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ASSESSMENT OF GENETIC DIVERSITY IN GARDEN PEA (*Pisum sativum* L.) GENOTYPES FOR VARIOUS QUANTITATIVE TRAITS

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Abstract

Pea (*Pisum sativum* L.) a member of the Fabaceae family is one of the most significant pulse crops due to its high nutritive values compared to other pulses. The yield potential of local varieties is very low as compared to varieties of other countries. The present study was sown under a randomized complete block design (RCBD) to explore the genetic variability of various quantitative parameters in 30 genotypes of peas with three replications. Data were collected for traits like days to first bloom, 50% flowering time, maturity, plant height (cm), distance between the nodes (cm), total number of nodes per plant, total number of pods per plant, pod size (cm), width of pods (cm), total number of seeds per pod, 100 seed weight (g) and yield per plant (g). The results revealed that all the genotypes revealed substantial differences for the traits under study. The estimates of broad sense heritability revealed that high heritability was observed among all the attributes and the number of pods per plant exhibited maximum heritability. The dendrogram constructed from the genotypic data grouped 30 genotypes into three major groups. Cluster one was the largest sub-divided into two sub-clusters containing 13 genotypes followed by cluster two includes 6 genotypes that are comparable to each other. The greatest inter-cluster distance was found among clusters 2 and 3 (87.87). Correlation analysis revealed that the height of the plant, nodes per plant, the width of the pod, number of pods per plant, pod size, number of seeds per pod, and 100-seed weight showed positive and extremely significant association by the yield per plant. Path coefficient analysis showed that 50% flowering time followed by pods per plant exhibited a maximum positive effect on plant yield.

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BAHÇE BEZELYESİ (Pisum sativum L.) GENOTİPLERİNDE ÇEŞİTLİ KANTİTATİF ÖZELLİKLER İÇİN GENETİK ÇEŞİTLİLİĞİN DEĞERLENDİRİLMESİ

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Özet

Bezelye (Pisum sativum L.), Fabaceae familyasının bir üyesi olup, diğer baklagillere kıyasla yüksek besin değerleri nedeniyle en önemli baklagil ürünlerinden biridir. Yerel çeşitlerin verim potansiyeli, diğer ülkelerin çeşitlerine kıyasla oldukça düşüktür. Bu çalışmada, bezelyenin 30 genotipi üzerinde, üç tekrarla yapılan rastgele tam blok desenine (RCBD) dayalı olarak çeşitli kantitatif parametrelerin genetik değişkenliği araştırılmıştır. İlk çiçeklenme günü, %50 çiçeklenme zamanı, olgunlaşma, bitki boyu (cm), düğümler arasındaki mesafe (cm), bitki başına toplam düğüm sayısı, bitki başına toplam kapsül sayısı, kapsül büyüklüğü (cm), kapsül genişliği (cm), kapsül başına toplam tohum sayısı, 100 tohum ağırlığı (g) ve bitki başına verim (g) gibi özellikler için veriler toplanmıştır. Sonuçlar, incelenen tüm genotiplerin özellikler bakımından önemli farklılıklar gösterdiğini ortaya koymuştur. Geniş anlamda kalıtım tahminleri, tüm özelliklerde yüksek kalıtım bulunduğunu ve bitki başına kapsül sayısının maksimum kalıtım gösterdiğini ortaya koymuştur. Genotip verilerinden oluşturulan dendrogram, 30 genotipi üç ana grupta sınıflandırmıştır. Birinci grup, 13 genotipi içeren iki alt küme halinde en büyük grup olarak yer alırken, ikinci grup ise birbirine benzer 6 genotip içermektedir. En büyük inter-grup mesafesi, grup 2 ve 3 arasında (87,87) bulunmuştur. Korelasyon analizi, bitki boyu, bitki başına düğüm sayısı, kapsül genişliği, bitki başına kapsül sayısı, kapsül büyüklüğü, kapsül başına tohum sayısı ve 100 tohum ağırlığının, bitki başına verim ile pozitif ve son derece önemli bir ilişki gösterdiğini ortaya koymuştur. Yol katsayısı analizi, %50 çiçeklenme zamanı ve bitki başına kapsül sayısının, bitki verimi üzerinde maksimum pozitif etkiye sahip olduğunu göstermiştir.

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Introduction

Field pea (*Pisum sativum* L.) is a significant temperate region crop belonging to family Fabaceae with other essential crops such as faba bean, chickpea, and lentil [1]. It is grown for its dried seeds and green pods and has a considerable amount of quality protein like lysine [2]. They have been used in human consumption for a long time as peas contain an exceptional source of protein, minerals, vitamins and other nutrients with no cholesterol while having maximum fiber and low fat [3]. Dry protein is a comparatively amusing and unique protein that is diverse from other naturally occurring protein sources. If the regular basis intake of pea protein increases, it helps reduce the danger of different diseases such as diabetes, obesity, and heart diseases which also reveals a positive effect in the inhibition of many forms of cancer [4]. Peas have a great digestibility (90-95%) rate with no health controversy having a less allergenic response (compared to soybean) with high nutritional value which offers a fresh mark for food products [5].

