Screening of Field Pea (*Pisum sativum* L.) Germplasm against Powdery Mildew (*Erysiphe polygoni*) Disease at Kulumsa, Arsi, South East Ethiopia

Kedir Yimam[1,*],Gizachew Yilma[1], Deresa Tesfaye[1] and Aliyi Robsa[1]

1Kulumsa Agricultural Research Center, P.O. Box 489, Asella, Ethiopia; *Author for correspondence

Field Pea (*Pisum sativum* L.) is an important food crop ranks fourth among pulse crops in Ethiopia. The yield of field pea is hampered due to the prevalence of powdery mildew disease. In view of the cost-effective solution for powdery mildew disease, host plant resistance is one of the most widely used control measure for this disease. Sixty nine field pea gene pools including one released variety were screened against Powdery Mildew using an Augmented Block Design with four blocks in Kulumsa Agricultural Research Center during 2018/19 main cropping season. Results from present study revealed that considerable variation was found for resistance against powdery mildew disease. High degree of severity showed at late (after pod setting) stage than earlier stage. Out of the total 69 genotypes 12 were resistant, 27 were moderately resistant, 25 were moderately susceptible and 5 were susceptible to powdery mildew disease. Among 12 resistant genotypes; GPHA-9 and GPHA-19 were high yielder and GPHA-29, GPHA-48, GPHA-45 and GPHA-42 genotypes were found to be high yielding among 27 moderately resistant genotypes. For more confirmation with the present result it is better to repeat for more seasons and locations for checking their stability of yield and disease resistant and to use for further breeding purpose.

Key words: Germplasm**,** powdery mildew, host plant resistance, cost-effective

INTRODUCTION

Economically, Pulses are the second most important crops after cereals in the world's crop production. Field pea (*Pisum sativum* L.) is one of the most widely grown pulse crop in the world with annual production of 16205448 tonnes (FAOSTAT, 2017). The major field pea-producing countries include Canada, Russian Federation, China, Ukraine, India, United States of America, France, Australia, Ethiopia and Germany (FAOSTAT, 2017).

In Ethiopia, field pea stands fourth next to faba bean, haricot bean and chickpea among pulse crops in total production and areas coverage (CSA, 2018). It is grown on 220,508.39 hectares of land with total production of 368,519.065 tonnes and productivity of 1.671 t/ha; which accounts 13.79 % from pulses total area coverage and 12.37 % from total production in Ethiopia. (CSA, 2018). It is widely cultivated in potential mid and high altitude areas of the country at elevations of 1800-3000 m with 700-1100 mm annual rainfall.

Field pea has a great economic merit in the livelihood of the agricultural societies of the country. It contains high protein content, favorable amino acids composition and low trypsin inhibitor levels and there by supply the essential nutrients to various age groups (Aysh *et al*., 2013). Due to its pertinent atmospheric nitrogen fixing capacity; field pea serves as a break crop suitable for rotation in areas where cereal monocropping is abundant.

Even though it has huge importance in the country, the national average production of field pea is low compared with the production of the crop in the advanced countries like India, USA, France (FAOSTAT, 2017). This may be due to inherent low yielding potential of the landrace cultivars, biotic factors (diseases ,insect pest, weed) and abiotic (frost) factors, inadequate land allocation, poor attention for the crop, instability of cultivars, poor adaptation and poor crop management (Mussa *et al*., 2008 ; Sahile *et al*., 2008).

From the biotic category, fungal diseases are important factors limiting the production of food-legume crops as a whole and field pea specifically in Ethiopia (Nigussie *et al.*, 2008).
Among the fungal diseases, powdery mildew (*Erysiphe polygoni*) and Ascochyta blight (*Ascochyta pisi*) are the major constraints, causing substantial yield loss (Teshome and Tegegn, 2017). Powdery mildew is one of the largest and the most important group affecting all parts of the plant of field pea (Nigussie *et al.*, 2008 ; Shahid *et al*., 2010).

Powdery mildew is caused by the biotrophic, ascomycete fungus *Erysiphe polygoni*; which form colonies on leaves, stems and pods and the disease is severe in many areas of the world, particularly in climates with warm, dry days and cool nights. (Ghafoor and Mcphee, 2012). Powdery mildew disease affects the yield potential, causing 86% loss in field pea germplasm growing in different parts of the world (Nisar *et al*. 2006).

