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EVALUATION OF CHICKPEA GERMPLASM AGAINST ASCOCHYTA RABIEI (PASS) LAB

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ABSTRACT

Evaluation of germplasm against chickpea blight (*Ascochyta rabiei* (Pass) Lab) is an effective method to characterize the resistance and susceptibility level of gram varieties. In present study, 48 varieties/lines collected from Ayub Agriculture Research Institute, (ARRI) Faisalabad were screened by artificial inoculation, at research area of Plant Pathology, University of Agriculture, Faisalabad. Among 48 genotypes, 16, 8, 3, 10, 11 were found highly susceptible, susceptible, moderately susceptible, resistant and moderately resistant, respectively. The lines showed highly susceptible reaction were: K-97006, K-97007, K-98009, K-94002, K-98014, K-98012, K-52721, K-60028, K-93001, K-92030, K-96022, D-CM98, D-CAM68, D-91013, D-97074, D-96022 and Punjab-1(check), while, genotypes showed susceptible reaction were viz: K-95058, K-60016, K-60034, K-60048, D-91224, D-03019, D-05028 and D-03006. There were only 3 lines (K-98007, K-50076 and K-95041) displayed moderately susceptible response. Whereas, K-96033, K-89169, K-90395, D-91017, D-89044, D-05006, D-96018, D-86030, D-96032, D-1CC-5127 and D-03009 exhibited moderately resistant response against chickpea blight. While lines, K-60013, K-98008, D-97092, K-96001, K-96022, D-91055, D-90272, D-96050, D-Pb2008 and D-Pu502-362 showed resistant reaction. Results clearly mentioning that most of the genotypes collected from ARRI were susceptible against Ascochyta blight.

Key words: Screening, chickpea, genotypes, *Ascochyta rabiei.*

INTRODUCTION

Chickpea (*Cicer arietinum* L.), is the most essential and chief rabi crop in different parts of the world. Chickpeas are of two types; Desi (black) types are usually small size, having rough surface and yellow to black testa. Black grams are cultivated in South Asians countries, Iran, Ethopia and Mexico. The other types of chickpeas are white or Kabuli. These are broad sized, tender surface and having light creamy colour, mostly cultivated in Mediterranean countries, Australia, North America, North Africa and West Asia (FAO., 2010).

In Pakistan, chickpea is the largest rabi crop, cultivated on an area of 1050 thousand hectares with yield 571 tones, (Anon., 2010). It is self-pollinated, diploid and worldwide most vital crop after dry beans and field peas (Pande *et al*., 2005). It is rich source of high-class protein and also used for animal feed.. Chickpeas sustain biological nitrogen fixation and cereal-legume rotations in cropping systems. In low temperature areas, grams are more forbearing to fungal blight, drought, heat and low fertility. However, fungal blight has been proven more upsetting factor for yield decline (Pande *et al*., 2005).

Chickpea blight caused by *Ascochyta rabiei* (Pass.) Lab. (telomorph: *Didymella rabiei*) (Kovachevski) v. Arx, is the most devastating check for the gram production around the globe (Bretag *et al*., 2008; Chandirasekaran *et al*., 2009). The disease in sever form may result yield losses up to 100% (Pande *et al*., 2005). In Pakistan, chickpea blight epidemics reasoned for heavy yield losses, whereas, under normal conditions it causes 20-25% yield loss per annum (Jamil *et al*., 2010).

The pathogen over-summers on diseased crop residues as anamorph (asexual) in the form of pycnidia having conidia, and teleomorph (sexual) psedothecia with ascospores. Conidia are proliferated by rain splashes, while ascospores through both wind and water (Shtienberg *et al*., 2005). Subsequently, primary infection takes place and necrotic spots establish with conidia at the center. These conidia work as inoculum for secondary infection during rain (Shtienberg, 2010).

Chickpea blight is mainly controlled through fungicides. As the fungicides are not eco-friendly, and increase input costs when applied on larger area, therefore not recommended. Further, pathogen of *A. rabiei* is highly variable and comprises of various pathotypes or races (Ilyas *et al*., 2007). Hence, resistant or tolerant varieties of chickpea may be the most effective tool to control gram blight (Ilyas *et al*., 2007). But, present cultivated varieties with desirable agronomic traits are vulnerable to blight disease, presumably because of emergence new pathotypes or races (Jamil *et al*., 2010). Therefore, there is a dire need for the identification of durable resistant genotypes and incorporation of their resistance genes into commercial

cultivars. For this reason, present study was designed to screen chickpea germplasm collected from Ayub Agriculture Research Institute (ARRI), Faisalabad.

