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Diversity Analysis and Identification of Promising Powdery Mildew Resistance Genotypes in Field Pea (*Pisum sativum* L.)

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Abstract: In the present study, seventy-one field pea gene pools including three released varieties were evaluated in an augmented block design for assessing genetic divergence and level of resistance to powdery mildew for exploitation in a breeding program aimed at improving yield potential of field pea by using cluster and principal component analysis. Among the 10 studied traits, four (Eigenvalue >1.0) contributed more than 68.45% variability among the materials. Cluster analysis grouped the 71 field pea genotypes into seven distinct classes. The genetic divergence between all possible pairs of clusters were highly significant (P<0.01). The inter-cluster D^2 value ranged from 311.63 to 2850.61 indicated that the evaluated gene pools were highly divergent. The genetically more divergent materials present in cluster five and six as indicated by inter-cluster distance value (2850.61). Selecting genotypes of these clusters and crossing them probably provide promising recombinants and better sergeants for future breeding program. Considerable variation was also found for resistance against the powdery mildew diseases. Out of the total 71 genotypes 12 were resistant, 29 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 29 moderately resistant genotypes. The resistant genotypes identified could be exploited directly and/or may be transferred through hybridization to high yielding disease susceptible genotypes after checking their yield and disease stability in a number of locations and seasons for more confirmation with the present finding, since the present result was from one location and one season (year) data.

Keywords: Cluster, Diversity, *Pisum sativum*, Powdery Mildew, Principal Component, Resistance

1. Introduction

Pulses are the second most important crops after cereals in the world's crop production. Among pulses, field pea (*Pisum sativum* L.) is one of the most widely cultivated crop in the world with annual production of 16205448 tonnes produced on 8141031 ha with productivity of 1.99 t/ha [8]. The top field pea-producing countries include Canada, Russian Federation, China, Ukraine, India, United States of America, France, Australia, Ethiopia and Germany [8].

Field pea ranks fourth next to faba bean, haricot bean and chickpea among pulse crops in Ethiopia in terms of total production and areas coverage [6]. 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. Field pea accounts 13.79% from pulses total area coverage and 12.37% from total production in Ethiopia. [6]. It is widely cultivated in potential mid and high altitude areas in different parts of the country at elevations of 1800-3000 m with 700-1100 mm annual rainfall.

Even though wild and primitive forms of field pea species are known to exist; *P. sativum* is more dominant in the production system at the high land of the country [15].

Ethiopia, Western and Central Asia and the Mediterranean region are proposed as possible centers of origin of field pea because of the high pea genetic diversity sampled in these regions [13].

Field pea has a major economic advantage in the livelihood of the farming societies of the country. It is an important crop consumed in different forms with high protein content as a complement to cereals for the majority of the poor population, especially for those who cannot afford to use proteins from animal source. 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 [4]. It serves as a break crop suitable for rotation in areas where cereal monocropping is abundant due to its high atmospheric nitrogen fixing capacity.

Even if it has huge importance, the national average productivity of the country (1.67 t ha^{-1}) is low compared with a number of cereals in the country [6] and advanced field pea producing countries in the world [8]. This is primarily due to inherent low yielding potential of the indigenous cultivars, biotic factors (diseases like powdery mildew and Ascochyta blight, insect pest, weed etc.) and abiotic (frost) factors, inadequate land allocation, poor attention for the crop, instability of cultivars, poor adaptation and poor crop management [20, 3, 22, 1].

Fungal diseases are important factors limiting the production of food-legume crops as a whole and field pea specifically in Ethiopia [17].

Powdery mildew (*Erysiphe polygoni*) and Ascochyta blight (*Ascochyta pisi*) are the major fungal diseases causing substantial yield loss [22, 1].

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 [10].

According to [18] Powdery mildew disease affects the yield potential, causing 86% loss in field pea germplasm growing in different parts of the world. 20-30% of field pea yield reduction has been reported by powdery mildew disease in the mid-altitudes under moderate severity. Powdery mildew is a troublesome disease when days are warm and dry; nights are cool enough for dew formation.

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 [16].

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 [22].

Farmers often use chemical agents for controlling the disease, which may cause environmental pollution [5].

Spore release also can cause breathing and allergic reactions in farm workers [7]. It is better to seek other alternative means of disease control methods due to high cost of fungicides, social and health related and environmental impacts. Genetic based resistance is the best option for crop breeding [9].

