Genetic Variability Studies in Some Peas (*Pisum sativum* L.) Populations

Hazem A.O. Ali[1], Khaled A.A. El Shaikh[1], Abo-Bakr A.A. El-Dakkak[2],
Haitham M.A. Elsayed[3] and Monera A.M. Abdein[1]*
[1]*Horticulture Department, Faculty of Agriculture, Sohag University, Sohag, Egypt.*
[2]*Horticulture Research Institute, Agricultural Research Center, Giza, Egypt.*
[3]*Genetics Department, Faculty of Agriculture, Sohag University, Sohag, Egypt.*

(Corresponding author: Haitham M.A. Elsayed*)

ABSTRACT: A field experiment was conducted on three F_3 and F_4 Peas populations used to study genetic variability, heritability on ten agronomic at Faculty of Agriculture, Sohag university during two winter seasons 2021/2022 and 2022/ 2023. Results showed highly significant different were found between all examined families for all studied traits in both seasons. In F_3 populations, the Phenotypic Coefficient of Variation (PCV) values were higher than The Genotypic Coefficient of Variation (GCV) values for all studied traits. Moderate to high heritability ranged from 42.33% for seed set trait (population 1) to 76.12% for dry pods weight/plant trait (population 3). Moreover, PCV and GCV values in F_4 were close to each other. Heritability in broad sense estimated in F_4 were much higher than F_3 and had a range from 34.22% for seed set trait (population 2) to 88.90% for height of plant trait (population 3) that refers to the selected families tend towards genetic stability and the influence of the environment on them is low. Moreover, the families in the third population of F_4 generation were ranked the first population in traits height of plant, branches plant number, pods plant number, dry pod weight/plant and plant dry seed yield followed by the families in the first population of F_4 generation and then the families in the second population of F4 generation. While, populations order in traits, seed set % and length of pod was second population, then third population then first population, respectively. The families in the third populations of F_4 generation were ranked the second population in traits seed set % and pod length followed by the families in the third population and then the families in the first population. Therefore, continuing the selection process in the following generations will help in obtaining high-yielding and early-flowering peas lines from the superior families of the three studied populations.

Keywords: Peas, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability, Genetic Advance (GA) and Genetic advance over mean (GAM).

INTRODUCTION

Peas (*Pisum sativum* L.) is an important vegetable crop with a rich history in genetic research dating back to the classical work by Mendel the father of genetics science. Pea is commonly consumed in several countries as fresh vegetables or dry seeds. Pea seed has high value of nutrition, proteins content ranges from 16% to 30% (Harmankaya *et al*., 2010; Lam *et al.,* 2018), several vitamins (A, B_1, B_2, B_3, C, and K) and complex vitamins such as folic acid, thiamine, and niacin. It is the second productive legume worldwide after common bean. It is an annual herbaceous crop of the family Fabaceae. The major objective of pea breeders is increasing seed yield to maximize the productivity of pea plants and have new cultivars it can widespread use of pea in many agricultural production systems especially in new reclaimed soils. Seed yield is a quantitative trait that is complexly inherited, and its expression depends on genetic factors and environment (Bedawy and Mohamed 2018).

The success of crop breeding programme depends on the nature of genetic variability existing in the breeding material. Genetic variability is the amount of genotypic variation present in a population, forms a basis for the crop breeding program (Kalloo *et al.,* 2005; Akhilesh *et al.,* 2007). Genetic variability stays unchanged with the environmental conditions on the contrary of phenotypic variability which is strongly affected by the environment. The plant breeder uses both genotypic and phenotypic to estimate the heritability and genetic advance in the selection or crossing. Heritability is the ratio of genetic variance to phenotypic variance

(Falconer, 1985). The genetic variability explains information on genetic parameters (Tasnim *et al.,* 2022; Chauhan *et al.,* 2023; Pandey *et al.,* 2023). Estimating the genetic variability parameters, especially PCV, GCV, heritability and genetic advance are important indicators for perfection of traits via selection. The selection for highly heritable traits is more effective for a successful breeding programme (Pandey *et al.,* 2023). The progress of any crop is symmetrical to the magnitude of its genetic variability present in the studied plant material. Therefore, the main objectives of the present investigation are to assess magnitude of genetic variability and genetic advance for ten different traits in three F_3 and F_4 pea populations, to study performance of selected genotypes and families of the same three pea populations and their parents.

MATERIALS AND METHODS

The present investigation was done in the field experiment during two successful winter seasons 2021/2022 and 2022/2023 at the Research farm of Faculty of Agriculture, Sohag University. The plant material was consisted of three F_3 and F_4 Pea populations, the first population derived from the cross (Cash × Sweet1), the second population derived from the cross (Sweet1 × Sweet2) and the third population derived from the cross (Progress × Sweet2). The selected plants of F_2 genotypes for each population were sown with their parents in season of 2021/2022. The experiment was designed in RCBD with three replications for each population separately. Each individual selected genotype was represented in one row in the plot (each plot was consisted of all selected individual from one population). Each row was 3 m long, 60 cm apart and 20 cm between hills within a row. The traits were recorded for each plant and the average of ten plants from each family. In the second season 2022/2023, the best plants (one or two plants from each family) of families from each population were selected for evaluate the first pedigree selection cycle (F_4 population) (the number of selected families in each generation for each population presented in Table 1 and 2). The experiment was designed as the previous year. The traits were recorded as in the previous season for each plant and the average of ten plants from each family.

The studied traits were; flowering date (number of days to first flower), height of plant (cm), plant branches number, plant pods number, length of pod (cm), pod width (cm), seed set percentage=Total number of seeds/ pod per plant/ Total number of ovules/ pods per plant *100, dry pods weight / plant (g), plant dry seed yield (g), shell-out percentage = plant dry seed yield / dry pods weight / plant. The collected data were statistically analyzed by using SAS program 9.2 (SAS Institute 2008). Genetic parameters were calculated for each generation separately (F_3 and F_4) as follow:

❖ Genotypic variance (δ^2 g) = MSg – Mse / r
   Where: MSg: mean square genotype, MSe: Error mean square and r: replication number.
❖ Phenotypic variance (δ^2 p) = δ^2 g + δ^2 e