MATERIALS AND METHODS

1. Isolation of *A. rabiei* and preparation of Mass culture: Severely blight infected pods of chickpea were collected from chickpea fields and refrigerated at 5-8^{0}C. The isolation carried out by the procedure adopted by (Ghazanfar *et al*., 2010). The culture of *A. rabiei* was purified through spore streak method on chickpea seed agar medium and maintained at 5^{0}C (Ghazanfar *et al*., 2010). Mass culture of the fungus was prepared by the method described by (Ghazanfar *et al*., 2010).

2. Inoculation of Nursery: Forty eight varieties both comprising of black and white genotypes were screened against chickpea blight disease under Augmented design, at the Research Area of Plant pathology, University of Agriculture, Faisalabad. Disease was produced through artificial inoculation and expedited by maintaining moisture above 80% by giving two fresh water sprays during afternoon and evening. Genotypes were sown in double rows with three meter length keeping row to row distance 30 cm and plant to plant 15 cm, respectively. Punjeab-1 (Pb-1) the most susceptible variety was planted after every two test lines as spreader. When the crop reached at booting stage nursery was sprayed daily with spore suspension of *A. rabiei* (1x 10^5 spores /ml). The spore suspensions spray continued until check lines of Pb-1 become fully susceptible. Development of Ascochyta disease was tried to enhance by doing continuous fresh water spray on daily basis.

3. Disease Rating: Data were recorded by using two scales; 9 point rating scale modified by (Pande *et al*., 2011) and 1-10 rating scale (Gowen *et al*., 1989). According to Pande *et al*., 2011 scale comprised of 1–9 ratings (modified from Jan and Wiese, 1991); 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 killed; 7=lesions as in 5, defoliation, broken, dry branches very common, up to 25% of plants killed; 8= symptoms as in 7 but up to 50% of the plants killed and 9= symptoms as in 7 but up to 100% of the plants killed. Test lines 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).

RESULTS AND DISCUSSION

Forty eight advanced lines (Black and White) collected from Ayub Agriculture Research Institute, (ARRI) Faisalabad, most of them were highly susceptible and susceptible, while, other demonstrated moderately susceptible, moderately resistant and resistant response. The number of highly susceptible and susceptible lines were 16 and 8, respectively. 3 lines displayed moderately susceptible response. There were 10 and 11 lines which showed resistant and moderately resistant response, respectively. No genotype was found highly resistant. The average maximum disease severity (up to 81.25%) was recorded on Punjab-1(check) (Table.1). The average disease severity on highly susceptible to susceptible lines were very high in contrast to moderately resistant and resistant. Responses of all genotypes is given in Table.1. Advanced lines showed highly susceptible response were viz; K-97006, K-97007, K-98009, K-94002, K-98014, K-98012, K-52721, K-60028, K-93001, K-92030, K-96022, D-CM98, D-CAM68, D-91013, D-97074, D-96022 and Punjab-1(check). Whereas, with susceptible level included; K-95058, K-60016, K-60034, K-60048, D-91224, D-03019, D-05028 and D-03006. Only three lines, K-98007, K-50076 and K-95041 showed moderately susceptible response. Chickpea lines exhibited moderately resistant response against blight were; K-96033, K-89169, K-90395, D-91017, D-89044, D-05006, D-96018, D-86030, D-96032, D-1CC-5127 and D-03009. While lines, K-60013, K-98008, D-97092, K-96001, K-96022, D-91055, D-90272, D-96050, D-Pb2008 and D-Pu502-362 displayed resistant reaction (Table.1).

During screening, it was found that most of genotypes were highly susceptible to susceptible. This shows that most of chickpea germplasm did not have resistance genes. In Pakistan, present available germplasm is mostly susceptible against chickpea blight. Iqbal *et al*. (2010) screened out one hundred and forty five genotypes against Ascochyta blight and wilt diseases. Most of the genotypes showed susceptible to highly susceptible reaction. Similarly, Bokhari *et al*. (2011) evaluated the resistance level of ten cultivars of gram and observed that maximum number of varieties were susceptible under field conditions. To date the different varieties of different research institutes are mostly susceptible to present races of *Ascochyta rabiei* (Ghanzanfar *et al*., 2010). Thus, only those genotypes having resistance genes of both local and exotic can be released as commercially grown varieties (Nasir *et al*., 2000).