Pea production and consumption differ according to cultural and ethnic groups in various countries and areas [6]. Therefore, a variety of growth kinds and morphologies are present among pea varieties and landraces that have been suited to various environmental circumstances, end uses and cropping systems [7]. It is widely grown in tropical and sub-tropical areas such as Pakistan, Colombia, Burma, India, and the Equator [8]. In plain areas, the pea is cultivated in winter, while in highlands, it is grown in summer [9]. Matter is the local name for pea with maximum nutritious qualities in Pakistan and cultivated in all provinces of Pakistan [10]. Pakistan's yield is low in comparison to other countries due to a dearth of high-yielding potential genotypes as well as pea fungus and viral infections [11]. Globally, it ranks 5th in production after soybean, peanut, dry bean, and chickpea, while 3rd significant leguminous crop after soya bean and common bean. Pea maintains agricultural ecological sustainability by fixing atmospheric nitrogen via a symbiotic association, eliminating the need for nitrogen fertilizers [12]. It provides organic matter and nitrogen to soil which iswhy pea is a very important legume crop for rotation [13].

94 countries around the world are producing dry peas [14]. Dry peas were cultivated in Pakistan on 34,036 hectares with a total outcome of 22,316 tonnes and 656 kg/ha of yield in the year 2021 [15]. In Pakistan, the pea is very important because its demand and utilization are increasing daily owing to its elevated nutritive values and it plays an essential role in a farmer's economy, but different constraints reduce the yield of pea. Plants have evolved specific mechanisms that allow them to acclimate and survive in a variety of environmental challenges [16].

Overall production of peas is less due to a lack of genotypes with high yield in diverse environmental conditions [17] and lack of disease resistance against different stresses [18] such drought [19, 20, 21], salinity [22, 23], low and high-temperature effects [24]. In a population high variability is useful for the selection of a genotype having desirable characteristics and coefficient of variation helps understand the unpredictability existing among the population [25]. In breeding, genetic variability among different traits is essential as these are used in the selection of desirable genetic material [26]. For the improvement of high-yielding varieties and improvement of crops, genetic variability is an important factor in obtaining improvement [27]. The parameters of variability especially genetic gain and heritability are estimated for the improvement of traits in the crop through the selection method [28]. Cluster analysis divides genotypes into similar genotypes clusters, with high variety among clusters, while the assortment inside two clusters is generally low. Clusters could be used in a hybridization scheme depending on the goal of breeding [29]. Selecting suitable divergent parents for hybridization makes it easier to get desirable segregants in successive generations [30].

Correlation and path analysis are used to measure the association between two parameters and separate the direct and indirect influence of various characters to identify high-yielding genotypes [31]. Finding the attribute that is connected with yield is crucial for plant breeders in order to further crop genetic development [32].

The proposed research work was conducted to estimate genetic variability in pea germplasm on different quantitative traits by using cluster analysis, correlation, and path coefficient analysis. The particular genotypes may be used further to develop better varieties of peas in breeding programs.

Materials and methods

Experimental area

The current study was led in the field area of the Plant Breeding and Genetics Department, University of Agriculture, Faisalabad, during the year 2021–22. The plant materials were collected from the National Agriculture Research Center (NARC). A total of thirty pea genotypes were included in this study (Table 1).

Table 1. List of genetic material utilized in research

Sr. no	Genotypes	Source
1	19755	NARC
2	19763	NARC
3	19766	NARC
4	19768	NARC
5	19771	NARC
6	19772	NARC
7	19774	NARC
8	19780	NARC
9	19781	NARC
10	19782	NARC
11	19783	NARC
12	19784	NARC
13	19785	NARC
14	19786	NARC
15	26849	NARC
16	26850	NARC
17	26852	NARC
18	26854	NARC
19	26858	NARC
20	26869	NARC
21	26870	NARC
22	26876	NARC
23	26928	NARC
24	26951	NARC
25	26960	NARC
26	26989	NARC
27	29249	NARC
28	29250	NARC
29	29260	NARC
30	29264	NARC

A total of thirty pea genotypes were sown for assessment of genetic variability for quantitative characters in a randomized complete block design (RCBD) having three replications. All replications consisted of a single row of each genotype having ten plants. The space between plants and rows was kept at 10 cm and 70 cm, respectively. Standard agronomic practices were used to raise the crop to maturity.

Data collection

At maturity total of five plants per replication for each genotype were carefully chosen for data recording and averages were calculated for the following parameters. Days to the first flower were recorded in each replication from sowing to the first blossom in each selected plant.50% flowering was counted from sowing until 50% of plants flowering in a genotype per replication. Maturity days were counted from seedling to the stage where pods have reached their dryness and final color. Plant height was calculated from the soil surface to the tip of the plant in centimeters with the help of a meter rod. The distance from one node to another was calculated with a meter rod in centimeters. Nodes/plants, seeds/pods, and pods/plants were counted manually. The width of the pod and length were recorded in centimeters by using vernier calipers. Hundred seeds from the total seed production of the five certain plants were weighted in grams by use of an electric balance. By using electric balance total obtained seeds of each plant were weighed in grams after sun drying.

