

Genetic Variability, Heritability and Correlation Coefficient in Production Traits of Pea (*Pisum sativum* L.) Genotypes

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To cite this article:

Barkat Ali, Sujon Kumar, Waleed Ahmed. Genetic Variability, Heritability and Correlation Coefficient in Production Traits of Pea (*Pisum sativum* L.) Genotypes. *International Journal of Genetics and Genomics*. Vol. 9, No. 4, 2021, pp. 78-88. doi: 10.11648/j.ijgg.20210904.13

Received: October 29, 2021; Accepted: November 15, 2021; Published: November 27, 2021

Abstract: An experiment was carried out to measure variability, heritability, genetic advance and correlation coefficient for yield and yield related traits in ten Pea (*Pisum sativum* L.) genotypes at Tarnab-Peshawar, during cropping season 2016-17. To identify the best genotypes for further breeding these genotypes were evaluated in a randomized complete block design with three replications. All genotypes were grown in 3m long ridges, which were kept 60cm apart where plant to plant distance was 30cm. To reduce experimental error, cultural practices were performed uniformly for all genotypes. Data was collected from ten randomly selected plants from each genotype in each replication. Highly significant ($p \leq 0.01$) differences were observed for days to 50% flowering, plant height, primary branches plant⁻¹, days to maturity, pods plant⁻¹, pod length, fresh pod shelling percentage, 100-seeds fresh and dry weight, seeds pod⁻¹ and seed yield plant⁻¹. Among genotypes Sultan was best for 50% flowering (50.38), days to maturity (122.08) and fresh pod shelling percentage (65.29%). Genotype PL-4 had maximum plant height (142.08 cm), pods plant⁻¹ (39.96) and seed yield plant⁻¹ (52.04 g). Anmol had maximum 100-seed fresh (43.90 g) and dry (21.29 g) weight. Genotype Sarsabz had maximum primary branches plant⁻¹ whereas Adventa Selection had maximum pod length (8.86 cm) and seeds pod⁻¹ (6.26). The estimates of heritability and genetic advance were high for days to 50% flowering (0.99, 35.38%), plant height (0.95, 46.88%) and seed yield plant⁻¹ (0.97, 62.47%). High heritability with moderate genetic advance were observed for days to maturity (0.97, 20.20%), pod length (0.95, 15.37%) fresh pod shelling percentage (0.82, 21.58%), 100-seed fresh (0.90, 29.52%) and dry weight (0.93, 22.68%). Significant and positive phenotypic coefficient of correlation was exhibited by seed yield plant⁻¹ with plant height ($r_p = 0.64$), days to 50% flowering ($r_p = 0.63$), days to maturity ($r_p = 0.78$), pods plant⁻¹ ($r_p = 0.72$), pod length ($r_p = 0.66$), fresh pod shelling percentage ($r_p = 0.64$), 100-seed fresh weight ($r_p = 0.65$) and 100-seed dry weight ($r_p = 0.62$). Significant and positive genotypic coefficient of correlation was exhibited by seed yield plant⁻¹ with plant height ($r_g = 0.81$), days to maturity ($r_g = 0.70$) and pods plant⁻¹ ($r_g = 0.84$). Among tested genotypes Sultan, PL-4, Anmol and Sarsabz performed better, therefore could be used in future breeding programs.

Keywords: Peas, Variability, Heritability, Genetic Advances and Correlation Coefficient

1. Introduction

Pea (*Pisum sativum* L.) is an annual herbaceous leguminous crop belonging to family Fabaceae or bean family. It is adapted to cool moist climate with moderate temperature. Pea is a grain legume and is cultivated during winter in plains and summer in highlands of Pakistan [1]. Genus *Pisum* comprises two species, *Pisum sativum* and *Pisum fulvum* of which *Pisum sativum* L. is

cultivated pea. *Pisum sativum* has high nutritive value and dietary proteins and is considered as an important vegetable crop. Dry pea is a widely consumed grain legume in many countries of the world. Pea is becoming popular in human foods due to its hypo-cholesterolaemic properties. It is a safe food material with no problems of mycotoxin, pesticide or fungicide residues [2].

Pea is cultivated for many purposes like its grains are eaten fresh or processed as canned food. Its grains are used to make

soup whereas some pea varieties known as feed peas are used for the purpose of green forage production, dry forage and green manure production. Pea seed contains 21 to 25% proteins and therefore considered alternative to soybean. It also contains high levels of carbohydrates and total digestible nutrients which makes it as good livestock feed [3]. Pea seed is also rich in phosphorus, calcium and vitamins A and D.

Pea production ranked 11th in the world valuing production worth of 27548 thousand US dollars in year 2008-09 [4]. China, India, US, France and Egypt are the largest producers whereas, France and Canada are the largest exporting countries while Spain and Germany are the biggest importers of pea [5]. During 2011-12, 7456 tons of peas (dried, fresh and frozen) were exported from Pakistan. These figures demonstrated the export potential of pea due to its higher yield and higher economic returns per unit area as compared to other food crop. Pea crop ranks 5th area wise and 6th production wise during 2008-09 amongst all types of vegetables grown in Pakistan. In Khyber Pakhtunkhwa, pea crop ranks third area wise and sixth production wise amongst the rabbi vegetable crops during 2013-2014 [6]. Considerable breeding efforts have been made with pea over the years to develop high yielding varieties around the world [2]. As other vegetable crops, yield of pea is also lower than its potential yield, which needs serious breeding efforts.

Presence of high variability in the field pea provides much more scope for its improvement. A great diversity is present in pea that may be used to develop new high yielding varieties [7]. A great proportion of variability has been observed in different agronomic characters of pea [8]. Local and exotic germplasm can be used in hybridization program for pea improvement [1].

Before starting any effective breeding program it is necessary to get some basic information about the available germplasm. The information includes the estimates of heritability and genetic advance. Heritability is defined as the proportion of total variance in a population for a particular trait at a particular time. Two types of heritability can be estimated, the broad sense heritability is the ratio of total genetic variance to total phenotypic variance while the narrow sense heritability is the ratio of additive genetic variance to the total phenotypic variance. Heritability estimates shows that either the phenotype is controlled by environment or genotype. High heritability coupled with high genetic advance indicates that there is the major role of genotypes in the expression of

character rather than the environment.

For an effective breeding program, it is necessary to know the importance and association of various components with yield and yield related traits. Correlation studies provide an opportunity to study the magnitude and direction of association of one character with another. The nature and magnitude of correlation coefficient helps breeders to determine the selection criteria for progress of various characters with yield. Pea yield could be enhanced by an understanding the interrelationship of yield and other traits at both phenotypic and genotypic levels. Unfavorable association between yield and its contributing components for the selection of desired attributes may result genetic slippage, and reduce the genetic advance and yield. The selection of highly heritable and positively correlated characters would be more effective.

The experiment was conducted with the following objectives to:

- 1) Study genetic variability among pea genotypes for important traits.
- 2) Estimate heritability and genetic advance of important traits in pea genotypes.
- 3) Estimate coefficient of correlation among yield and yield related traits in pea genotypes.
- 4) Identify best pea genotypes for further breeding.