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.
Powdery mildew on peas is a widely distributed disease. It is a troublesome disease when days are warm and dry; nights are cool enough for dew formation.
Sever powdery mildew infection is reported to adversely affect plant and seed weight, number of seed per pod and per plant, plant height and number of nodes per plant (Musa *et al*.,2009) .
It causes yield loss up to 37% in Ethiopia. This disease is of less effect in high rainfall areas of Ethiopia where its spores are removed from the plant tissue by rain and cannot cause infection. However, late sown and off-season fields were reported to be severely affected by the disease(Musa *et a*l.,2009).
21.09% of yield losses have been reported due to powdery mildew severity on local field pea cultivar from plot without fungicide application at Sinana South Eastern Ethiopia (Teshome and Tegegn, 2017).
Powdery mildew is becoming a continuous threats in Ethiopia in general and particularly in midland of field pea growing areas of South Eastern Ethiopia.
Currently, different attempts have been made for control of this disease including fungicide sprays. Farmers often use chemical agents for controlling the disease, which may cause environmental pollution (Bhattacharjee and Dey, 2014).

Furthermore, spore release can cause breathing and allergic reactions in farm workers (Eklund *et al*., 2005). Thus 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 powdery mildew disease, genetic based resistance is the best option for crop breeding (Fondevilla and Rubiales, 2012).
There are reported sources of genetic resistance available, which were controlled by single recessive gene.

Hence; there is a need to develop high yielding and powdery mildew resistant varieties (Ghafoor and Mcphee, 2012). 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 screen different field pea genotypes against powdery mildew diseases at Kulumsa Agricultural Research Center for further utilization.

Materials and Methods

Experimental sites

Field experiment was carried out during the main cropping season (June to November) of the year 2018/19 at Kulumsa Agricultural Research Center. The center is located at 80 01' 10''N latitude and 390 09'13'' E longitudes and at an altitude of 2200 meter above sea level.

The agro-ecology of the area is characterized by an average annual rain-fall of 850 mm, with short rain between March and April and long rain between June and September, and with annual mean minimum and maximum temperatures of 7.9 º C and 23.1 º C respectively (Tamene, 2017). Kulumsa is naturally hot spot area for powdery mildew disease occurrence.

Experimental Materials

Sixty nine field pea materials including Sixty-eight single plant selected from bulked gene pool field pea materials and one released variety were considered for the study (Table 1). The one commercial variety (letu) that was included in the study which was released as moderate resistance to powdery mildew.

Table 1.list of field pea genotypes

No	Genotype	Source	Origin/Remark
1	GPHA-36	HARC	SPS
2	GPHA-3	HARC	SPS
3	GPHA-38	HARC	SPS
4	GPHA-68	HARC	SPS
5	GPHA-2	HARC	SPS
6	GPHA-58	HARC	SPS
7	GPHA-17	HARC	SPS
8	GPHA-7	HARC	SPS
9	GPHA-60	HARC	SPS
10	GPHA-11	HARC	SPS
11	GPHA-42	HARC	SPS
12	GPHA-48	HARC	SPS
13	GPHA-37	HARC	SPS
14	GPHA-15	HARC	SPS
15	GPHA-10	HARC	SPS
16	GPHA-67	HARC	SPS
17	GPHA-52	HARC	SPS
18	GPHA-1	HARC	SPS
19	GPHA-33	HARC	SPS
20	GPHA-8	HARC	SPS
21	GPHA-49	HARC	SPS
22	GPHA-21	HARC	SPS
23	GPHA-12	HARC	SPS
24	GPHA-14	HARC	SPS
25	GPHA-16	HARC	SPS
26	GPHA-39	HARC	SPS
27	GPHA-55	HARC	SPS
28	GPHA-9	HARC	SPS
29	GPHA-22	HARC	SPS
30	GPHA-20	HARC	SPS
31	GPHA-31	HARC	SPS
32	GPHA-5	HARC	SPS
33	GPHA-66	HARC	SPS
34	GPHA-41	HARC	SPS
35	GPHA-57	HARC	SPS
36	GPHA-13	HARC	SPS
37	GPHA-28	HARC	SPS
38	GPHA-59	HARC	SPS
39	GPH-27	HARC	SPS
40	GPHA-53	HARC	SPS
41	GPHA-32	HARC	SPS
42	GPHA-30	HARC	SPS
43	GPHA-63	HARC	SPS

