



# Relationship of Quantitative Traits in Different Morphological Characters of Pea (*Pisum Sativum* L.)

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## Abstract

An experiment was undertaken to elucidate the genetic relationship between different quantitative traits for commercial cultivation and to evaluate selection criteria in pea breeding programs in five inbred parents. Their 17 F<sub>4</sub>'s derivatives in pea (*Pisum sativum* L.) evaluated ten characters during the winter season (November to February) of 2017-18 at the research farm, BSMRAU, Gazipur, Bangladesh. Analysis of variance explored significant differences among the genotypes for all the characters. Phenotypic coefficients of variation (PCV) were close to genotypic coefficients of variation (GCV) for all the characters indicating less influence on the environment and potentiality of selection. A high heritability relationship with high genetic advance was observed for plant height, pod per plant, hundred seed weight, and seed yield per plot. Pod length showed a highly significant positive correlation with pod width and hundred seeds weight. Only days to first flowering showed a highly negative correlation with pod length and hundred seed weight. Path coefficient analysis revealed that plant height, pod per plant, and seeds per pod had a highly positive effect on yield per plant. Therefore, associating and selecting those traits, yield improvement must be possible in pea, and the days to maturity, plant height, pods per plant, pod length, and seed showed a considerable positive and highly significant correlation with plant height, pod per plant, seed per pod, and yield per plant at both genotypic and phenotypic levels indicating yield could be increased with the increase of days to maturity, plant height, pods per plant, pod length, and seed.

**Keywords:** Pea, *Pisum sativum*, plant height, flower, pod, seed, PVC, GCV

## 1. INTRODUCTION

Pea (*Pisum sativum* L.) is an annual herbaceous important member crop that belongs to the family Leguminosae. Among legumes, *Pisum sativum* is the oldest common pea and it is a self-pollinated ( $2n=2x=14$ ) food crop [1]. It has initiated in the Mediterranean region, primarily in the Middle East [2]. It is an imperative, highly productive, and nutritionally rich cool-season legume crop, grown across the world, consumed as food, feed, and fodder [3][4]. Pea is cultivated for green pod seeds as vegetable and dry seeds in Bangladesh.

It is a vital crop with a rich history in genetic study seeing back to the classical work by the father of genetics Gregor J. Mendel. Genetic deviation more gives an idea about the scope of development in a character through simple selection based on grouping. Generally, the mature dry seeds are used as dhal and the green seeds are used as fresh,

frozen, or canned vegetables. It is an excellent source of dietary protein, nutritious feed for humans and livestock. This plant is a great source of nitrogen having a profound ameliorative effect on soil. It is widely used as a supplement feed, fresh vegetables, grains, and green manure, due to its amusing source of healing properties and nutritional value [5]. It is a starchy vegetable with high nutritional value, high in fibers, proteins, vitamin A, vitamin B6, vitamin C, vitamin K, iron, zinc, phosphorus, magnesium, copper, and lutein [6]. The protein of peas contains all the essential amino acids important for the normal activity of living organisms [7][8].

Pathak and Jamwal [9] stated that the high genotypic coefficient of variation (GCV) was noted for pod yield per plant, moderate to high GCV were verified for several days to 50% flowering and plant height. Sureja and Sharma [10] reported that a considerable amount of phenotypic coefficient of variation and genotypic coefficient of variation was observed for most of the characters such as the plant height, number of pods per plant, and weight of grains per pod, while the variation was low for the other characters tested. Breeding efforts have contributed substantially to improving yield potential, regional adaptation through resistance or tolerance to abiotic, and is a highly complex character and is controlled by a large number of genes and greatly influenced by the environment

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**Table 1.** Analysis of variance for yield and yield related characters in pea.