2. Materials and Methods

2.1. Description of the Study Site

Experiment was conducted at Department of Plant Breeding and Genetics form the University of Agriculture, Peshawar, Pakistan during the winter season 2016-2017. The experimental location are 34.04°N and 71.35°E with an altitude of 350m above sea level. Field soil is silty loam with a pH of 7.6 and climate of the experimental location is subtropical with precipitation ranges 500-700mm and daily temperature ranges 24±6.24°C to 40.7±6.29°C.

2.2. Experimental Materials

The ten pea genotypes Green Gold, PL4, PL5, Pea 2009, Sarsabz, Green Cross, Adventa Selection, Anmol, Mateor and Sultan (Table 1) were obtained from the Oil Seed Section, Agricultural Research Institute (ARI) Tarnab, Peshawar, Pakistan.

Table 1. Source of diverse genotypes used in the current study.

S. No.	Name	Source
01	Green Gold	Imported Pea variety from New Zealand.
02	PL-4	Deptt of Botany, University of Malakand.
03	PL-5	Deptt of Botany, University of Malakand.
04	Pea-2009	Ayub Agriculture Research Institute (AARI) Faisalabad
05	Sarsabz	Ayub Agriculture Research Institute (AARI) Faisalabad
06	Sultan	ICI Pakistan (Pvt) Ltd.
07	Green cross	Variety imported by Star Seed company, Gujranwala (pvt)
08	Adventa selection	ICI Pakistan (Pvt) Ltd.
09	Anmol	Rashid Seeds, Gujranawala Pakistan (Pvt)
10	Meteor	Ayub Agriculture Research Institute (AARI) Faisalabad

2.3. Experimental Design and Trial Management

These genotypes were evaluated in a randomized complete block design with three replications. All genotypes were grown in 3m long ridges which were kept 60cm apart where plant-to-plant distance was 30cm. To reduce experimental error, cultural practices were performed uniformly for all genotypes. Data was collected from ten randomly selected plants from each genotype in each replication on the following parameters.

2.4. Data Collected

Data was collected from ten randomly selected plants from each genotype in each replication on the following parameters.

- 1) *Days to 50% flowering*: Days to 50% flowering were counted from the sowing date to the days when 50% flowers produced by the plant in each genotype in each replication.
- 2) *Plant height (cm)*: Plant height was recorded in centimeter with meter rod from the ground level up to the tip of the main stem on each selected plant of each genotype.
- 3) *Primary branches plant⁻¹*: Primary branches plant⁻¹ which arose from the main stem of each selected plant of each replication were counted.
- 4) *Pod length (cm)*: For taking data on pod length, five pods from each selected plant was collected and their lengths were measured in cm and average was taken.
- 5) *Pods plant⁻¹*: Total pods produced by each selected plant of each replication were counted and data were recorded.
- 6) *Fresh pod shelling percentage*: The ratio of total fresh seed weight pod⁻¹ to fresh pod weight in percentage is known as shelling percentage. Ten fresh pods from each selected plant from each replication were taken, weighed using electronic balance and shelled for fresh pea seed weight to determine shelling percentage.
- 7) *100-seed fresh weight (g)*: Hundred seeds from each selected plant were counted and weighed with the help of electronic balance.
- 8) *100-seed dry weight (g)*: Hundred seeds at physiological maturity from the seeds of selected plants were taken and weighed with the help of electronic balance. For this, fresh seeds (weighed) were air dried for one week under shed in normal temperature and then their weight were again taken and recorded as dry weight.
- 9) *Seeds pod⁻¹*: Number of seeds from each selected pod of each selected plant were counted and then average was taken.
- 10) *Days to maturity*: Days to maturity was counted from the date of sowing till the date when physiological maturity reached and then days were recorded.
- 11) *Seed yield plant⁻¹ (g)*: Total pods produced by each selected plant of each replication were harvested and

then total seeds were collected by hand threshing. All seeds were then weighed and data was recorded as seed yield plant⁻¹ in grams.

2.5. Statistical Analysis

The data thus collected were statistically analyzed using method proposed by Steel and Torrie [9]. Means were separated using LSD test.

Broad sense heritability

Broad sense heritability for particular trait was calculated according to Choudhary *et al.* [10].

$$\text{Genotypic Variance } (\delta^2 g) = \frac{(GMS - EMS)}{r}$$

$$\text{Phenotypic Variance } (\delta^2 p) = \delta^2 g + \delta^2 e$$

$$\text{Environmental Variance } (\delta^2 e) = EMS$$

$$\text{Broad sense heritability} = h^2 (BS) = \frac{\delta^2 g}{\delta^2 p}$$

Whereas

$\delta^2 g$ = Genotypic variance for traits.

$\delta^2 p$ = Phenotypic variance for traits.

$h^2 (BS)$ = Broad sense heritability for a trait.

Genetic advance (GA)

Genetic advance was computed by using the following formula given by Panse and Sukhatme [11].

$$GA = K. \sqrt{\delta^2 p} . h^2$$

Whereas

$K = 1.76$ for 10% selection intensity.

h^2 = Broad sense heritability.

$\delta^2 p$ = Phenotypic standard deviation.

GA = Genetic advance.

Correlation analysis

Phenotypic correlations (r_p) coefficient among various traits were computed according to Chaudhary *et al.* [12].

$$\text{Genotypic Co-variance } (\delta^2 g_1 g_2) = \frac{GMCP - EMCP}{r}$$

$$\text{Environmental Co-variance } (\delta^2 e_1 e_2) = EMCP$$

$$\text{Phenotypic Co-variance } (\delta^2 p_1 p_2) = \delta^2 g_1 g_2 + \delta^2 e_1 e_2$$

Where,

$$\text{Genotypic correlation } (r_G) = \frac{\text{COV } G(X_1 X_2)}{\sqrt{\delta^2 G(X_1) \delta^2 G(X_2)}}$$

$$\text{Phenotypic correlation } (r_P) = \frac{\text{COV } P(X_1 X_2)}{\sqrt{\delta^2 P(X_1) \delta^2 P(X_2)}}$$

Where,

$\text{COV } G(X_1 X_2)$ = Genotypic covariance between traits x_1 and x_2

$\delta^2 g (x_1)$ = Genotypic variance of trait x_1 , $\delta^2 g (x_2)$ = Genotypic variance of trait x_2

$\text{COV } P(X_1 X_2)$ = Phenotypic covariance between trait x_1 and x_2

$\delta^2 p (x_1)$ = Phenotypic variance of trait x_1 , $\delta^2 p (x_2)$ = Phenotypic variance of trait x_2 .

3. Results and Discussion

Significant variations were observed for most of the characters among the ten pea genotypes of *Pisum sativum* L. The importance of Pea (*Pisum sativum* L.) as a vegetable crop an experiment was evaluate genetic variability, heritability, genetic advance and correlation among different genotypes during 2016-17.

3.1. Days to 50% Flowering

Mean squares revealed highly significant differences for days to 50% flowering among genotypes, indicating the existence of genetic variability in the tested material (Table 2). Mean values for 50% flowering ranged from 50.38 (Sultan) to 92.17 days (PL-5) with an overall mean of 66.93 days (Table 3). Early flowering in pea results in early maturity therefore early flowering is desirable while breeding for early maturity. Our results showed the existence of significant variation among the tested genotypes. Gudadinni *et al.* [13] also reported significant differences for days to 50% flowering while working with 26 Pea genotypes.