There is a requirement for improvement and to develop high yielding and powdery mildew resistant varieties to maximize and sustain production and productivity of field pea under small scale farmers [10].

Genetic diversity is an essential factor that determines expectation of yield improvement in the future. Knowledge of genetic diversity within a crop and association among the yield contributing characters is important for the long-term success of a breeding program and enhances the exploration of germplasm resources [19]. Evaluation of genetic diversity is essential to identify the source of genetic materials for an individual trait within the available germplasm [23]. Diversity analysis is a useful tool to identify the degree of divergence among the biological populations at genotypic level and to determine the relative contribution of different components to the total divergence both inters and intra cluster levels [12]. Therefore, the present study was undertaken to assess the genetic divergence of important morpho-agronomic traits, and to evaluate the performance of different genotypes of field pea and thereby to identify powdery mildew resistant materials evaluated under natural infection for future breeding program.

2. Materials and Methods

2.1. Experimental Site

Field experiment was carried out at Kulumsa Agricultural Research Center during the main cropping season (June to November) of the year 2018/19. 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 Experimental site 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°C and 23.1°C respectively. Kulumsa is hot spot area for powdery mildew disease occurrence under natural infection.

2.2. Experimental Materials

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

Table 1. *List of field pea genotypes.*

No	Genotype	Origin/Remark
1	GPHA-36	SPS
2	GPHA-3	SPS
3	GPHA-38	SPS
4	GPHA-68	SPS
5	GPHA-2	SPS
6	GPHA-58	SPS
7	GPHA-17	SPS
8	GPHA-7	SPS
9	GPHA-60	SPS
10	GPHA-11	SPS

No	Genotype	Origin/Remark
11	GPHA-42	SPS
12	GPHA-48	SPS
13	GPHA-37	SPS
14	GPHA-15	SPS
15	GPHA-10	SPS
16	GPHA-67	SPS
17	GPHA-52	SPS
18	GPHA-1	SPS
19	GPHA-33	SPS
20	GPHA-8	SPS
21	GPHA-49	SPS
22	GPHA-21	SPS
23	GPHA-12	SPS
24	GPHA-14	SPS
25	GPHA-16	SPS
26	GPHA-39	SPS
27	GPHA-55	SPS
28	GPHA-9	SPS
29	GPHA-22	SPS
30	GPHA-20	SPS
31	GPHA-31	SPS
32	GPHA-5	SPS
33	GPHA-66	SPS
34	GPHA-41	SPS
35	GPHA-57	SPS
36	GPHA-13	SPS
37	GPHA-28	SPS
38	GPHA-59	SPS
39	GPH-27	SPS
40	GPHA-53	SPS
41	GPHA-32	SPS
42	GPHA-30	SPS
43	GPHA-63	SPS
44	GPHA-46	SPS
45	GPHA-47	SPS
46	GPHA-51	SPS
47	GPHA-24	SPS
48	GPHA-40	SPS
49	GPHA-64	SPS
50	GPHA-56	SPS
51	GPHA-6	SPS
52	GPHA-35	SPS
53	GPHA-25	SPS
54	GPHA-61	SPS
55	GPHA-44	SPS
56	GPHA-50	SPS
57	GPHA-19	SPS
58	GPHA-26	SPS
59	GPHA-23	SPS
60	GPHA-43	SPS
61	GPHA-29	SPS
62	GPHA-4	SPS
63	GPHA-62	SPS
64	GPHA-54	SPS
65	GPHA-65	SPS
66	GPHA-34	SPS
67	GPHA-45	SPS
68	GPHA-18	SPS
69	Adi	RV
70	Megeri	RV
71	Letu	RV

Where; SPS - Single plant selection from bulked gene pool, RV –Released Variety.

Source: - Holeta Agricultural Research Center for bulked gene pool and Kulumsa Agricultural Research Center for Released Variety.

2.3. Experimental Design and Treatments

Seventy one test germplasm including three control (check) varieties were evaluated in the field in an augmented block design, with four blocks containing seventeen different test germplasm per blocks. The control (check) varieties (Adi, Megeri and letu) were 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.

2.4. Data Collection

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.