Source of Variation	df	DFP	DFPF	DM	PH	PPP	PL	PW	SPP	HSW	SYPP
Replication	2	21.511	48.966	60.045	0.14	0.2306	0.07	0.00002	0.0093	0.0017	0.0002
Genotype	21	109.513**	114.37**	200.779*	3250.99**	57.372**	1.513**	0.048**	1.462**	54.276**	42.858**
Error	42	4.13	1.502	0.474	0.27	0.102	0.011	0.0001	0.017	0.001	0.0001
CV%		5.67	2.86	0.78	0.47	2.62	1.73	0.65	2.53	0.16	0.13

Note: \*\* and \* Significant at 1% and 5% level of probability, respectively.

DFP = Days to First Flowering, DFPF = Days to 50% flowering, PH = Plant Height (cm), PPP = Pods per Plant (no.), PL = Pod Length (cm), PW = Pod Width (cm), SPP = Seeds per Pod (no.),

DM = Days to Maturity, HSW = Hundred Seed Weight (g).

SYPP = Yield per Plant (g).

and quality traits influence the yield directly and indirectly. These traits are simply inherited and less influenced by the environment as compared to yield. So, selection based on these traits has a better chance of success in comparison to selection for yield alone. The genotypic correlation indicates the extent to which the two characters are under the control of the same set of genes are having the physiological basis of their expression [11][12].

In the pea gene pool, genotypes with new mutant traits have looked, changing the plant body. It has led to a substantial change in the constraints of the morphostructure of the new variations and increasing the limit of the changeability of the quantitative traits. Many researchers differently evaluate the role of the individual characteristics in plant thrupt formation. Hamed et al. [12] found that positive heterosis over the better parent for plant length was ranged from 6.44% to 104.21%. El -Dakkak [13] found negative heterosis (-16.82%) based on the tallest parent for this trait. Significant positive heterosis based on an early parent was observed in all garden pea crosses for days to the flowering trait [14], while, Askander and Osman [15] found negative heterosis in some crosses and positive heterosis values in the others. The data from these studies provide an opportunity to combine appropriate traits in one genotype and increase the efficiency of the breeding activity [16]. Zayed et al. [17] reported that the maximum significant heterosis in desirable direction was recorded for the number of seeds/pod. Genanasekaran and Padmavathi [18] found that average heterosis was observed for plant height, pods per plant, pod length, and seeds per pod. The plant height, pods per plant, pod length, seed number and seed weight were effect of yield of pea.

El Hanafi et al. [19] found that the maximum significant mid-parent heterosis in desirable direction was recorded for stem length trait. Hussein [20] confirmed the partial dominance for earliness and overdominance for the remainder growth trait stem length and number of branches. The inheritance of quantitative characters in peas has long been investigated. Suman et al. [21] and Manjunath et al. [22] observed that both general and specific combining abilities were important for hundred seed weight and the number of seeds per pod. Also, Askander et al. [23] reported that general

combining ability was significant for the traits plant height, 100 seeds weight, and pod weight but non-significant for seeds pod, while SCA for most characters was significant in pea. This correlation study along with path coefficient analysis is more useful to study the yield conducive traits [12]. This study aims to find out the relationship between different quantitative traits for commercial cultivation and to evaluate selection criteria in pea breeding programs.

## 2. MATERIALS AND METHODS

### 2.1. Materials

#### 2.1.1. Study Period and Site

The experiment was conducted at the experimental field of Genetics and Plant Breeding Department, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur during the winter season (November to February) of 2017-2018. The experimental site is located at the center of the Madhupur tract (latitude- 24.09°N and longitude- 90.26°E) with an elevation of 8.4 meters from the sea level.