Among pea genotypes, genotypic variance (182.77) for days to 50% flowering was more than environmental variance (1.75) (Table 5). The estimates of heritability in the broad sense and genetic advance for days to 50% flowering were 0.99, 35.38%, respectively indicating greater genetic influence in comparison to environmental influence (Table 5). Present findings are in agreement with the results of Singh [14] estimated high heritability (98.3) for days to 50%

flowering. High broad sense heritability with high genetic advance (0.99, 32.92%) for days to 50% flowering among pea genotypes was reported [15].

Days to 50% flowering exhibited significant positive phenotypic correlation with days to maturity ($r_p = 0.630^{**}$), fresh pod shelling percentage ($r_p = 0.707^{**}$), 100 seeds fresh weight, seeds pod⁻¹ and seed yield plant⁻¹ ($r_p = 0.630^{**}$). 50% flowering showed phenotypic negative association with primary branches plant⁻¹ ($r_p = -0.125$). Days to 50% flowering showed significant positive genotypic association with fresh pod shelling percentage ($r_g = 0.768^{**}$) and seed yield plant⁻¹ ($r_g = 0.587^{**}$) while negative genotypic association with primary branches plant⁻¹ ($r_g = -0.152$) and days to maturity ($r_g = -0.202$). Days to 50% flowering showed non-significant correlation with all other traits both at genotypic and phenotypic levels (Table 6). The Current findings are in agreement with the results of Singh [14] conducted experiment on 30 varieties of pea and reported positive significant association of days to 50% flowering with days to maturity and seed yield plant⁻¹. The current results are further in support to the findings of Singh and Singh [16] conducted experiment on 37 advance lines of pea and reported positive significant association between days to 50% flowering and days to maturity. The results of significant positive correlation of days to 50% flowering with days to maturity and seed yield plant⁻¹ are also in agreement with the results reported [17]. Non-significant correlation of days to 50% flowering both at phenotypic and genotypic levels with plant height, pod plant⁻¹ and 100-seeds fresh weight were reported [18].

Table 2. Mean squares for yield and yield associated traits of Pea genotypes studied in Peshawar during 2016-17.

Source	Replication df = 2	Genotypes df = 9	Error df = 29	CV
Days to 50% flowering	1.24	550.06**	1.75	1.98
Plant height (cm)	1.19	1539.89**	27.87	6.44
Primary branches plant ⁻¹	0.20	1.36**	0.25	14.38
Days to maturity	0.69	848.09**	9.39	2.14
Pods plant ⁻¹	16.48	107.03**	27.59	18.11
Pod length (cm)	0.02	1.35**	0.02	2.08
Fresh pod shelling (%)	10.00	180.72**	12.64	6.45
100-seed fresh weight (g)	0.44	103.34**	3.62	5.83
100-seed dry weight (g)	0.04	14.36**	0.33	3.57
Seeds pod ⁻¹	1.28	0.85*	0.31	10.11
Seed yield plant ⁻¹	12.16	361.12**	3.72	6.37

Table 3. Mean values for days to 50% flowering, plant height, primary branches plant⁻¹, days to maturity and pods plant⁻¹ of Pea genotypes studied in Peshawar during 2016-17.

Genotypes	Days to 50% flowering	Plant height (cm)	Primary branches ⁻¹	Days to maturity	Pods plant ⁻¹
Green gold	52.46	68.59	2.63	143.50	21.13
PL-4	80.67	136.13	3.00	150.00	40.00
PL-5	92.17	85.56	3.25	142.00	24.25
Pea 2009	63.92	63.25	3.13	138.25	26.38
Sarsabz	71.21	64.38	3.75	149.63	31.50
Sultan	50.38	67.38	3.50	122.00	24.75
Green cross	61.92	77.13	3.88	135.00	30.88
Adventa selection	71.67	81.88	4.00	180.25	37.00
Anmol	73.11	86.88	3.63	147.50	33.50
Meteor	51.83	87.50	3.63	122.50	29.25
Mean	66.93	81.87	3.44	143.06	29.86
LSD (0.05)	2.26	9.05	0.86	5.25	9.01

3.2. Plant Height

Mean squares indicated significant differences for plant height among pea genotypes (Table 2). Mean values for plant height ranged from 63.33 cm (Pea-2009) to 136.13 cm (PL-4) with the mean value of 81.87 cm (Table 3). Our results showed the existence of significant variation for plant height among the tested genotypes. Genetic differences for plant height among pea genotypes have also been reported by Gudadinni *et al.* [13] while working with 26 Pea genotypes. Our results are similar to the findings of Singh and Singh [16] found significant differences for plant height while working with 37 pea lines. Fikreselassie [17] and Jaiswal *et al.* [19] also observed significant differences for plant height among pea genotypes.

Among pea genotypes genotypic variance (504.01) for plant height was greater than environmental variance (27.87) in pea genotypes. The estimates of heritability in the broad sense and genetic advance for plant height were high (0.95, 46.88% respectively) indicating greater genetic influence in comparison to environmental influence in plant height (Table 5). These results are in accordance with the results of Singh [14] reported high heritability with high genetic advance (95.54, 69.92%) for plant height among pea genotypes. Gudadinni *et al.* [13] also reported high heritability with high genetic advance (99.23, 25.59%) for plant height among pea genotypes. Singh and Singh [16] estimated high heritability with high genetic advance (95.70, 25.55%) for plant height among pea genotypes.

Plant height exhibited significant positive phenotypic association with pods plant⁻¹ ($r_p = 0.536^*$) and seed yield plant⁻¹ ($r_p = 0.630^{**}$) and significant positive genotypic correlation with seed yield plant⁻¹ ($r_g = 0.807^{**}$) while it showed genotypic negative association with primary branches plant⁻¹ ($r_g = -0.202$), pod length ($r_g = -0.030$) and 100-seeds fresh weight ($r_g = -0.038$). Plant height showed non-significant coefficient of correlation both at genotypic and phenotypic levels with other traits (Table 6). Our results are in agreement with the findings of Singh [14] observed significant association of plant height with seed yield plant⁻¹ both at phenotypic and genotypic levels among 30 pea varieties. Current findings are similar with the results of Gul *et al.* [20] reported significant positive association of plant height with seed yield plant⁻¹. Fikreselassie [17] and Habtamu and Million [21] also reported significant correlation between plant height and seed yield plant⁻¹. Siddika *et al.* [18] reported non-significant correlation both at phenotypic and genotypic levels of plant height with pods plant⁻¹ and pod length which may be due to different environments.

3.3. Primary Branches Plant⁻¹

Mean square for primary branches plant⁻¹ showed highly significant differences ($p \leq 0.01$) (Table 2). Among genotypes mean values for primary branches plant⁻¹ ranged from 2.63 (Green Gold) to 4.00 (Adventa Selection) with an

overall mean of 3.44 branches (Table 3). Our results showed the existence of significant variation among the tested genotypes which is in accordance with the earlier findings of Singh and Singh [16] also conducted an experiment on pea lines and found significant differences for primary branches plant⁻¹.