❖ Genotypic coefficient variance (GCV%) = $\sqrt{\frac{Vg}{\bar{x}}} * 100$

❖ Phenotypic coefficient variance (PCV%) = $\sqrt{\frac{Vp}{\bar{x}}} * 100$

❖ Heritability in the broad (H_b) = (V_G/ V_p) ×100
❖ Genetic Advanced (GA)= K*H_b*(V_p)
Where, k is the intensity of selection (k =2.06 at 5% selection intensity).
❖ Genetic advance over mean (GAM) = (GA/x) *100

RESULTS AND DISCUSSION

Genetic variability and main performance of F_3 families

Population 1: The analysis of variance and genetic components of the selected genotypes in F_3 families with ten studied traits in the three studied population presents in Table 1. All studied traits were highly significant for the selected twenty families of population 1. The Phenotypic Coefficient of Variation (PCV) values were higher than The Genotypic Coefficient of Variation (GCV) values for all studied traits. PCV values varied from 2.55% for seed set % to 27.85 %for trait branches plant number. GCV values recorded lower values (> 5 %) for traits of seed set% (1.66%), shell-out % (2.36%), flowering date (2.87%) and the length of pod (4.84%). The Heritability ranged from 42.33% for seed set traits to 75.05% for height of plant trait. Three studied traits recorded Heritability in broad sense values lower than 50%, they were pod length,(47.88%), seed set%(42.33%) and shell-out%(46.60%). The higher Genetic Advanced (GA) values were record for height of plant trait with values of 8.6. While, the lowest GA were recorded for trait pod width with values 0.1. The best Genetic Advance as percentage over Mean (GAM) was found for pods plant number trait with values of (33.6%).

The flowering date character ranged from 37.33 days for family No. 47 to 42.34 days for family No. 29 (Table 3). Six families out of 20 had a flowering date earlier than parent 1 "Cash". These families were (10, 30, 47, 62, 70, and 128). All families were earlier than second parent "Sweet-1". The first population is considered the earliest population in this work. Height of plant character had a range from 34.33 cm for family No. 78 to 54.22 cm for family No. 70. All families had mean values of pods plant number higher than 10 (P1 mean). Moreover, all selected families had plant pods number mean value higher than parent 2 "Sweet-1" (17) except family No. 78. Only three families (78,110 and 125) had lower length of pod mean values the shortest pod length parent 1 "Cash" in this character with values of (8.35, 8.37 and 7.99 cm). No family had length of pod mean higher than parent 2 "Sweet-1" (10.73 cm).

The seed set % for almost all selected families was very high and nearest to reaching 100 % seed set %. All selected families had mean values of dry pods weight/plant character higher than the mean of parent 1 "Cash" (14.39 g) except family No. 78 (12.83 g). Furthermore, there were two families (No. 18 and 78) could not exceed the lowest mean parent "Cash" for the plant dry seed yield character with values of 10.70 and 9.87 g, respectively. The shellout % character had a range 66.79 – 82.16 % for families (68 and 47) this range is wide and means of shellout % for the first population is low.

Population 2: Analysis of variance for the second population showed highly significant variance for all studied traits of 17 selected families there was a big difference between (PCV) values and (GCV) for traits, height of plant, branches plant number, plant pods number, dry pods weight and plant dry seed yield. Flowering date, pod width, seed set % and shell-out % have lower PCV and GCV values lower than 6%.Hertability in broad sense values varied in wide range between studied traits between 49.47%for flowering date to 69.73% for length of pod trait. The highest GA recorded also in Pop.2 for plant height trait with value 7.8. While, the highest GAM value was recorded for branches plant number with values of 24.01.

The results showed that families No. 5, 8, 15, 142, and 205 were superior in flowering date with a mean value of 42.94, 44.93, 45.14, 46.49, and 45.78 days, respectively. They were earlier than the parent (Sweet-2) and flowered before 47 days (Table 4). Plant height trait means values ranged from 37.61 cm for family 5 to 58.09 cm for family 142. All selected families in F3 from the second population had plant pods number higher than parent Sweet-1 (11.18), at the same time, no family had plant pod number mean higher than the other parent "Sweet-2". Only one family (No. 52) exceeded the high parent "Sweet-2" in length of pod value with mean value of 12.04 cm. Seven families (No. 15, 34, 46, 52, 134, 142, 177 and 192, respectively) exceeded the other parent "Sweet-1" with an average value of 11.21, 10.91, 11.03, 12.04, 11.00, 10.86, 10.77 and 11.35, respectively. All selected families had seed set % mean value higher than the parent 2 "Sweet-2" (93 %) except two families No. 52 and 214 with means of 90.67 and 92.67 %, respectively. Only three families (No. 8, 142 and 177) out of the 17 families of the second population had mean dry pods weight/plant and plant dry seed yield higher than the highest parent "Sweet-2" with values of (26.06 and 19.21), (25.08 and 18.20) and (23.62 and 18.30), respectively.

Population 3: Highly significant differences were recorded for all studied traits in Pop.3 on the ten of F3 generation families. The height PCV and GCV values were recorded for plant dry seed yield, dry pods weight,

branches plant number and pods plant number. Heritability in broad sense estimates varied from 35.29% for seed set% trait to 76.12% for trait of dry pods weight. Moreover, the highest GA values for pop 3 were recorded for traits of dry pods weight with value 10.8. While, the highest GAM 39.31% were recorded for plant dry seed yield followed by dry pods weight trait then pods plant number trait.

All selected families had mean values earlier than parent 2 "Progress" (58 days). Only two families No. 18 and 50, had flowering date mean value close to parent 1 "Sweet-1". Family No. 18 was the earliest flowering date with a mean value of 43.33 days (Table 4). Out of the 10 families of the third population, only one family (No. 91) was recorded with the highest height of plant mean value of 65.40 cm. It was taller than the tallest parent 2 "Progress". Only three families (No. 58, 74 and 110) gave the highest branches plant number in the third population with mean values of 6.83, 5.54 and 5.70, respectively. Seven families (No. 24, 40, 50, 51, 58, 74, and 91) out of ten in the third population had pods number higher than the high parent 2 "Progress" (20.67), with mean values (20.80, 20.84, 23.75, 23.82, 29.65, 23.05 and 21.61, respectively). Three families exceeded the parent "Sweet-1" mean for trait length of pod with means of (10.81,11.01, and 10.90cm) there were families No. (40, 74 and 110), respectively. Three families (No. 40, 74 and 110) exceeded the parent 1"Sweet-1" mean for trait length of pod with means of (10.81, 11.01, and 10.90 cm), respectively. All studied families in the third population had seed set % lower than the two parents (95 and 93.3 %). Six families out of ten had dry pods weight/plant means and plant dry seed yield higher than the best parent "Progress". The best two families out of these six were families No. 58 and 74, they had dry pods weight/plant means (35.65 and 35.29 g) and means of values (30.19 and 28.72 g) for plant dry seed yield trait. The shellout % trait means for families of the second and third populations were higher than the first population.

