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RESPONSE OF FIELD PEA (PISUM SATIVUM L.) GENOTYPES TO ASCOCHYTA BLIGHT (MYCOSPHAERELLA PINODES) DISEASE IN ARSI HIGHLANDS, SOUTHEASTERN ETHIOPIA

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Abstract:-

The yield of field pea in Ethiopia is hampered due to the prevalence of Ascochyta Blight disease. 49 field pea materials including 21 introduced field pea materials; 19 single plants selected from bulked gene pool materials and 9 released varieties were evaluated under field condition of two environments using simple lattice design to identify resistant genotypes. The current study revealed that considerable variation was found for response against ascochyta blight diseases and yield performance even if high level of resistance materials were not identified. High degree of disease severity was observed at Kofele site than Bekoje. Out of the total 49 genotypes; 16 genotypes (GPHA03, GPHA019, GPHA06, GPHA01, GPHA018,P-313-010 , P-313-045 ,P-313-086, P-313-082, P-313-071 , P-313-065 , P-313-098 , P-313-061 , P-313-068 , P313-067 and PDFPT-BEK) were moderately resistant and the remaining 33 materials were susceptible to ascochyta blight disease. Genotypes PDFPT-BEK, P-313-067,P-313-010, and P-313-082 were relatively high yielder and moderately resistant materials. It is better to repeat this trial in multi-location and season to check disease and yield stability for further breeding purpose.

Keywords:-*Ascocayta blight, disease severity,host, Pisum sativum, resistance.*

INTRODUCTION

Pulses are the second most important crops both in terms of area coverage and in terms of total production after cereals. Field pea (*Pisum sativum* L.) is the fourth most important legume crop in Ethiopia after faba bean, haricot bean and chick pea in terms of both area and total amount of production. (CSA, 2018).

It is grown on 220,508.39 hectares of land with total production of 368,519.065 ton and productivity of 1.67t/ha; which accounts for 13.79 % of the total area covered by pulses and 12.37 % of the total pulses production in the country (CSA, 2018).The crop is widely cultivated in potential mid and high altitude areas of the country characterized with elevations of 18003000 meters above sea level and receiving average annual rainfall of 700-1100mm. Field pea is grown by small-scale farmers on marginal lands with minimum management practices as compared to cereals

It has a great economic merit in the country. It serves as a source of food and feed with valuable and cheap sources of protein as a complement to cereals for the majority of the poor population mainly for those who cannot afford to use proteins from animal source. It is also a good source of cash to the farmers. Due to its pertinent atmospheric nitrogen fixing capacity (up to 60 kg ha^{-1} $year^{-1}$); field pea is suitable rotation crop with nationally important cereal crops like wheat, barley and teff. It also plays an important role in soil fertility restoration and controlling disease epidemics as a suitable rotation and break crop where cereal mono-cropping is predominant at areas like Bale and Arsi, Ethiopia(Angaw and Asakew, 1994).

Despite its importance; the average production and productivity of field pea under smallholder farmers is very low (1.67 t ha^{-1}) (CSA, 2018) even if there is availability of high yielding varieties (>3 t ha^{-1}) (MoALR, 2017).

The low productivity of the crop is attributed to susceptibility to many biotic and abiotic stresses (Sahile *et al*., 2008 and Mussa *et al*., 2008). From the biotic category, diseases are important factors limiting the production of food-legume crops as a whole and field pea specifically in Ethiopia (Nigussie *et al.,* 2008). Fungi diseases are among major production constraints in field pea and particularly Ascochyta blight is destructive disease in Ethiopia (Gorfu, 2000). Most diseases of field pea caused by fungi includes Ascochytapinodes (teleomorph 4 = Mycosphaere.Uapinodes), A. pisi, Septoriapisi, Phomamedicaginis var. pinodella, Erysiphepoligoni, and Fusarium spp. (Jennifer, 2012).

Ascochyta blight distracts all stages of field pea crop causing stem, leaf and pod spots and lesions, foot and stem girdling and lesions that finally leads to brightening of the whole crop. It also causes serious quality losses and decreases plant growth and biomass. This destruction of foliage and the ultimate effects on productivity of field pea crop are mostly dependent on time and level of infection, host reaction and prevailing local climatic conditions (Nasir and Hoppe, 1998). Ascochyta has there three species that cause disease of field pea viz. Ascochytapisi, Mycosphaerellapinodes, and Phomamedicaginis var. pinodes, of which M. pinodes is the most damaging of the three worldwide pathogens too as cited by Musa *et al* (2009) . It contributes to grain yield instability and reduces farmers' confidence in growing field pea. It occurs every year in all major field pea growing areas (Musa *et al.*,2009). It is stubble and seed born pathogen where inoculum infecting plant parts and adhering on seed surface as dormant mycelia, spores and fruiting bodies of the fungus, could be responsible for disease transmission.

