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Assessment of genetic variability, genetic advance and correlation coefficient in quantitative traits of field pea (*Pisum sativum L.*) Genotypes

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Field pea (*Pisum sativum* L.) is an economically valuable pulse crop grown around the globe for its protein rich seed and other soil restorative purposes. Improvements in genetic diversity are obligatory in order to develop crop cultivars with desirable traits including resistance to stresses, higher yields or improved nutritive value. Therefore, the present research study was designed to examine genetic variability, heritability, genetic advance and correlation coefficient for yield and yield related traits in ten pea genotypes at Tarnab-Peshawar, during cropping season 2016–2017. Highly significant ($p \leq 0.01$) differences among the tested genotypes were observed. Genotype Sultan flowered earlier (50.38), matured earlier (122.08) and had maximum fresh pod shelling percentage (65.29%). Genotype PL-4 produces taller plants (142.08 cm), more pods plant^{-1} (39.96) and produced maximum yield plant^{-1} (52.04 g). Anmol had maximum 100-seed fresh (43.90 g) and dry (21.29 g) weight. Genotype Adventa selection produced maximum primary branches plant^{-1} (4.0) lengthy pods (8.86 cm) and maximum number of seeds pod^{-1} (6.26). The estimates of heritability and genetic advance were high for flowering (0.99%, 35.38%), plant height (0.95%, 46.88%) and seed yield (0.97%, 62.47%). High heritability with moderate genetic advance were observed for 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 also exhibited for seed yield plant^{-1} with plant height (r_p = 0.64), days to flowering (r_p = 0.63), 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 for 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 Adventa selection performed better for representing earlier flowers, taller plants, more pods plant^{-1}, higher yield plant^{-1}, 100-seed dry and fresh weight, more branches plant^{-1} and lengthy pods.

Keywords: Genetic advance, Genetic diversity, Genotype, Heritability, *Pisum sativum*, Variability.

INTRODUCTION

To modern breeding program encompasses creating genetic variability, selection, and utilization variation found in selected genotypes to generate new breeding materials. To reveal the genetic control of any trait heritability, variance component and genotypic and environmental variance are key parameters of interest unravelling the gene action governing the desired trait. In order to initiate the efficient breeding program, information on estimation of variability and heritable elements of traits of particular genetic material is utmost necessary. Phenotypic and genotypic components of variation, heritability, and correlation would provide valuable information for breeding of desirable traits (Bekele et al., 2013). Genetic variability among traits is essential for breeding and in selecting desirable genetic material (Atlin, 2003). Heritability, a measure of the phenotypic variance that is attributed due to genotype, has predictive function of breeding crops (Songsri et al., 2008). Generally, heritability represents the effectiveness of selection of genotypes that could be based on phenotypic performance (Bitew, 2006). Field pea (*Pisum sativum* L.) is an annual herbaceous leguminous crop that belongs to family Fabaceae or bean family, a group named for the butterfly-like appearance of their flowers. Pea is a grain legume and is cultivated during winter in plains and summer in highlands of Pakistan (Javaid et al., 2002). Genus *Pisum* comprises two species, *Pisum sativum* and *Pisum fulvum* of which *Pisum sativum* L. is cultivated specie. *P. 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 (Santalla et al., 2001). Pea seed contains 21% to 25% proteins and therefore, is considered an alternative to soybean. Presence of high variability in the field pea germplasm provides much more scope for its improvement. A great diversity is present in pea that may be used to develop new high yielding cultivars (Georgieva et al., 2016). A great proportion of variability has been observed in different agronomic characters of pea (Pallavi, Pandey, 2013). Local and exotic germplasm can be used in hybridization program for pea improvement (Javaid et al., 2002). Pea yield could be enhanced by understanding the interrelationship of yield and other traits at both phenotypic and genotypic levels. Unfavourable 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. Hence the present study was conducted with the objectives is to estimate genetic variability, heritability and correlation among the various quantitative traits of pea in order to aid the effective selection for successful breeding program. The findings of this study would help to identify the highly suitable genetic material and assist to design the subsequent breeding program to foster the varietal improvement program.

MATERIALS AND METHODS

Experimental Site and Treatments

The present research was carried out at the Experimental Farm, Agriculture Research Institute Tarnab-Peshawar (70°41'48 E, 33°30'43 N, 1042 meters) during the cropping season 2016–2017. The experimental station is characterized by a hot climate and low annual rainfall with a clay loam soil. These genotypes were evaluated in a Randomized Complete Block Design with three replications. Ten field pea (*Pisum sativum* L.) genotypes: Green Gold, PL4, PL5, Pea 2009, Sarsabz, Green Cross, Adventa Selection, Anmol, Mateor and Sultan, were obtained from the Oil Seed Section, ARI Tarnab (Table 1).