Statistical analysis

Collected data were evaluated for analysis of variance [33]. Phenotypic and genotypic variation coefficients were determined by using the method described by Burton [34]. Broad sense heritability and genetic advance as a percent of the mean were calculated according to the method advocated by Burton and Devane [35] and Johnson [36] respectively. Genotypic and phenotypic correlations were performed as suggested by Al-Jibouri [37]. Association among yield and yield-related parameters was estimated by path coefficient analysis [38]. The genetic diversity was studied by cluster analysis [38].

Results and Discussion

To increase production, it is very important to improve the genetic makeup of crop plants. Thus, it is very necessary for breeders to select parents to develop the genotypes with high-yielding capacity by identifying the genetic nature of yield as well as yield-related traits.

Recorded data were statistically analyzed and subjected to analysis of variance. Analysis of variance (Table 2) disclosed that all the twelve characters viz days to first bloom, 50% flowering time, plant height, maturity, internodal distance, number of nodes per plant, pod size, pods/plant, width of pod, yield per plant, number of seeds/pod and 100-seed weight had significant variability among the genotypes. Days to first bloom, 50% flowering and nodes number per plant ranged from 48.00-90.33, 56.33-98.00 and14.17-28.83 respectively. The highest variation was observed in maturity (85.33-120.0), plant height (86.33-210.3), 100 seed weight (9.20-21.98), and yield per plant (15.11-36.71). Inter nodal distance (6.83-14.00), pod size (4.55-6.03), and width of the pod (0.35-0.68) had minimum variation according to range values.

Phenotypic coefficient of variation (PCV) was greater than the coefficient of variation of the genotype (GCV) for some of the calculated characters in this study, representing notable degree of genetic variability that was not just influenced by genotypic effect but also by environmental factors (Table 3). The phenotypic coefficient of variation was relatively maximum for characters such as days to first bloom, maturity, plant height, yield per plant and, 50% flowering time. A minor difference was found between GCV and PCV in terms of inter-nodal distance, nodes/plant, width of pod, number of pods per plant, pod size, number of seed/pod, and 100-seed weight. PCV was found high in pod size (22.77), days to first bloom (27.56), number of pods per plant (25.10), and 50% flowering time (33.56), while GCV was maximum in terms of pod size (22.30) and pods/plant (25.04). It suggests the existence of a large genetic basis that would be open to additional selection. The characters viz maturity (15.91, 17.16), internodal distance (17.74, 17.81), number of nodes per plant (13.46, 13.52), width of pod (15.47, 15.92), and yield per plant (12.90, 16.98) had moderate values for GCV and PCV. This indicates that these attributes were equally important in both non-additive and additive gene action. Low PCV and GCV were found in 100 seed weight (7.33, 8.80) and plant height (8.04, 13.74). Low GCV and PCV estimates demonstrated the minimal impact of the environment on the manifestation of this character.

Heritability estimations serve as a leader for the breeder's selection process for enhancing certain qualities in a particular environment. The magnitude of the heritable component of variation can be determined by estimating heritability in a broad sense. The heritability was detected maximum for traits such as pods/plant (99.55%) followed by inter-nodal distance (99.20), number of nodes per plant (99.15), number of seeds per pod (98.29), pod size (95.94), width of pod (94.34) and maturity (86.03).

Days to first bloom (19.10), 50% flowering time (37.77), plant height (34.26) and yield/plant (57.72) had low broad sense heritability.

The genetic advance varied from 0.097 to73.79% (Table 3). The higher-level genetic advance was found in a number of nodes per plant (73.79%) while moderate in plant height (25.98) and internodal distance (23.38). Maturity (1.485), pods/plant (4.99), days to first bloom (5.80), pod size (6.14), 50% flowering time (10.10), width of pod (16.12), seeds per pod (0.654), 100 seed weight (0.097) and yield/plant (1.434) showed lowest genetic advance. The highest evaluation of heritability fixed with high genetic advances (as % mean) was found in traits like a number of nodes and width of the pod showing the influence of additive gene action. Maximum heritability with moderate values of GAM was recorded for traits pod size, internodal distance and, pods/plant. Characters like seeds/pod and maturity days had the highest heritability and decreased genetic advances as a percentage of the mean.

Table 2. Analysis of variance for 12 characters in Pea (*Pisum sativum* L.).

Traits	Replication Df=2	Genotype Df=29	Error Df=58	CV (%)
Days to first bloom	32.033	482.377	1.286	1.58
50% flowering time	34.300	390.920	1.116	1.24
Maturity	297.744	266.885	1.055	0.97
Plant height	15.54	3872.67	5.83	1.69
Inter nodal distance	0.0279	18.6104	0.2590	4.59
Nodes/plant	0.7792	28.8387	0.5651	3.79
Pods/plant	1.066	187.915	1.079	4.43
Pod size	0.41423	0.50095	0.06445	4.88
Width of pod	0.01108	0.01422	0.00279	11.04
Number of seed/pod	7.0228	16.0340	0.8232	6.41
100 seed weight	0.0003	34.9034	0.7269	6.16
Yield per plant	3.849	142.279	3.840	8.73

Table 3. Parameters for yield and yield attributing traits in pea.