Musa *et al* (2009) cited that no field resistance of field pea cultivars to this disease. Breeding field pea for M. pinodes resistance is complicated because it is inherited as a complex polygenic trait (Wroth, 1998). However, at Holetta, there are some lines identified as moderately resistant to Ascochyta blight (e.g., IFPI series introduced from Australia) that could be used in the breeding program as source of resistance gene (Musa *et al.*, 2009) . The pathogen causes significant losses when the cropping system and environmental conditions favor disease developments that include frequent rain and high humidity regimes (Jennifer, 2012).

Yield loss on field pea due to this disease was reported to be 50-75% in USA, 45% in England, 15-75% in Australia and 25-45% in Canada (Jennifer, 2012). In Ethiopia, A. pinodes plays a major role in the destruction of the crops and reduces seed yield up to 53%, especially in the major production areas of the central highlands (Gorfu and Hiskias, 2001)

Ascochyta blight and Powdery mildew has been reported to be the major field pea disease in the mid-altitudes and may reduce yields by 20-30% under moderate severity.

26% of yield losses have been reported due to ascocayta blight severity on local field pea cultivar from plot without fungicide application at sinana south eastern Ethiopia.(Adisu and Ermias, 2017).

Ascochyta blight is becoming a continuous threat in Ethiopia in general and particularly in high land of Arsi and west Arsi field pea growing areas of South Eastern Ethiopia next to powdery mildew.

Currently, different attempts have been made for control of this disease including fungicide sprays. But due to high cost of fungicides, social and health related and environmental impacts. it is better to seek other alternative means of disease control methods. In view of the cost-effective solution for Ascochyta blight, Host resistance is one of the most widely used Control measure for this disease.

Hence; there is a need to develop high yielding and ascochyta blight resistant varieties. Thus, developing Resistant and high yielder field pea genotypes are widely recognized as the safest, most economical and most effective method for protecting crops from this disease. Therefore, the present study was designed to evaluate different field pea genotypes

against ascochyta blight disease to identify resistant genotypes naturally under field condition of Bekoje and Kofele substation for further utilization.

Materials and Methods Experimental sites

Field experiments were carried out during the main cropping season (June to November) of the year 2018/19 at Bekoji and Kofele sub-station of Kulumsa Agricultural Research Center.

Table 1: Description of the test environments.

Locations	Locations	Locations
Latitude	Bekoji (07º31′22″N)	Koffale (07º04′27″N)
Longitude	39º14′46″E	38º46′45″E
Altitude (m.a.s.l.)	2780	2660
Mean annual rainfall (mm)	1010	1211
Minimum temperature (0C)	7.9	7.1
Maximum temperature (0C)	16.6	18
Agro-ecologies	CHMH	CHMH

CHMH: Cool Humid Mid Highland
Source (Tamene, 2017)

Experimental Materials

Forty-nine field pea materials including, twenty-one introduced field pea materials; nineteen single plants selected from bulked gene pool materials and nine released varieties were evaluated at Bekoji and Kofele substation of Kulumsa Agricultural Research Center.

