X S01098	3.00±0.00	R	3.50±0.70	R
FLIP-10-371C	X04TH175/FLIP95-51XFLIP97-165	3.50±0.70	R	3.50±0.70	R
FLIP-10-372C	X04TH176/FLIP95-68XFLIP97-205	3.50±0.70	R	4.50±0.70	MR
FLIP-10-373C	X04TH177/FLIP97-90XFLIP97-229	5.50±0.70	R	4.50±0.70	MR
FLIP-10-377C	X04TH178/FLIP97-91XFLIP98-137	4.00±0.00	MR	4.50±0.70	MR
FLIP-10-378C	X04TH180/FLIP97-205XFLIP97-229	3.50±0.70	R	4.00±0.00	MR
FLIP-11-113C	X04TH127/FLIP98-230XFLIP97-116	3.00±0.00	R	4.50±0.70	MR
FLIP-11-114C	X04TH128/FLIP98-232XFLIP99-34	3.50±0.70	R	4.50±0.70	MR
FLIP-11-130C	X04TH135/FLIP97-205XFLIP97-83	4.00±0.00	MR	3.50±0.70	R
FLIP-11-131C	X04TH135/FLIP97-205XFLIP97-83	4.00±0.00	MR	4.50±0.70	MR
FLIP-11-137C	X04TH136/FLIP97-229XFLIP97-126	4.00±0.00	MR	4.50±0.70	MR
FLIP-11-139C	X04TH136/FLIP97-229XFLIP97-126	4.00±0.00	MR	5.00±0.00	MR
FLIP-11-13C	X04TH53/X03TH-53XFLIP97-116	6.50±0.70	MS	8.50±0.70	S
FLIP-11-141C	X04TH136/FLIP97-229XFLIP97-126	4.00±0.00	MR	5.00±0.00	MR
FLIP-11-146C	X04TH146/FLIP00-16XFLIP98-229	7.50±0.70	S	9.00±0.00	HS
FLIP-11-148C	X04TH147/FLIP00-17XFLIP98-230	3.50±0.70	R	5.00±0.00	MR
FLIP-11-153C	X04TH156/ S01205XFLIP97-229	4.00±0.00	MR	3.50±0.70	R
FLIP-11-154C	X04TH162/Pusa 1053XFLIP96-154	3.50±0.70	R	4.00±0.00	MR
FLIP-11-155C	X04TH164/FLIP 87-59CXFLIP99-34	4.00±0.00	MR	5.50±0.70	MR
FLIP-11-171C	X05TH106/FLIP97-131XFLIP00-14	7.00±1.41	MS	9.00±0.00	HS
FLIP-11-177C	X05TH192/ICCV03108XFLIP00-06	4.00±0.00	MR	5.50±0.70	MR
FLIP-11-17C	X04TH56/X03TH-56XFLIP96-154	3.50±0.70	R	4.00±0.00	MR
FLIP-11-203C	X05TH56/X04TH-183XX04TH-184	3.50±0.70	R	4.50±0.70	MR
FLIP-11-20C	X04TH56/X03TH-56XFLIP96-154	4.00±0.00	MR	5.50±0.70	MR
FLIP-11-221C	X04TH93/X03TH-161XS01076	4.00±0.00	MR	5.50±0.70	MR
FLIP-11-222C	X04TH136/FLIP97-229XFLIP97-126	4.00±0.00	MR	4.50±0.70	MR
FLIP-11-228C	X05TH141/FLIP97-5XSeI03TH10089	3.50±0.70	R	4.50±0.70	MR
FLIP-11-234C	X04TH72/X03TH-140XFLIP99-48	3.50±0.70	R	4.50±0.70	MR
FLIP-11-25C	X04TH60/X03TH-60XFLIP96-154	4.00±0.00	MR	4.50±0.70	MR
FLIP-11-80C	X04TH79/X03TH-147XFLIP96-154	4.00±0.00	MR	5.00±0.00	MR
FLIP-11-81C	X04TH79/X03TH-147XFLIP96-154	4.00±0.00	MR	3.50±0.70	R
ILC-263	PI 339223 (Susceptible)	9.00±0.00	HS	9.00±0.00	HS
Genotype		**		**	
Grand mean		4.23		5.06	
CV		12.17		12.40	
LSD (0.05)		1.043		1.270	
Error		0.149		0.175	

Key: HS= highly susceptible, S= susceptible, MS= moderately susceptible, MR= moderately resistant and R= resistant.

Table 2. Combined mean severity for *Ascochyta* blight on chickpea genotype over locations 2018.