2.4.1. 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 [11] where 1 stands for immune, 2 for highly resistant, 3 for resistant, 4 for moderately resistant, 5 and 6 for moderately susceptible, 7 for susceptible, and 8 and 9 highly susceptible.

2.4.2. 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 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.

2.5. Data Analysis

The disease ratings were subjected to Friedmans non-parametric analysis of variance.

The analysis was computed based on multivariate analysis using cluster, divergence and principal component analysis.

(i) Cluster Analysis

Cluster analysis was performed based on average linkage method with Euclidean distance measure using Minitab release 17 to cluster the genotypes based on their morpho-agronomic traits.

(ii) Divergence Analysis

Genetic distances between clusters as standardized

Mahalanobis's D^2 statistics were calculated as:

$$D2ij=(xi - xj)' \text{ cov-1 } (xi - xj)$$

Where, D2ij=the distance between cases i and j; xi and xj=vectors of the values of the variables for cases i and j; and cov-1=the pooled within groups variance-covariance matrix. The D2 values obtained for pairs of clusters were considered as the calculated values of Chi-square (X^2) and were tested for significance both at 1% and 5% probability levels against the tabulated value of X^2 for 'P' degree of freedom, where P is the number of characters considered [21].

(iii) Principal Component Analysis (PCA)

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

3. Result and Discussion

3.1. Performance of the 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). 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. But GPHA-23 showed high yielding potential and moderately susceptible (Table 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).

Table 2. *Average Performance of the genotypes for the characters.*

Entry	genotype	SCAE	FD	MD	PH	PPP	SPP	TSW	GYKGH	AB	PM
1	GPHA-36	90	72	120	140	9	5	185	1160	4	6
2	GPHA-3	86	73	121	150	13	6	191	2109	4	5
3	GPHA-38	48	78	126	143	14	7	214	2522	3	4
4	GPHA-68	90	78	125	138	15	5	220	2251	2	3
5	GPHA-2	96	72	126	135	11	6	207	2530	3	4
6	GPHA-58	91	72	117	120	11	5	154	2204	2	3
7	GPHA-17	68	72	121	140	12	5	191	2210	4	5
8	GPHA-7	80	77	118	120	11	5	189	2726	4	5
9	GPHA-60	76	70	118	128	8	6	200	1628	3	4
10	GPHA-11	80	73	119	137	9	5	151	2931	3	4
11	GPHA-42	90	79	122	130	10	6	206	3164	4	4
12	GPHA-48	90	79	122	160	13	6	211	3565	3	4
13	GPHA-37	88	75	122	135	12	5	211	2311	4	5
14	GPHA-15	92	74	119	137	8	5	191	2214	3	4
15	GPHA-10	90	75	124	133	16	5	159	1852	4	6
16	GPHA-67	90	78	125	133	11	5	134	1858	4	7
17	GPHA-52	86	79	126	128	12	5	177	1135	3	5
18	GPHA-1	90	79	125	120	10	6	143	2006	2	4
19	GPHA-33	30	76	124	100	14	5	152	1349	4	5
20	GPHA-8	85	80	123	133	9	5	150	2982	3	4
21	GPHA-49	80	79	126	123	8	5	122	1112	3	7
22	GPHA-21	93	80	125	117	8	4	124	1517	4	6
23	GPHA-12	90	79	124	150	11	5	196	1878	3	3
24	GPHA-14	94	79	124	137	12	6	163	1926	3	4
25	GPHA-16	95	73	116	118	8	5	179	2583	4	6
26	GPHA-39	65	79	121	133	12	6	161	1868	4	6
27	GPHA-55	96	78	125	140	13	7	206	2336	3	4
28	GPHA-9	94	79	124	130	9	7	216	3083	3	3
29	GPHA-22	95	69	117	123	12	4	155	2312	3	3
30	GPHA-20	95	75	118	137	15	5	155	2224	4	6
31	GPHA-31	93	73	118	128	11	6	185	2862	4	6
32	GPHA-5	51	74	121	108	10	5	174	1627	4	7
33	GPHA-66	96	78	120	110	10	6	200	2538	3	5
34	GPHA-41	83	75	125	118	7	6	224	2026	3	5
35	GPHA-57	48	78	123	110	9	6	162	1494	3	5
36	GPHA-13	40	81	125	128	10	6	156	2152	3	4
37	GPHA-28	93	76	118	135	17	5	169	2502	2	3
38	GPHA-59	96	74	118	125	11	6	179	2271	2	3
39	GPH-27	93	78	126	120	9	7	211	2238	3	4
40	GPHA-53	63	77	124	123	11	6	190	1956	3	4
41	GPHA-32	90	78	123	130	17	6	167	2225	4	5