Table 2 Description of field pea Genotypes used in the Study

No	Genotype	Source	Pedigree /Origin
1	GPHA-05	HARC	SPS
2	GPHA-013	HARC	SPS
3	GPHA-03	HARC	SPS
4	GPHA-019	HARC	SPS
5	GPHA-02	HARC	SPS
6	GPHA-010	HARC	SPS
7	GPHA-07	HARC	SPS
8	GPHA-08	HARC	SPS
9	GPHA-06	HARC	SPS
10	GPHA-012	HARC	SPS
11	GPHA-04	HARC	SPS
12	GPHA-016	HARC	SPS
13	GPHA-09	HARC	SPS
14	GPHA-01	HARC	SPS
15	GPHA-018	HARC	SPS
16	GPHA-017	HARC	SPS
17	GPHA-014	HARC	SPS
18	GPHA-011	HARC	SPS
19	GPHA-015	HARC	SPS
20	P -313-010	ICARDA	Australia
21	P -313-045	ICARDA	Australia
22	P -313-086	ICARDA	Australia
23	P -313-082	ICARDA	Australia
24	P -313-042	ICARDA	Australia
25	P -313-071	ICARDA	Australia
26	PDFPTBEK	ICARDA	Australia
27	G227 63-2C	HARC	G22763-2c
28	P -313-053	ICARDA	Australia
29	P -313-070	ICARDA	Australia
30	P -313-027	ICARDA	Australia
31	P -313-065	ICARDA	Australia
32	P -313-026	ICARDA	Australia
33	P -313-090	ICARDA	Australia
34	P -313-046	ICARDA	Australia
35	MILKEY	HARC	NEP634 X1801
36	P-313-098	ICARDA	Australia
37	HASABE	HARC	JI No 116
38	HOLETA	HARC	Holeta local-90/
39	WALMERA	HARC	FpExDzX 305PS2108-22-1
40	p-313-059	ICARDA	Australia
41	p-313-061	ICARDA	Australia
42	p-313-068	ICARDA	Australia
43	p-313-089	ICARDA	Australia
44	p-313-067	ICARDA	Australia
45	p-313-003	ICARDA	Australia
46	ADI	HARC	G22763-2CX
			305PS210813-2
47	BURKITU	HARC	EH-92004-02
48	BILALO	KARC	
49	BURSA	KARC	

Where, SPS= single plant selection from gene pool, KARC=Kulumsa Agricultural Center, HARC= Holeta Agricultural Center, ICARDA =International Center of Agricultural Research for Dry Areas.

Experimental design and treatments

The experiment was laid out in a 7 x 7 simple lattice design with two replication. Each plot consists two rows of 4m length with spacing of 20cm between rows and 10cm between plants. Each genotype was planted in a plot size of 1.6 m^2. The space between plots within block was 1 m and between blocks was 1.5m. Each row was sown 80 seed and each plots contained total of 160 seeds.100kg/ha DAP fertilizer was applied during planting time and all other recommended agronomic practice was followed for both locations

Disease scoring
Ascochyta blight Disease reactions of individual genotypes were recorded (1-9 scale) on whole plot basis 70 days after Planting
Based on the disease score, test genotypes were categorized for their reaction to AB infection according to (Paul *et al.*, 2013) scale where,
1, asymptomatic (A);
1.1–3.0, resistant (R);
3.1-5.0, moderately resistant (MR);
5.1–7.0, susceptible (S); and 7.1–9.0, highly susceptible (HS).

The whole plant disease ratings were averaged across replicates to generate a mean disease rating for each genotype before analysis.

Determination of grain yield
The data for grain yield and other agronomic traits were taken following the standard practice for field pea trial used. Grain yield adjustment was made based on oven dried seeds and adjusted to constant moisture level of 10%. The total grain yield was recorded on a plot basis and converted to Kg ha^{-1} for statistical analysis.

Data analysis
The disease ratings were subjected to Friedmans non-parametric analysis of variance while yields was subjected to ANOVA using General Linear Model (PROC GLM) of the SAS
Procedure using version 9.0 of the software (SAS, 2002). The significance of variance effects was considered at $P \leq 0.05$, $P \leq 0.01$, and $P \leq 0.001$, respectively Homogeneity of error mean square between the two locations was tested by F-test (Hartley, 1950) and combined analyses were performed for parameters whose error mean squares were homogenous Mean comparison among genotype were carried out using Duncan Multiple range Test(DMRT) (Duncan, 1955).

Result and Discussion
The present study indicated that,there were significant differences in AB responses between the genotypes at kofele site and combined over the two locations(Table 3). The significant differences obtained in the present experiment indicated the presence of considerable variation in the response to ascochyta blight in the genetic materials studied. Tamene (2017) reported Significant variations among twenty five field pea genotypes for ascochyta blight response and grain yield (kg/ha) in the study of genetic variability, heritability and genetic advance from Selection in Elite Breeding Materials of Field Pea (*Pisum sativum L.*) genotypes.

Test locations (sites) exerted very highly significant effect on ascochyta blight response which means the environment affected the disease development. It indicates the phenotypic expression of these traits were different at both locations. The interaction effects of locations and genotypes were exerted significant effects for ascochyta blight response. (Table 3). Significant of genotype (G) x location (L) interaction observed in this study indicated the differential response of genotypes for this trait at each location.

High degree of disease severity was observed at kofele site than bekoje. This could be due to frequent rain and high humidity happened at pod setting stage at kofele and the environmental conditions favored disease developments (high degree of disease severity) .The disease severity was also increased from initial stage to grain filling (pod setting) stage and the symptoms showed on plant parts like leaf,stem and pod. Hence; the tested genotypes were evaluated for ascochyta blight response depend on highest location severity (kofele site).