#### 2.1.2. Planting Materials

Five inbred parents viz. IPSA Motorshuti 1, IPSA Motorshuti 2, IPSA Motorshuti 3, Natore, Zhikargacha along with seventeen F<sub>4</sub>'s viz IPSA Motorshuti 1 × IPSA Motorshuti 2, IPSA Motorshuti 1 × IPSA Motorshuti 3, IPSA Motorshuti 3 × IPSA Motorshuti 1, IPSA Motorshuti 1 × Natore, IPSA Motorshuti 1 × Zhikargacha, Zhikargacha × IPSA Motorshuti 1, IPSA Motorshuti 2 × IPSA Motorshuti 3, IPSA Motorshuti 3 × IPSA Motorshuti 2, IPSA Motorshuti 2 × Natore, IPSA Motorshuti 2 × Zhikargacha, Zhikargacha × IPSA Motorshuti 2, IPSA Motorshuti 3 × Natore, Natore × IPSA Motorshuti 3, IPSA Motorshuti 3 × Zhikargacha, Zhikargacha × IPSA Motorshuti 3, Natore × Zhikargacha, Zhikargacha × Natore produced from crossing of the inbred parents were included in the experiment. The F<sub>4</sub>'s were synthesized in the previous year of the experiment. All the seeds of the mentioned genotypes were collected from the Department of Genetics and Plant Breeding Department, Bangabandhu Sheikh Mujibur Rahman

Agricultural University (BSMRAU).

### 2.2. Methods

#### 2.2.1. Experimental Design

Each plot consisted of a single row of 1.5 m long. The rows were spaced at 25 cm in which seeds were sown continuously. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications.

#### 2.2.2. Data Collection

Five randomly selected competitive plants from parents and 20 plants of F<sub>4</sub>'s were used for recording observations on the following parameters. Genotypic and phenotypic coefficients of variations were estimated by using those formulas.

##### 2.2.2.1. Univariate Analysis

The data were statistically analyzed. The mean, range, and standard deviation for each character have been calculated and analysis of variance for each of the characters was performed, and mean values were separated by DMRT. The mean square (MS) at error and phenotypic variances were estimated as per [24]. The error MS was considered as error variance ( $\sigma_e^2$ ), Genotypic variances ( $\sigma_g^2$ ) were derived by subtracting error MS from the variety MS and dividing by the number of replications as shown below:

$$\sigma_g^2 = \frac{\text{GMS} - \text{EMS}}{r} \quad (1)$$

Where GMS and EMS are the varietal and error can square and r is the number of replications. The phenotypic variance ( $\sigma_p^2$ ), were derived by adding genotypic variances with the error variance ( $\sigma_e^2$ ), as given by the formula 2.

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad (2)$$

##### 2.2.2.2. Estimation of Genotypic and Phenotypic Coefficient of Variation

Genotypic and phenotypic coefficient of variation (GCV) was calculated by the formula 3.

$$\text{GCV} = \frac{\sigma_g \times 100}{\bar{X}} \quad (3)$$

where,  $\sigma_g$  = Genotypic standard deviation,  $\bar{X}$  =

**Table 2.** Genotypic (G) and phenotypic (P) correlation coefficient of ten different characters of pea.

Traits		DFP	DFPF	DM	PH	PPP	PL	PW	SPP	HSW
DFPF	G	0.923**								
	P	0.895**								
DM	G	0.454*	0.687**							
	P	0.325	0.568**							
PH	G	0.288	0.563**	0.885**						
	P	0.129	0.409*	0.828**						
PPP	G	0.248	0.496**	0.634**	0.676**					
	P	0.155	0.411*	0.591**	0.633**					
PL	G	-0.655**	-0.418*	0.042	0.162	-0.115				
	P	-0.728**	-0.543**	-0.054	0.110	-0.164				
PW	G	-0.522**	-0.477*	-0.297	-0.202	-0.332	0.737**			
	P	-0.469*	-0.415*	-0.179	-0.075	-0.274	0.800**			
SPP	G	0.194	0.478*	0.749**	0.790**	0.513**	0.428*	0.091		
	P	0.027	0.307	0.631**	0.702**	0.425*	0.420*	0.266		
HSW	G	-0.648**	-0.576**	-0.441*	-0.237	-0.264	0.620**	0.841**	-0.080	
	P	-0.587**	-0.489*	-0.290	-0.046	-0.168	0.718**	0.830**	0.133	
YPP	G	-0.155	0.196	0.484*	0.657**	0.788**	0.390	0.205	0.599**	0.281
	P	-0.261	0.084	0.425*	0.636**	0.769**	0.371	0.292	0.557**	0.418*