Entry	genotype	SCAE	FD	MD	PH	PPP	SPP	TSW	GYKGH	AB	PM
42	GPHA-30	96	78	119	133	11	7	228	1695	3	4
43	GPHA-63	96	71	122	118	15	6	209	1898	3	4
44	GPHA-46	66	76	120	130	9	5	149	1537	2	3
45	GPHA-47	93	76	126	140	12	6	214	2521	3	4
46	GPHA-51	84	77	125	150	15	5	211	1817	4	5
47	GPHA-24	93	72	115	100	9	6	148	1922	2	3
48	GPHA-40	50	76	125	135	10	6	151	886	3	4
49	GPHA-64	73	79	118	133	7	6	180	1880	3	4
50	GPHA-56	90	74	121	138	11	5	158	1307	3	4
51	GPHA-6	80	76	120	140	10	6	195	1735	2	3
52	GPHA-35	16	76	123	110	10	6	173	1227	4	5
53	GPHA-25	93	76	123	150	7	5	167	2182	4	7
54	GPHA-61	90	76	118	130	10	6	190	2443	2	4
55	GPHA-44	62	78	124	110	11	4	138	2243	2	3
56	GPHA-50	65	80	125	120	11	5	209	1851	3	6
57	GPHA-19	93	70	118	115	10	5	213	3412	2	3
58	GPHA-26	90	77	124	160	14	5	195	2943	3	4
59	GPHA-23	86	76	121	128	13	5	148	3724	3	5
60	GPHA-43	76	79	124	125	14	5	140	1772	3	4
61	GPHA-29	87	74	119	130	10	5	182	3720	3	4
62	GPHA-4	94	76	123	153	10	5	191	2446	3	5
63	GPHA-62	90	76	122	144	11	6	221	2294	4	5
64	GPHA-54	87	73	122	145	14	5	183	2547	3	4
65	GPHA-65	86	73	123	135	15	5	157	1702	4	6
66	GPHA-34	38	80	125	120	11	5	179	753	4	7
67	GPHA-45	83	72	118	118	16	5	164	3306	3	4
68	GPHA-18	80	76	124	145	14	6	212	2075	3	4
69	Adi	86	72	110	135	9	6	148	3068	3	3
70	Megeri	90	71	116	140	11	6	115	1871	3	4
71	Letu	83	73	114	130	10	6	139	2043	3	6

Where**;** SCAE=Stand count at emergency (%), DF=Days to 50% flowering (days), DM=Days to maturity (days), PH=Plant heigh (cm), PPP=Pods per plant (number), SPP=Seeds per pod (number), TSW=Thousand seed weight (grm), GYKGH=Grain yield (Kg/ha), AB=Ascochyta blight (1-9 scale), PM=Powdery mildew (1-9 scale).

3.2. Divergence Analysis

3.2.1. Cluster Analysis

Cluster analysis grouped the 71 field pea genotypes into seven distinct classes (Figure 1). Cluster C_1 constituting 8.45% of the total genotypes. This cluster constituted smaller seed size, relatively moderately resistance to ascochayta blight and moderately susceptible to powdery mildew. Cluster C_2 and C_3 was the largest constituting 36.5% and 35.2% of the total genotypes respectively. Clusters C_2 and C_3 were characterized by genotypes with an intermediate number of pods plant^{-1} and medium maturity. Clusters C_4, C_5 and C_6, and C_7 constituted 9.86%, 4.23% and 2.82% of the total genotypes, respectively. Genotypes with more number of stands, low number of pods plant^{-1} and high number of seeds pod^{-1} were grouped in C_4. Cluster five constituted high yielding genotypes with taller plant height and an intermediate number of pods plant-^{1}. Genotypes with less number of stands, lately flower and, mature and low yielding genotypes were categorized under C_6. Whereas, the seventh cluster characterized by short plant height, a higher number of pods plant^{-1}, larger seed size but a lower number of seeds pod^{-1}, early flower and, mature, relatively high yielding potential, relatively resistance and moderately resistance to ascochayta blight and powdery mildew respectively (Table 3).

