



RESEARCH ARTICLE

## Phenotypic Dissection of *Pisum sativum* Germplasm for Yield and Yield Components: Potential Genetic Resource

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Article History: 24-53

Received: 15-Nov-2024

Revised: 30-Dec-2024

Accepted: 21-Jan-2025

### ABSTRACT

Pea is the most important temperate grain legume grown globally, and in Pakistan, it is cultivated in large areas, predominantly in Punjab and other provinces. The variations present in the germplasm provide the raw material for any plant breeding program on which selection acts to develop improved cultivars. This study evaluated 30 pea genotypes in the field area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The trial was conducted under a randomized complete block design with three replications. Different morphological traits such as days to first blossom, days to 50% blooming, plant height (cm), number of pods/plant, number of seeds/pod, number of nodes/plant, 100-grain weight (g), pod width (cm), pod length (cm), seed yield/plant (g), internodal distance (cm) and days to maturity were noted. Collected data were analyzed for variance (ANOVA), correlation, and path analysis. Phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), and cluster analysis. Correlation analysis revealed that the Plant height, nodes per plant, inter-nodal distance and seeds per pod are positively associated with seed yield per plant. The estimates of genotypic coefficients of variation (GCV) were slightly lower than phenotypic coefficients of variation (PCV) for all traits under consideration. Cluster analysis grouped the 30 pea accessions into three main clusters based on various phenotypic traits. Path analysis showed that days to maturity had a maximum positive effect on yield/plant. The range of variation in the observed variables indicated the genotypes' suitability for use in variety development and breeding research.

**Key words:** Peas, Genetic Diversity, Seed Yield

### INTRODUCTION

Pea is one of the pulses with a huge genome (4.45 Gb), which is diploid ( $2n = 14$ ). (Kreplak et al., 2019). Following cereals, pulses are the second-most significant crop in terms of global agricultural output. Field pea is one of the pulses grown most frequently in the world. Peas are substantial due to their flavor in vegetable curries when combined with other vegetables and because they are often used as pulses in everyday diets. It is a superb food source with many applications, such as food, feed, and fodder. It contains a healthy amount of vitamins, such as vitamins A (139

IU), B (0.25 mg/100 g), and C (9 mg/100 g), as well as ionic minerals like phosphorus (139 mg/100 g), iron (1.5 mg/100 g) and magnesium (34 mg/100 g). It also contains a significant amount of consumable protein (7.2 g/100 g), lysine, and tryptophan, essential amino acids in large amounts. Plant-derived proteins have reportedly become more prevalent in recent years as a result of concerns about human health, the environment, and animal safety, with pea and soybean proteins dominating the marketplace (Asghar et al., 2010; Bashi et al., 2019; He et al., 2020; Choudhury et al., 2020; Vatansever et al., 2020; Boukid, 2021), According to Vatansever et al. (2020), the global market for meat

**Cite This Article as:** Aslam U, Manzoor Z, Mumtaz A, Khalid I, Haider M, Shakeel A and Usman M, 2024. Phenotypic dissection of *Pisum sativum* germplasm for yield and yield components: potential genetic resource. Trends in Animal and Plant Sciences 5: 4-11. <https://doi.org/10.62324/TAPS/2025.059>

for meat replacements, for example, was valued at US\$4.1 billion in 2017 and is predicted to grow to US\$3.5 billion by 2026. Pea protein has many health advantages, including lowering blood pressure and serum cholesterol and the risk of chronic diseases (Shen *et al.*, 2016; Lu *et al.*, 2020; Zhao *et al.*, 2020). It is also recommended because of its excellent digestibility and gluten-free nature (Boukid *et al.*, 2021).

