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[Short Communication]

Response of Chickpea Lines to *Ascochyta rabiei* at Two Growing Stages

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ABSTRACT
During winter 2004 and 2005, two field and glasshouse experiments were conducted to evaluate the response of 471 chickpea genotypes to *Ascochyta rabiei*, as Ascochyta blight (AB) disease in Chickpea (*Cicer aurietimum*). Frequent rainfall at flowering and pod formation stages made favorite conditions conducive for the infection and symptoms expression. So, the genotypes with high level of tolerance at seedling stage proved response to the pathogen under field condition. Disease at seedling and adult plant stage exhibited high association, although level of infection was higher at adult plant stage. In glasshouse 65 genotypes at seedling stage and in field experiment 14 genotypes at pod formation stage were resistant to the pathogen. Following green house and field screening methods, six genotypes FLIP98-229C, FLIP82-150C,NCS 950204, NCS 950219, NCS 9903 and PaidarxParbat from NARC and six lines (FLIP 00-20C, FLIP 02-18C, FLIP 02-44C, FLIP 97-120C, FLIP 02-39C and FLIP 97-102C) from ICARDA found resistant for multilocational / agronomic evaluation and use as resistant parent trials for high yielding AB resistance breeding varieties.

Key words: Germplasm, greenhouse, pod formation, resistant sources, chickpea and Ascochyta blight.

INTRODUCTION

Chickpea is an important food legume crop in Pakistan. It serves as a source of inexpensive high quality protein in the diets of many people and provides a rich crop residue for animal feed. Average yield of chickpea (615 kg/ha) in Pakistan is very lower than its actual yield potential because of environmental fluctuations (Haqqani *et al*., 2000). Ascochyta blight (*Ascochyta rabiei*) is the most wide spread and economically destructive disease of chickpea and is major limiting factor in low average yield (Iqbal *et al*., 2003). This disease has been reported in almost all chickpea growing countries including Pakistan (Nene *et al*., 1996). The disease was occurred in epidemic form in three consecutive years from 1980 to 1982, which resulted in the crop losses between 48 to 70% (Malik, 1984).

Management practices including seed fungicide dressing of the seeds, foliar application of fungicides, destruction of crop residues and rotation with non host crops such as cereals can be effective to minimize the disease perpetuation and incidence (Bashir and Ilyas., 1983; Reddy and Kabbabeh, 1984). However, these approaches are not feasible at farmer's fields. The only practical control of Ascochyta blight is thought producing resistant varieties against the pathogen. Researchers have identified numbers of resistant chickpea genotypes to Ascochyta blight at National and International levels (Hawtin and Singh, 1984; Nene and Reddy, 1987). The genotype of fungal pathogen has a tendency to produce new forms through mutation and random mating of virulent forms in nature as a consequence new virulent forms or races appear that are not daunted by the existing resistant genes in the released chickpea cultivars. The objective of present study was screening chickpea germplasm and breeding

Table 1. Analysis of variance and correlation between two stages of Ascochyta Blight in local and exotic chickpea germplasm

Source of germplasm	Number of genotypes	Genotypes	Stages	Error	Correlation between 2-stages
Arid Zone Research Institute (AZRI) Bhakkar	90	2.44	285.90	1.25	0.419** (df=88)
Arid Zone Research Institute (AZRI) Bahawalpur	10	1.56	81.00	0.80	0.218ns (df=8)
Nuclear Institute of Agriculture and Biology (NIAB), Faisalabad	99	1.62	179.73	1.73	0.253* (df=97)
International Centre for Agriculture Research in Dry Areas (ICARDA), Syria	82	2.30	4.99	1.95	0.394** (df=80)
National Agriculture Research Centre (NARC), Islamabad	190	2.75	40.17	1.72	0.473** (df=188)

* and ** are significant at 5 and 1 percent level of probability, respectively.

lines to AB resistance under field and glasshouse conditions and identifies agronomically superior AB resistant chickpea genotypes.