Amongst test genotypes, GPHA03, GPHA019, GPHA06, GPHA01, GPHA018,P-313-010 , P313-045 ,P-313-086, P-313-082, P-313-071 , P-313-065 , P-313-098 , P-313-061 , P-313-068 , P-313-067 and PDFPT-BEK had moderate disease rating between 3.1 – 5.0 (moderate disease resistance) than other genotypes(Table 3). Majority of the introduced materials were moderately resistant relatively compared with others. This finding was in agreement with Musa *et al* (2009); who reported some introduced materials were moderately resistance to ascocayta blight.
Majority of other genotypes were susceptible to AB (mean disease rating >5.0) (Table 3).Unfortunately, there were no resistance genotypes to AB with mean disease scores <3.0 in kofele and combined over the two sites,similarly to other reports (Boros and Wawer, 2007 ; Musa *et al*.,2009 ; Lech B,2010). However, some genotypes moderately resistant were identified (Table 3).

There were highly significant (P<0.01) differences in yield performance of test genotypes in both sites and combined over the two locations. (Table 4).
The interaction between genotype and environment (sites) also significantly (P<0.01) affected the grain yield production amongst test genotypes. Grain yield performances of most of the genotypes were varied across the two locations.
Genotypes PDFPT-BEK, P-313-053, P-313-010, P-313-046, P-313-067, GPHA-015 and GPHA06 were relatively the highest yielding genotypes in their performance of grain yield and other yield related traits at both sites and combined over the two locations. Genotype PDFPT- BEK yielded of 6089kg ha-1 at the location Bekoji, whereas BILALO yielded the best of 6627kg ha1at the location kofele (Table 4).

The mean location grain yield across genotypes ranged from 3722kg ha-1 in bekoje to 3884kg ha-1 in kofele . The mean grain yield of field pea genotypes ranged from1820 to 6081 kg ha^{-1} and 1618 to 6627 kg ha^{-1} at bekoie and kofele respectively (Table 4). The mean grain yield of field pea genotypes across/combined locations varied from 1955kg ha^{-1} for genotype GPHA-011 to 5997 ha-1 for PDFPT-BEK, with an overall location mean of 3802.84 kg ha-1 (Table 4).

Table 3. Mean Ascochyta blight scores (scale 1–9 where 1, no disease and 9, dead plants) for 49 test field pea genotypes in Bekoji and kofele.

No.	Genotype	Bekoje	Kofele	Mean	Response based on highest location severity (kofele)
1	GPHA-05	4	5.5	4.8	S
2	GPHA-013	3	6	4.5	S
3	GPHA-03	2.7	3.5	3.1	MR
4	GPHA-019	4	5	4.5	MR
5	GPHA-02	4	6	5.0	S
6	GPHA-010	3	6	4.5	S
7	GPHA-07	3	6	4.5	S
8	GPHA-08	2.5	5.5	4.0	S
9	GPHA-06	3.5	5	4.3	MR
10	GPHA-012	3.5	6	4.8	S
11	GPHA-04	4	6	5.0	S
12	GPHA-016	3	5.5	4.3	S
13	GPHA-09	4	5.5	4.8	S
14	GPHA-01	3.5	5	4.3	MR
15	GPHA-018	3.5	5	4.3	MR
16	GPHA-017	3.5	6.5	5.0	S
17	GPHA-014	3	6.5	4.8	S
18	GPHA-011	4	5.5	4.8	S
19	GPHA-015	3.5	7	5.3	S
20	P -313-010	3	5	4.0	MR
21	P -313-045	3.5	4.5	4.0	MR
22	P -313-086	3	4.5	3.8	MR
23	P -313-082	3	3.5	3.3	MR
24	P -313-042	3.5	5.5	4.5	S
25	P -313-071	3	5	4.0	MR
26	PDFPTBEK	3	3.5	3.3	MR
27	G 227 63-2c	2.5	5.5	4.0	S
28	P -313-053	3	6.5	4.8	S
29	P -313-070	3	5.5	4.3	S
30	P -313-027	3	6	4.5	S
31	P -313-065	3	5	4.0	MR
32	P -313-026	2.5	6.5	4.5	S
33	P -313-090	4	6	5.0	S

*, **, *** and NS indicate significance levels at 0.05, 0.01, 0.001 and non- significance, respectively. SE =standard error MR =moderately resistance and S = susceptible

Table 4. Mean grain yield (Kg ha-1) for 49 test Field pea genotypes in Bekoje and Kofele .