Genotype	Pedigree	Mean±SD	Reaction
FLIP-10-317C	X04TH13/X03TH-13XFLIP96-154	7.25±1.25	S
FLIP-10-320C	X04TH86/X03TH-154XS01116	5.00±0.81	MR
FLIP-10-335C	X04TH57/X03TH-57XFLIP97-116	4.50±0.57	MR
FLIP-10-336C	X04TH63/X03TH-131XFLIP99-34	4.75±0.95	MR
FLIP-10-356C	X04TH131/FLIP95-68XFLIP97-83	3.75±0.95	R
FLIP-10-359C	X04TH138/FLIP98-22XFLIP95-51	4.00±0.81	MR
FLIP-10-361C	X04TH151/S01020XFLIP95-68	4.25±0.50	MR
FLIP-10-363C	X04TH152/S01069XFLIP97-90	3.75±0.50	R
FLIP-10-369C	X04TH172/ICCV-2X S01098	3.25±0.50	R
FLIP-10-371C	X04TH175/FLIP95-51XFLIP97-165	3.50±0.57	R
FLIP-10-372C	X04TH176/FLIP95-68XFLIP97-205	4.00±0.81	MR
FLIP-10-373C	X04TH177/FLIP97-90XFLIP97-229	5.00±0.81	MR
FLIP-10-377C	X04TH178/FLIP97-91XFLIP98-137	4.25±0.50	MR
FLIP-10-378C	X04TH180/FLIP97-205XFLIP97-229	3.75±0.50	R
FLIP-11-113C	X04TH127/FLIP98-230XFLIP97-116	3.75±0.95	R
FLIP-11-114C	X04TH128/FLIP98-232XFLIP99-34	4.00±0.81	MR
FLIP-11-130C	X04TH135/FLIP97-205XFLIP97-83	3.75±0.50	MR
FLIP-11-131C	X04TH135/FLIP97-205XFLIP97-83	4.25±0.50	MR
FLIP-11-137C	X04TH136/FLIP97-229XFLIP97-126	4.25±0.50	MR
FLIP-11-139C	X04TH136/FLIP97-229XFLIP97-126	4.50±0.57	MR
FLIP-11-13C	X04TH53/X03TH-53XFLIP97-116	7.50±1.29	S
FLIP-11-141C	X04TH136/FLIP97-229XFLIP97-126	4.50±0.57	MR
FLIP-11-146C	X04TH146/FLIP00-16XFLIP98-229	8.25±0.95	S
FLIP-11-148C	X04TH147/FLIP00-17XFLIP98-230	4.25±0.95	MR
FLIP-11-153C	X04TH156/ S01205XFLIP97-229	3.75±0.50	R
FLIP-11-154C	X04TH162/Pusa 1053XFLIP96-154	3.75±0.50	R
FLIP-11-155C	X04TH164/FLIP 87-59CXFLIP99-34	4.75±0.95	MR
FLIP-11-171C	X05TH106/FLIP97-131XFLIP00-14	8.00±1.41	S
FLIP-11-177C	X05TH192/ICCV03108XFLIP00-06	4.75±0.95	MR
FLIP-11-17C	X04TH56/X03TH-56XFLIP96-154	3.75±0.50	R
FLIP-11-203C	X05TH56/X04TH-183XX04TH-184	4.00±0.81	MR
FLIP-11-20C	X04TH56/X03TH-56XFLIP96-154	4.75±0.95	MR
FLIP-11-221C	X04TH93/X03TH-161XS01076	4.75±0.95	MR
FLIP-11-222C	X04TH136/FLIP97-229XFLIP97-126	4.25±0.50	MR
FLIP-11-228C	X05TH141/FLIP97-5XSel03TH10089	4.00±0.81	MR
FLIP-11-234C	X04TH72/X03TH-140XFLIP99-48	4.00±0.81	MR
FLIP-11-25C	X04TH60/X03TH-60XFLIP96-154	4.25±0.50	MR
FLIP-11-80C	X04TH79/X03TH-147XFLIP96-154	4.50±0.57	MR
FLIP-11-81C	X04TH79/X03TH-147XFLIP96-154	3.75±0.50	R
ILC-263	PI 339223 (Susceptible)	9.00±0.00	HS
Genotype		**	
Location		**	
Genotype x Location		NS	
Grand mean		4.65	
CV		13.60	
LSD (0.05)		0.903	
Error		0.632	

Key: HS= highly susceptible, S= susceptible, MS= moderately susceptible, MR= moderately resistant and R= resistant.

Table 3. Mean severity for Ascochyta blight on chickpea genotypes in 2019 growing season in Alem Tena and Dhera.