The highly significant differences between F3 families in pea found for all studied traits. This suggesting that these traits are genetically controlled by additive (Rashwan and El-Shaieny 2016), they reported highly significant differences between F_3 families in two populations under study. El-Dakkak (2016 b) found medium heritability values in the end of selection cycle for number of seeds/pods in the wrinkled (52.33%), round (50.65%) of green seed and only round of mottled seed (56.74%). Kumar *et al.* (2013); Gudadinni *et al.* (2017) reported high heritability coupled with moderate genetic advance was observed for plant height. Moreover, Vinayaka *et al.* (2022) ; Ban *et al.* (2019) had a similar finding for PCV and GCV they recorded PCV and GCV values(> 20 %) for traits number of branches per plant and No. of pod plant, dry

pods weight/ plant and total dry seed yield/ plant indicated additive gene action this helps the breeder in producing promising pea lines via selection.

Genetic variability and main performance of F_4 families:

Population 1: The best plants in each F_3 families in the three populations, which had early flowering date and had high dry seed yield same time were selected and planted to provide the F_4 generation. The analysis of variance and genetic components for 10 studied traits in F_4 families of population 1, 2 and 3 represented in Table 2. The analysis of variance showed highly significant difference between 25 families and ten studied traits in the first population. PCV values ranged from 2.75% for seed set% to 25.32% for trait branches plant number. GCV values ranged from 2.13–20.70 % for traits of seed set % and plant branches number. The highest heritability estimates recorded for flowering date (79.30%), height of plant (81.01%) length of pod (85.57%) and pod width (87.11%) traits. The GA values ranged from 0.3 for pod width trait to 8.6 for height of plant trait. Higher values of GAM; 34.85, 31.10 and 30.82 % were found for traits of branches plant number, dry pods weight/plant and plant dry seed yield, respectively.

The mean performance of 25F4 selected families and 10 studied traits is shown in Table 5. Seventeen F4 families had mean values of flowering date earlier than the "Cash" parent (39.33 days). The best seven earliest families out of this seventeen were No. (10.1.3,27.1.1,47.1.2,68.1.4,70.1.4,74.3.1 and74.3.4) which had flowering date mean of less than 37 days. Eleven families exceeded the tallest population parent "Sweet-1" mean (46.02 cm). These families were No. (17.2.2, 19.1.1, 19.2.3, 27.1.1, 29.1.1, 48.1.1, 62.1.1, 63.1.2, 47.83, 70.1.4, and 145.1.5). All selected families had branches plant number mean values higher than parent "Cash" (1.00) except one family No. (48.1.1). All families had plant pods number mean value higher than parent 2 "Sweet-1" (12.33). All families have plant pods number mean value higher than parent 2 "Sweet-1" (12.33) except for four families No. (68.1.3, 74.3.1, 110.1.2 and 125.1.2). Six families; No. (10.1.3,27.1.1, 29.1.1, 29.1.2, 63.1.2 and 70.1.4) had the longest pod length higher than parent 2 "Sweet-1"(10.24cm) with meanvalues(10.65,10.39, 10.80, 10.72, 10.83 and 10.57 cm). Seventeen F_4 families had mean values of pod width higher than the "Cash" parent 1 (1.2 cm). The best six families higher in pod width out of this seventeen were No. (17.2.1, 48.1.1, 70.1.4, 110.1.2, 125.1.2 and 145.1.5) which had a pod width higher than 1.40 cm.

All studied F_4 families had seed set % higher than 90 % but no family had a mean value of 100% seed set %. Five families had dry pods weight/plant lower than the parent 2Sweet-1 (17.82 g), this means 20 families had a dry pods weight/plant higher than both of the population parents. Therefore, we can say that most of the selected families in the first population in the F_4 are considered high yielding families compared with their parents. The best five families plant dry seed yield trait were; (10.1.3, 17.2.2, 19.2.3, 27.1.1 and 70.1.4) with mean values of plant dry seed yield (19.17, 19.52, 25.28, 20.64 and 19.85g, respectively). Family No. 19.2.3 had the highest dry pods weight/plant and plant dry seed yield with mean values of 32.06 and 25.28 g, respectively. This family was also recorded (37.94 days) for flowering date mean, this family surpassed all selected F_4 families on the first population. Three families No. (10.1.3, 30.2.5 and 47.1.2) had shellout % higher than the best parent 2 "Sweet-1" (78.90 %). with a mean value of 79.28, 83.23 and 81.46, respectively.

Population 2: Highly significant differences were found between 17 examined F_4 families in population 2. Variance components revealed that, PCV and GCV values for five traits didn't reach 6%, these traits were flowering date (5.66 and 5.17%), length of pod (5.72 and 5.06%), pod width (5.81 and 4.50%), seed set % (2.44 and 1.43%) and shell-out % (3.07 and 2.24%). High heritability estimated values were recorded for flowering date (83.32 %) and plant height (83.27%). The highest GA values found for height of plant trait (12.6). The GAM values ranged from1.72% for seed set % to 26.67 % to plant pods number trait.

The mean performance for selected families in the second population in the F_4 generation is shown in Table 6. Four families No. (5.2.2, 8.1.2, 8.1.3 and 175.3.2) out of 17 families had flowering date earlier than 46 days with means of (42.33, 45.42, 45.44, and 45.36 days), respectively. Unfortunately, no family had an early mean flowering date than parent 1 "Sweet-1". Four families (8.1.2, 134.2.2, 177.1.3 and 185.2.1) are considered the tallest families with a means of 61.33, 64.58, 63.53 and 61.69 cm, respectively. Two families (8.1.2 and 134.2.2) had pods plant number higher than 20 with a means of 21.50 and 22.42, respectively. All selected families had long pods more than 10.34 cm. Families No. (46.1.3, 175.3.2 and 192.1.3) were higher in length of pod than the parent 2 "Sweet-2" (11.88 cm). All selected families in the second population in F4 generation had the longest pods among the three studied population. Eight superior families (5.2.2, 8.1.2, 134.2.2, 167.2.1, 175.3.2, 185.2.1, 186.2.2 and 192.1.3) had highly dry pods weight/ plant exceeded the mean values of the parents by means values of 22.34, 26.53, 25.71, 20.94, 22.39, 22.65, 24.44 and 22.23 g, respectively. Eight superior families (5.2.2, 8.1.2, 134.2.2, 167.2.1, 175.3.2, 185.2.1, 186.2.2 and 192.1.3) had highly dry pods weight/ plant exceeded the population parents mean values with means of (22.34, .26.53, 25.71, 20.94, 22.39, 22.65, 24.44 and 22.23 g, respectively). Otherwise, four families No. (8.1.2, 134.2.2, 167.2.1 and 185.2.1) out of 17 had plant dry seed yield higher than parent 2 "Sweet-2" with mean

values of 20.12, 19.53, 18.56 and 18.59 g, respectively. All selected families had seed set % mean higher than 93 %. Whereas, all selected families had shellout % means lower than both population parents.