Traits	Mean value	Range	SE	CD (5%)	GCV %	PCV %	H^2	GA	GAM%
Days to first bloom	22.21	48.00-90.33	3.396	9.509	12.05	27.56	19.10	5.80	26.12
50% flowering time	104.12	56.33-98.00	6.700	18.76	20.63	33.56	37.77	10.10	9.701
Maturity	13.69	85.33-120.0	1.959	5.49	15.91	17.16	86.03	1.485	10.85
Plant height	71.40	86.33-210.3	0.655	1.833	8.04	13.74	34.26	25.98	36.390
Inter nodal distance	84.67	6.83-14.00	0.609	1.708	17.74	17.81	99.20	23.38	27.616
Nodes/plant	143.34	14.17-28.83	1.395	3.905	13.46	13.52	99.15	73.79	51.481
Pods/plant	11.09	8.00-41.50	0.294	0.823	25.04	25.10	99.55	4.99	45.002
Pod size	19.85	4.55-6.03	0.434	1.215	22.30	22.77	95.94	6.14	30.95
Width of pod	23.44	0.35-0.68	0.599	1.679	15.47	15.92	94.34	16.12	68.75
Number of seeds/pod	5.205	3.11-6.11	0.147	0.410	33.66	33.95	98.29	0.654	12.57
100 seed weight	0.478	9.20-21.98	0.031	0.085	7.33	8.80	69.30	0.097	20.19
Yield per plant	4.716	15.11-36.71	0.175	0.489	12.90	16.98	57.72	1.434	30.40

H2 – Broad sense heritability, GA- Genetic advance, GCV- Genotypic co-efficient of variation, GAM- Genetic advance as per cent of mean, PCV- Phenotypic co-efficient of variation

The range of relationship between two or more independent variables is measured by correlation. It is very helpful in breeding as genotypic and phenotypic association determine the influence of the environmental effects on characters and provides the interrelationship between the variables which is very helpful for the direct selection of the high-yielding varieties and other important traits. The correlations of genotypic and phenotypic among all the quantitative parameters were estimated and are presented in Tables 4 and 5 respectively. A positive and very significant association was observed among yield/plant by plant height, 100-seed weight, nodes/plant, pod size, number of pods per plant, width of pod, and number of seed/pod whereas, negative non-significant by days to first bloom at genotypic level (Table 4). At the phenotypic level yield per plant revealed an extremely significant and positive link through several nodes per plant, width of pod, pods/plant, pod size and, 100-seed weight while positive and significant with plant height and number of seeds/pod (Table 5).

Table 4. Genotypic correlation coefficients of various quantitative traits in Pea Genotypes

	DB	**FT**	**DM**	**PH**	**IND**	**NP**	**NPP**	**PL**	**PW**	**NSP**	**SW**
FT	0.746**										
DM	0.758**	0.961**									
PH	-0.070	0.202*	0.097								
IND	-0.272**	-0.004	-0.094	0.462**							
NP	0.423**	0.427**	0.346**	0.359**	0.033						
NPP	0.099	0.125	0.058	0.079	-0.081**	0.583**					
PL	0.197	-0.005	0.074	0.017	0.062**	0.093	0.077				
PW	-0.077	0.031	0.031	0.252**	0.133	0.253**	0.506	0.412**			
NSP	-0.359**	-0.155**	-0.196	-0.207*	0.030**	-0.021	0.322**	-0.037	0.053		
SW	-0.188	-0.130	-0.134	0.161	0.291**	0.135	0.303**	0.624**	0.458	0.215*	
YP	-0.017	0.150	0.082	0.256**	0.118	0.512**	0.838**	0.363**	0.720**	0.249**	0.584**

**=Highly significant, *=Significant, DB=Days to first bloom, FT=50% flowering time, DM= Maturity, PH=Plant height, IND= Inter nodal distance, NP= Number of nodes per plant, NPP=Number of pods per plant, PL=Pod size, PW=Width of pod, , NSP=Number of seeds per pod, SW=100-Seed weight, YP=Yield per plant

Table 5. Phenotypic correlation coefficients of various quantitative traits in Pea Genotypes

	DB	**FT**	**DM**	**PH**	**IND**	**NP**	**NPP**	**PL**	**PW**	**NSP**	**SW**
FT	0.739**										
DM	0.752	0.951**									
PH	-0.069	0.200*	0.096								
IND	-0.265	-0.004	-0.090	0.450**							
NP	0.408**	0.415**	0.333**	0.349**	0.030						
NPP	0.097	0.124	0.057*	0.080	-0.083	0.566**					
PL	0.167	-0.006	0.063	0.012	0.037	0.035	0.062				
PW	-0.068	0.032	0.020	0.189	0.111	0.214*	0.402**	0.266**			
NSP	-0.328**	-0.143	-0.183	-0.186	0.012	0.009	0.297**	-0.082	0.015		
SW	-0.181	-0.127	-0.129	0.156	0.293**	0.132	0.298**	0.459**	0.367**	0.175	
YP	-0.019	0.139	0.079	0.243*	0.109	0.476**	0.819**	0.278**	0.548**	0.209*	0.556**