Note: \*\* and \* Significant at 1% and 5% level of probability, respectively

PH = Plant Height (cm), PPP = Pod Per Plant (no.), PL = Pod Length (cm), PW = Pod Width (cm), SPP = Seed Per Pod (no.), DFP = Days to First Flowering, DFPF = Days to 50% flowering, DM = Days to Maturity, HSW = Hundred Seed Weight (g), SYPP = Seed Yield Per Plant

Population mean similarly, the phenotypic coefficient of variation (PVC) was calculated from the following formula 4.

$$PVC = \frac{\sigma_p \times 100}{\bar{X}} \tag{4}$$

Where,  $\sigma_p$  = Phenotypic standard deviation;  $\bar{X}$  = Population mean

### 2.2.2.3. Estimation of Heritability

Broad sense heritability was estimated by the formula 5 suggested by [24].

$$h^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100\% \tag{5}$$

Where,  $h^2$  = Heritability;  $\sigma_g^2$  = Genotypic variance;  $\sigma_p^2$  = Phenotypic variance.

### 2.2.2.4. Estimation of Genetic Advance

The expected genetic advance for different characters under selection was estimated using the formula 6 suggested by Silpashree et al. [24].

$$Genetic\ advance\ (GA) = K \times h^2 \times \sigma_p$$

$$= K \times \frac{\sigma_g^2}{\sigma_p^2} \times \sigma_p \tag{6}$$

### 2.2.2.5. Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficient for all possible combinations the formula 7 and 8 suggested by Silpashree et al. [24] and Hanson et al. [25].

$$Genotypic\ correlation\ (r_g) = \frac{\sigma_{gxy}^2}{\sqrt{(\sigma_{gx}^2 \times \sigma_{gy}^2)}} \tag{7}$$

Where,  $\sigma_{gxy}^2$  = Genotypic covariance between the traits x and y;  $\sigma_{gx}^2$  = Genotypic variance of the trait x;  $\sigma_{gy}^2$  = Genotypic variance of the trait y.

$$Phenotypic\ correlation\ (r_p) = \frac{\sigma_{pxy}^2}{\sqrt{(\sigma_{px}^2 \times \sigma_{py}^2)}} \tag{8}$$

Where,  $\sigma_{pxy}^2$  = phenotypic covariance between the traits x and y;  $\sigma_{px}^2$  = phenotypic variance of the trait x;  $\sigma_{py}^2$  = phenotypic variance of the trait y.

#### 2.2.2.6. Estimation of Path Coefficient Analysis

Path analysis was carried out using the genotypic correlation coefficients to know the direct and indirect effects of the components on yield as suggested and illustrated [26][27].

#### 2.2.3. Statistical Analysis

The collected data were analyzed by the Analysis of variance (ANOVA) technique using the computer package program MSTAT and mean differences were adjudged by the least significant difference (LSD) test at a 5% level of significance.

### 3. RESULTS AND DISCUSSIONS

#### 3.1. Mean Performance for Yield and Yield-Related Characters in Pea

Analysis of variance for all the characters showed significant differences between the treatments viz., days to first flowering, days to 50% flowering, plant height (cm), pods per plant (no.), pod length (cm), pod width (cm), seeds per pod (no.), days to maturity, hundred seed weight (g), yield per plant (g). Thus, there was considerable genetic variability in the material chosen for investigation (Table 1).