3.2.2. Estimation of Inter and Intra Cluster Distance

The genetic divergence between all possible pairs of clusters were highly significant ($P<0.01$). Different members within a cluster being assumed to be more closely related in terms of the trait under consideration with each other than those members in different clusters [14]. The maximum distance was found between cluster five and six ($D^2=2850.61$) (Table 4). Cluster five constitutes three genotypes while cluster six constitutes two genotypes. The second most divergent clusters were cluster six and seven ($D^2=2540.12$). Cluster seven constitutes two genotypes. The third most divergent clusters were cluster one and five ($D^2=2454.89$). Cluster one constituting from six genotypes. The forth most diver-gent clusters were between cluster four and six ($D^2=2185.50$). Cluster four contain seven genotypes and so on, indicated the wide diversity of the genotypes. Genotypes grouped into the same cluster also presumably diverge little from one another as the aggregate characters are measured. Different authors reported the presence of diversity among field pea genotypes classifying in different number of distinct clusters. In the present study; therefore, crossing of genotypes from cluster five and six will give rise to maximum genetic segregation. All clusters showed zero intra-cluster D^2 value (Table 4). This

result revealed; the genotypes grouped within the cluster are more similar with each other.

Table 3. *Mean of genetic divergence in morpho-agronomic traits of the seven clusters of 71 field pea genotypes studied.*

Character	I	II	III	IV	V	VI	VII	Grand Mean
SCAE	65.33	80.27	86.04	88.29**	87.67	44.0*	88	81.34
FD	76	76.04	75.56	76.14	76.33	78.0**	71.00*	75.8
MD	123.33	121.73	121.52	120	120.67	125.0**	118.00*	121.56
PH	123.17	129.19	132.24	136.14	139.33**	127.5	116.50*	130.46
PPP	10.67	11.12	11.64	10.14*	12	10.5	13.00**	11.24
SPP	5.17	5.62	5.48	5.71**	5.33	5.5	5.00*	5.51
TSW	161.17*	173.58	186.32	178.71	180.33	165	188.50**	177.99
GYKGH	1215.05	1828.63	2361.04	3004.48	3669.71**	819.5*	3359.09	2172.65
AB	3.50**	3.15	3.08	3.29	3	3.5**	2.50*	3.15
PM	5.33	4.69	4.32	4	4.33	5.5**	3.50*	4.52

Where; SCAE=Stand count at emergency (%), DF=Days to 50% flowering (days), DM=Days to maturity (days), PH=Plant heigh (cm), PPP=Pods per plant (number), SPP=Seeds per pod (number), TSW=Thousand seed weight (grm), GYKGH=Grain yield (Kg/ha), AB=Ascochyta blight (1-9 scale), PM=Powdery mildew (1-9 scale).

Table 4. *Pair wise generalized squared distance (D^2) among 7 clusters constructed from seventy one field pea genotypes.*

	C_1	C_2	C_3	C_4	C_5	C_6	C_7	Average D^2
C_1	0	613.91**	1146.49**	1789.71**	2454.89**	396.18**	2144.35**	92.472
C_2		0	532.61**	1175.92**	1841.14**	1009.82**	1530.62**	143.644
C_3			0	643.5**	1308.7**	1542.28**	998.19**	143.93
C_4				0	665.24**	2185.5**	355.34**	92.708
C_5					0	2850.61**	311.63**	75.743
C_6						0	2540.12**	68.815
C_7							0	58.376