Among pea genotypes the genotypic variance (0.37) was greater than environmental variance (0.25) for primary branches plant⁻¹ (Table 5), showing the greater role of genetic factors in the expression of traits. The estimates of heritability in the broad sense was moderate with high genetic advance (0.59, 23.35%) indicating equal importance of both genotype and environment in controlling primary branches plant⁻¹ (Table 5). Our results are supported by Afreen *et al.* [22] estimated moderate heritability with low genetic advance (65.83, 1.22) for primary branches plant⁻¹ among different pea genotypes. However, Gudadinni *et al.* [13] estimated high heritability with low genetic advance (89.65, 4.12%) for primary branches plant⁻¹ in pea.

Primary branches plant⁻¹ revealed significant positive phenotypic correlation with pod length ($r_p = 0.422^*$) and negative phenotypic correlation with seed yield plant⁻¹ ($r_p = -0.010$) while it showed genotypic negative correlation with fresh pod shelling% ($r_g = -0.308$) and plant height ($r_g = -0.202$) and seed yield plant⁻¹ ($r_g = -0.097$). Primary branches plant⁻¹ had non-significant association both at genotypic and phenotypic levels with rest of the traits (Table 6). Singh and Singh [16] found non-significant association between primary branches plant⁻¹ and seed yield plant⁻¹. These results are not in conformity with the findings of [14]. Our results for negative correlation of primary branches plant⁻¹, with days to 50% flowering, plant height, and seed yield plant⁻¹ are justified because when the number of primary branches increases there is more vegetative growth rather than reproductive growth, seeds size, pods, pod shelling percentage and 100 seeds weight get decreased which results in lower seed yield.

3.4. Days to Maturity

In the present study mean squares showed significant differences for days to maturity ($p \leq 0.01$) among pea genotypes indicating the existence of genetic variability among the germplasm (Table 2). Mean values among pea genotypes ranged from 122.00 days (Sultan) to 180.25 days (Adventa Selection) with a mean value of 143.06 days (Table 3). Our results showed the existence of sufficient variation among the tested genotypes. The results of present findings are in accordance with the earlier findings of Gudadinni *et al.* [13], Fikreselassie [17], Avci and Ceyhan [23], Singh and Singh [16] found significant differences for maturity among various pea genotypes.

Among pea genotypes genotypic variance (279.57) was greater than environmental variance (9.39) for days to maturity among pea genotypes. Heritability in the broad sense was high (0.97) while genetic advance was low (20.20%) for days to maturity (Table 5). The results of high

heritability with low genetic advance for days to maturity are in accordance with the results of Jaiswal *et al.* [19] conducted experiment on 12 pea genotypes and estimated high heritability with low genetic advance (0.70, 4.03%). Our results are further strengthened by Kumar *et al.* [24] estimated high heritability with low genetic advance (0.62, 5.09%) for days to maturity while working on 58 pea genotypes.

Days to maturity exhibited significant positive phenotypic relationship with pods plant⁻¹ ($r_p = 0.629$), pod length ($r_p = 0.819$), fresh pod shelling percentage ($r_p = 0.678$), 100-seeds fresh weight ($r_p = 0.636$) 100-seeds dry weight ($r_p = 0.424$),

seeds pod⁻¹ ($r_p = 0.498^*$) and seed yield plant⁻¹ ($r_p = 0.777$) and pods plant ($r_p = 0.629$). Days to maturity had negative genotypic association with days to 50% flowering ($r_g = -0.202$) while rest of the traits showed non-significant associations both at phenotypic and genotypic levels with days to maturity (Table 6). The current findings are in agreement with the results of Habtamu and Million [21] and Singh [14] they reported significant positive phenotypic relationship of days to maturity with seed yield plant⁻¹. Fikreselassie [17], and Singh and Singh [16] also reported significant positive relationship of days to maturity with seed yield plant⁻¹.

Table 4. Mean values for seeds pod⁻¹, fresh pod shelling%, 100 seeds fresh weight, 100 seeds dry weight, seeds pod⁻¹ and seed yield plant⁻¹ of Pea genotypes studied in Peshawar during 2016-17.

Genotypes	Pod length (cm)	Fresh pod shelling%	100-seed fresh weight (g)	100-seed dry weight (g)	Seeds pod ⁻¹	Seed yield plant ⁻¹ (g)
Green gold	6.85	47.96	24.23	14.48	4.63	25.45
PI-4	7.11	58.60	28.97	16.32	5.00	48.22
PI-5	6.74	65.23	32.58	14.89	5.25	28.66
Pea 2009	6.87	63.39	30.98	15.50	5.25	23.64
Sarsabz	7.57	53.36	33.04	16.81	5.00	24.59
Sultan	7.08	44.31	30.51	14.97	4.38	15.07
Green cross	7.68	45.52	28.71	13.79	5.63	24.94
Adventa selection	8.84	63.16	41.25	17.82	4.13	46.23
Anmol	7.96	59.96	44.81	21.30	6.13	38.71
Meteor	7.16	42.39	30.05	16.40	5.25	25.91
Mean	7.38	54.39	32.51	16.23	5.06	30.14
LSD (0.05)	0.26	6.09	3.26	0.99	0.94	3.30

Table 5. Genotypic variance, phenotypic variance, heritability and genetic advance for different traits in Pea (*Pisum sativum*) L. genotypes during 2016-17.

Parameters	Genotypic variance (Vg)	Environmental variance (Ve)	Heritability (h^2_{BS})	Genetic advance (%)
Days to 50% flowering	182.77	1.75	0.99	35.38
Plant height (cm)	504.01	27.87	0.95	46.88
Primary branches plant ⁻¹	0.37	0.25	0.59	23.35
Days to maturity	279.57	9.39	0.97	20.20
Pods plant ⁻¹	26.48	27.59	0.49	21.85
Pod length (cm)	0.44	0.02	0.95	15.37
Fresh pod shelling (%)	56.03	12.64	0.82	21.58
100-seed fresh weight (g)	33.24	3.62	0.90	29.52
100-seed dry weight (g)	4.67	0.33	0.93	22.68
Seeds pod ⁻¹	0.18	0.31	0.37	8.36
Seed yield plant ⁻¹	119.13	3.72	0.97	62.47

Table 6. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient among various traits of 10 pea genotypes evaluated at Peshawar during 2016-2017.