#### 3.2. Genetic Parameters of Pea

##### 3.2.1. Days to first flowering

Days to first flowering showed a considerable positive and highly significant correlation with days to 50% flowering and days to maturity at both genotypic and phenotypic levels. In contrast days to first flowering showed a positive but non-significant correlation with plant height, seed per pod, and pod per plant. On the other hand, pod length, pod width, hundred seed weight have highly negative and significant correlations with days to first flowering and it showed a negative and non-significant relationship with yield per plant in both genotypic and phenotypic levels (Table 2). Gudadinni et al. [28] observed days to first flowering (30.07 to 64.45), days to 50% flowering (35.71 to 75.55), days to first pod setting (33.92 to 68.23), days to first pod picking (45.85 to 82.36), and those results were supported to this results.

##### 3.2.2. Days to 50% flowering

Days to 50% flowering showed a considerable positive and highly significant correlation with days to maturity, plant height, seed per pod, pod per plant at both genotypic and phenotypic levels. Besides days to 50% flowering showed considerable positive but non-significant correlation with yield per plant. On the other hand, pod length, pod width, hundred seed weight have a highly negative and significant correlation with days to 50% flowering in both genotypic and phenotypic levels (Table 2). Lagiso et al. [29] found days to 50% flowering were positively associated with days to maturity.

##### 3.2.3. Days to Maturity

Days to maturity showed a considerable positive and highly significant correlation with plant height, pod per plant, seed per pod, and yield per plant at both genotypic and phenotypic levels. On the contrary days to maturity showed considerable negative and significant correlation with hundred seed weight. On the other hand, pod length, pod width has a highly negative and non-significant correlation with days to maturity in both genotypic and phenotypic level (Table 2). According to Singh et al. [30], days to maturity was a major yield and yield contributing character in field pea. Motte et al. [31] studied on the correlation between yield and yield components of a pea.

##### 3.2.4. Plant Height

Plant height showed a considerable highly significant positive correlation with pods per plant, seeds per pod, and yield per plant at a genotypic and phenotypic level indicating yield could be increased with the increase of plant height. Quite the opposite, plant height exhibited an insignificant positive association with pod length. On the other hand, pod width, hundred seed weight have an insignificant negative correlation with plant height in both genotypic and phenotypic levels (Table 2). Riaz et al. [32] reported that plant height showed a positive correlation with seed yield per plant.

##### 3.2.5. Pods per Plant

Pods per plant showed a considerable significant positive correlation with seeds per pod, yield per plant at both genotypic and phenotypic levels indicating yield could be increased with the

increase of pods per plant. Furthermore, pods per plant exhibited an insignificant negative association with pod length, pod width, and hundred seed weight (Table 2). Siddika et al. [33] assessed pods per plant exerted a positive direct effect on yield.

### 3.2.6. Pod Length

Pod length showed a significant positive correlation with pod length, pod width, hundred seed weight at both genotypic and phenotypic levels. Quite the reverse, pod length exhibited an insignificant positive association with yield per plant (Table 2). Character association studies of Sharma et al. [34] in pea indicated a positive and insignificant association with seed yield per plant. Similar results were also observed by Khan et al. [35] in legume crop country bean during 2017-2018 in Sylhet, Bangladesh.

### 3.2.7. Pod Width

Pod width showed a significant positive correlation with hundred seed weight at both genotypic and phenotypic levels. In contrast, pod width showed an insignificant positive correlation with seed per pod and yield per plant at both genotypic and phenotypic levels (Table 2). Similar results were also observed by Khan et al. [36] in legume crop country bean during 2017-2018 in Sylhet, Bangladesh.

### 3.2.8. Seeds per Pod

Seeds per pod showed a significant positive

correlation with yield per plant at both genotypic and phenotypic levels. In addition to seeds per pod showed a considerable negative insignificant correlation with hundred seed weight (Table 2). Gayacharan et al. [37] found a positive correlation with seed yield and seeds per pod in black gram. Karyawati and Puspitaningrum [38] got the similar result in lentil. Tiwari and Lavanya [39] found a significant and positive correlation between seed yield per plant and the number of seeds per pod. Similar results were also observed [35] in legume crop country bean during 2017-2018 in Sylhet, Bangladesh.