Table 1; Source of diverse pea genotypes used in the current study

S. No.	Name	Source
01	**Green Gold**	Imported pea cultivar 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**	Imported pea cultivar 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

Field preparation and other cultural practices:

All genotypes were grown in three meter long ridges, where row to row and plant to plant distance (60 and 30 cm) were kept. To reduce experimental error, different cultural practices were performed uniformly for all genotypes.

Attributes studied:

Data were collected from ten randomly selected plants from each genotype in each replication on the following parameters i.e. 50% flowering (days from the date of transplanting to first flowering were recorded, plant height (The tallest shoot of each plant was measured from the soil surface to the apical top with a measuring tape), primary branches, days to maturity, Number of pods plant^{-1}, pod length (when the fruit attained certain maturity then the length was measured with the help of measuring tap in cm), fresh pod shelling percentage, 100-seed fresh (It was measured with the help of balance and their average was taken), dry weight, Number of seeds pod^{-1} and seed yield.

Correlation analysis:

Genotypic (r_g) and phenotypic (r_p) correlations among various traits were worked out from genotypic, phenotypic and environmental co-variances following Singh and Chaudhary (1985) as under:

Genotypic Co-variance $(\delta^2{}_{g1g2}) = \frac{GMCP-EMCP}{r}$

Phenotypic Co-variance $(\delta^2{}_{p1p2}) = \delta^2{}_{g1g2} + \delta^2{}_{e1e2}$

$$\textbf{Genetic correlation } (r_g) = \frac{COV_{gx_1x_2}}{\sqrt{\delta^2 g(x_1)\ \ \delta^2 g(x_2)}}$$

$$\textbf{Phenotypic correlation}(r_p) = \frac{COV_{px_1x_2}}{\sqrt{\delta^2 p(x_1)\ \ \delta^2 p(x_2)}}$$

Where

GMCP = Genotypic mean cross product

EMPC = Environmental mean cross product

$COV_{G(X1X2)}$ = Genetic covariance among 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 traits X_2

$COV\ _{p\ (X1X2)}$ = Phenotypic covariance among traits X_1 and X_2

$\delta^2{}_{P\ (X1)}$ = Phenotypic variance of traits X_1

$\delta^2{}_{P\ (X2)}$ = Phenotypic variance of traits X_2

Statistical analysis:

All the data of all the above mentioned parameters were individually subjected to the analysis of various techniques subsequently the significant means were separated by the least significant difference test by using the programme *MSTATC* (Steel et al., 1997).

RESULTS AND DISCUSSION

Mean squares revealed highly significant differences for all the characters among 10 pea genotypes (Table 2) and the mean values of various genotypes had also indicated sufficient range of variability for various traits in the present study (Table 3).

The mean values among pea genotypes noted for days to 50% flowering (66.93 days), plant height (81.87 cm), primary branches plant^{-1} (3.44), days to maturity (143.06), Pods plant^{-1} (29.86), pod length (7.38 cm), Fresh pod shelling percentage (54.39%), 100-seed fresh weight (32.51g), 100-seed dry weight (16.23), seeds pod^{-1} (5.06), seed yield plant^{-1} (30.14 g) (Figure 1). The traits under study were analysed for variance, heritability and genetic advance. Genotypic variance calculated for 50% flowering was (182.77), plant height (504.01), primary branches plant^{-1} (0.37), days to maturity (279.57), number of pods plant^{-1} (26.48), pod length (0.44), fresh pod shelling percentage (56.03), 100-seed fresh weight (33.24), 100-seed dry weight (4.67), number of seeds pod^{-1} (0.18), seed yield plant^{-1}(119.13) respectively. While the environmental variance for 50% flowering (1.75), plant height (27.87), primary branches plant^{-1} (0.25), days to maturity (9.39), number of pods plant^{-1} (27.59), pod length (0.44), fresh pod shelling percentage (12.64), 100-seed fresh weight (3.62), 100-seed dry weight (0.33), number of seeds pod^{-1} (0.31), seed yield plant^{-1} (3.72) respectively.