	DTF	PH	PBP	DTM	PP	PL	FPS%	100-SFW	100-SDW	SP	SYP
DTF	—	0.297	-0.125	0.630**	0.355	0.333	0.707**	0.438*	0.355	0.395*	0.630**
PH	0.449*	—	-0.187	0.169	0.536**	0.066	0.146	0.090	0.187	0.151	0.637**
PBP	-0.152	-0.202	—	0.029	0.275	0.422*	-0.220	0.204	0.188	0.061	-0.010
DTM	-0.202	0.210	0.074	—	0.629**	0.819**	0.678**	0.636**	0.424*	0.498*	0.777**
PP	0.434*	0.717**	0.332	0.590*	—	0.659**	0.371	0.435*	0.350	0.344	0.716**
PL	0.123	-0.030	0.611**	0.703**	0.580**	—	0.402*	0.756**	0.559*	0.568*	0.656**
FPS%	0.768**	0.180	-0.308	0.604**	0.291	0.209	—	0.658**	0.529*	0.364	0.644*
100SFW	0.343	-0.038	0.397	0.526*	0.369	0.770**	0.547**	—	0.899**	0.484*	0.654**
100 SDW	0.266	0.147	0.341	0.435*	0.421*	0.608**	0.457*	0.873**	—	0.411*	0.624*
SP	0.382	0.072	0.217	0.677**	0.534*	0.797**	0.485*	0.709**	0.606**	—	0.452*
SYP	0.587*	0.807**	-0.097	0.696**	0.842**	0.413*	0.523*	0.381	0.517*	0.551*	—

*, ** = significant at 5% and 1% probability level, respectively

DTF= Days to 50% flowering, PH= Plant height, PBP= Primary branches plant⁻¹, DTM= Days to maturity, PP= Pods plant⁻¹, PL= Pod length, FPS%= Fresh pod shelling percentage, 100SFW= 100-seed fresh weight, 100 SDW= 100-seed dry weight, SP= seeds pod⁻¹ and SYP= seed yield plant⁻¹.

3.5. Pods Plant⁻¹

In the present study mean squares showed significant differences ($p \leq 0.01$) among pea genotypes for pods plant⁻¹ (Table 2). On overall basis, data for pods plant⁻¹ ranged from 21.13 (Green Gold) to 40.00 (PL-4) with an overall mean of 29.86 (Table 3). The results of present findings are in accordance with Gudadinni *et al.* [13], Fikreselassie [17], Avci and Ceyhan [23] and Singh and Singh [16] observed significant differences among various pea genotypes.

Among pea genotypes genotypic variance (26.48) for pods plant⁻¹ was less than environmental variance (27.59) (Table 5) resulting in moderate estimates of heritability. Heritability in the broad sense was moderate with low genetic advance for pods plant⁻¹ (0.49, 21.85%) (Table 5). Our results are in agreement with the findings of Georgieva *et al.* [7] conducted experiment on 5 pea genotypes and found moderate heritability with low genetic advance (0.39, 0.400) for pod plant⁻¹. Low heritability with low genetic advance may be mainly due to non-additive gene action [14].

Pods plant⁻¹ exhibited significant positive phenotypic correlation with pod length ($r_p = 0.659$), 100-seed fresh weight ($r_p = 0.435$) and seed yield plant⁻¹ ($r_p = 0.716$). Significant positive genotypic association were observed for pods plant⁻¹ with pod length ($r_g = 0.580$), 100-seed dry weight ($r_g = 0.421$), seeds pod⁻¹ ($r_g = 0.534$) and seed yield plant⁻¹ ($r_g = 0.842$). Rest of the traits had non-significant association both at phenotypic and genotypic levels with pods plant⁻¹ (Table 6). The current results are in agreement with the results of Fikreselassie [17] reported highly significant phenotypic and genotypic association of pods plant⁻¹ with plant height, days to 50% flowering, days to maturity, seeds pod⁻¹ and seed yield plant⁻¹. Singh [14] also observed significant association of pods plant⁻¹ with seed yield plant⁻¹ both at phenotypic and genotypic levels among 30 pea varieties.

3.6. Pod Length

Mean squares showed significant differences among pea genotypes for pod length, indicating the existence of genetic variability among 10 pea genotypes (Table 2). Mean values for pod length among genotypes varied between 6.85 cm to 8.84 cm with the overall mean of 7.38 cm. (Table 4). Shorter pods (6.85 cm) were observed in genotype Green gold while longer pods (8.84 cm) were in genotype Advanta selection. The results of present findings are in accordance with Gudadinni *et al.* [13] observed significant differences for pod length among 26 pea genotypes. Our results are further strengthened by the earlier findings of Singh and Singh [16] observed significant differences for pod length among 37 advanced lines of pea.

Genotypic variance (0.44) for pod length was greater than environmental variance (0.02). Heritability in the broad sense was high (0.95) with low genetic advance (15.33%) for pod length (Table 5). Our results for high heritability and low genetic advance are in agreement with Afreen *et al.* [22] conducted experiment on 21 different genotypes of garden

pea and estimated high heritability with low genetic advance (0.90, 22.42%) for pod length. Jaiswal *et al.* [19] estimated high heritability with low genetic advance (0.66 10.37%) for pod length while working on 12 field pea genotypes.

In the present study pod length exhibited significant positive phenotypic association with fresh pod shelling percentage ($r_p = 0.402$), 100-seed fresh weight ($r_p = 0.756$), 100-seed dry weight ($r_p = 0.559$), seeds pod⁻¹ ($r_p = 0.568$) and seed yield plant ($r_p = 0.656$). Pod length showed significant genotypic positive association with 100-seed fresh weight ($r_g = 0.770$), 100-seeds dry weight ($r_g = 0.608$), seeds pod⁻¹ ($r_g = 0.797$) and seed yield plant⁻¹ ($r_g = 0.413$). The remaining traits showed non-significant association both at phenotypic and genotypic levels with pod length (Table 6). The current findings are in accordance with the results of Habtamu and Million [21] reported significant genotypic positive association of pod length with days to maturity and 1000-seed weight and significant phenotypic positive association with 1000-seed weight and seed yield plant⁻¹. Siddika *et al.* [18] showed non-significant correlation both at phenotypic and genotypic levels of pod length with plant height.

3.7. Fresh Pod Shelling Percentage

Analysis of variance indicated significant differences ($p \leq 0.01$) among pea genotypes for fresh pod shelling percentage (Table 2). On overall basis, data for fresh pod shelling percentage ranged from 42.39% (Meteor) to 65.23% (PL-5) with the mean value of 54.39% (Table 4). The results of present findings are in accordance with Gudadinni *et al.* [13] observed significant differences for fresh pod shelling percentage among 26 pea genotypes. Our results are further in support to the findings of Ramzan *et al.* [25] revealed significant differences for fresh pod shelling percentage among 13 pea genotypes.

Among pea genotypes genotypic variance (56.03) for fresh pod shelling percentage was greater than environmental variance (12.64) indicating the greater role of genotype in controlling the trait. Heritability in the broad sense was high (0.82) while genetic advance was low (21.58%) for fresh pod shelling percentage (Table 5). Our results for high heritability and low genetic advance are in agreement with the results of Kumar *et al.* [24] estimated high heritability with low genetic advance (0.62, 29.35%) for fresh pod shelling percentage among various pea genotypes.

The association of fresh pod shelling percentage was phenotypically significant positive with 100-seed fresh weight ($r_p = 0.658$), 100-seed dry weight ($r_p = 0.529$) and seed yield plant⁻¹ ($r_p = 0.644$). Fresh pod shelling percentage exhibited significant positive genotypic association with 100-seed fresh weight ($r_g = 0.547$), 100-seed dry weight ($r_g = 0.457$), seeds pod⁻¹ ($r_g = 0.485$) and seed yield plant⁻¹ ($r_p = 0.523$) negative genotypic association with primary branches plant⁻¹ ($r_g = -0.308$). Rest of the traits showed non-significant association both at phenotypic and genotypic levels with fresh pod shelling percentage (Table 6).