According to research by Ikram *et al.* (2019), peas are a widely grown crop in Pakistan and globally. In addition to potatoes, it is a significant summer cash crop and vegetable in Pakistan's upper Kaghan Valley. In Pakistan, dry peas were farmed in Punjab over roughly 14,400 hectares, yielding 11,600 tons of dry pea seed (Anon. 2018-19). The breeding program at Pulses Research Institute, Faisalabad, intends to produce high-yielding, rust-tolerant, and powdery mildew-resistant varieties of dry peas appropriate for irrigated and rain-fed areas. Iqbal *et al.* (2017) reported this is a broadly dispersed pulse crop. It often suffers from numerous biotic and abiotic stresses. Therefore, creating high-yielding cultivars with high protein content, tolerance to the most important abiotic and biotic stresses, and compatibility for various agro-climatic conditions and cropping configurations is essential. Since the potential of genetic modification in any crop relies significantly on the range of available genetic diversity. The fact that this crop had such a wide range of variations suggested much room for its development since any crop with a wide range of variability usually provides the best chance of selecting the desired forms. According to Kaur *et al.* (2018) the degree of genetic heritable variability and necessary qualities are prerequisites for crop improvement and a successful breeding program; in line with this, genetic advancement, heritability, and genetic variability all play crucial roles in the development of crops. Several genetic variables that interacted with the environment strongly influenced the complicated parameter yield. Therefore, the accomplishment of any breeding effort to improve it relies on the effectiveness of selection and the genetic variety that is now present in the base population. A detailed biological understanding of yield and its components and knowledge of genetic diversity are necessary for developing an aggressive improvement and breeding program. According to Pathak *et al.* (2019), field peas can increase their quality and yield, increasing their export potential. The essentials for a successful breeding program are genetic diversity and the genetic processes that govern the genes responsible for a character. This research was carried out to evaluate genetic variation, the relationship between various seed yield features, and the impacts of these parameters on the yield of plants.

## MATERIALS AND METHODS

The current experiment was conducted during the season 2021-2022 in the experimental field of the

Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, with 30 pea genotypes: 4 checks and 26 lines (Table 1) and seeded in a randomized complete block design (RCBD) with three replications to evaluate genomic diversity for quantitative traits. The crop was raised to maturity with standard production practices. Five plants per replication of each genotype were chosen at the maturity stage for data recording and the averages were computed.

The data were noted for 12 morpho-agronomic traits such as plant height (Pht), days to first blossom (DFsF), days to maturity (DM), days to 50% blooming (DFF), internodal distance (ID), number of seeds per pod (NSP), number of nodes/plant (NNP), number of pods per plant (NPP), pod length (PL), pod width (PW), seed yield per plant (SYP) and 100-seeds weight (SW) respectively.

A statistical analysis was performed and compared to standard statistical methods. Composed data was subjected to analysis of variance (ANOVA) (Steel *et al.*, 1997) and the Tuckey HSD Test to evaluate significant differences among genotypes (Silva and de Azevedo, 2016). Genetic diversity was studied using cluster analysis, as Johnson (1967) outlined. Broad sense heritability, phenotypic and genotypic coefficients of variation, and genetic advance as a percentage of mean were calculated following Singh and Choudhary (1979). Al-Jibouri *et al.*, (1958), and Dewey and Lu (1959) methods were followed to measure the correlation coefficients and path analysis, respectively.

## RESULTS & DISCUSSION

ANOVA was performed distinctly for all traits presented in (Table 2). The mean sum of squares between treatment/genotype was highly significant for all of the parameters. In other words, the genotypes' performances on these parameters were statistically dissimilar, indicating plenty of room for selection in the field of pea genotypes available. The findings are consistent with previous research, such as Pathak *et al.* (2019).

**Table 1:** List of genetic material utilized in the experiment

Sr. No.	Genotype	Sr. No.	Genotype
1	9034	16	19579
2	10615	17	19585
3	18372	18	19589
4	18384	19	19599
5	18373	20	19605
6	19306	21	19685
7	19537	22	19688
8	19540	23	19699
9	19553	24	19713
10	19565	25	19723
11	19566	26	19739
12	Supreme	27	19742
13	Sarsabz	28	19744
24	Meteor	29	19746
15	Pea-2009	30	19752