Genotype	Pedigree	Alem Tena Mean±SD	Reaction	Dhera Mean±SD	Reaction
Dhera	X98TH30/FLIP-93-55CXS-96231	4.50±0.70	MR	4.00±1.41	MR
FLIP10-234C	X04TH72/X03TH-140XFLIP99-48	4.00±0.00	MR	4.00±1.41	MR
FLIP10-361C	X04TH151/S01020XFLIP95-68	3.50±0.70	R	5.00±0.00	MR
FLIP10-363C	X04TH152/S01069XFLIP97-90	3.50±0.70	R	6.00±4.24	MS
FLIP10-371C	X04TH175/FLIP95-51XFLIP97-165	3.50±0.70	R	6.00±4.24	MS
FLIP10-372C	X04TH176/FLIP95-68XFLIP97-205	4.00±0.00	MR	7.00±2.82	S
FLIP10-377C	X04TH178/FLIP97-91XFLIP98-137	3.50±0.70	R	6.00±1.41	MS
FLIP11-114C	X04TH128/FLIP98-232XFLIP99-34	4.00±0.00	MR	6.50±3.53	MS
FLIP11-130C	X04TH135/FLIP97-205XFLIP97-83	4.00±0.00	MR	3.00±0.00	R
FLIP11-153C	X04TH156/ S01205XFLIP97-229	3.50±0.70	R	3.00±0.00	R
FLIP11-154C	X04TH162/Pusa 1053XFLIP96-154	3.50±0.70	R	5.00±2.82	MR
FLIP11-155C	X04TH164/FLIP 87-59CXFLIP99-34	3.50±0.70	R	3.50±0.70	R
FLIP11-177C	X05TH192/ICCV03108XFLIP00-06	5.00±0.00	MR	6.00±0.00	MS
FLIP11-17C	X04TH56/X03TH-56XFLIP96-154	4.00±1.41	MR	4.00±1.41	MR
FLIP11-203C	X05TH56/X04TH-183XX04TH-184	4.00±0.00	MR	7.50±2.12	S
FLIP11-20C	X04TH56/X03TH-56XFLIP96-154	4.50±0.70	MR	3.50±0.70	R
FLIP11-222C	X04TH136/FLIP97-229XFLIP97-126	4.00±0.00	MR	6.50±3.53	MS
FLIP11-228C	X05TH141/FLIP97-5XSel03TH10089	5.00±0.00	MR	5.00±2.82	MR
FLIP11-80C	X04TH79/X03TH-147XFLIP96-154	4.50±0.70	MR	6.00±4.24	MS
FLIP11-81C	X04TH79/X03TH-147XFLIP96-154	3.50±0.70	R	3.00±0.00	R
Grand mean		3.97		5.07	
LSD		0.626		1.196	
CV		14.16		15.29	
Genotype		NS		**	
Error		0.107		0.351	

Key: HS= highly susceptible, S= susceptible, MS= moderately susceptible, MR= moderately resistant and R= resistant.

Table 4. Combined mean severity of Ascochyta blight on chickpea genotype over locations 2019.

Genotype	Pedigree	Mean±SD	Reaction
Dhera	X98TH30/FLIP-93-55CXS-96231	4.70 ± 1.36	MR
FLIP10-234C	X04TH72/X03TH-140XFLIP99-48	3.50± 0.70	R
FLIP10-361C	X04TH151/S01020XFLIP95-68	4.25± 0.95	R
FLIP10-363C	X04TH152/S01069XFLIP97-90	4.75± 2.87	R
FLIP10-371C	X04TH175/FLIP95-51XFLIP97-165	4.75 ± 2.87	R
FLIP10-372C	X04TH176/FLIP95-68XFLIP97-205	5.50± 2.38	MR
FLIP10-377C	X04TH178/FLIP97-91XFLIP98-137	4.75±1.70	MR
FLIP11-114C	X04TH128/FLIP98-232XFLIP99-34	5.25 ± 2.50	MR
FLIP11-130C	X04TH135/FLIP97-205XFLIP97-83	3.50±0.57	R
FLIP11-153C	X04TH156/ S01205XFLIP97-229	3.25± 0.50	R
FLIP11-154C	X04TH162/Pusa 1053XFLIP96-154	4.25± 1.89	MR
FLIP11-155C	X04TH164/FLIP 87-59CXFLIP99-34	3.50±0.57	R
FLIP11-177C	X05TH192/ICCV03108XFLIP00-06	5.50±0.57	MR
FLIP11-17C	X04TH56/X03TH-56XFLIP96-154	4.00±1.15	MR
FLIP11-203C	X05TH56/X04TH-183XX04TH-184	5.75± 2.36	MS
FLIP11-20C	X04TH56/X03TH-56XFLIP96-154	4.00±0.81	MR
FLIP11-222C	X04TH136/FLIP97-229XFLIP97-126	5.25±2.50	MS
FLIP11-228C	X05TH141/FLIP97-5XSel03TH10089	5.00±1.63	MR
FLIP11-80C	X04TH79/X03TH-147XFLIP96-154	5.25±2.62	MR
FLIP11-81C	X04TH79/X03TH-147XFLIP96-154	3.50±0.50	R
Grand mean		4.51	
Genotype		**	
Location		NS	
Genotype x Location		NS	
LSD		0.834	
CV		15.6	
Error		0.107	

Key: HS= highly susceptible, S= susceptible, MS= moderately susceptible, MR= moderately resistant and R= resistant.