3.8. 100-seed Fresh Weight

In the present investigation mean squares showed significant differences ($p \leq 0.01$) among pea genotypes for 100-seed fresh weight (Table 2). Mean values for 100-seed fresh weight ranged from 24.23g to 44.81g with the mean value of 32.51g (Table 4). Minimum 100-seed fresh weight was observed in genotype Green gold while maximum 100-seed fresh weight was observed for Anmol. The current results indicated the existence of genetic variation in the tested germplasm. Singh and Singh [16] also observed significant differences for 100-seed weight among 37 pea genotypes. Our results are further strengthened by Avci and Ceyhan [23] observed significant differences for 100-seed weight. Siddika *et al.* [18] also observed significant differences for 100-seed fresh (green) weight among 26 lines of pea.

Genotypic variance (33.24) for 100-seed fresh weight was greater than environmental variance (3.62). Heritability in the broad sense was estimated high 0.90 while genetic advance was low 29.52% for 100-seed fresh weight (Table 5). Similar results of high heritability were reported by Siddika *et al.* [18] observed high heritability with low genetic advance (0.77, 13.98%) for 100-seed fresh (green) weight while working with 26 lines of pea. Our results are further in support with earlier findings of Singh and Singh [16] observed high heritability with low genetic advance (0.89, 26.61%) for 100-seed weight among 37 lines Pea.

The association of 100-seed fresh weight was positive significant with 100-seed dry weight ($r_p = 0.899$), seeds pod^{-1} ($r_p = 0.484$) and seed yield plant^{-1} ($r_p = 0.654$) while significant positive genotypic association with 100-seed dry weight ($r_g = 0.873$) and seeds pod^{-1} ($r_g = 0.709$). 100-seed fresh weight had negative genotypic association with plant height ($r_g = -0.038$). Rest of the traits showed non-significant association both at phenotypic and genotypic levels with 100-seed fresh weight (Table 6). The current results of negative correlation of 100-seed fresh weight with plant height and genotypic significant positive association of 100-seed fresh weight with 100-seed dry weight and yield plant^{-1} are in agreement with the results reported [25].

3.9. 100-seed Dry Weight

In the present study mean squares specified significant differences ($p \leq 0.01$) among pea genotypes for 100-seed dry weight (Table 2). Mean value for 100-seed dry weight ranged from 13.63g to 21.30g with the overall mean of 16.23g (Table 4). Minimum 100-seed dry weight was observed in genotype Green cross while maximum 100-seed dry weight was observed for Anmol. Our results for significant differences are confirmed by Georgieva *et al.* [7] observed significant differences for 100-seed weight in 5 pea genotypes. Our results are further supported by Singh and Singh [16] observed significant differences among 37 pea genotypes for 100-seed dry weight.

Genotypic variance (4.67) for 100-seed dry weight was greater than environmental variance (0.33). Heritability in the broad sense was 0.93 whereas genetic advance was 22.68%

for 100-seed dry weight (Table 5). Similar results of high heritability in the broad sense and low genetic advance (0.95, 11.30%) for 100-seed weight were reported [7]. Our results of high heritability and low genetic advance are also in agreement with the results of Siddika *et al.* [18] observed high heritability with low genetic advance (0.77, 13.98%) for 100-seed weight among pea lines.

In the present findings 100-seed dry weight exhibited significant positive phenotypic correlation with seeds pod^{-1} ($r_p = 0.484$) and seed yield plant^{-1} ($r_p = 0.624$) and genotypic positive correlation with days to maturity ($r_g = 0.435$), pods plant^{-1} ($r_g = 0.421$), pod length ($r_g = 0.608$), fresh pod shelling percentage ($r_g = 0.457$) and 100-seed fresh weight ($r_g = 0.873$). Rest of the traits showed non-significant association both at phenotypic and genotypic levels with 100-seed dry weight (Table 6). Current results of genotypic significant association of 100-seed dry weight with 100-seed fresh weight are in agreement with the results of Singh and Singh [16] reported highly significant association between 100-seed dry weight and 100-seed fresh weight.

3.10. Seeds Pod^{-1}

In the existing investigation mean squares showed significant differences ($p \leq 0.01$) among pea genotypes for seeds pod^{-1} , indicating the existence of genetic variability in the tested germplasm (Table 2). Mean values for seeds pod^{-1} ranged from 4.13 to 6.13 with the mean value of 5.06 (Table 4). Minimum seeds pod^{-1} was observed in genotype Adventa Selection while maximum seeds pod^{-1} was observed in genotype Sultan. Present findings are in accordance with the results of Gudadinni *et al.* [13] observed significant differences for seeds pod^{-1} among pea genotypes. Our results are further supported by Avci and Ceyhan [23] observed significant differences for seeds pod^{-1} among pea genotypes. Fikreselassie [17] also observed significant differences for seeds pod^{-1} among 25 elite pea genotypes.

An estimated genotypic and environmental variance for seeds pod^{-1} were 0.18 and 0.31 (Table 4) showing greater value of environmental variance than genetic variance, suggesting the greater role of environment in the expression of seeds pod^{-1} . Heritability in the broad sense was 0.37 while genetic advance was 8.36% for seeds pod^{-1} (Table 5). Low heritability with low genetic advance shows that there is the major role of environment in the expression of character. Low heritability with low genetic advance also showed non additive gene action. Our results for low heritability and low genetic advance are in agreement with the results of Fikreselassie [17] estimated low heritability with low genetic advance (0.39, 0.77%) for seeds pod^{-1} among 25 elite pea genotypes. Our results are also similar to the findings of Tolessa [26] estimated low heritability with low genetic advance for seeds pod^{-1} among pea genotypes.

In the present conclusions seeds pod^{-1} exhibited significant phenotypic positive association with seed yield plant^{-1} ($r_p = 0.452$) and significant genotypic positive correlation with days to maturity, ($r_g = 0.677$), pods plant^{-1} ($r_g = 0.534$), pod length ($r_g = 0.797$), fresh pod shelling percentage ($r_g = 0.485$),

100-seed fresh weight ($r = 0.709$) and 100-seed dry weight ($r_g = 0.606$). Rest of the traits showed non-significant genotypic association with seeds pod^{-1} (Table 6). Current results are in agreement with the results of Fikreselassie [17] reported highly significant genotypic association between seeds pod^{-1} and days to maturity. Our results are also in agreement with the results of Habtamu and Million [21] also reported highly significant genotypic positive association between seeds pod^{-1} and pod length in pea genotypes.

4. Seed Yield Plant⁻¹

In the present study mean squares showed significant differences ($p \leq 0.01$) among genotypes for seed yield plant⁻¹ (Table 2). Mean values for seed yield plant⁻¹ ranged from 15.07g to 48.22g with the overall mean of 30.14 g (Table 4). Lowest seed yield plant⁻¹ was observed in genotype Sultan while highest seed yield plant⁻¹ was reached in genotype PL-4. The results of present findings are in accordance with the earlier findings of Gudadinni *et al.* [13] observed significant differences for seed yield plant⁻¹ among pea genotypes. Our results are further in support of Singh and Singh [16] observed significant differences for seed yield plant⁻¹ among 37 pea genotypes. Avci and Ceyhan [23] also reported significant differences for seed yield plant⁻¹ among pea genotypes.