**=Highly significant, *=Significant, DB=Days to first bloom, FT=50% flowering time, DM= Maturity, PH=Plant height, IND= Inter nodal distance, NP= Number of nodes per plant, NPP=Number of pods per plant, PL=Pod size, PW=Width of pod, , NSP=Number of seeds per pod, SW=100-Seed weight, YP=Yield per plant

Table 6. Direct and indirect effects of different traits on yield and yield related traits

	DB	FT	DM	PH	IND	NP	NPP	PL	PW	NSP	SW
DB	-0.442	-0.330	-0.346	0.031	0.120	-0.187	-0.044	-0.087	0.034	0.159	0.083
FT	0.610	0.818	-0.439	0.165	-0.003	0.350	0.103	-0.004	0.025	-0.126	-0.106
DM	-0.346	-0.346	-0.457	-0.045	0.043	0.089	-0.027	-0.034	-0.014	0.089	0.061
PH	0.003	-0.007	-0.045	-0.035	-0.016	-0.012	-0.003	-0.001	-0.009	0.007	-0.006
IND	0.013	-0.002	0.043	-0.022	-0.047	-0.002	0.004	-0.003	-0.006	-0.001	-0.001
NP	0.018	0.018	-0.158	0.015	0.001	0.041	0.024	0.004	0.010	0.001	0.006
NPP	0.067	0.084	-0.027	0.053	-0.054	0.392	0.676	0.052	0.340	0.216	0.204
PL	0.055	-0.001	-0.034	0.005	0.018	0.026	0.022	0.282	0.116	-0.011	0.176
PW	-0.013	0.005	-0.014	0.043	0.023	0.043	0.087	0.071	0.172	0.009	0.079
NSP	0.043	0.019	0.089	0.025	-0.004	0.003	-0.004	0.005	-0.006	-0.012	-0.026
SW	0.024	0.016	0.062	0.020	0.037	0.017	0.038	0.079	0.058	0.027	0.127

DB=Days to first bloom, DF=50% flowering time, DM= Maturity, PH=Plant height, IND= Inter nodal distance, NP= Number of nodes per plant, NPP=Number of pods per plant, PL=Pod size, PW=Width of pod, , NSP=Number of seeds per pod, SW=100-Seed weight, YP=Yield per plant

In plant breeding path analysis is mostly used to regulate the nature of the relationship among the yield and its contributive characteristics which is used for the selection of genotypes. Path analysis was done with eleven characters using evaluations of direct and indirect influence on yield/plant while yield per plant was dependent and other were independent characters (Table 6, Fig 1). It was exposed that 50% flowering time (0.818) and number of pods per plant (0.673) had a maximum positive direct effect on yield/plant. 50% flowering time had positive indirect effect on yield/plant by number of nodes per plant (0.018), pods/plant (0.084), width of pod (0.005), number of seed/pod (0.019) and 100-seed weight (0.016) while, negative by days to first bloom (-0.330), maturity (-0.346), plant height (-0.007), inter nodal distance (-0.002) and pod size (-0.001). (Table 6.)