Population 3: Highly significant differences found for all studied traits and families in the third population. Highest values of PCV and GCV found for pods plant number (27.96% and 25.60 %) followed by plant dry seed yield trait (25.36 % and 22.85%) and dry pods weight/plant traits (24.59 and 22.52%). High heritability values of (80.74, 88.90, 83.87, 80.51, 83.89, 81.23 and 84.61 %) were found for flowering date, height of plant, plant pods number, pod width, dry pod weight /plant, plant dry seed yield and shell-out %. Height of plant had highest GA value (16.7), while the lowest GA value (0.1) found for pod width trait. GAM values reached 48.30 % for pods plant number trait, follow by 42.49 % value for pod dry weight/ plant trait. The mean traits of 15 selected families in the third population from the F_4 generation were studied and shown in Table 6. Two-year pedigree selection gave a high response in the third population for the flowering date trait. This is very evident from three families No. (18.2.1, 50.3.1 and 50.2.2) that had an early flowering date (44.67, 44.57 and 44.39 days respectively) and earlier than 45 days. The third Population included three families (91.1.2, 91.2.2 and 100.2.4) that had the tallest plant means value (73, 75.38 and 71.53, respectively). The majority of families in the third population of F4 generation had means more than three branches plant number. Only three families (40.2.4, 51.1.5 and 58.1.6) had the lowest plant branches number with mean values of 2.20, 2.89, and 2.39, respectively. The widest pod width was found in two families (50.2.2 and 40.3.1) of the third population cm with a mean value of 1.52 and 1.49 cm, respectively.

The third population came first in pod width, followed by the first and then second populations, as averages for pod width trait. The highest family mean of pods plant number, dry pods/plant and plant dry seed yield in the third population was recorded for family 91.1.2 with mean values of 29.59, 35.06 and 27.87 g, respectively. All families in the third population of F_4 generation had seed set % higher than 90 % but no family had a mean value of 100% seed set %. Four families No. (24.3.1, 91.1.2, 91.2.2 and 110.1.2) had shellout % higher than the parent 1 "Sweet-1" (78.90 %). with a mean value of 80.70, 79.49, 79.91 and 79.28, respectively.

The genetic components in F_4 generation are differed than F3 generation in the three studied populations and ten traits. Heritability in broad sense estimated were much higher in F_4 than F_3 (Fig. 1 and 2) that refers to the selected families tend towards genetic stability and the influence of the environment on them is low. Similar finding found by El-Dakkak (2016a and b); Rashwan and El-Shaieny (2016); Jagadeesh *et al.* (2023); Pandey *et al.* (2023). The highest heritability values were found in population number three in F_3 and F_4 and for traits plant dry seed yield, dry pods weight/ plant and pod width. PCV and GCV values in F4 were close to each other, these also support the idea about the low effect of environment in this generation, El-Dakkak (2016b); Tasnim *et al.* (2022); Gudadinni *et al.* (2017); Patil and Lokesha (2018); Bedawy and Mohamed (2018) supported these results. Vinayaka *et al.* (2022); Bhardwaj *et al.* (2020); Jagadeesh *et al.* (2023) had high values for PCV and GCV higher than 20% for traits; flowering date, number of branches per plant, plant height, and seed yield which were, these results matching with PCV and GCV values which recorded for some traits in first and second studied population in F_4.

Table 1: Analysis of variance and genetic components for studied traits of F₃ populations.

Trait		Flowering date	Height of plant, cm	Plant branches number	Plant pods number	Length of pod, cm	Pod width, cm	Seed set %	Dry pods weight / plant, g	Plant dry seed yield, g	Shellout %
Population 1											
S.O. V	**DF**					Mean Square					
Replication	2	1.36 NS	33.62 *	0.35 NS	39.61 **	0.49 NS	0.002	0.27 NS	72.68 **	24.29 **	3.52 NS
Families	19	4.80**	77.71 **	0.90 **	33.63 **	0.78**	0.02 **	10.35 **	54.03 **	17.73 **	11.46 **
Error	38	0.85	7.75	0.20	4.22	0.21	0.002	3.23	8.08	3.93	3.17
Mean		39.68	42.83	2.36	16.05	9.00	1.11	92.97	20.04	14.6	70.52
PCV		3.69%	13.01%	27.85%	23.33%	7.00%	8.20%	2.55%	22.18%	20.10%	3.45%
GCV		2.87%	11.27%	20.45%	19.51%	4.84%	6.97%	1.66%	17.94%	14.76%	2.36%
Heritability		60.70%	75.05%	53.92%	69.91%	47.88%	72.28%	42.33%	65.46%	53.92%	46.60%
GA		1.8	8.6	0.7	5.4	0.6	0.1	2.1	6.5	3.2	2.3
GAM		4.61%	20.12%	30.94%	33.61%	6.90%	12.21%	2.22%	29.91%	22.33%	3.32%
Population 2											
S.O. V	**DF**					Mean Square					
Replication	2	1.67 NS	53.04 *	0.35 NS	0.74 NS	0.55 *	0.0006 NS	2.14 NS	0.38 NS	1.03 NS	4.08 NS
Families	16	7.11 **	80.99 **	1.17 **	20.98 **	1.02 **	0.01 **	13.19 **	22.14 **	13.19 **	39.82 **
Error	32	1.81	12.85	0.26	4.78	0.13	0.00	2.55	3.95	2.65	5.22