Correspondingly, Iqbal et al. (2002) assessed 356 genotypes and recorded that none of the 356 genotypes was showed highly resistant, whereas 7 genotypes were resistant and 75 moderately resistant. Furthermore, Pande et al., (2006) screened 148 wild accessions from 7 *Cicer spp.* viz., *C. bijugum*, *C. cuneatum*, *C. echinospermum*, *C. judaicum*, *C. pinnatifidum*, *C. reticulatum* and *C. yamashitae* for resistance to *A. rabiei* and 5 accessions found of *Cicer judaicum* exhibited resistant to the pathogen under controlled environmental conditions.

Similarly, Nasir et al., (2000) was comparable with present work they evaluated 14 chickpea cultivars, 29 land races of chickpea lines and 38 local breeding lines and establish that all of the Australian chickpea cultivars showed susceptible to *A. rabiei*, however 7 indigenous lines and 3 local advance lines were revealed resistant to *A. rabiei*. (Iqbal et al., 2010) screened 398 chickpea lines/verities only 18 were found resistant at seedling stage and among 277 advanced lines of chickpea only 2 lines were found highly resistant (Ghazanfar et al., 2010).

These studies showed that environmental conditions affect the resistance level of the same genotypes at different location in different growing season which is depends on microclimatic condition at that particulars season. Even at different growth stage genotypes express different resistance level. The similar result was obtained by Abdul et al., (2014), that resistance of most genotypes are depends on environmental conditions for different resistance levels. Hence, *A. rabiei* resistance is a multipart attempt suggesting that there is a series of different sources of resistance with different genes. *Ascochyta rabiei* has a inclusive range of resistance from different sources partaking different genes of resistance (Collard et al., 2003).

Most of the genotypes are not stable and consistent source of resistance with the same location at different growing season and with different location of the same genotypes even in similar planting time that seems environmental influenced such as temperature, disease gradient, and relative humidity. Consequently, our output was long-established these sensitivity reactions. Although the relevance of use the resistant varieties to control the disease, it's difficult to obtain a stable and durable source of resistance which is agreement as suggested by Malik et al. (2005). This result was confirmed by Singh & Reddy (1990) and Dolar et al. (1994) who proved the sensitivity behaviour of chickpea genotypes.

Our observation from results of the studies described as resistant by previous researchers like (Sheikh et al., 2010; Ilyas et al., 1991) have been stated that it is important to note that although similar distribution of rainfall and uniform inoculation was applied for both testing sites but resistance reactions was noted on different sets of genotypes that might be due different genes involved in *A. rabiei* resistance in the material screened. Infection might be due to different genes involved in mechanism of resistance at different plant growth stages or distinction in mode of infection at various stages (Reddy and Singh, 1993).

Many scholars have also testified the occurrence of moderate resistance to *Ascochyta* blight. Many sources of resistance to *Ascochyta rabiei* have been documented during the last five decades and these reports were founded either under natural conditions during natural epidemics or on artificial inoculation tests in the field or controlled environment (Alam et al., 2003; Iqbal et al., 2004; Chaudhary et al., 2005; Bashir et al., 2006).

Recommendation

Ascochyta blight is a destructive disease of chickpea in major chickpea growing area of the region. The existing result elaborate most of genotypes exhibited moderately resistant to moderately susceptible and only five promising genotypes were identified as resistant. The moderately resistant genotypes can be verified under natural conditions that not intensify the *A. rabiei* in absence of resistant genotypes.

The identification of resistance in Kabuli chickpea is a considerable importance to development of high yielding cultivars where *Ascochyta blight* is serious problem. There was high difference of environmental conditions, difference in disease pressure and distribution in each location and season. Therefore, intensive work is necessary on durable sources of resistance and stable adaptability as well as for the exploration of the mode of inheritance and mechanism of resistance. We are should have to concentrate our breeding efforts on genotypes that remain durable resistant at different locations and season.

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Conflict of interest statement

Authors declare that there is no conflict of interest in this work.

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