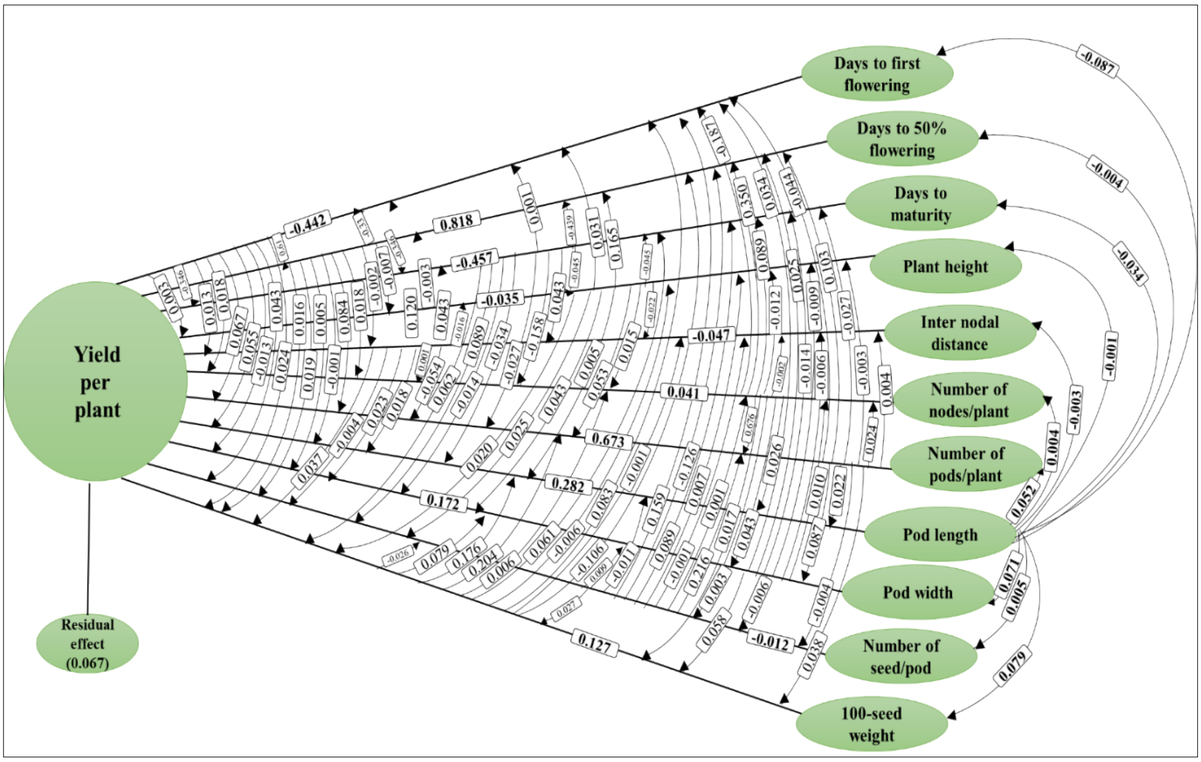

Figure 1. Path diagram for-yield and yield related components in thirty pea genotypes. Straight lines represent the direct effects and arrow lines show the indirect effects

Dendrogram revealed that 30 pea genotypes were divided into three major groups: Cluster 1, Cluster 2, Cluster 3, and four sub-clusters based on various morphological characters (Fig 2). Cluster analysis showed that cluster 1 is the largest comprised of 13 genotypes, 19755, 19763, 19774, 26850, 19782, 19780, 26928, 26951, 26989, 19781, 26854, 26850, 26852, and 26876 that are similar to each other and further divides into two sub-clusters. Cluster 2 included 6 genotypes 19766, 26869, 19771, 26870, 19768, and 19786 found similar to each other. The second main cluster 3 consisted of 11 varieties that were related to each other and were further subdivided into two sub-clusters (Table 9). Genetic diversity can be attained through the crossing of similar genotypes with dissimilar ones.

The data showed that various clusters had different mean values for nearly all of the traits (Table 7). Cluster analysis showed that the genotypes of cluster 1 had maximum mean for days to 1st bloom, 50% flowering time, and maturity whereas it produced the lowest mean values for inter nodal distance, 100 seed weight, pods/plant, pod size, number of seeds/pod, and yield per plant. Cluster 2 carried 6 genotypes found similar to each other and produced the highest plant height, internodal distance, number of nodes per plant, the width of the pod, number of pods per plant, pod size, 100-seed weight, and yield/plant. The genotypes in cluster 2 were of the early maturing type and had the shortest days to 1st bloom and 50% flowering time. Cluster 3 consists of the remaining 11 genotypes, 19785, 19784, 19783, 29260, 19772, 26858, 29264, 26854, 26898, 29249, 29250, and scored first position for the number of seeds per pod. These groups can be employed in hybridization programs to generate high-producing genotypes along with early maturing types.

The inter-genotypic distance was used to calculate the intra-cluster distance (Table 8). Cluster 2 and 3 had the highest inter-cluster distance (87.87), followed by Cluster 1 and 2 (49.24). The higher inter-cluster distance among these clusters showed a wide range of variability in the population. The intra-cluster distances in each of the three groups were smaller than the inter-cluster distances, indicating a close relationship between genotypes in the same cluster. The genotypes included in clusters 3 and 1 had the lowest inter-cluster distance (43.15), indicating a close link between them. The entire cluster showed zero intra-cluster distance which means genotypes within the same cluster are similar to each other. The larger inter-cluster distance indicates greater genetic diversity between the genotypes of dissimilar clusters.

Table 7. Cluster mean values of 12 characters of 30 genotypes in pea

Variables	**Cluster 1**	**Cluster 2**	**Cluster 3**
Days to first bloom	75.79	68.44	66.49
50% flowering time	89.23	88.33	76.55
Maturity	109.31	106.78	99.88
Plant height	148.15	195.53	109.19
Inter nodal distance	10.74	12.44	10.77
Number of nodes per plant	19.15	22.92	19.00
Number of pods per plant	21.19	28.14	23.55
Pod size	5.17	5.25	5.22
Width of pod	0.47	0.51	0.47
Number of seeds per pod	4.41	4.72	5.08
100-seed weight	13.36	14.67	13.94
Yield per plant	20.57	27.76	21.76

Table 8. Distances between the cluster centroids among 30 genotypes of pea

Cluster	1	2	3
1	0	49.25	43.15
2		0	87.87
3			0

Table 9. Distribution of 30 varieties of pea in different clusters

Clusters	No. of accessions	Genotypes
1	13	19755, 19763, 19774, 26850, 19782, 19780, 26928, 26951, 26989, 19781, 26854, 26850, 26852, 26876
2	6	19766, 26869, 19771, 26870, 19768, 19786
3	11	19785, 19784, 19783, 29260, 19772, 26858, 29264, 26854, 26898, 29249, 29250