**Table 2:** Analysis of variance for 12 parameters in pea (*Pisum sativum* L.)

Source of variation	DF	Mean square	Sum of square	DFsF	DFF	DM	Pht (cm)	ID (cm)	NNP	PL (cm)	PW (cm)	NPP	NSP	SYP	SW
Replication	2	2.13	1.87	1.40	3.01	0.006	0.077	0.595	0.001	3.33	2.39	3550.95	0.017		
Genotypes	29	226.03**	307.45**	202.48**	4523.11**	33.53**	104.58**	2.134**	0.063**	334.69**	1.925**	189.61**	20.57**		
Error	58	3.89	0.80	3.13	158.41	0.35	2.423	0.057	0.003	2.51	0.24	24.81	1.11		

**Table 3:** Estimates of genetic parameters for growth, yield, and quality parameters in garden pea genotypes

Variable	Grand Mean	GCV%	PCV%	h <sup>2</sup> %	GA	GAM
Days to 1 <sup>st</sup> Flower	61.9667	13.8892	14.2416	95.1123	17.2910	27.9038
Days to 50% flowering	74.9167	13.4956	13.5476	99.2326	20.7474	27.6940
Days to maturity	121.7500	6.6953	6.8518	95.4839	16.4087	13.4773
Plant height	109.1493	34.9471	36.7948	90.2087	74.6317	68.3758
Inter nodal distance	7.9778	41.6866	42.3509	96.8878	6.7434	84.5276
Number of nodes/plant	23.7169	24.6072	25.4662	93.3678	11.6168	48.9810
Number of pods/plant	25.4661	41.3187	41.7908	97.7535	21.4310	84.1550
Pod length	5.5883	14.8833	15.5030	92.1653	1.6449	29.4341
Pod width	0.4840	29.1369	31.7795	84.0605	0.2663	55.0309
Number of seed/pod	5.0593	14.8034	17.7226	69.7699	1.2887	25.4720
100-seed weight	16.7469	15.2096	16.4601	85.3822	4.8484	28.9513
Seed yield/plant	23.3499	40.8579	43.2699	89.1621	18.5575	79.4756

**h<sup>2</sup>** – Broad sense heritability, **GCV**- Genotypic co-efficient of variation, **GA**- Genetic advance, **GAM**- Genetic advance as percent of the mean, **PCV**- Phenotypic coefficient of variation.

The mean performance of different lines also presented a fair range of genetic diversity for the features examined in the current experiment (Table 3). The PCV was slightly higher than the GCV for all attributes studied. Some influences of the environment on phenotypic expression were also responsible for the superior magnitudes of PCV over GCV for all characters. Our results conform with Iqbal *et al.* (2015), Katoch *et al.* (2016); Gudadinni *et al.* (2017), Pandey *et al.* (2017), Barcchiya *et al.* (2018). The maximum PCV and GCV values were observed for inter-nodal distance (42.65/41.68), pods/plant (41.79/41.31), and seed yield/plant (43.26/40.85) respectively. The findings suggest that breeders can choose desirable plants by screening for characteristics with greater PCV/GCV magnitudes. Our results are parallel to Pal and Singh (2012), Saxesena *et al.* (2014), and Gudadinni *et al.* (2017).

A population's or gene's quantity of transmissible variability can be estimated and assessed using heritability. It is one of the most crucial fundamental elements determining whether a population's or genotypes superior plants will exhibit genetic progress or respond to selection. For all the characters under consideration in the current analysis, the heritability values in a broad sense ranged from 69.76 % to 99.23 %. The above calculations suggested that these traits may undergo significant genetic improvement and that environmental factors had little effect on these parameters. Low selection pressure is needed to improve these. Comparable verdicts were also reported by Georgieva *et al.* (2015), Gupta *et al.* (2018), and Kumar *et al.* (2019).

According to reports, traits with high genetic advancement and heritability may be caused by genes that work additively and respond vigorously to

selection. These features should be prioritized during breeding selection, whereas traits with little genetic progress and moderate to high heritability suggest non-additive gene action; as a result, selection should be carried out carefully about low heritable characteristics. About this, Sardana *et al.* (2007), supplementary explanation revealed that features with high heritability could not always result in more genetic advances. The variation in GCV and PCV values across characters suggested that the environment impacts how traits show variability. If there is little difference, it indicates that the characters' inconsistent performances are primarily influenced by their environment. However, if the difference is more significant, it suggests that the environment significantly impacts how features are expressed.