MATERIALS AND METHODS

During winter 2004-05, the seeds of 471 chickpea germplasm lines were obtained from national and international institutes were disinfected with Clorox solution (0.1% available chlorine) for 2 minutes. The seeds of each line were sown separately in disposable pots (7.5x15 cm) filled with sterilized soil and sand mixture (2:1) to obtain five seedlings. The susceptible line named C727 was considered as control. Pots were kept under glasshouse at 20±2 ^{0}C in sun light for 15 days before inoculation. Pots were watered from the top prior to inoculation. *A. rabiei* was grown on chickpea grains according to the procedure developed by Ilyas and Khan (1986) to produce spores. Two week old seedlings were inoculated by spraying aqueous spore suspension having concentration of 5x10^5 spores/ml.

The inoculum was prepared from 15 days old culture of *A. rabiei* multiplied on chickpea grains according to the procedure developed by Ilyas and Khan (1986). The inoculated seedlings were incubated in humid chamber (temperature 20-25 ^{0}C and RH< 80%) for 72 hours in the glasshouse. Disease observations were taken when susceptible check was killed on 1- 9 disease rating scale where 1 was highly resistant, 3 resistant, 5 tolerant, 7 susceptible and 9 highly susceptible (Singh *et al*., 1981).

The same germplasm lines were screened under field conditions during simultaneous crop season of 2004-2005. One 4m row of a susceptible line C 727 was planted after every two rows of the germplasm for better dispersion of pathogen and comparison of symptom expression. Each genotype was planted for in two replications. In addition, at early flowering stage, the field was sprayed with spore suspension of *A. rabiei* at 5x10^5 spores per ml. The spraying carried out daily in the evening till the appearance of blight. Spray of water with knapsac sprayer was carried out when needed to enhance RH for better disease development. The data for blight at vegetative stage was recorded according to Singh *et al*. (1981). Data for both sets of experiments were analyzed for variance and correlation for each source to compare genotypes and disease at two stages within and between germplasm sources using computer software MS Excel for Windows following the methods by Singh and Chaudhry (1985).

RESULTS AND DISCUSSION

Chickpea lines obtained from different locations showed various responses to pathogen (Table 1). The genotypes obtained from Arid Zone Research Institute (AZRI), Bahawalpur showed similar response. The material from National Agricultural Research Centre (NARC), Islamabad, International Centre of Agricultural Research for Dry

Table 2. Resistant (R) and Tolerant (T) genotypes selected from germplasm obtained from local and exotic sources screened in green house at seedling stage and in field at pod formation stage.

Source	Stages	Number	Genotype
AZRI. Bhakkar	Seedling	21 (R)	04A004, 04A005, PC2000, 04A006, 04A007, 04A008, 04A009, 04A010, 04A013, 04A014, 04A022, 04A023, 04A026, 04A027, 03A020, 03A010, 91A001, 96A4522, NCS98KG, 96A2004, 96A4580.
	Pod Formation	13 (T)	04A004, 04A006, 04A009, 04A026, 03A020, 02A005, 03A001, 03A010, 03A002, 96A2004, 96A4504, NCS98K49, 96A007
AZRI, Bahawalpur	Seedling	5 (R)	BRC-1, BRC-62, BRC-64, BRC-69, BRC-213
	Pod Formation	0	
NIAB, Faisalabad	Seedling	15 (R)	04101, 04103, 04106, 04109, 04110, 04127, 04128, 04130, 04138, 04160, 04161, 04169, 04170, 04187, 04190.
	Pod Formation	6 (T)	04101, 04102, 04117, 04137, 04181, 04187.
ICARDA, Syria	Seedling	4 (R)	Flip00-24C, Flip01-36C, Flip02-24C, Flip97-217C
	Pod Formation	12 (R)	Flip00-20C, Flip02-18C, Flip02-39C, Flip02-44C, Flip02-45C, Flip97-102C, Flip97-120C, Flip97-221C, Flip98-206C, Flip02-28C, Flip02-47C, ICC12004
NARC, Islamabad	Seedling	16 (R)	ICCV03402, ilc482, F98-133C, F82-150C, F99-28C, F01-5C, NCS950204, NCS9903, Pb1xCM72-1, CM89/90xPaidar 91, 86120xCM88, 89021xPb91, E101xPb91, L86120xPk519491, PaidarxParbat, E.32
	Pod Formation	2 (R)	F-98-229C, F82-150C
		35 (T)	BalkasarxPb1, F97-174C, F99-54C, F98-107C, F00-55C, F00-50C, F98-38C, F00-35C, F82-150C, F88-85C, F98-80C, F82-150C, F88-55C, F00-23C, F00-40C, F98-130C, F00-17C, F98-198C, F99-31C, F99-35C, F99-28C, F01-54C, F01-5C, NCS9914, NCS950204, NCS950219, NCS2005, NCS9903, , CM89/90xPaidar 91, CMC55-S, E101XPb1, L86120xPk519491, NCS950195, NCS9906, NCS950235