44	GPHA-46	HARC	SPS	**57**	GPHA-19	HARC	SPS
45	GPHA-47	HARC	SPS	**58**	GPHA-26	HARC	SPS
46	GPHA-51	HARC	SPS	**59**	GPHA-23	HARC	SPS
47	GPHA-24	HARC	SPS	**60**	GPHA-43	HARC	SPS
48	GPHA-40	HARC	SPS	**61**	GPHA-29	HARC	SPS
49	GPHA-64	HARC	SPS	**62**	GPHA-4	HARC	SPS
50	GPHA-56	HARC	SPS	**63**	GPHA-62	HARC	SPS
51	GPHA-6	HARC	SPS	**64**	GPHA-54	HARC	SPS
52	GPHA-35	HARC	SPS	**65**	GPHA-65	HARC	SPS
53	GPHA-25	HARC	SPS	**66**	GPHA-34	HARC	SPS
54	GPHA-61	HARC	SPS	**67**	GPHA-45	HARC	SPS
55	GPHA-44	HARC	SPS	**68**	GPHA-18	HARC	SPS
56	GPHA-50	HARC	SPS	**69**	Letu	KARC	RV

Where; HARC - Holeta Agricultural Research Center, KARC - Kulumsa Agricultural Research Center,
SPS - Single plant selection from bulked gene pool

Experimental design and treatments

The test germplasm were evaluated in the field in an augmented block design, with four blocks containing seventeen different test germplasm per blocks. The control (check) variety (letu) was replicated four times in an experiment.

Each plot consisted of four rows of 4m length with spacing of 20cm between rows and 5cm between plants with a total plot area of $3.2m^2$. The space between plots within block was 1 m and between blocks was 1.5m. Each row was sown 80 seeds and each plots contained total of 320 seeds.100 Kg/ha Diammonium-phosphate (DAP)

fertilizer was applied during planting. weeding and all other recommended agronomic practice was followed.

Data collection and Analysis

Data on days to 50% flowering, days to 95% physiological maturity, 1000 seed weight (g), grain yield (kg ha-1), Ascochyta blight (1-9), and powdery mildew (1-9) were assessed on plot bases, while plant height (cm), pods plant-1 and seeds pod-1 were recorded from five sample plants randomly selected from each plot. Mean values of the five random samples of plants plot-1 were then used for the analysis of data collected on an individual plant basis.

Disease data scoring

Disease reaction of individual genotypes were recorded on whole plot basis 70 days after Planting at three times (early stage, flowering and pod setting stage) based on 1-9 scale following (Little and Hills, 1978)

Table: 2. Disease scoring scale.

Disease scale (1- 9)	Response
1	Immune
2	highly resistant
3	Resistant
4	moderately resistant
5	Moderately susceptible
6	moderately susceptible
7	Susceptible
8	highly susceptible
9	highly susceptible

The data for grain yield and other agronomic traits were taken following the standard practice for field pea trial used. Grain yield was taken as weight of seeds from all rows per plot. 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.

Statistical Analysis

The analysis was computed based on multivariate analysis using principal component analysis.

Principal component (PC) analysis was made based on the mean values for the ten traits of field pea genotypes using the PRINCOMP of the R software package in order to identify the traits that most contributed to the total variation among the genotypes

Result and Discussion

The field pea genotypes were screened against powdery mildew disease caused by *Erysiphe polygoni* at three growth stages in hot spot condition. The symptoms of the disease started to appear at 70 days after planting. The severity of the disease was increased from early to flowering and to pod setting stages. All tested genotypes differed significantly for their response to *powdery mildew* disease. Hence forward, it was found that out of the total 69 field pea genotypes, twelve genotypes (GPHA-12,