### 3.2.9. 100 seed weight

The character 100 seed weight showed a positive and phenotypically non-significant correlation with seed yield per plant (Table 2). A significant and positive correlation was observed with days to maturity, plant height, pods per plant at both genotypic and phenotypic levels. The character showed a nonsignificant positive correlation with days to 50% flowering, pod length, pod width, and this character showed a nonsignificant negative correlation with days to first flowering at both levels. Siddika et al. [33] observed a positive correlation between seed yield per plant and 100 seed weight. Similar results were also observed by Khan et al. [35], Khan et al. [40], and Khan et al. [41] in legume crop country bean during 2017-2018 in Sylhet, Bangladesh.

**Table 3.** Partitioning of genotypic correlation ( $r_g$ ) into its direct and indirect effects for seed yield components in pea.

Traits	DFP	DFPF	DM	PH	PPP	PL	PW	SPP	HSW	YPP
DFP	<b>-0.233</b>	0.216	-0.061	0.080	0.175	-0.067	-0.078	-0.005	-0.172	-0.146
DFPF	-0.201	<b>0.251</b>	-0.095	0.159	0.360	-0.044	-0.074	-0.013	-0.156	0.188
DM	-0.103	0.172	<b>-0.138</b>	0.256	0.472	0.006	-0.047	-0.021	-0.122	0.475*
PH	-0.063	0.136	-0.120	<b>0.294</b>	0.514	0.018	-0.032	-0.022	-0.067	0.657**
PPP	-0.053	0.119	-0.085	0.198	<b>0.762</b>	-0.013	-0.053	-0.014	-0.074	0.786**
PL	0.139	-0.099	-0.007	0.047	-0.086	<b>0.112</b>	0.117	-0.012	0.173	0.385
PW	0.114	-0.115	0.040	-0.059	-0.252	0.082	<b>0.161</b>	-0.003	0.237	0.205
SPP	-0.041	0.112	-0.099	0.228	0.381	0.046	0.014	<b>-0.029</b>	-0.022	0.589**
HSW	0.142	-0.139	0.060	-0.070	-0.200	0.069	0.135	0.002	<b>0.283</b>	0.281

Note: Residual effect (R) = 0.05430826

PH = Plant Height (cm), PPP = Pods Per Plant (no.), PL = Pod Length (cm), PW = Pod Width (cm), SPP = Seeds Per Pod (no.), DFP = Days to First Flowering, DFPF = Days to 50% flowering, DM = Days to Maturity, HSW = Hundred Seed Weight (g), YPP = Yield Per Plant (g).

### 3.3. Path Coefficient Analysis

Association of character determined by correlation coefficient may not provide an exact picture of the relative importance of the direct and indirect influence of each yield component on yield. As a fact, to find out a clear picture of the interrelationship between yield per plant and other yield attributes, direct effects were worked out using path analysis at a genotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and plant height, pods per plant, pod length, pod width, seeds per pod, days to first flowering, days to 50% flowering, days to maturity, and hundred seed weight as a causal (independent) variable.

The cause and effect of the relationship of yield per plant and yield-related characters have been presented in Table 3. Residual effects of their independent variables, which have influenced yield to a small extent, have been denoted as 'R'.

#### 3.3.1. Days to First Flowering

Days to first flowering showed negative direct effects with yield per plant (-0.233). This trait showed the maximum positive indirect effect in days to 50% flowering (0.216), pods per plant (0.175), plant height (0.080). In contrast, this trait showed a negative indirect effect through seeds per pod (-0.005), days to maturity (-0.061), pod length (-0.067), pod width (-0.078), yield per plant (-0.146), hundred seed weight (-0.172) (Table 3 and Figure 1).