		47.72	48.17	3.46	15.28	10.66	1.04	95.31	20.31	15.14	74.86
Mean		47.72	48.17	3.46	15.28	10.66	1.04	95.31	20.31	15.14	74.86
PCV		3.93%	12.38%	21.67%	15.84%	6.12%	5.32%	2.59%	15.58%	16.74%	5.57%
GCV		2.77%	9.89%	15.89%	11.53%	5.11%	3.94%	1.98%	12.13%	12.64%	4.62%
Heritability		49.47%	63.87%	53.78%	53.05%	69.73%	54.86%	58.12%	60.56%	57.01%	68.82%
GA		1.9	7.8	0.8	3.5	0.9	0.1	3.0	3.9	2.9	5.8
GAM		4.01%	16.29%	24.01%	17.31%	8.79%	6.02%	3.10%	19.44%	19.66%	7.90%
Population 3											
S.O. V	**DF**					**Mean Square**					
Replication	2	5.92 NS	10.31 NS	0.41 NS	9.25 NS	0.90 **	0.004 NS	7.30 NS	6.06 NS	12.32 NS	20.10 **
Families	9	21.84 **	100.79**	3.32 **	60.84 **	0.46 **	0.01 **	6.55 *	120.5 **	84.97 **	17.78 **
Error	18	2.50	16.75	0.76	8.19	0.10	0.001	2.49	11.40	10.68	2.36
Mean		48.06	53.90	4.97	21.22	10.51	1.24	90.73	29.15	22.10	75.40
PCV		6.22%	12.41%	25.55%	23.91%	4.45%	4.84%	2.15%	23.71%	27.31%	3.53%
GCV		5.28%	9.82%	18.62%	19.74%	3.28%	3.98%	1.28%	20.69%	22.83%	2.85%
Heritability		72.02%	62.58%	53.08%	68.19%	54.34%	67.60%	35.29%	76.12%	69.87%	65.47%
GA		4.4	8.6	1.4	7.1	0.5	0.1	1.4	10.8	8.6	3.5
GAM		9.24%	16.00%	27.94%	33.58%	4.98%	6.75%	1.56%	37.18%	39.31%	4.76%

Where**, NS*** and ******: are non-significant, Significant and highly significant, respectively. **PCV** and **GCV:** are Phenotypic and Genotypic Coefficient of Variations. **GA**: Genetic Advance. **GAM**: Genetic Advance as percentage over Mean.

Table 2: Analysis of variance and genetic components for studied traits of F₄ populations.

Trait		**Flowering date**	**Height of plant, cm**	**Plant branches number**	**Plant pods number**	**Length of pod, cm**	**Pod width, cm**	**Seed set %**	**Dry pods weight / plant, g**	**Plant dry seed yield, g**	**Shellout %**
Population 1											
S.O. V	**DF**					**Mean Square**					
Replication	2	0.86 NS	41.86 **	0.008 NS	4.27 NS	0.06 NS	0.0007 NS	0.04 NS	9.90 NS	13.16 *	1.87 NS
Genotypes	24	13.27 **	69.59 **	0.79 **	15.37 **	1.84 **	0.06 **	15.23 **	48.80 **	30.45 **	19.84 **
Error	48	1.06	5.04	0.11	2.52	0.10	0.003	2.77	4.89	3.40	2.16
Mean		38.41	45.36	2.27	14.92	9.62	1.27	91.79	21.99	16.87	76.72
PCV		5.86%	11.39%	25.32%	17.58%	8.55%	11.23%	2.75%	19.96%	20.79%	3.67%
GCV		5.22%	10.25%	20.70%	13.96%	7.91%	10.48%	2.13%	17.28%	17.72%	3.14%
Heritability		79.30%	81.01%	66.81%	63.00%	85.57%	87.11%	59.97%	74.97%	72.62%	73.21%
GA		3.7	8.6	0.8	3.4	1.5	0.3	3.3	6.8	5.3	4.3
GAM		9.57%	19.00%	34.85%	22.82%	15.07%	20.15%	3.40%	30.82%	31.10%	5.54%
Population 2											
S.O. V	**DF**					**Mean Square**					
Replication	2	0.96 NS	5.10 NS	0.61 NS	10.26 *	0.21 NS	0.0003 NS	0.61 NS	24.69 *	16.02 *	0.02 NS
Genotypes	16	19.79 **	142.88 **	0.74 **	22.75 **	1.09 **	0.001 **	9.19 *	30.85 **	17.96 **	11.01 **
Error	32	1.24	8.97	0.24	2.36	0.09	0.001	3.59	4.92	3.72	2.50
Mean		47.74	52.12	3.33	17.36	11.39	1.03	95.69	21.11	15.78	74.64
PCV		5.66%	14.05%	19.07%	17.43%	5.72%	5.81%	2.44%	17.45%	18.54%	3.07%
GCV		5.17%	12.82%	12.27%	15.02%	5.06%	4.50%	1.43%	13.93%	13.88%	2.24%
Heritability		83.32%	83.27%	41.42%	74.26%	78.14%	60.13%	34.22%	63.73%	56.06%	53.17%
GA		4.7	12.6	0.5	4.6	1.0	0.1	1.6	4.8	3.4	2.5
GAM		9.72%	24.10%	16.27%	26.67%	9.21%	7.20%	1.72%	22.90%	21.42%	3.36%
Population 3											
S.O. V	**DF**					**Mean Square**					
Replication	2	0.05 NS	19.41 NS	0.02 NS	28.24 **	0.03 NS	0.0006 NS	5.76 NS	15.31 NS	13.81 *	2.47 NS
Genotypes	14	14.41 **	231.3 **	0.69 **	71.96 **	0.87 **	0.02 **	9.26 **	85 **	47.62 **	30.25 **
Error	28	1.06	9.24	0.09	4.34	0.07	0.001	2.18	5.11	3.41	1.73
Mean		46.93	60.33	3.27	18.54	10.18	1.40	93.76	22.92	17.20	74.59
PCV		4.94%	15.13%	16.46%	27.96%	5.70%	5.50%	2.27%	24.59%	25.36%	4.53%
GCV		4.44%	14.26%	13.58%	25.60%	5.07%	4.93%	1.64%	22.52%	22.85%	4.17%
Heritability		80.74%	88.90%	68.13%	83.87%	79.15%	80.51%	51.92%	83.89%	81.23%	84.61%
GA		3.9	16.7	0.8	9.0	0.9	0.1	2.3	9.7	7.1	5.8
GAM		8.21%	27.71%	23.10%	48.30%	9.29%	9.12%	2.43%	42.49%	42.43%	7.90%