The traits under study were also analyzed for coefficient of correlation. Pods plant^{-1} exhibited significant and 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 plan^{-1} with pod length (r_g = 0.580), 100-seed dry weight (r_g = 0.421), seeds pod^{-1} (r = 0.534) and seed yield plant^{-1} (r_g = 0.842) 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 phenotypic association of fresh pod shelling percentage was positively significant 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).

Table 2; Mean squares for morphological, yield and yield associated traits of pea genotypes during 2016–2017

Source	Replication	Genotypes	Error	CV
	df = 2	df = 9	df = 29	
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*;* Genotypic variance, phenotypic variance, heritability and genetic advance for different traits in pea genotypes during 2016–2017

Parameters	Genotypic variance (Vg)	Environmental variance (Ve)	Heritability (h2 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 4; Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient among various traits of 10 pea genotypes 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*	_

DTF – Days to flowering, PH – Plant height, PBH – Primary branches plant^{-1}, DTM – Days to maturity, PP – Pods plant^{-1}, PL – Pod length, FPS% – Fresh pod shelling percentage, 100-SFW – 100 seeds fresh weight, 100-SDW – 100 seeds dry weight, SP –Seeds pod^{-1}, SY – Seed yield; * – LSD ≤ 0.05,** – LSD ≤ 0.01

The association of 100-seed fresh weight was positive and 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 it revealed 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). 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). Seeds pod^{-1} exhibited significant and positive phenotypic association with seed yield plant^{-1} (r_p= 0.452) and significant positive genotypic 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). 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) (Table 4).

The estimates of heritability in the broad sense and genetic advance for 50% flowering were 0.99% and 35.38%, respectively, which indicates a greater genetic influence in comparison to environmental influence on this trait. High broad sense heritability with high genetic advance for 50% flowering among pea genotypes was also reported by Ahmad et al. (2014). Present findings are also in agreement with the results of Singh (1984) who estimated high heritability (98.3) for 50% flowering. The estimates of heritability in the broad sense and genetic advance for plant height were high (0.95% and 46.88%), respectively, indicating greater genetic influence in comparison to environmental influence. Gudadinni et al., (2017) also reported high heritability with high genetic advance for plant height among pea genotypes. Singh and Singh (2006) estimated high heritability with high genetic advance for plant height among pea genotypes. Primary branches plant^{-1} indicated moderate heritability with moderate genetic advance (0.59% and 23.35%) respectively indicating equal importance of both genotype and environment in controlling primary branches plant^{-1}. The present results are supported by Afreen et al. (2017) who estimated moderate heritability with low genetic advance for primary branches plant^{-1} among different pea genotypes. Heritability in the broad sense was high (0.97) while genetic advance was low (20.20%) for days to maturity. The results of high heritability with low genetic advance for days to maturity are in accordance with the results of Jaiswal et al. (2015) who conducted experiment on 12 pea genotypes and estimated high heritability with low genetic advance. Heritability in the broad sense was moderate with low genetic advance for pods plant^{-1} (0.49 and 21.85%). Our results are in agreement with the findings of Georgieva et al. (2016) who conducted experiment on five pea genotypes and found moderate heritability with low genetic advance (0.39 and 0.40) for pod plant^{-1}.

Heritability in the broad sense was high (0.95) with low genetic advance (15.33%) for pod length. Our results for high heritability and low genetic advance for pod length are in agreement with Afreen et al. (2017) who conducted experiment on 21 different genotypes of garden pea and estimated high heritability with low genetic advance (0.90% and 22.42%) for pod length. Heritability in the broad sense was high (0.82) while genetic advance was low (21.58%) for fresh pod shelling percentage. Our results for high heritability and low genetic advance are in agreement with the results of Kumar et al. (2014) who estimated high heritability with low genetic advance (0.62% and 29.35%) for fresh pod shelling percentage among various pea genotypes. Heritability in the broad sense was estimated high (0.90), while genetic advance was low (29.52%) for 100-seed fresh weight. Similar results of high heritability were also reported by Siddika et al. (2013) who observed high heritability with low genetic advance (0.77% and 13.98%) for 100-seed fresh (green) weight while working with 26 lines of pea. Heritability in the broad sense was high (0.93), whereas genetic advance was (22.68%) for 100-seed dry weight. Similar results of high heritability in the broad sense and low genetic advance (0.95% and 11.30%) for 100-seed weight were reported by Georgieva et al., (2016). Low heritability in broad sense (0.37) and genetic advance (8.36%) was estimated for seeds pod^{-1}. Low heritability with low genetic advance revealed 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 accordance with the results of Fikreselassie (2012) who estimated low heritability with low genetic advance (0.39% and 0.77%) for seeds pod^{-1} among 25 elite pea genotypes. Heritability in the broad sense was estimated to be (0.97) with high genetic advance (62.47%) for seed yield plant^{-1}. 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., (2016) in pea genotypes. Our results for high heritability and high genetic advance are also supported by Kumar et al., (2014) who estimated high heritability with high genetic advance (0.83% and 67.87%) for seed yield plant^{-1} in pea genotypes.