#### 3.3.2. Plant Height

Plant height showed a positive direct effect on yield per plant (0.294). This trait projected maximum positive indirect effects on biological yield via yield per plant (0.657), pods per plant (0.514), days to 50% flowering (0.136), and pod length (0.018). In contrast, this trait projected negative indirect effects on biological yield through seeds per pod (-0.022), pod width (-0.032), days to first flowering (-0.063), hundred seed weight (-0.067), and days to maturity (-0.120) (Table 3).

#### 3.3.3. Pods per Plant

Pods per plant showed a positive direct effect on yield per plant (0.762). Pods per plant showed the

maximum positive indirect effect through yield per plant (0.786), followed by plant height (0.198) and days to first flowering (0.119). In contrast, this trait showed the negative indirect effect via pod length (-0.013), seeds per pod (-0.014), pod width (-0.053), days to first flowering (-0.053), hundred seed weight (-0.074), and days to maturity (-0.085) (Table 3). In path coefficient analysis of revealed that the number of pods per plant had the greatest direct effect on yield per plant.

#### 3.3.4. Days to 50% Flowering

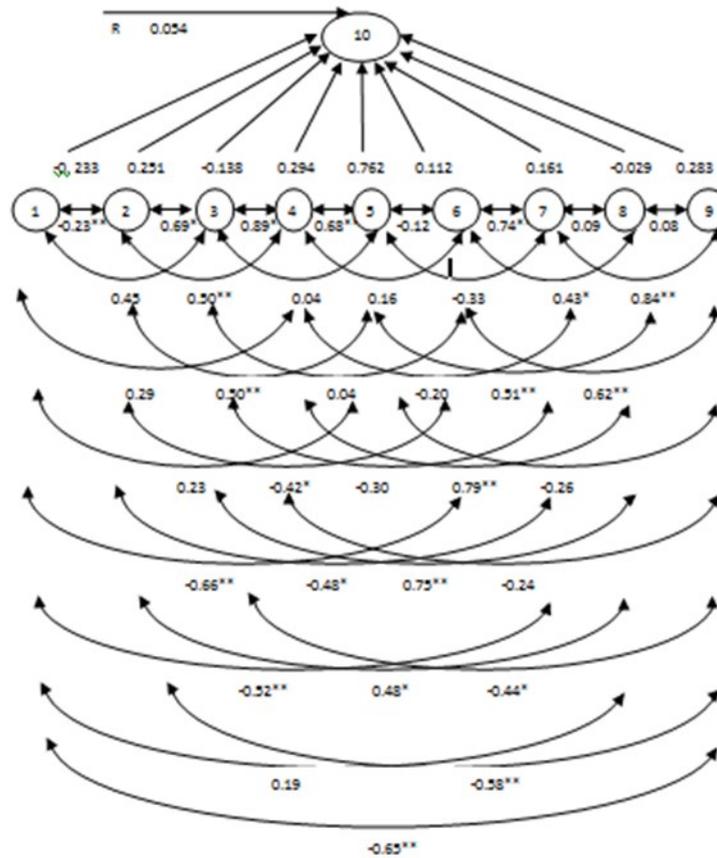
Days to 50% flowering showed a positive direct effect on yield per plant (0.251). This trait showed the maximum positive indirect effect through pods per plant (0.360) followed by yield per plant (0.188), plant height (0.159). In contrast, this trait showed a negative indirect effect through seeds per pod (-0.013), pod length (-0.044) pod width (-0.074) days to maturity (-0.095) hundred seed weight (-0.156) and days to first flowering (-0.201) (Table 3). Hageblad [42] showed that yield had positive associations with days to 50% flowering.

#### 3.3.5. Days to Maturity

Days to maturity showed positive direct effects with yield per plant (-0.138). This trait showed the maximum positive indirect effect through yield per plant (0.475) which was significantly followed by pods per plant (0.472), plant height (0.256), days to 50% flowering (0.172), and pod length (0.006). In contrast, this trait showed a negative indirect effect through seed per pod (-0.021), width (-0.047), days to first flowering (-0.013), and hundred seed weight (-0.122) (Table 3 and Figure 1).