GPHA-9, GPHA-22, GPHA-44, GPHA-19, GPHA-68, GPHA-58,GPHA-28,GPHA-59,GPHA-46, GPHA-24 and GPHA-6) were resistant (DSS-3), twenty seven (GPHA-14, GPHA-55,GPHA-61, GPHA-26, GPHA-43, GPHA-29, GPHA-54, GPHA-45, GPHA-18,GPHA-38, GPHA-2, GPHA-60, GPHA-11,GPHA-42, GPHA-48, GPHA-15, GPHA-1, GPHA-8,GPHA-13, GPHA-27, GPHA-53,GPHA-30, GPHA-63, GPHA-47, GPHA-40,GPHA-64,GPHA-56) were moderately resistant (DSS-4), twenty five (GPHA-21, GPHA-16, GPHA-39, GPHA-20, GPHA-31, GPHA-66, GPHA-41, GPHA-57, GPHA-50 ,GPHA-23, GPHA-4, GPHA-62, GPHA-65, GPHA-36, GPHA-3, GPHA-17, GPHA-7,GPHA-37,GPHA-10, GPHA-52, GPHA-33, GPHA-32, GPHA-51, GPHA-35 and LETU) were moderately susceptible (DSS-5 &6), and seven (GPHA-49, GPHA-5, GPHA-34, GPHA-67,GPHA-25) were susceptible (DSS-7) (Table 3 and 5). Ajmal *et al* . (2017) was found that out of the 24 pea lines, three lines (PL-4, PL-5 and PL-23) were highly resistant, seven (PL-1, PL-2, PL-3, PL-6, PL-11, PL-16 and PL-19) were rated as resistant and three (PL-10, PL-12 and PL-13) were moderately resistant. Research reports also indicated that some materials introduced from Australia, especially cultivar cooke that have resistance for powdery mildew in Ethiopia and there is genetic diversity in resistance to powdery mildew in Ethiopian landrace collections (Musa *et al*.,2009).

Performance of genotypes

The result of the range of parameters suggested that there were considerable differences observed in all of the traits under investigation and especially for yield, seed size, pod setting and disease response. The grain yield of the field pea genotypes ranged from 753 to 3724 kg/ha. The highest grain yield was produced by GPHA-23 (3724Kg/ha) followed by GPHA-29 (3720Kg/ha) (Table 6). GPHA-9 and GPHA-19 were high yielding and resistant .Where as; GPHA-29, GPHA-48, GPHA-45 and GPHA-42 were high yielding and moderately resistant (Table 3 &6). But GPHA-23 showed high yielding potential and moderately susceptible (Table 3 &6).

Some genotypes were larger in their seed size GPHA-30,GPHA-41,GPHA-62,GPHA-68,GPHA-9,GPHA-38,GPHA-47,GPHA-19,GPHA-18,GPHA-48,GPHA-37,GPHA-27,GPHA-57) (Table.6)

All the traits were subjected to principal component analysis (PCA) for estimation of weight contribution of each trait and to evaluate the total level of genetic diversity. Four components gave Eigenvalues >1.0, thus they were important in consideration of genetic variability amongst all the genotypes. Four components (PC1-PC4) contributed 68.45% genetic variability (Table 4). The importance of this technique has been reported appreciably for selecting field pea lines for high yielding and powdery mildew resistance and explained 70% of genetic variability by this technique (Ajmal *et al.*,2017). The PC1 explained 23.4% of the total variability. Powdery mildew, days to mature, days to flower, Ascocayta blight were the variables with the largest positive loadings in their order. However, grain yield and stand count with negatively loading was observed for this component. The PC2 explained 18.5% of the total contribution toward variability. Thousand seed weight, plant height, days to mature,days to flower and seed per pod were the variables in their order with high positive loading. The third component (PC3) contributed 15% of variability with Ascocayta blight, powdery mildew and plant height was variables in their order with high positive loading but negatively for days to flowering and seed per pod. The PC4 explained 11.5% of the total variance and related to high positive loadings for seeds pod^{-1} and powdery mildew along with negative loadings for pods $plant^{-1}$ and days to maturity.

Table.3 response of different field pea genotypes screened against *Erysiphe polygoni at* three growth stages (1-9 scale).

Genotype	Disease severity at flowering stage (1-9)	Disease severity at pod setting stage (1-9)	Disease severity at seed setting stage (1-9)	Disease Response
GPHA-49	2	6	7	S
GPHA-21	3	5	6	MS
GPHA-12	2	3	3	R
GPHA-14	3	4	4	MR
GPHA-16	3	5	6	MS
GPHA-39	3	5	6	MS
GPHA-55	3	4	4	MR
GPHA-9	3	3	3	R

Table 3 cont.