The current study concluded that GCV and PCV were high for inter-nodal distance, pods/plant, and seed yield/plant. This demonstrated the character's high degree of variability and highlighted the potential for increasing yield by selecting these features.

Correlation coefficient analysis makes effective selection and hybridization programs possible, which provides a better understanding of the yield component. Identifying suitable yield components and drawing information about their interactions with yield and one another will be beneficial to developing a variety with high yield potential.

The correlation coefficient provides a symmetrical estimate of the interaction between two features, helping describe the extent of the interaction between yield and its constituent parts. According to this perspective, understanding the relationships between seed yield and related variables is required to develop an effective selection strategy to increase seed yield.

**Table 4:** Simple correlation coefficient of various quantitative traits in peas cultivar

DFsF	DFsF	DFF	DM	Pht	ID	NNP	NPP	PL	PW	NSP	SW	SYP
1												
DFF	0.763316	1										
DM	0.530932	0.772472	1									
Pht	0.209267	0.161619	0.329312	1								
ID	0.295712	0.19515	0.258802	0.646436	1							
NNP	0.146359	0.068056	0.210519	0.539768	0.347488	1						
NPP	0.171645	-0.17049	-0.02382**	0.169113	0.125056	0.383084	1					
PL	-0.38007	-0.29099	-0.26683	-0.36847	-0.33992	-0.23585	0.060128	1				
PW	0.094036	0.163324	0.231676	0.093191	0.004557**	-0.25292	-0.10941	0.299605	1			
NSP	-0.15793	-0.10729	-0.05248*	-0.27321	-0.25453	-0.09303	-0.01314**	0.292887	-0.01611**	1		
SW	-0.16516	-0.14208	0.028079**	0.163978	-0.05122*	0.047051*	0.080489	0.2035	0.312863	-0.10697	1	
SYP	-0.07735	-0.36327	-0.12242	0.021518**	0.036993*	0.044352*	0.626806	0.29272	0.132871	-0.0321*	0.22646	1

**Table 5:** Genotypes grouped into different clusters

Observations	Class/ cluster	Genotype
Obs1	1	9034
Obs2	2	10615
Obs3	2	18372
Obs4	1	18384
Obs5	2	18373
Obs6	2	19306
Obs7	3	19537
Obs8	3	19540
Obs9	3	19553
Obs10	3	19565
Obs11	2	19566
Obs12	1	Supreme
Obs13	1	Sursabz
Obs14	1	Meteor
Obs15	1	Pea-2009
Obs16	2	19579
Obs17	1	19585
Obs18	3	19589
Obs19	3	19599
Obs20	2	19605
Obs21	2	19685
Obs22	2	19688
Obs23	2	19699
Obs24	3	19713
Obs25	3	19723
Obs26	2	19739
Obs27	2	19742
Obs28	2	19744
Obs29	3	19746
Obs30	3	19752

It was noted that seed yield/plant had a highly significant strong positive correlation with plant height (0.021) and 100 seed weight (0.028). It also had a significant positive correlation with inter-nodal distance (0.036), nodes/plant (0.044), and seeds/pod (0.032) (Table 4). Consequently, the current study recommends enhancing seed yield/plant by selecting these characters in native pea germplasm. Lal *et al.* (2018) and Kumawat *et al.* (2018) and Pratap *et al.*, (2024) also documented comparable results for seed yield with one or more of the above characters. Parallel to the current investigation, seed yield/plant showed a significant positive association with these parameters in field pea (Parihar *et al.*, 2014; Srivastava *et al.*, 2018; Singh *et al.*, 2018; Ton *et al.*, 2018).