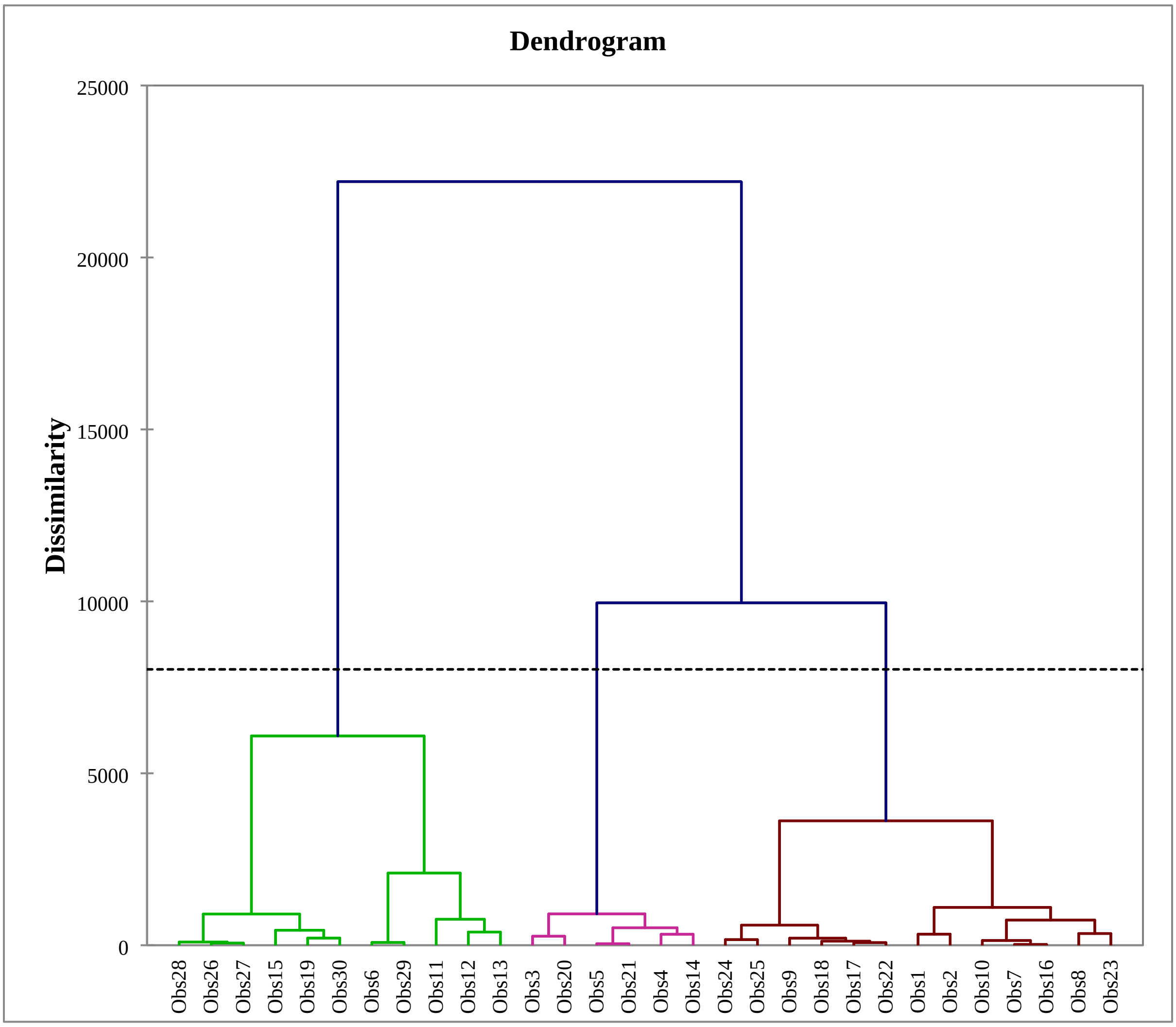

Figure 2. Dendrogram of 30 field pea genotypes based on 12 traits using Euclidean distance matrix

Table 10. Genotypes group into different cluster

Observations	Clusters	Genotypes
Obs1	1	19755
Obs2	1	19763
Obs3	2	19766
Obs4	2	19768
Obs5	2	19771
Obs6	3	19772
Obs7	1	19774
Obs8	1	19780
Obs9	1	19781
Obs10	1	19782
Obs11	3	19783
Obs12	3	19784
Obs13	3	19785
Obs14	2	19786
Obs15	3	26849
Obs16	1	26850
Obs17	1	26852
Obs18	1	26854
Obs19	3	26858
Obs20	2	26869
Obs21	2	26870
Obs22	1	26876
Obs23	1	26928
Obs24	1	26951
Obs25	1	26960
Obs26	3	26989
Obs27	3	29249
Obs28	3	29250
Obs29	3	29260
Obs30	3	29264

It is preferable to have a high degree of variability in the germplasm collection when adding new sources of variation to breeding programs. The identification of phenotypic clusters among large geographic groupings can be enhanced by the evaluation and characterization of inherited agronomic features. Genetic variation analysis helps the breeder choose the best approach and selection criteria to employ to develop the desired qualities. All characters revealed high genetic variation in the present study [39, 40, 41].