GPHA-22	**2**	**3**	**3**	**R**
GPHA-20	2	5	6	MS
GPHA-31	3	5	6	MS
GPHA-5	3	6	7	S
GPHA-66	2	4	5	MS
GPHA-41	2	4	5	MS
GPHA-57	3	4	5	MS
GPHA-61	2	3	4	MR
GPHA-44	3	3	3	R
GPHA-50	2	6	6	MS
GPHA-19	2	3	3	R
GPHA-26	3	4	4	MR
GPHA-23	2	5	5	MS
GPHA-43	2	4	4	MR
GPHA-29	3	4	4	MR
GPHA-4	3	5	5	MS
GPHA-62	3	5	5	MS
GPHA-54	3	4	4	MR
GPHA-65	3	6	6	MS
GPHA-34	3	6	7	S
GPHA-45	2	4	4	MR
GPHA-18	3	4	4	MR
GPHA-36	2	5	6	MS
GPHA-3	2	5	5	MS
GPHA-38	3	4	4	MR
GPHA-68	3	3	3	R
GPHA-2	3	3	4	MR
GPHA-58	2	3	3	R
GPHA-17	2	5	5	MS
GPHA-7	3	4	5	MS
GPHA-60	2	3	4	MR
GPHA-11	3	4	4	MR
GPHA-42	3	4	4	MR
GPHA-48	3	4	4	MR
GPHA-37	2	4	5	MS
GPHA-15	3	4	4	MR
GPHA-10	2	5	6	MS
GPHA-67	3	7	7	S
GPHA-52	3	4	5	MS
GPHA-1	3	4	4	MR
GPHA-33	3	5	5	MS
GPHA-8	3	4	4	MR
GPHA-13	3	4	4	MR
GPHA-28	3	3	3	R
GPHA-59	3	3	3	R
GPHA-27	3	4	4	MR
GPHA-53	3	4	4	MR
GPHA-32	2	4	5	MS
GPHA-30	3	4	4	MR
GPHA-63	3	3	4	MR
GPHA-46	2	3	3	R
GPHA-47	3	4	4	MR
GPHA-51	3	4	5	MS
GPHA-24	3	3	3	R
GPHA-40	3	4	4	MR
GPHA-64	3	4	4	MR
GPHA-56	3	4	4	MR

GPHA-6	2	3	3	R

Table 3 cont.

GPHA-35	**2**	**4**	**5**	MS
GPHA-25	3	5	7	S
letu	4	5	6	MS

Where R=Resistant,MR=Moderately Resistant ,
MS= Moderately Susceptible, S= Susceptible

Table 4. Disease response, frequency and percentage of the field pea genotypes screened against *Erysiphe polygoni*

Disease response	**DSS (1-9)**	**field Pea genotypes**	**F**	**%**
Resistant	3	GPHA-12, GPHA-9, GPHA-22, GPHA-44 , GPHA-19, GPHA-68, GPHA-58 ,GPHA-28,GPHA-59, GPHA-46, GPHA-24,GPHA-6	**12**	**17.39**
Moderately resistant	4	GPHA-14, GPHA-55, GPHA-61, GPHA-26, GPHA-43, GPHA-29, GPHA-54, GPHA-45, GPHA-18, GPHA-38, GPHA-2, GPHA-60, GPHA-11,GPHA-42, GPHA-48, GPHA-15, GPHA-1, GPHA-8 ,GPHA-13, GPHA-27, GPHA-53, GPHA-30, GPHA-63, GPHA-47, GPHA-40, GPHA-64,GPHA-56	**27**	**39.13**
Moderately susceptible	5 &6	GPHA-21, GPHA-16, GPHA-39, GPHA-20, GPHA-31, GPHA-66, GPHA-41, GPHA-57, GPHA-50 ,GPHA-23, GPHA-4, GPHA-62, GPHA-65, GPHA-36, GPHA-3, GPHA-17, GPHA-7, GPHA-37, GPHA-10, GPHA-52, GPHA-33, GPHA-32, GPHA-51, GPHA-35, LETU	**25**	**36.23**
Susceptible	7	GPHA-49, GPHA-5, GPHA-34, GPHA-67,GPHA-25	**5**	**7.24**

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

Table.5. Grain yield performance and seed size of field pea genotypes.