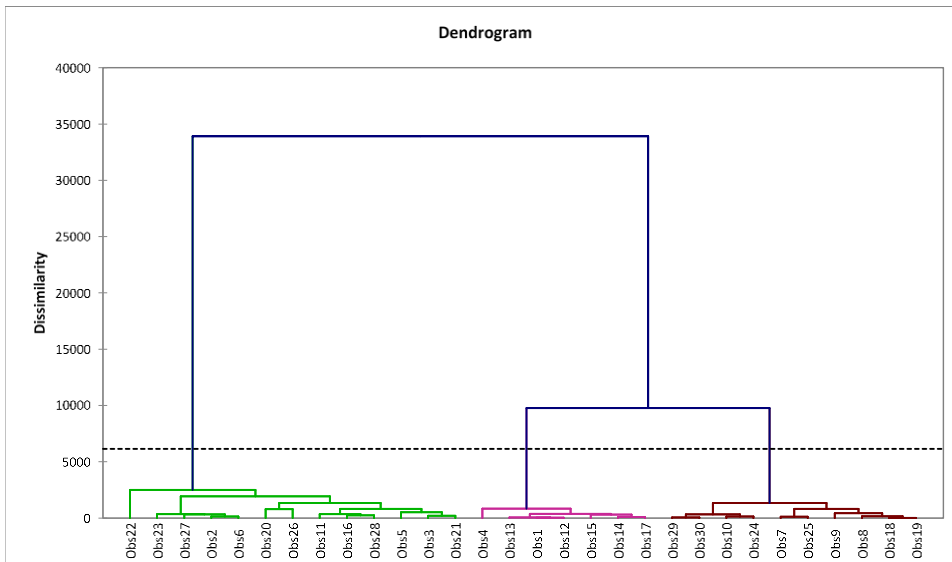
The correlation coefficient aids in describing the extent of the relationship between the yield and its constituent parts by providing a symmetrical evaluation of the magnitude of the interaction between two features. According to this perspective, understanding the relationships between seed yield and related variables is required to develop an effective selection strategy to increase seed yield.

Hierarchical cluster analysis forms a discrete set of nested clusters/categories by analytically matching clusters and variables. The wide-ranging linkages among the value of the clustering criteria and categories related with each are shown on a graph that is formed similarly to the taxonomical dendrogram of the biological systematist.

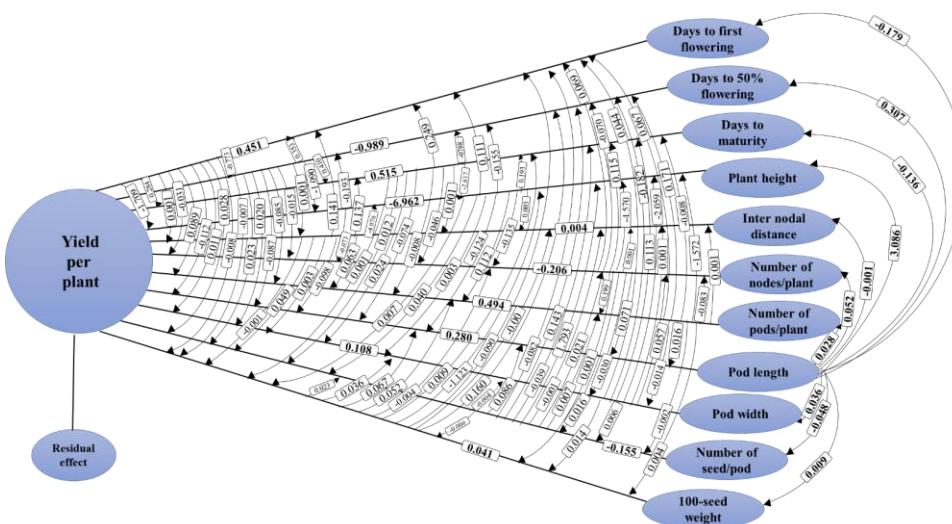
According to the cluster analysis shown as a dendrogram in (Fig. 1), genotypes were divided into three major groups; 1, 2, and 3 based on similarities and differences in several morphological features. It clearly illustrates the similarities and differences among the assessors. Cluster analysis revealed that clusters 1, 2, and 3 each included seven, thirteen, and ten genotypes, respectively (Table 5).