Where**, NS*** and ******: are non-significant, Significant and highly significant, respectively. **δ²e, δ² g** and **δ²p**; are environment, genetic and phenotypic variances, respectively. **PCV** and **GCV**: are Phenotypic and Genotypic Coefficient of Variations. **GA**: Genetic Advance. **GAM**: Genetic Advance as percentage over Mean.
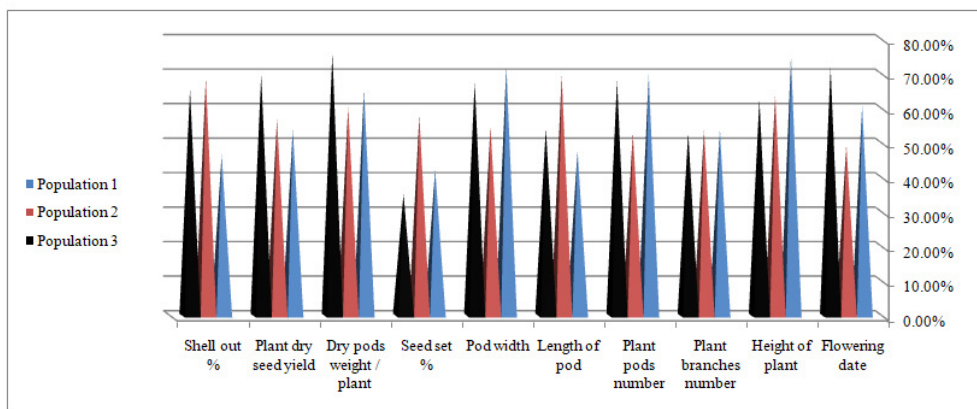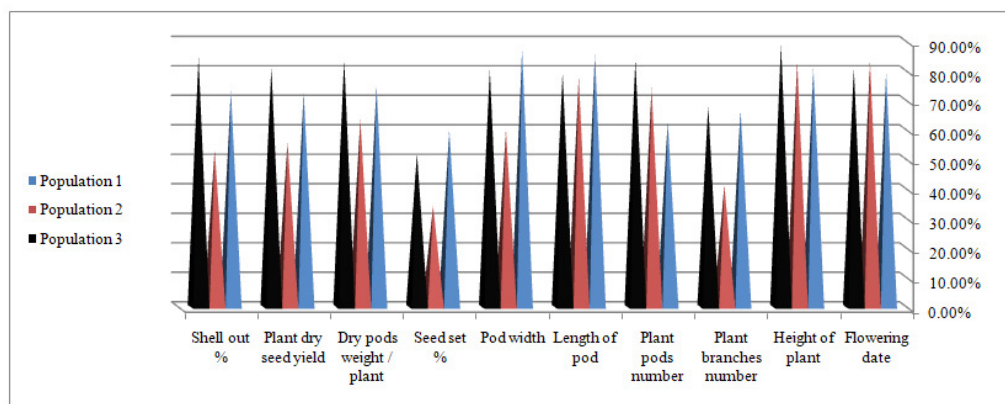
Fig. 1. Heritability estimates of the three populations for ten studied traits in F_3.

Fig. 2. Heritability estimates of the three populations for ten studied traits in F_4.

Table 3: Performance of F₃ families for the first population.

Family	Flowering date	Height of plant, cm	Branches plant number	Pods plant number	Length of pod, cm	Pod width, cm	Seed set %	Dry pods weight /plant, g	Plant dry seed yield, g	Shell out %
10	36.67	38.93	1.70	14.63	9.22	0.92	93.00	17.77	12.13	68.26
17	41.26	37.67	1.97	18.67	8.78	1.24	93.00	21.54	16.38	76.04
18	41.07	42.03	1.89	13.83	8.72	0.94	92.33	15.69	10.70	68.20
19	40.84	50.17	3.16	19.26	8.67	1.10	95.33	25.05	16.88	67.39
27	40.21	49.50	3.00	13.76	9.19	1.09	92.67	21.19	14.30	67.48
29	42.34	43.02	3.08	16.00	9.82	1.15	90.33	19.75	13.79	69.82
30	37.50	36.56	1.84	14.00	9.21	1.11	94.33	18.60	13.46	72.37
47	37.33	39.60	2.17	18.50	9.06	1.11	92.33	19.90	16.35	82.16
48	39.67	42.25	1.61	13.08	9.20	1.10	93.33	20.55	15.50	75.43
62	37.12	48.39	2.84	16.79	8.89	1.13	96.00	20.02	14.07	70.28
63	40.67	40.33	1.61	12.47	9.84	1.06	91.00	19.90	15.18	76.28
68	40.52	45.69	3.33	17.73	9.92	1.10	89.33	21.05	14.06	66.79
69	39.49	44.73	2.67	17.91	8.44	1.25	93.33	26.27	19.63	74.72
70	38.42	54.22	2.53	19.33	8.95	1.07	94.33	25.13	17.37	69.12
74	39.50	41.30	1.96	15.67	8.94	1.16	90.00	19.46	13.06	67.11

Family	Flowering date	Height of plant, cm	Branches plant number	Pods plant number	Length of pod, cm	Pod width, cm	Seed set%	Dry pods weight /plant, g	Plant dry seed yield, g	Shell out %
78	39.84	34.33	2.89	11.08	8.35	1.07	91.67	12.83	9.87	76.93
110	41.10	39.91	2.27	18.11	8.37	1.20	95.33	23.10	17.51	75.80
125	41.26	38.14	2.28	25.03	7.99	1.19	95.33	20.48	16.63	81.20
128	38.00	42.83	2.28	12.78	9.29	1.06	93.00	17.24	11.94	69.26
145	40.77	47.02	2.06	12.33	9.13	1.15	93.33	16.89	12.79	75.73
P₁ Cash	39	43.67	1.22	10	8.53	1.2	93.33	14.39	11.31	78.60
P₂ Sweet1	43	48.7	4	11.18	10.73	1.40	95	16.8	12.81	76.25
LSD5%	1.588	4.756	0.761	3.508	0.777	0.082	3.070	4.855	3.386	3.039

Table 4: Performance of F₃ families for Population 2 and 3.