Significant and positive phenotypic correlation and genotypic association among the pea genotypes for all the attributes indicates that that simple selection Scheme would be sufficient for these traits to bring genetic improvement in desired direction. The current results are in agreement with the results of Fikreselassie (2012) who 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 (1984) also observed significant association of pods plant^{-1} with seed yield plant^{-1} both at phenotypic and genotypic levels among 30 pea cultivars. The current findings are in accordance with the results of Habtamu and Million (2013) who reported significant genotypic positive association of pod length with days to maturity and 1000-seed weight and significant positive phenotypic association with 1000-seed weight and seed yield plant^{-1}. Siddika et al., (2013) showed non-significant correlation both at phenotypic and genotypic levels of pod length with plant height. The current results of negative correlation of 100-seed fresh weight with plant height and positive significant genotypic association of 100-seed fresh weight with 100-seed dry weight and yield plant^{-1} are in agreement with the results of Ramzan et al., (2014). 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 (2006) who reported highly significant association between 100-seed dry weight and 100-seed fresh weight. Current results are in agreement with the results of Fikreselassie (2012) who 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 (2013) who also reported highly significant and positive genotypic association between seeds pod^{-1} and pod length in pea genotypes. Current results are in line with Singh and Singh (2006) who reported significant positive correlation of seed yield plant^{-1} with plant height and pod plant^{-1} in pea genotypes. Mean squares revealed highly significant differences for all the characters among 10 pea genotypes (Table 2) and the mean values of various genotypes had also indicated sufficient range of variability for various traits in the present study (Table 3).

The mean values among pea genotypes noted for days to 50% flowering (66.93 days), plant height (81.87 cm), primary branches plant^{-1} (3.44), days to maturity (143.06), Pods plant^{-1} (29.86), pod length (7.38 cm), Fresh pod shelling percentage (54.39%), 100-seed fresh weight (32.51g), 100-seed dry weight (16.23), seeds pod^{-1} (5.06), seed yield plant^{-1} (30.14 g) (Figure 1). The traits under study were analysed for variance, heritability and genetic advance. Genotypic variance calculated for 50% flowering was (182.77), plant height (504.01), primary branches plant^{-1} (0.37), days to maturity (279.57), number of pods plant^{-1} (26.48), pod length (0.44), fresh pod shelling percentage (56.03), 100-seed fresh weight (33.24), 100-seed dry weight (4.67), number of seeds pod^{-1} (0.18), seed yield plant^{-1}(119.13) respectively. While the environmental variance recorded for 50% flowering (1.75), plant height (27.87), primary branches plant^{-1} (0.25), days to maturity (9.39), number of pods plant^{-1} (27.59), pod length (0.44), fresh pod shelling percentage (12.64), 100-seed fresh weight (3.62), 100-seed dry weight (0.33), number of seeds pod^{-1} (0.31), seed yield plant^{-1} (3.72) respectively.

The traits under study were also analysed for coefficient of correlation. Pods plant^{-1} exhibited significant and 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 plan^{-1} with pod length (r_g = 0.580), 100-seed dry weight (r_g = 0.421), seeds pod^{-1} (r = 0.534) and seed yield plant^{-1} (r_g = 0.842) 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 phenotypic association of fresh pod shelling percentage was positively significant 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). The association of 100-seed fresh weight was positive and 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 it revealed 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). 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). Seeds pod^{-1} exhibited significant and positive phenotypic association with seed yield plant^{-1} (r_p= 0.452) and significant positive genotypic 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). 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) (Table 4).