As the aggregate features are assessed, genotypes placed into the same cluster are likely to differ very little. Field pea genotype diversity was noted by many writers, who classified it into a variety of unique groups. Among all genotypes, Cluster C1, C2, and C3 account for 23.33 percent, 43.33 percent, and 33.33 percent, respectively. It is thought that members of a cluster are more closely connected than members of other clusters in terms of the attribute under discussion, how the 30 genotypes of peas are divided into three major groups based on a variety of morpho-agronomic parameters. Cluster analysis results and the creation of individual groups revealed that genotypes with similar ancestry do not always belong to the same cluster (Gixhari *et al.*, 2014; Ouafi *et al.*, 2016). Our findings are parallel to the results of Kumar *et al.* (2019), Mohamed *et al.* (2019), Hanci & Cebeci (2019), Kalapchieva *et al.* (2020), Arif *et al.* (2020), Assen (2020) and Ton *et al.* (2022).

Cluster 1 and Cluster 2 depicted maximum inter-cluster distance. Consequently, combining lines from clusters one and two will produce the highest genetic segregation. Assen, (2020) also reported the same



**Fig. 1:** Dendrogram of 30 pea genotypes based on agromorphological characters using Euclidean distance matrix. The original names of genotypes are shown in supplementary table 5.



**Fig. 2:** Evaluations of direct/diagonal and indirect effects of different traits on seed yield/plant in field pea.

results. In line with our findings, earlier documentation showed that alterations in inter-cluster for agromorphological traits were found in pea genotypes (Khan *et al.*, 2016; Prasad *et al.*, 2018). Some other investigations documented parallel results. (Parihar *et al.*, 2014; Ouafi *et al.*, 2016). The current study showed that pea genotypes of diverse geographical regions were clustered in the identical group in agreement with the preceding reports (Srivastava *et al.*, 2018).

The phenotypic expression of the traits can be used to estimate the genetic distance between genotypes. It is also acknowledged to gauge phenotypic variety by fundamental traits employed in technical questionnaires for distinctness, homogeneity, and stability (Hanci & Cebeci 2019). The genotypes in cluster 1 demonstrated the highest seed yield per plant, 100 seed weight, and number of seeds per pod (Table 6). This suggested that the lines corresponding to this group could be utilized in imminent breeding programs for the enhancement of seed yield attributes. Parallel outcomes were also documented by Kalapchieva *et al.* (2021) and Azmat *et al.*, (2011). They also reported a significant increase in seed yield, 100 seed weight.

**Table 6:** Cluster analysis of different morphological traits in *Pisum sativum*

Variable	Cluster 1	Cluster 2	Cluster 3
DFsF	56.0000	63.6154	64.0000
DFF	65.9286	75.5000	80.4500
DM	112.5714	124.0000	125.2500
Pht	55.5595	146.9231	97.7694
ID	4.9165	10.4567	6.8958
NNP	19.8571	27.6154	21.3500
NPP	25.6905	29.5128	20.0500
PL	5.3635	6.3571	5.3400
PW	0.4464	0.4846	0.5075
NSP	5.3221	4.8481	5.1492
SW	16.5986	17.3877	16.0165
SYP	27.3700	26.7912	16.5875

Cluster 2 was characterized by genotypes showing a significant enhancement in plant height, inter-nodal distance, nodes/plant, pods/plant, and pod length. Kalapchieva *et al.* (2021) documented the same results for pod length. Azmat *et al.* (2011) stated the same findings for pods/plants. Gixhari *et al.* (2016) and Ton *et al.* (2022) confirmed the same pods/plant and plant height findings.