Family	Flowering date	Height of plant, cm	Branches plant number	Pods plant number	Length of pod, cm	Pod width, cm	Seed set%	Dry pods weight /plant, g	Plant dry seed yield, g	Shell out %
					Population 2						
5	42.94	37.61	1.89	12.11	9.73	1.03	98.00	16.62	12.06	72.56
8	44.93	43.87	3.38	17.13	10.21	0.98	96.33	26.06	19.21	73.71
15	45.14	53.83	2.59	13.89	11.21	1.03	96.33	18.08	12.67	70.08
34	49.22	47.55	2.67	13.60	10.91	1.15	96.33	19.95	13.74	68.87
46	50.33	50.92	3.58	14.75	11.03	1.03	94.00	18.66	13.60	72.88
52	49.14	50.69	4.22	14.33	12.04	1.06	90.67	19.31	13.54	70.12
134	47.70	46.40	3.83	16.52	11.00	1.10	93.67	20.11	15.90	79.07
142	46.49	58.09	3.67	17.17	10.86	1.08	93.00	25.08	18.20	72.57
153	48.43	44.08	3.28	14.98	10.26	1.03	95.67	19.84	16.21	81.70
167	49.50	47.33	3.33	15.83	10.42	1.10	96.00	22.27	17.09	76.74
175	47.57	46.15	3.62	16.58	10.61	1.07	98.00	19.00	13.73	72.26
177	50.89	55.44	3.44	18.22	10.77	1.07	96.67	23.62	18.30	77.48
185	48.67	43.58	4.10	14.87	10.46	1.05	98.33	16.61	12.50	75.26
186	47.97	44.83	3.78	15.97	9.97	0.96	93.67	21.16	17.07	80.67
192	47.06	52.67	4.33	15.44	11.35	0.98	95.67	21.12	15.88	75.19
205	45.78	44.22	3.22	13.56	9.91	0.98	95.33	17.46	13.00	74.46
214	49.50	51.58	3.88	14.85	10.53	1.06	92.67	20.26	14.60	72.06
P1 Sweet 1	43	48.70	4.00	11.18	10.73	1.40	95	16.8	12.81	76.25
P2 Sweet 2	53	56.70	5.00	18.5	11.89	0.95	93	23.02	18.08	78.54
LSD5%	2.325	6.201	0.882	3.782	0.621	0.064	2.765	3.438	2.815	3.954
					Population 3						
18	43.33	50.25	3.00	13.83	10.33	1.25	91.67	19.27	13.78	71.51
24	47.07	52.00	4.07	20.80	10.54	1.26	90.00	28.71	20.32	70.78
40	47.23	60.41	4.35	20.84	10.81	1.18	91.67	33.03	26.06	78.90
50	44.13	53.04	5.67	23.75	10.54	1.24	88.00	30.87	22.50	72.89
51	48.92	54.94	4.90	23.82	9.81	1.27	92.00	33.31	22.63	67.94
58	47.88	47.33	6.83	29.65	10.67	1.21	93.00	35.65	30.19	84.68
74	49.57	57.64	5.54	23.05	11.01	1.35	90.33	35.29	28.72	81.38
91	51.17	65.40	4.83	21.61	10.58	1.28	91.67	32.64	24.75	75.83
100	48.25	47.67	4.77	15.07	9.94	1.17	92.00	18.66	14.08	75.46
110	50.80	50.30	5.70	19.80	10.90	1.23	92.67	24.04	17.94	74.63
P₁ Sweet1	43	48.70	4.00	11.18	10.73	1.40	95	16.8	12.81	76.25
P₂ Progresss	58	60.58	5.00	20.67	10.4	1.5	93.3	29.9	23.80	79.59
LSD5%	2.920	7.555	1.604	5.282	0.583	0.063	3.734	6.233	6.031	2.835

Table 5: Performance of F4 families for the first population.

Family	Flowering date	Height of plant, cm	Branches plant number	Pods plant number	Length of pod, cm	Pod width, cm	Seed set %	Dry pods weight /plant, g	Plant dry seed yield, g	Shellout %
10.1.3	36.64	43.85	2.76	13.88	10.65	1.16	96.67	24.18	19.17	79.28
17.2.1	39.44	39.25	2.50	14.79	9.33	1.42	90.00	22.77	16.91	74.26
17.2.2	40.44	58.37	1.89	17.11	9.35	1.35	94.00	26.66	19.52	73.22
18.1.1	38.67	45.00	2.50	16.28	9.47	1.04	97.00	20.60	15.83	76.84
19.1.1	39.05	46.18	2.13	16.33	9.55	1.07	98.67	21.61	16.13	74.64
19.2.3	37.94	52.12	2.70	19.12	8.28	1.17	96.33	32.06	25.28	78.85
27.1.1	36.72	46.72	2.39	17.88	10.39	1.12	93.67	27.21	20.64	75.85
29.1.1	43.17	51.27	2.73	16.56	10.80	1.25	93.00	23.92	18.86	78.85
29.1.2	43.23	43.60	2.89	16.47	10.72	1.16	94.67	24.29	18.74	77.15
30.2.5	37.17	44.61	2.11	16.33	8.94	1.23	96.67	20.87	17.37	83.23
47.1.2	35.67	44.33	2.83	12.83	10.32	1.20	97.00	21.03	17.13	81.46
48.1.1	39.38	48.44	1.67	17.33	10.08	1.49	92.00	23.94	17.49	73.06
62.1.1	37.58	48.13	1.96	15.07	8.96	1.21	97.33	22.60	16.42	72.65
63.1.2	39.42	49.83	2.50	13.58	10.83	1.00	98.00	22.53	16.98	75.37
68.1.3	37.50	39.61	2.28	11.28	9.23	1.33	96.67	14.99	11.59	77.32
68.1.4	36.83	47.83	1.83	13.83	9.41	1.37	92.67	17.95	13.91	77.49
69.1.1	38.50	43.42	2.62	13.89	9.00	1.36	98.00	23.74	18.64	78.52
70.1.4	35.70	46.48	2.30	13.47	10.57	1.43	96.00	25.19	19.85	78.80
74.3.1	35.76	39.90	1.88	11.09	8.47	1.28	97.00	17.16	13.43	78.26
74.3.4	36.56	40.33	3.00	16.67	9.66	1.36	97.33	23.30	16.21	69.57
78.1.3	38.18	38.55	2.57	14.08	9.73	1.28	95.67	20.95	16.33	77.95
110.1.2	39.62	42.84	2.06	12.16	9.37	1.42	93.00	17.39	13.68	78.67
125.1.2	42.28	40.39	1.72	11.17	8.47	1.42	96.67	14.32	10.74	75.00
128.1.2	37.42	42.28	1.65	14.75	9.23	1.15	95.67	17.56	13.32	75.85
145.1.5	37.47	50.68	2.20	17.08	9.66	1.44	95.33	23	17.47	75.96
P1 Cash	39.33	47.75	1.00	10	8.63	1.2	95	15.95	12.40	77.74
P2 Sweet1	42	46.02	2.00	12.33	10.24	1.48	95	17.82	14.06	78.90
LSD5%	1.736	3.782	0.564	2.672	0.527	0.086	2.803	3.723	3.106	2.474

Table 6: Performance of F4 families for the second population.