**=highly significant at ($P \leq 0.01$) chi-square ($\chi 2$)=23.21.

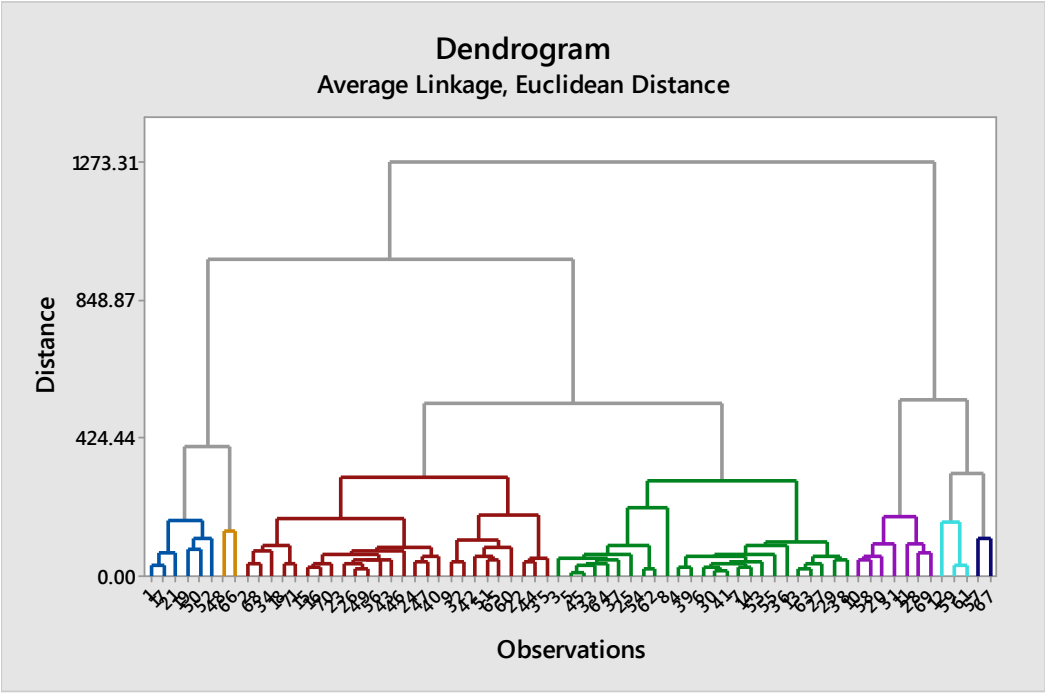

Figure 1. *Dendrogram of 71 field pea genotypes based on ten morpho-agronomic traits using Euclidean distance matrix (The dendrogram represent cluster one=6 genotypes, cluster six=2 genotypes, cluster two=26 genotypes, cluster three=25 genotypes, cluster four=7 genotypes, cluster five=3 genotypes and cluster seven=2 genotypes respectively).*

3.3. Contribution of the Component Characters to Genetic Diversity

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 5). The importance of this technique has been reported appreciably for selecting field

pea lines for high yielding and powdery mildew resistance [2]. 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 ascochayta 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 seed per pod and powdery mildew along with negative loadings for pod per plant and days to maturity.

Table 5. *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	0.358732*	0.348916*	-.250219**	-0.0966
Days to mature	0.375201*	0.432508*	-0.16865	-.277857**
Plant height (cm)	-0.13362	0.444120*	0.372104*	-0.04028
No. of pods per plant	-0.06033	0.251607	0.22596	-.644759**
No. of seeds per pod	-0.088	0.340741*	-.336310**	0.515947*
Thousend Seed weight (gm)	-0.18747	0.519140*	-0.10924	0.245362
Grain yield/ha (Kg)	-.434838**	0.144765	0.168257	0.034232
Ascocayta blight (1-9 score)	0.353656*	0.089166	0.520427*	0.226313
Powdery mildew (1-9 score)	0.423891*	-0.00355	0.441257*	0.338225*
Eigenvalue	2.34014	1.84884	1.50694	1.14878
Percent variability	0.234	0.1849	0.1507	0.1149
Commulative variability	0.234	0.4189	0.5696	0.6845

3.4. Response of Genotypes for Powdery Mildew Resistance

The field pea genotypes were screened under field condition for natural infection against powdery mildew disease caused by *Erysiphe pisi* at three growth stages. 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 71 field pea genotypes, thirteen genotypes (GPHA-12, GPHA-9, GPHA-22, GPHA-44, GPHA-19, GPHA-68, GPHA-58, GPHA-28, GPHA-59, GPHA-46, GPHA-24, GPHA-6, ADI) were resistant (Disease Severity Scale-3), twenty nine (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, Adi and Megeri) were moderately resistant (Disease Severity Scale -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, LETU) were moderately susceptible.