The members of the 3<sup>rd</sup> cluster were categorized by early first flowering and 50% flowering, days to

**Table 7:** Direct/diagonal and indirect effects of different parameters on seed yield/plant in field pea

	DFsF	DFF	DM	Pht	ID	NNP	NPP	PL	PW	NSP	SW
DFsF	<b>0.451</b>	-0.773	0.284	-1.709e-04	0.001	-0.031	0.089	-0.112	0.011	0.028	-0.008
DFF	0.353	<b>-0.989</b>	0.410	-1.090e-04	0.001	-0.015	-0.085	-0.087	0.020	0.023	-0.007
DM	0.249	-0.788	<b>0.515</b>	-2.617e-04	0.001	-0.046	-0.008	-0.074	0.024	0.012	0.001
Pht	0.111	-0.155	0.193	<b>-6.962e-04</b>	0.003	-0.135	0.112	-0.124	0.003	0.040	0.007
ID	0.141	-0.193	0.137	-4.976e-04	<b>0.004</b>	-0.073	0.063	-0.098	0.003	0.049	-0.001
NNP	0.069	-0.070	0.115	-4.570e-04	0.001	-0.206	0.199	0.071	-0.030	0.016	0.001
NPP	0.067	0.171	-0.008	-1.572e-04	0.001	-0.083	<b>0.494</b>	0.016	-0.014	-0.002	0.004
PL	-0.179	0.307	-0.136	<b>3.086e-04</b>	-0.001	0.052	0.028	<b>0.280</b>	0.036	-0.048	0.009
PW	0.044	-0.182	0.113	-2.059e-04	0.001	0.057	-0.062	0.092	0.108	0.006	0.014
NSP	-0.082	0.143	-0.039	<b>1.793e-04</b>	-0.001	0.021	0.007	0.086	-0.004	-0.155	-0.006
SW	-0.090	0.160	0.009	-1.123e-04	-0.000	-0.004	0.052	0.067	0.036	0.023	0.041

Residual effect: 0.259 ; bold italic figures denote the direct effect.

maturity and pod width. Our findings are in consistence with the reports of Azmat *et al.* (2011) and Gixhari *et al.* (2016). The cluster analysis efficiently categorized genotypes by genetic similarity and genetic distance based on the researched characteristics and can be used to organize initial parent combinations in selection. A crossbreeding strategy can effectively use genotypes with the researched traits from ecologically distinct locations.

In terms of agro-morphological traits, clustering analysis showed significant variance among the genotypes of the examined pea. According to the results of the current study, significant local genetic diversity can be employed in selection/hybridization programs to enhance the yield of pea genotypes. Therefore, future pea breeding will benefit from this potential to obtain desirable recombinants.

In the current studies, the path coefficient analysis showed that days to maturity (0.515) had the highest positive direct effect on seed yield/plant followed by pods/plant(0.494), days to 1st flowering(0.451), pod length(0.280), pod width(0.108), 100- seed weight(0.041) and internodal distance(0.004) respectively as shown in (Table 7, Fig 2). While maximum direct negative effect was contributed by days to 50% flowering (-0.98) followed by a number of nodes/plant (-0.20) and seed/pod (-0.15).

The maximum indirect positive effect was contributed by days to 50% flowering via days to 1st flowering (0.35) followed by days to 1st flowering via days to maturity (0.28). The maximum negative indirect effect was exerted by inter nodal distance via days to 50% maturity (-0.19). It indicates that direct selections for these traits would bring an inclusive improvement of seed yield/plant in peas. Our results are parallel to the findings of (Selvi *et al.*, 2016, Devi *et al.*, 2017 and Khan *et al.*, 2017), in their studies also revealed high direct effects for pod/plant, seeds/pod width, and pod length internodal distance and 100-seed weight. The maximum indirect positive effect on seed yield/plant was imposed by pod length via plant height and internodal distance had the highest negative indirect effect via plant height on seed yield/plant.

## Conclusion

The range of variation in the variables that were found indicated the genotypes' suitability for use in variety development and breeding research.

The entire research shows that a breeding program should take advantage of the wide range of genetic erraticism in yield and its contributory traits to maximize genetic gain in field peas. Through heterosis/transgressive breeding, the genotypes 19685 and 19688 can be used to maximize genetic gain in field peas.

## Conflict of Interest

The authors claim no conflicts of interest.

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