genotype	Grain yield ($kgha^{-1}$)	Thousand seed weight (g)	Genotype	Grain yield ($kgha^{-1}$)	Thousand seed weight (g)	Genotype	Grain yield ($kgha^{-1}$)	Thousand seed weight (g)
GPHA-49	1112	122	GPHA-62	2294	221	GPHA-33	1349	152
GPHA-21	1517	124	GPHA-54	2547	183	GPHA-8	2982	150
GPHA-12	1878	196	GPHA-65	1702	157	GPHA-13	2152	156
GPHA-14	1926	163	GPHA-34	753	179	GPHA-28	2502	169
GPHA-16	2583	179	GPHA-45	3306	164	GPHA-59	2271	179
GPHA-39	1868	161	GPHA-18	2075	212	GPHA-27	2238	211
GPHA-55	2336	206	GPHA-36	1160	185	GPHA-53	1956	190
GPHA-9	3083	216	GPHA-3	2109	191	GPHA-32	2225	167
GPHA-22	2312	155	GPHA-38	2522	214	GPHA-30	1695	228
GPHA-20	2224	155	GPHA-68	2251	220	GPHA-63	1898	209
GPHA-31	2862	185	GPHA-2	2530	207	GPHA-46	1537	149
GPHA-5	1627	174	GPHA-58	2204	154	GPHA-47	2521	214
GPHA-66	2538	200	GPHA-17	2210	191	GPHA-51	1817	211
GPHA-41	2026	224	GPHA-7	2726	189	GPHA-24	1922	148
GPHA-57	1494	162	GPHA-60	1628	200	GPHA-40	886	151
GPHA-61	2443	190	GPHA-11	2931	151	GPHA-64	1880	180
GPHA-44	2243	138	GPHA-42	3164	206	GPHA-56	1307	158
GPHA-50	1851	209	GPHA-48	3565	211	GPHA-6	1735	195
GPHA-19	3412	213	GPHA-37	2311	211	GPHA-35	1227	173
GPHA-26	2943	195	GPHA-15	2214	191	GPHA-25	2182	167
GPHA-23	3724	148	GPHA-10	1852	159	Letu	2043	139
GPHA-4	2446	191	GPHA-1	2006	143			

Table 6. Principal component analysis (PCA) of 10 traits among pea genotypes, Eigen values, percentage variability explained by first four components.

Trait	**PC1**	**PC2**	**PC3**	**PC4**
Stand count	-.415107**	0.126941	0.317062	0.054206
Days to flower (number)	0.358732*	0.348916*	.250219**	-.096597
Days to mature (number)	0.375201*	0.432508*	-.168650	-.277857**
Plant height (cm)	-.133618	0.444120*	0.372104*	-.040282
pods plant $^{-1}$ (number)	-.060334	0.251607	0.225960	-.644759**
seeds pod $^{-1}$ (number)	-.087999	0.340741*	-.336310**	0.515947*
Thousand seed weight (g)	-.187466	0.519140*	-.109243	0.245362
Grain yield ha $^{-1}$ (kg ha $^{-1}$)	-.434838**	0.144765	0.168257	0.034232
Ascochyta blight (1-9 scale)	0.353656*	0.089166	0.520427*	0.226313
Powdery mildew (1-9 scale)	0.423891*	-.003553	0.441257*	0.338225*
Eigenvalue	2.34014	1.84884	1.50694	1.14878
Percent Variability	0.234	0.1849	0.1507	0.1149
Cumulative variability	0.234	0.4189	0.5696	0.6845

*High positive loading and **High negative loading

Conclusion

Results from present study revealed that considerable variation was found for resistance against powdery mildew diseases and grain yield indicating the potential of selection for promising gene pools and which could be exploited as direct sources or may be transferred through hybridization to high yielding but disease susceptible genotypes. GPHA-29, GPHA-48, GPHA-45 and GPHA-42 genotypes were found to be high yielding and powdery mildew moderately resistant and GPHA-9 and GPHA-19 genotypes were also high yielding and resistant; they could be selected as elite genotypes pass to the next yield trial stage or for breeding (crossing) purposes. These genotypes are to be evaluated under wider range of agro-climatic condition in the field pea potential areas of the country as to evaluate their yielding potential, disease and yield stability for general cultivation. High yielding and resistant gene pools (GPHA-9 and GPHA-19) and low yielding and resistant gene pools (GPHA-12,GPHA-22,GPHA-44,GPHA-68,GPHA-58,GPHA-28,GPHA-59,GPHA-46,GPHA-24,GPHA-6) could be selected as elite genotypes for breeding (crossing) purposes.

Conflict of Interests

The authors have not declared any conflict of interests

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