Areas (ICARDA), Syria, Arid Zone Research Institute (AZRI), Bhakkar and Nuclear Institute of Agriculture and Biology (NIAB), Faisalabad showed significant differences ($p< 0.01$) for genotypes.

Among all lines obtained from different locations, 75 genotypes which were scored 3, considered as resistant genotype, 54 lines which were scored 4-5 showed tolerance (Table 2) and 341 lines with scoring 6-9 were recognized as susceptible/highly susceptible genotypes. Out of total resistant genotypes, 61 genotypes were tolerant in glasshouse and only 14 genotypes were resistant in field. The lower number of resistant genotypes at pod formation stage in field conditions compared to glasshouse may be attributed to high susceptibility of chickpea at flowering stage and conducive environmental condition for blight incidence at NARC, Islamabad was another factor (Figure 1). The correlation between diseases at two stages for all the sources is shown in Table 1.

The frequency of chickpea lines grouped based on their response to pathogen at seedling and pod formation stages are shown in Figure 2. Disease tolerant (4- 5 disease rating) lines were amassed at seedling stage in all sources. Due to favorable environmental conditions for blight and high susceptibility of genotypes at flowering and pod formation stages only 14 genotypes were found resistant. Out of total resistant genotypes 12 were from ICARDA and 2 from NARC. Large number of resistant/tolerant genotypes at pod formation stage indicated the efforts made by chickpea breeders for developing resistant cultivars.

The moderately tolerant lines can be tested for the areas where the environment does not favor the blight. Chickpea lines developed at NARC withstood high levels of inoculum.

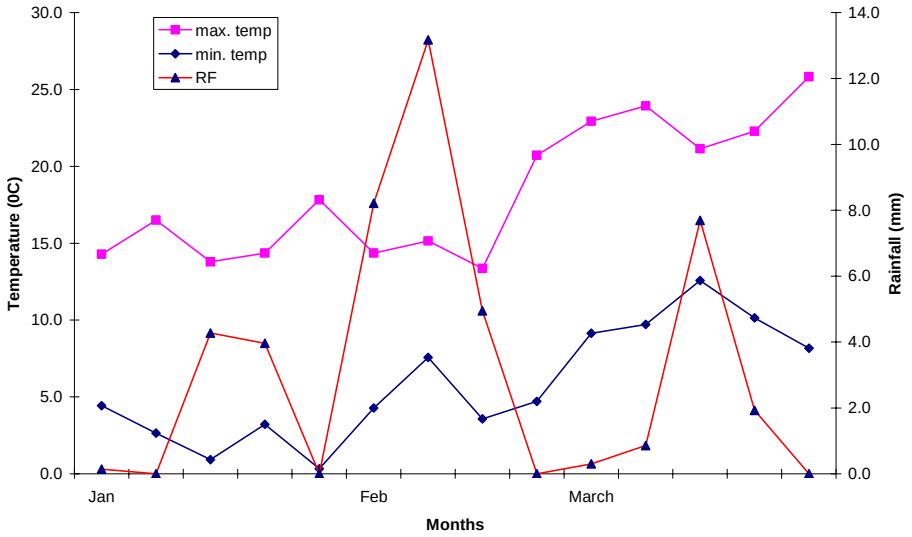

Fig 1. Precipitation, maximum and minimum temperatures at NARC Islamabad during the disease prone period.