No.	Genotype	Bekoje	Kofele	Mean
1	GPHA-05	3854	1726	2790jklmnop
2	GPHA-013	2941	2564	2753lmnop
3	GPHA-03	1820	2508	2164op
4	GPHA-019	2862	4904	3883hijkl
5	GPHA-02	4827	3441	4134fghij
6	GPHA-010	4305	3171	3738hijkl
7	GPHA-07	3713	1632	2672lmnop
8	GPHA-08	3858	2926	3392jklmnop
9	GPHA-06	4032	4669	4351fghi
10	GPHA-012	2792	3180	2986jklmnop
11	GPHA-04	4593	2707	3650hijklmn
12	GPHA-016	3050	1618	2334nop
13	GPHA-09	3735	3301	3518hijkl
14	GPHA-01	3862	2347	3105klmnop
15	GPHA-018	4192	1801	2997jklmnop
16	GPHA-017	3104	2642	2873lmnop
17	GPHA-014	3578	1678	2628lmnop
18	GPHA-011	2017	1894	1955p
19	GPHA-015	4731	5050	4891efg
20	P -313-010	3078	5582	4330ghijk
21	P -313-045	2676	3754	3215jklmno
22	P -313-086	3422	3973	3697hijkl
23	P -313-082	3702	5582	4642fgh
24	P -313-042	3752	3408	3580ijklmn
25	P -313-071	3804	2510	3157klmnop
26	PDFPT-BEK	6081	5913	5997a
27	G 227 63-2C	4062	2170	3116hijklmn
28	P -313-053	5474	6100	5787cde
29	P -313-070	3525	3807	3666hijklm
30	P -313-027	1855	3671	2763lmnop
31	P -313-065	2544	3950	3247jklmnop
32	P -313-026	3928	4414	4171fghi
33	P -313-090	3489	4425	3957hijkl
34	P -313-046	4329	4454	4392fghi
35	MILKEY	4546	5724	5135ef
36	P-313-098	2080	2914	2497mnop
37	HASABE	2721	3223	2972jklmnop
38	HOLETA	3550	3792	3671fghij
39	WALMERA	4683	3621	4152fgh
40	p-313-059	2800	2738	2769klmnop
41	p-313-061	4175	3513	3844hijkl
42	p-313-068	3503	3740	3621hijklmn
43	p-313-089	2477	3118	2797mnop
44	p-313-067	3040	5850	4445ef
45	p-313-003	3869	2882	3375hijklm
46	ADI	5631	5886	5758bcd
47	BURKITU	4513	5734	5123def
48	BILALO	5141	6627	5884ab
49	BURSA	6043	5397	5720abc
	Mean	3038	3884	3803
	Site			NS
	Genotype	**	**	***
	Site x genotype			***
	R-square (%)	89	94	93
	CV (%)	16.75	16.6	16.6

*, **, *** and NS indicate significance levels at 0.05, 0.01, 0.001 and non- significance, respectively.

Table 5. Disease response, frequency and percentage of the field pea genotypes evaluated against ascochyta blight.

Disease response	DSS (1-9)	Pea genotypes	F	%
Moderately resistant (MR)	**3.1 – 5.0**	GPHA03, GPHA019, GPHA06, GPHA01, GPHA018,P-313-010 , P-313-045 ,P-313-086, P-313-082, P-313-071 , P-313-065 , P-313-098 , P-313-061 , P-313-068 , P-313-067 , PDFPT-BEK	**16**	32.65
Susceptible(S)	**5.1 – 7.0**	All others genotypes except the above listed moderately resistant materials	**33**	**67.35**

DSS-disease severity scale; *F*- frequency; %- percentage

CONCLUSION

Results from present study revealed that considerable variation was found for response against ascochyta blight diseases even if there were no resistant materials identified.

Out of 49 materials evaluated; 16 genotypes (32.65%) were showed moderate resistance and 33 materials (67.35%) were susceptible. This figure shows that field pea for resistance to AB is often limited due to the absence of high levels of resistance gene in the studied genotypes of field pea , which along with the highly variable pathogen, has precluded the development of varieties with both high and durable resistance. The present finding is from one year and two locations data. Hence, expanded multi-location and multi-season field trials are essential before varieties are released to farmers to widen the scope of available AB resistant genotypes.

The development/severity / of ascochyta blight disease depends on the conduciveness of the environment and growing season. Therefore; it is advisable to repeat this trial in multi-location and multi-season to check its disease and yield stability for more confirmation and then to exploit as direct sources to the next stage for general cultivation or may be transferred through hybridization.

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