The estimates of heritability in the broad sense and genetic advance for 50% flowering were 0.99% and 35.38%, respectively, which indicates a greater genetic influence in comparison to environmental influence on this trait. High broad sense heritability with high genetic advance for 50% flowering among pea genotypes was also reported by Ahmad et al. (2014). Present findings are also in agreement with the results of Singh (1984) who estimated high heritability (98.3) for 50% flowering. The estimates of heritability in the broad sense and genetic advance for plant height were high (0.95% and 46.88%), respectively, indicating greater genetic influence in comparison to environmental influence. Gudadinni et al*.,* (2017) also reported high heritability with high genetic advance for plant height among pea genotypes. Singh and Singh (2006) estimated high heritability with high genetic advance for plant height among pea genotypes. Primary branches plant^{-1} indicated moderate heritability with moderate genetic advance (0.59% and 23.35%) respectively indicating equal importance of both genotype and environment in controlling primary branches plant^{-1}. The present results are supported by Afreen et al. (2017) who estimated moderate heritability with low genetic advance for primary branches plant^{-1} among different pea genotypes. Heritability in the broad sense was high (0.97) while genetic advance was low (20.20%) for days to maturity. The results of high heritability with low genetic advance for days to maturity are in accordance with the results of Jaiswal et al. (2015) who conducted experiment on 12 pea genotypes and estimated high heritability with low genetic advance. Heritability in the broad sense was moderate with low genetic advance for pods plant^{-1} (0.49 and 21.85%). Our results are in agreement with the findings of Georgieva et al. (2016) who conducted experiment on five pea genotypes and found moderate heritability with low genetic advance (0.39 and 0.40) for pod plant^{-1}.

Heritability in the broad sense was high (0.95) with low genetic advance (15.33%) for pod length. Our results for high heritability and low genetic advance for pod length are in agreement with Afreen et al., (2017) who conducted experiment on 21 different genotypes of garden pea and estimated high heritability with low genetic advance (0.90% and 22.42%) for pod length. Heritability in the broad sense was high (0.82) while genetic advance was low (21.58%) for fresh pod shelling percentage. Our results for high heritability and low genetic advance are in accordance with the results of Kumar et al. (2014) who estimated high heritability with low genetic advance (0.62% and 29.35%) for fresh pod shelling percentage among various pea genotypes. Heritability in the broad sense was estimated high (0.90), while genetic advance was low (29.52%) for 100-seed fresh weight.