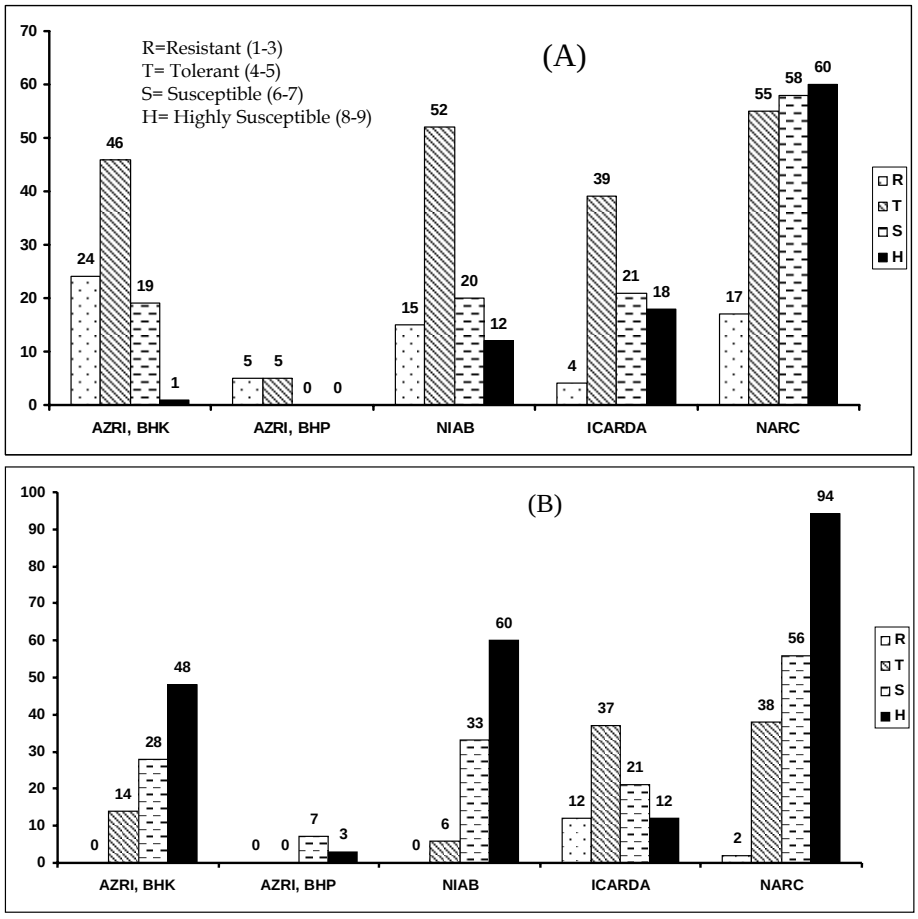

Fig 2. Frequency of genotypes obtained from local and alien sources for disease ratings at seedling (A) and pod formation stage (B)

pathogen in current research were reported as resistant by earlier researches (Reddy and Singh, 1990; Crino *et al*., 1985; Ilyas *et al*., 1991; Hussain *et al*., 2002; Iqbal *et al*., 2002).

The genotypes with indifference reaction at two stages are needed to be investigated for mode of resistance at particular stage as not to loose genes for yield potential. Infection might be due to different genes involved for resistance mechanism at various plant stages or may be because of variation in mode of infection at various stages (Reddy and Singh, 1993).

The information on the resistance to *A. rabiei* generated in the present study indicated that there is sufficient genetic variation in chickpea for this trait that can be exploited for disease control by building disease resistance pyramids. Six genotypes including viz., FLIP- 98- 229C, FLIP82-150C, NCS 950204, NCS 950219, NCS 9903 AND Paidarx Parbat from NARC and six lines (FLIP 00-20C, FLIP 02-18C, FLIP 02- 44C, FLIP 97-120C, FLIP 02- 39C AND FLIP 97-102C) from ICARDA were identified to be resistant/ tolerant at both growing stages and are suggested to test under multilocational/ agronomic trials for varietal development.

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