Genotypic variance (119.13) was greater than environmental variance (3.72) for seed yield plant⁻¹ indicating the greater role of genetics in controlling this trait. Heritability in the broad sense was estimated 0.97 with high genetic advance 62.47% for seed yield plant⁻¹ (Table 5). High heritability coupled with high genetic advance for seed yield plant⁻¹ suggested that effective selection may be possible for this trait. Similar results were estimated by Georgieva *et al.* [7] in pea genotypes. Our results for high heritability and high genetic advance are also supported by Kumar *et al.* [24] estimated high heritability with high genetic advance (0.83, 67.87%) for seed yield plant⁻¹ in pea genotypes.

Significant positive genotypic relationship was observed for seed yield plant⁻¹ with days to 50% flowering ($r_g = 0.587$), plant height ($r_g = 0.807$), days to maturity ($r = 0.696$) pods plant⁻¹ ($r_g = 0.842$), pod length ($r_g = 0.413$), fresh pod shelling percentage ($r_g = 0.523$) and 100-seed dry weight ($r_p = 0.517$). Negative genotypic relationship was exhibited by seed yield plant⁻¹ and primary branches plant⁻¹ ($r_g = -0.097$). Rest of the traits showed non-significant genotypic association with seed yield plant⁻¹ (Table 6). Current results are in agreement with Singh and Singh [16] reported significant positive correlation of seed yield plant⁻¹ with plant height and pod plant⁻¹ in pea genotypes.

5. Summary, Conclusions and Recommendations

5.1. Summary

The research was conducted to estimate heritability,

genetic advance and traits association among quality and yield attributes in Pea (*Pisum sativum*) L. genotypes. This experiment was carried out at the Agriculture research institute, Tarnab Peshawar, during the cropping season 2016-2017. In this experiment 10 Pea genotypes were used in a randomized complete block design with three replications. Sowing was done in four rows for each entry on 3m long ridges which were 60 cm apart. To reduce experimental error, cultural practices were performed uniformly for all genotypes. Data were recorded on 10 randomly selected plants from each genotype in each replication with proper time on days to 50% flowering, plant height, primary branches plant⁻¹, days to maturity, pods plant⁻¹, pod length, fresh pod shelling percentage, 100-seed fresh weight, 100-seed dry weight, seeds pod^{-1} and seed yield plant⁻¹.

Analysis of variance showed significant differences among pea genotypes for all studied traits. Early flowering (50.38 days), maximum 100-seed fresh weight (43.90 g) and maximum 100-seed dry weight (21.29 g) were recorded for genotype Anmol. Taller plants (142.08 cm) with more pods plant⁻¹ (39.96) and maximum seed yield plant⁻¹ (52.04 g) were recorded for genotype PL-4. Maximum primary branches plant⁻¹ (4.85) were recorded for Sarsabz. Late maturity (181.75 days), longer pods (8.86 cm) and maximum seeds pod^{-1} (6.26) was recorded for genotype Advanta selection. Early maturity (122.08 days), less fresh pod shelling percentage (44.32%), minimum seeds pod^{-1} (4.49) and minimum seed yield plant⁻¹ (15.02 g) was recorded for Genotype Sultan. Late flowering (92.17 days), maximum fresh pod shelling percentage (65.29%) and smaller pods (6.79 cm) were recorded for genotype PL-5. Minimum primary branches plant⁻¹ (2.71), minimum pods plant⁻¹ (21.21) and minimum 100-seed fresh weight (24.31 g) were observed for Green gold. Shorter plants (63.33 cm) were observed for Pea-2009. Minimum 100-seed dry weight (13.63 g) was noted for Green cross.

Genotypic variance was high (182.77) for flowering, plant height (504.01), maturity (279.57) and seed yield plant⁻¹ (119.13), while it was low for primary branches plant⁻¹ (0.37), pods plant⁻¹ (29.48), pod length (0.44), fresh pod shelling percentage (56.03), 100-seed fresh weight (33.24), 100-seed dry weight (4.67) and seeds pod^{-1} (0.18). Environmental variance was moderate (27.87) for plant height and (27.59) for pods plant⁻¹, while for rest of the genotypes it was minimum.

High broad sense heritability with high genetic advance was estimated for flowering (0.99) plant height (0.95) and seed yield plant⁻¹ (0.97) Most of the traits showed high heritability with moderate genetic advance like days to maturity, pod length, fresh pod shelling percentage, 100-seed fresh weight and 100-seed dry weight, while moderate heritability with low genetic advance was observed for primary branches plant⁻¹, pods plant⁻¹ and seeds pod^{-1} .

Correlation analysis showed that flowering, plant height, days to maturity pod plant⁻¹, pod length, fresh pod shelling percentage, 100-seed fresh and dry weight had positive significant phenotypic association with seed yield plant⁻¹. Seed yield plant⁻¹

had genotypic significant positive association with plant height and pods plant⁻¹ and genotypic significant positive association with days to maturity. Pod length had highly significant association with some traits at both phenotypic and genotypic levels. Fresh pod shelling percentage had also highly significant and significant association with some traits at both phenotypic and genotypic levels. Seeds pod⁻¹ had highly significant genotypic association with days to maturity, pod length, pods plant⁻¹, fresh pod shelling percentage, 100-seed fresh weight and 100-seed dry weight.

Significant and positive phenotypic coefficient of correlation was exhibited by seed yield plant⁻¹ with plant height ($r_p = 0.64$), days to 50% flowering ($r_p = 0.630$), days to maturity ($r_p = 0.78$), pods plant⁻¹ ($r_p = 0.72$), pod length ($r_p = 0.656$), fresh pod shelling percentage ($r_p = 0.64$), 100 seed-fresh weight ($r_p = 0.654$) and 100-seed dry weight ($r_p = 0.62$). Significant and positive genotypic coefficient of correlation was exhibited by seed yield plant⁻¹ with plant height ($r_G = 0.81$), days to maturity ($r_G = 0.70$) and pods plant⁻¹ ($r_G = 0.84$).

5.2. Conclusions

Significant differences were observed among Pea genotypes for all the studied traits.

Among genotypes, earliest flowering (50.38 days), maturity (122.08 days) and maximum fresh pod shelling percentage (65.29%) was observed for genotype Sultan. PL-4 had maximum plant height (142.08 cm), pods plant⁻¹ (39.96) and seed yield plant⁻¹ (52.04 g). Genotype Anmol had maximum 100-seed fresh (43.90 g) and dry weight (21.29 g). Sarsabz had maximum primary branches plant⁻¹ while Adventa selection had maximum pod length (8.86 cm) and seeds pod⁻¹ (6.26). Flowering, plant height and seed yield plant⁻¹ had high heritability coupled with high genetic advance indicating more genetic influence and lesser environmental influence. High heritability with moderate genetic advance was observed for days to maturity, pod length, fresh pod shelling percentage, 100-seed fresh weight and 100-seed dry weight. Moderate heritability with low genetic advance was observed for primary branches plant⁻¹, pods plant⁻¹ and seeds pod⁻¹ indicating non additive gene action. Low heritability with low genetic advance were observed for pods plant⁻¹, pod length and seeds pod⁻¹ indicating the effectiveness of these traits in later generations. Significant and positive coefficient of correlation was exhibited by seed yield plant⁻¹ with plant height, days to 50% flowering, days to maturity, pods plant⁻¹, pod length, fresh pod shelling percentage, 100-seed fresh weight and dry weight therefore for pea improvement, these traits could be given due consideration.