Characters showing the highest PCV and GCV values indicate that there is a high level of variability, which suggests the existence of a large genetic basis that would be open to additional selection [42, 43, 44, 45, 46]. Traits that revealed low GCV and PCV manifested low susceptibility to environmental factors and a bigger role of genetic variables influencing the appearance of these characters. Georgieva et al. (2018) observed low GCV and PCV in 100 seed weight [47]. Pujar iet al. (2021) described high GCV and PCV in pods/plant and plant height while least in 100 seed weight and moderate PCV and GCV were found in yield/plant [48]. Barcchiya et al. (2018) recorded moderate phenotypic and genotypic coefficient of variations for pods/plant, yield per plant, and maturity which indicates a need for refinement in the base population [39].

A breeder can choose greater genotypes based on the phenotypic expression of quantitative attributes when there is a high broad sense heritability, which aids in the identification of suitable characters for selection. High heritability was observed for pods/plant, internodal distance, number of nodes per plant, number of seeds per pod, pod size, and width of the pod [49, 28, 45, 48]. Characters with moderate heritability and low genetic advancement as a percentage of the mean were primarily governed by non-additive gene action, and direct selection might not be possible because the majority of variation is attributed to environmental factors. On the other hand, characters with high heritability and high genetic advancement as a percentage of the mean indicated the predominance of additive gene action for these characters. Therefore, by using simple selection techniques, the plant breeder may confidently base their selection on the phenotypic manifestation of these features in the particular plant.

Genetic advances are a useful indicator of efficient selection on the base of population. Characters like seeds/pod and maturity days had the highest heritability and decreased genetic advances as a percentage of the mean [44, 50, 51, 52], which suggests that non-additive gene action predominates in these characters' inheritance and may make selection ineffective in this case. Luthra et al. (2020) observed low genetic advances in pod size, number of seeds per pod, width of pod, pod yield, and number of pods per plant [45]. Characters with high heritability and modest genetic advancement in percentage of mean provided more room for qualities to be improved by selection than other characters, making it easier to develop these traits [53].

The link between individual characteristics and the impact of environmental variables condition the phenotypic correlation [54]. Direct selection of one feature will alter the other if there is a link between the two. Understanding the relationships between different qualities is essential before starting any successful selection program [55]. The traits that showed positive association with each other indicate a significant influence on yield [56, 41]. Since these associated characters are moving in the desired direction, it was clear that selecting these characters together would increase the yield. Furthermore, negative correlation between PH and NSP, also along with other traits may indicate a non-linear association among these traits [57].

Depending on selective breeding, the direction, and strength of the connection between yield and yield components are crucial for identifying the critical traits that may be included in the breeding plan as a crop enhancement strategy. Other connected yield component characteristics should be taken into consideration since direct selection for yield traits may not be very successful [17]. Katoch et al. (2021) and Lal et al. (2011) detected maximum direct effects for 50% flowering time and pods/plant. It means that an increase in the number of pods per plant causes a rise in the yield of seeds/plant, and these characteristics may be used as selection measures to recognize pea germplasm that will increase yield [32, 25].

Clustering analysis exposed significant variation among pea genotypes under study for agro-morphological characters. To enhance high seed-producing pea genotypes, the current study showed that significant variability among local genotypes may be employed for selection between the different genotypes from distant clusters. Thus, this will be a good chance to get desired recombinants for pea breeding in the future. Group assemblage of pea genotypes through genetic divergence has also been reported by [58, 44, 59, 60]. The cluster having maximum mean values and high cluster difference showed wide variation. Variable cluster means for many plant development and yield parameters have also been described by Ramzan and Bijalwan [61, 62].

Conclusion

The present study indicated considerable variability among all the genotypes as all the traits presented significant differences. Thirty genotypes of pea were sown under randomized complete block design (RCBD) with three replications for assessing the genetic diversity of various quantitative traits viz, days to first bloom, plant height, 50% flowering time, internodal distance, maturity, pod size, number of nodes per plant, 100-seed weight, number of pods per plant, number of seeds/pod, width of pod, and yield per plant. The material had a wide range of variability together with strong heritability and high genetic advance for crucial yield parameters. The magnitudes of phenotypic variances were greater than the equivalent genotypic variances, demonstrating the strong environmental influences. Some traits showed the same values for PCV and GCV which means these traits had minimal effect on the environment on the manifestation of this character. Keeping in view the variation present among germplasm and high estimates of broad sense heritability, it is suggested that the germplasm could be used in other breeding programs for improving pea seed yield in Pakistan. The genotypes were clustered into three clusters. Cluster 1 was largest followed by cluster 3 and cluster 2. Cluster 2 and 3 had the highest inter-cluster distance (87.87), followed by Cluster 1 and 2 (49.24). Therefore, selecting and combining genotypes from clusters two and three will give rise to maximum genetic segregation. The higher inter-cluster distance among these clusters showed find wide range of variability in the population. The maximum intra-cluster distance was noted as zero for all the major clusters. The larger inter-cluster distance specifies broader genetic diversity between the genotypes of diverse groups

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