#### 3.3.6. Pod Length

Pod length showed a positive direct effect on yield per plant (0.112). This trait showed the maximum positive indirect effect through yield per plant (0.385) followed by hundred seed weight (0.173), days to first flowering (0.139), pod width (0.117), and plant height (0.047). In contrast, this trait showed a negative indirect effect through days to maturity (-0.007), seeds per pod (-0.012), pods per plant (-0.086), and days to 50% flowering (-0.099) (Table 3).



**Figure 1.** Path diagram of yield contributing characters in vegetable pea (1. Days of first flowering; 2. Days of 50 flowering; 3. Days to maturity; 4. Plant height; 5. Pods per plant; 6. Pod length; 7. Pod width; 8. Seeds per pod; 9. 100 seed weight; 10. Yield per plant).

### 3.3.7. Pod Width

Pod width showed a positive direct effect on yield per plant (0.161). This trait showed the maximum positive indirect effect through hundred seed weight (0.237) followed by yield per plant (0.205), days to first flowering (0.114), pod length (0.082), and days to maturity (0.040). In contrast, this trait showed a negative indirect effect through seeds per pod (-0.033), plant height (-0.059), days to 50% flowering (-0.115), and pods per plant (-0.252) (Table 3).

### 3.3.8. Seeds per Pod

Seeds per pod showed a negative direct effect on yield per plant (-0.029). This trait showed the maximum positive indirect effect through yield per plant (0.589) followed by pods per plant (0.381), plant height (0.228), days to 50% flowering (0.112), pod length (0.046), and pod width (0.014). In contrast, this trait showed a negative indirect effect through hundred seed weight (-0.022), days to first flowering (-0.041), and days to maturity (-0.099) (Table 3). Tanni et al. [43] also observed similar

results in the okra promising genotypes in Sylhet during 2018.

### 3.3.9. 100 Seed Weight

Hundred seed weight showed positive direct effects with yield per plant (0.283). This trait showed the maximum positive indirect effect through yield per plant (0.281) followed by days to first flowering (0.142), pod width (0.135), pod length (0.069), days to maturity (0.060), and seeds per pod (0.002). In contrast, this trait showed a negative indirect effect on plant height (-0.070), days to 50% flowering (-0.139), and pods per plant (-0.200) (Table 3). Goulart et al. [44] investigated pigeon pea (*Cajanas cajan*) varieties revealed that 100-grain weight had the highest positive direct effect on grain yield.

### 3.3.10. Residual Effect

The residual effect of the present study was 0.054 indicating that 94.60% of the variability was accounted for 10 yield contributing traits included in the present study. The rest amount of the

variability might be controlled by other yield contributed traits that were not included in the present investigation.

#### 4. CONCLUSIONS

Based on the findings of the present investigation, it can be concluded that the analysis of variance revealed that all the characters showed significant differences between the treatments. Phenotypic coefficients of variation (PCV) were close to genotypic coefficients of variation (GCV) for all the characters. High heritability associated with high genetic advance per mean was observed for plant height, pod per plant, hundred seed weight, and seed yield per plot. The correlation analysis revealed that seed yield per plant showed a positive and significant correlation with the characters' days to maturity, plant height, and pods per plant and seeds per pod at both genotypic and phenotypic levels. Days to fifty percent flowering, plant height, pods per plant, pod length, pod width, 100 seed weight showed positive direct effects on yield per plant. Hence, yield improvement in pea would be achieved through the association and selection of these characters. We can observe the days to maturity, plant height, pods per plant, pod length, and seed showed a considerable positive and highly significant correlation with both genotypic and phenotypic levels indicating yield could be increased with the increase of the best performance in the experiment.

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