(Disease Severity Scale -5 &6), and seven (GPHA-49, GPHA-5, GPHA-34, GPHA-67, GPHA-25) were susceptible (Disease Severity Scale -7) (Table 6). [2] 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 [16].

table 6. *Response of different field pea genotypes screened against powdery mildew under field condition at different growth stages.*

Entry	Genotype	Disease severity at early stage (1-9)	Disease severity at flowering stage (1-9)	Disease severity at pod setting stage (1-9)	Disease Response (at the last stage)
1	GPHA-36	2	5	6	MS
2	GPHA-3	2	5	5	MS
3	GPHA-38	3	4	4	MR
4	GPHA-68	3	3	3	R
5	GPHA-2	3	3	4	MR
6	GPHA-58	2	3	3	R
7	GPHA-17	2	5	5	MS
8	GPHA-7	3	4	5	MS
9	GPHA-60	2	3	4	MR
10	GPHA-11	3	4	4	MR
11	GPHA-42	3	4	4	MR

Entry	Genotype	Disease severity at early stage (1-9)	Disease severity at flowering stage (1-9)	Disease severity at pod setting stage (1-9)	Disease Response (at the last stage)
12	GPHA-48	3	4	4	MR
13	GPHA-37	2	4	5	MS
14	GPHA-15	3	4	4	MR
15	GPHA-10	2	5	6	MS
16	GPHA-67	3	7	7	S
17	GPHA-52	3	4	5	MS
18	GPHA-1	3	4	4	MR
19	GPHA-33	3	5	5	MS
20	GPHA-8	3	4	4	MR
21	GPHA-49	2	6	7	S
22	GPHA-21	3	5	6	MS
23	GPHA-12	2	3	3	R
24	GPHA-14	3	4	4	MR
25	GPHA-16	3	5	6	MS
26	GPHA-39	3	5	6	MS
27	GPHA-55	3	4	4	MR
28	GPHA-9	3	3	3	R
29	GPHA-22	2	3	3	R
30	GPHA-20	2	5	6	MS
31	GPHA-31	3	5	6	MS
32	GPHA-5	3	6	7	S
33	GPHA-66	2	4	5	MS
34	GPHA-41	2	4	5	MS
35	GPHA-57	3	4	5	MS
36	GPHA-13	3	4	4	MR
37	GPHA-28	3	3	3	R
38	GPHA-59	3	3	3	R
39	GPHA-27	3	4	4	MR
40	GPHA-53	3	4	4	MR
41	GPHA-32	2	4	5	MS
42	GPHA-30	3	4	4	MR
43	GPHA-63	3	3	4	MR
44	GPHA-46	2	3	3	R
45	GPHA-47	3	4	4	MR
46	GPHA-51	3	4	5	MS
47	GPHA-24	3	3	3	R
48	GPHA-40	3	4	4	MR
49	GPHA-64	3	4	4	MR
50	GPHA-56	3	4	4	MR
51	GPHA-6	2	3	3	R
52	GPHA-35	2	4	5	MS
53	GPHA-25	3	5	7	S
54	GPHA-61	2	3	4	MR
55	GPHA-44	3	3	3	R
56	GPHA-50	2	6	6	MS
57	GPHA-19	2	3	3	R
58	GPHA-26	3	4	4	MR
59	GPHA-23	2	5	5	MS
60	GPHA-43	2	4	4	MR
61	GPHA-29	3	4	4	MR
62	GPHA-4	3	5	5	MS
63	GPHA-62	3	5	5	MS
64	GPHA-54	3	4	4	MR
65	GPHA-65	3	6	6	MS
66	GPHA-34	3	6	7	S
67	GPHA-45	2	4	4	MR
68	GPHA-18	3	4	4	MR
69	Adi	2	4	3	MR
70	megeri	3	4	4	MR
71	Letu	4	5	6	MS

4. Conclusion

Results from present study revealed that a considerable level of genetic diversity and variation for resistance against powdery mildew was found indicating the potential of selection for promising gene pools which could be exploited as direct sources or may be transferred through hybridization.

Among the 10 studied traits, four (Eigenvalue >1.0) contributed more than 68.45% variability among the materials Cluster analysis grouped the 71 field pea genotypes into seven distinct classes. The genetic divergence between all possible pairs of clusters were highly significant (P<0.01). The maximum distance was found between cluster five and six. Therefore, selecting and crossing of genotypes from cluster five and six will give rise to maximum genetic segregation.

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 stage. 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) purpose. However, the present result was from one location and one year (season) data; it is recommended to repeat under wide range of agro-climatic conditions in a number of locations and seasons to evaluate their yielding potential, yield and disease stability to confirm with the present finding.

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