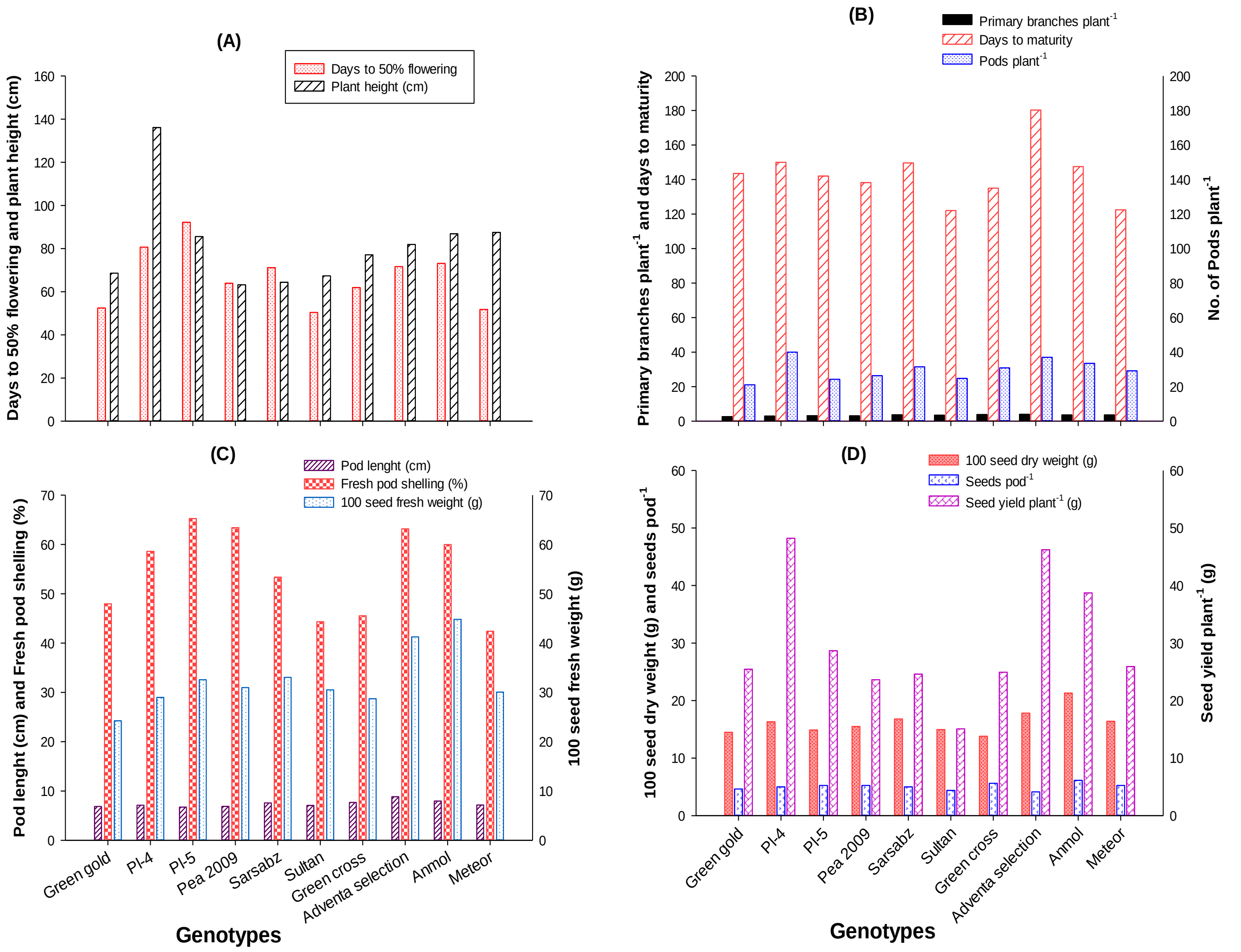

Figure 1. Means values of morphological and yield related traits of pea as influenced by different genotypes

Similar results of high heritability were also reported by Siddika et al*.,* (2013) who observed high heritability with low genetic advance (0.77% and 13.98%) for 100-seed fresh (green) weight while working with 26 lines of pea. Heritability in the broad sense was high (0.93), whereas genetic advance was (22.68%) for 100-seed dry weight. Similar results of high heritability in the broad sense and low genetic advance (0.95% and 11.30%) for 100-seed weight were reported by Georgieva et al., (2016). Low heritability in broad sense (0.37) and genetic advance (8.36%) was estimated for seeds pod^{-1}. 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 (2012) who estimated low heritability with low genetic advance (0.39% and 0.77%) for seeds pod^{-1} among 25 elite pea genotypes. Heritability in the broad sense was estimated to be (0.97) with high genetic advance (62.47%) for seed yield plant^{-1}. 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., (2016) in pea genotypes. Our results for high heritability and high genetic advance are also supported by Kumar et al., (2014) who estimated high heritability with high genetic advance (0.83% and 67.87%) for seed yield plant^{-1} in pea genotypes.

Significant and positive phenotypic correlation and genotypic association among the pea genotypes for all the attributes indicates that that simple selection Scheme would be sufficient for these traits to bring genetic improvement in desired direction. The current results are in agreement with the results of Fikreselassie (2012) who 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 (1984) also observed significant association of pods plant^{-1} with seed yield plant^{-1} both at phenotypic and genotypic levels among 30 pea cultivars. The current findings are in accordance with the results of Habtamu and Million (2013) who reported significant genotypic positive association of pod length with days to maturity and 1000-seed weight and significant positive phenotypic association with 1000-seed weight and seed yield plant^{-1}. Siddika et al., (2013) showed non-significant correlation both at phenotypic and genotypic levels of pod length with plant height. The current results of negative correlation of 100-seed fresh weight with plant height and positive significant genotypic association of 100-seed fresh weight with 100-seed dry weight and yield plant^{-1} are in agreement with the results of Ramzan et al., (2014). 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 (2006) who reported highly significant association between 100-seed dry weight and 100-seed fresh weight. Current results are in agreement with the results of Fikreselassie (2012) who 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 (2013) who also reported highly significant and positive genotypic association between seeds pod^{-1} and pod length in pea genotypes. Current results are in agreement with Singh and Singh (2006) who reported significant positive correlation of seed yield plant^{-1} with plant height and pod plant^{-1} in pea genotypes.

CONCLUSION

It was concluded that among pea genotypes, early flowering and maturity along with maximum fresh pod shelling percentage was observed for genotype Sultan. PL-4 had taller plants, maximum pods plant^{-1} and maximum seed yield plant^{-1}. Genotype Anmol had maximum 100-seed fresh and dry weight. Sarsabz had maximum primary branches plant^{-1} while Adventa selection had maximum pod length and seeds pod^{-1}. 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.

CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

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AUTHOR CONTRIBUTIONS

Conceived and designed the experiments: BA and RUD, Performed the experiments: BA. Analyzed the data: UI, KS, SST Contributed materials/ analysis/ tools: KH. Wrote the paper: UI. Reviewed the manuscript: UF, UZ, KMA. All authors read and approved the final version

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