A comprehensive study on the number of genes conferring resistance against chickpea blight, their nature, and diversity is essential for exploiting a particular resistance source in resistance breeding programme (Ilyas *et al*., 2007). Chickpea blight resistance in gram cultivars

Table-1:- Response of chickpea genotypes against *Ascochyta rabiei*

Sr. No	Genotypes	Disease Rating	% Average Severity	Reaction
1	K-97006	9.0	60	HS
2	K-97007	9.0	58.75	HS
3	K-60013	3.0	3.75	R
4	K-98009	9.0	56.25	HS
5	K-94002	9.0	63.75	HS
6	K-98007	6.0	36.25	MS
7	K-98008	3.0	7.5	R
8	K-98014	9.0	63.75	HS
9	K-98012	9.0	56.25	HS
10	K-52721	9.0	61.25	HS
11	K-50076	6.0	36.25	MS
12	K-95041	6.0	32.5	MS
13	K-95058	7.0	45	S
14	K-96033	4.0	16.25	MR
15	D-97092	3.0	10	R
16	K-96001	3.0	7.5	R
17	K-60016	7.0	41.25	S
18	K-60028	9.0	65	HS
19	K-93001	9.0	58.75	HS
20	K-60034	7.0	40	S
21	K-60048	7.0	43.75	S
22	K-89169	4.0	12.5	MR
23	K-90395	4.0	13.75	MR
24	K-92030	9.0	67.5	HS
25	K-96022	3.0	5	R
26	K-96022	9.0	58.75	HS
27	D-91224	7.0	45	S
28	D-CM98	9.0	58.75	HS
29	D-91055	3.0	10	R
30	D-91017	4.0	15	MR
31	D-CAM68	9.0	56.25	HS
32	D-90272	3.0	10	R
33	D-89044	4.0	15	MR
34	D-91013	9.0	63.75	HS
35	D-05006	4.0	17.5	MR
36	D-97074	9.0	56.25	HS
37	D-96050	3.0	10	R
38	D-96022	9.0	60	HS
39	D-96018	4.0	17.5	MR
40	D-86030	4.0	16.25	MR
41	D-03006	7.0	40	S
42	D-03019	7.0	43.75	S
43	D-05028	7.0	42.5	S
44	D-96032	4.0	15	MR
45	D-03009	4.0	17.5	MR
46	D-1CC-5127	4.0	20	MR
47	D-Pb2008	3.0	5	R
48	D-Pu502-362	3.0	3.75	R
49	Punjab-1(check)	10	81.25	HS

HS= Highly susceptible, S= Susceptible, MR= Moderately resistant, R= Resistant.

is controlled by single dominant gene or recessive gene (Singh and Reddy, 1991). Ali *et al*. (2011) conducted molecular marker study which revealed that resistance in chickpea is due to presence of three independently segregating dominant genes and a recessive gene. Additive genes and interallelic interaction influence resistance (Hina *et al*., 2008). Various Quantitative Trait loci (QTL) also contribute towards inheritance of blight resistance (Collard *et al*., 2003). Different biochemicals and physiological characters of varieties also control the resistance of the chickpea cultivars. Randhawa *et al*. (2009) worked on role of glandular hairs density, population and size of stomatal aperture in chickpea cultivars against Ascochyta blight. It was found that these characters played key role in cultivars resistance.

Ascochyta blight resistance is a complex venture controlled by various different resistant sources comprises of resistance genes. Under such situation, introducing diverse résistance genes into cultivars may assist in developing resistance stability in commercially grown varieties.

Conclusion: Sources of resistance identified during this study, can further be exploited in breeding programmes for the development of disease resistant commercial cultivars after determining their genetics. Most of genoytpes were highly susceptible to susceptible against chickpea blight indicating scarcity of resistance in Pakistani chickpea germplasm. To develop resistance, therefore, an intensive screening of chickpea germplasm is required to be conducted. Different résistance genes into commercial cultivars through pyramiding may facilitate in building up the level of resistance and increasing the durability of resistance in the commercial cultivars.

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