5.3. Recommendations

- 1) Sufficient work should be done for understanding and describing the nature and extent of genetic variability, heritability in broad sense, genetic advance, association between yield and yield related traits of vegetable pea varieties developed for high land of Pakistan.

- 2) The government and research centers should give attention on study and release of cultivars that have resistant to diseases and pests.
- 3) The large gap on yield obtained in research center and farmer's land should be minimized. The breeders do not give attention when compare to cereals crops.
- 4) This result being from single location, it is recommended for further testing in diverse environments to identify favorable environments for genotypes.
- 5) It needs further studies on field pea to identify and select genotypes that have important agronomic properties and use them in direct hybridization.
- 6) It should be worthwhile to study more available germplasm over years and locations to identify more accessions as well as to confirm the importance of the traits identified as predictors of yield.

References

- [1] Javaid, A., Ghafoorm, A and Anwar, R. (2002). Evaluation of local and exotic pea (*Pisum sativum* L.) germplasm for vegetable and dry grain traits. *Pak. J. Bot.* 34 (4): 419-427.
- [2] Santalla, M., Amurrio, J. M., & De Ron, A. M. (2001). Food and feed potential breeding value of green, dry and vegetable pea germplasm. *Canadian Journal of plant science*, 81 (4): 601-610.
- [3] Ouafi, L., Alane, F., Rahal-Bouziane, H., & Abdelguerfi, A. (2016). Agro-morphological diversity within field pea (*Pisum sativum* L.) genotypes. *African Journal of Agricultural Research*, 11 (40): 4039-4047.
- [4] Munir, K. (2013). Comparative advantage and competitiveness of pea crop in Khyber Pakhtunkhwa. *Sarhad Journal of Agriculture*, 29 (2): 299-306.
- [5] FAOSTAT. (2007). Food and Agricultural Organization of United Nations. UN statistics department report, top five green pea producing countries, New York.
- [6] PBS. 2015. Pakistan Bureau of Statistics, Government of Pakistan. Statistics House, G-9/1, Islamabad, Pakistan.
- [7] Georgieva, N., Nikolova, I., & Kosev, V. (2016). Evaluation of genetic divergence and heritability in pea (*Pisum sativum* L.). *Journal of BioScience & Biotechnology*, 5 (1): 61-67.
- [8] Pallavi, A. S., & Pandey, K. K. (2013). Estimation of heritability on pea (*Pisum sativum* L.). *Ad. Biores*, 4, 89-92.
- [9] Steel, R. G. and Torrie, J. H. (1980). Principles and Procedures of Statistics. 2nd Ed. New York. McGraw-Hill.
- [10] Choudhary, D. K., Sharma, R. R. and Sureja, A. K. (2004). Correlation and path analysis studies across the generations in garden pea. *Indian J. Hort.*, 61: 163-167.
- [11] Panse, V. G., & Sukhatme, P. V. (1954). Statistical methods for agricultural workers. Statistical methods for agricultural workers. *Indian Council Agric. Res.* New Dehli. 381.
- [12] Chaudhary S. P., Sharma S. S. N & Singh A. K. (1997). Line × tester analysis in Indian mustard (*Brassica juncea* L.). *Indian General Journal*, 57 (2): 168-173.

- [13] Gudadinni, P., Bahadur, V., Ligade, P., Topno, S. E and Prasad, V. M. (2017). Study on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* var. *hortense* L.). *Int. J. Biol. Appl. Sci.* 6 (8): 2384-2391.
- [14] Singh, R. K. (1984). Genotypic and phenotypic variability correlations in Pea. *Ind. J. Agric. Sci.* 55 (3): 147-50.
- [15] Ahmad, H. B., Rauf, S., Rafiq, C. M., Mohsin, A. U and Iqbal, A. (2014). Estimation of genetic variability in pea (*Pisum sativum* L.). *J. Glob. Inno. Agric. Soc. Sci.* 2 (2): 62-64.
- [16] Singh J. D & Singh I. A. (2006). Genetic variability, heritability, expected genetic advance and character association in field pea (*Pisum sativum* L.). *Legume Research.*, 29 (1): 65- 67.
- [17] Fikreselassie, M. (2012). Variability, heritability and association of some morpho-agronomic traits in field pea (*Pisum sativum* L.) genotypes. *Pakistan Journal of Biological Sciences*, 15 (8): 358-366.
- [18] Siddika, A., Islam, A. K. M. A., Rasul, M. G., Mian, M. A. K and Ahmed, J. U. (2013). Genetic variability in advanced generations of vegetable pea (*Pisum sativum* L.). *Int. J. Pl. Bree.*, 7 (2): 124-128.
- [19] Jaiswal, N. K., Gupta, A. K., Dewangan, H and Lavanya, G. R. (2013). Genetic variability analysis in field Pea (*Pisum sativum* L.). *Int. J. Sci. Res.*, 4 (1): 1-2.
- [20] Gul, I., Sumerli, M., Bicer, B. T., & Yilmaz, Y. (2005). Heritability and correlation studies in pea (*Pisum arvense* L.) lines. *Asian Journal of Plant Sciences*, 4 (2): 154-158.
- [21] Habtamu, S., & Million, F. (2013). Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes. *International Journal of Genetics and Molecular Biology*, 5 (6), 78-87.
- [22] Afreen, S., Singh, A. K., Moharana, D. P., Singh, V., Singh, P., & Singh, B. (2017). Genetic evaluation for yield and yield attributes in garden pea (*Pisum sativum* var. *hortense* L.) under North Indian gangetic plain conditions. *Int. J. Curr. Microbiol. App. Sci.*, 6 (2), 1399-1404.
- [23] Avci M. A & Ceyhan E. (2006). Correlations and genetic analysis of pod characteristics in pea (*Pisum sativum* L.). *Asian Journal of Plant Science.*, (5): 1-4.
- [24] Kumar, T. V., Alloli, T. B., Hadimani, H. P., Ajjappalavar, P. S., Satish, D., Abdul, K., & Hanchinamani, C. N. (2019). Studies on Genetic Variability, Heritability and Genetic Advance in Garden Pea (*Pisum sativum* L.) varieties. *Int. J. Curr. Microbiol. App. Sci.*, 8 (12): 3032-3038.
- [25] Ramzan A., Noor T., Khan T. N & Hina A. (2014). Correlation, cluster and regression analysis of seed yield and its contributing traits in pea (*Pisum sativum* L.). *Journal of Agricultural Research.*, 52 (4): 481-488.
- [26] Tolessa, T. T. (2017). Genetic variation, heritability and advances from selection in elite breeding materials of field pea (*Pisum sativum* L.) Genotypes. *Agri. Res. Tech.*, 8 (4): 55-57.