Family	Flowering date	Height of plant, cm	Branches plant number	Pods plant number	Length of pod, cm	Pod width, cm	Seed set %	Dry pods weight /plant, g	Plant dry seed yield, g	Shellout %
5.2.2	42.33	44.86	2.92	18.55	10.71	0.97	95.33	22.34	16.85	75.43
8.1.2	45.42	61.33	4.37	21.50	11.78	0.99	94.67	26.53	20.12	75.84
8.1.3	45.44	41.61	3.22	12.78	11.50	1.07	93.33	14.39	10.72	74.50
15.1.1	44.92	56.33	3.92	19.00	10.63	1.03	96.33	20.65	14.97	72.49
34.3.3	50.90	47.97	3.23	15.53	11.57	1.03	96.67	18.03	13.16	72.99
46.1.3	51.08	52.58	2.92	15.42	12.22	1.15	96.33	19.44	14.57	74.95
52.3.1	47.55	47.12	2.70	15.10	11.01	1.05	97.67	17.70	12.86	72.66
134.2.2	46.90	64.58	3.92	22.42	10.66	0.96	95.67	25.71	19.53	75.96
153.3.3	47.60	48.00	3.80	17.73	10.94	1.00	94.67	20.20	15.29	75.69
167.2.1	50.89	49.67	3.22	19.50	11.65	1.04	98.00	24.29	18.56	76.41
175.3.2	45.36	47.50	3.00	17.58	12.05	1.04	97.33	22.39	16.78	74.94
177.1.3	46.53	63.53	2.93	16.27	11.70	1.03	93.33	20.91	15.68	74.99
185.2.1	49.36	61.69	3.03	19.11	11.56	1.03	93.67	22.65	16.95	74.83
186.2.2	51.61	50.87	3.22	18.94	11.16	1.07	99.00	24.44	18.59	76.06
192.1.3	47.17	51.00	3.83	16.33	12.41	1.03	93.67	22.23	16.57	74.54
205.2.2	46.17	50.33	2.67	12.00	11.80	0.97	96.67	17.45	12.88	73.81
214.2.1	52.33	47.00	3.67	17.33	10.34	1.13	94.33	19.53	14.23	72.86
P1 Sweet1	42	46.02	2.00	12.33	10.24	1.48	95	17.82	14.06	78.90
P2 Sweet2	50	51	4.33	18.25	11.88	0.98	94	22.08	17.50	79.25
LSD5%	1.925	5.180	0.840	2.656	0.527	0.066	3.276	3.837	3.337	2.735

Table 7: Performance of F₄ families for the third population.

Family	Flowering date	Height of plant, cm	Branches plant number	Pods plant number	Length of pod, cm	Pod width, cm	Seed set %	Dry pods weight /plant, g	Plant dry seed yield, g	Shell out %
18.2.1	44.67	57.83	3.25	17.58	10.02	1.33	97.33	21.19	16.65	78.57
24.3.1	47.75	53.86	3.72	16.36	9.64	1.40	94.33	20.41	16.47	80.70
40.3.1	46.80	48.07	3.40	14.73	9.20	1.49	96.67	19.91	13.77	69.16
40.2.4	48.08	57.92	2.20	12.45	9.77	1.45	94.33	17.63	12.98	73.62
50.3.1	44.57	53.93	3.55	13.27	10.46	1.36	90.67	16.24	11.50	70.81
50.2.2	44.39	57.00	3.17	13.03	10.58	1.52	92.33	16.30	11.67	71.60
51.1.5	46.00	54.88	2.89	15.78	10.83	1.44	92.67	19.22	13.48	70.14
51.2.3	47.14	50.05	3.06	17.53	9.89	1.42	92.67	21.25	15.73	74.02
58.1.6	46.72	61.51	2.39	19.44	10.78	1.30	93.00	25.54	18.24	71.42
58.2.4	46.89	53.39	3.22	16.94	10.47	1.32	93.00	21.27	16.13	75.83
74.1.3	49.10	68.13	3.47	20.47	10.70	1.29	94.33	25.14	17.29	68.77
91.1.2	46.28	73.00	3.61	29.59	9.36	1.47	93.33	35.06	27.87	79.49
91.2.2	46.80	75.38	3.68	22.04	10.12	1.38	93.67	28.42	22.71	79.91
100.2.4	48.13	71.53	3.67	24.67	10.86	1.39	95.67	27.97	21.12	75.51
110.1.2	50.67	68.40	3.81	24.27	10.07	1.45	92.33	28.18	22.34	79.28
P₁ Sweet1	42	46.02	2.00	12.33	10.24	1.48	95	17.82	14.06	78.90
P₂ Progresss	56.21	61.5	4	22	10.4	1.45	93.3	26.74	21.6	80.77
LSD5%	1.803	5.322	0.532	3.645	0.464	0.059	2.587	3.958	3.231	2.301

CONCLUSIONS

Families in the third population of F4 generation were ranked the first population in traits height of plant, branches plant number, pods plant number, dry pod weight/plant and plant dry seed yield followed by families in the first population of F4 generation. Additionally, families in the third populations of F₄ generation were ranked the second population in traits seed set % and pod length followed by the families in the third population.

FUTURE SCOPE

Continuing selection process in the next generations will help in obtaining high-yielding and early-flowering peas lines from the superior families. This will facilitate development of breeding programs in the future.

Conflict of Interest. None.

REFERENCES

Akhilesh, S., Meenakshi, S., Ashwini, R. and Yudhvir S. (2007). Genetic variability and association studies for green pod yield and component horticultural traits in garden pea under high hill dry temperate conditions. *Ind. J. Hort, 64,* 349-354.

Ban, S. J., Jagtap, V. S., Ghorpade, S. B. and Ghatul, I. D. (2019). Genetic variability studies in pea (*Pisum sativum* L.). *International Journal of Chemical Studies, 7*(5), 1975-1978.

Bedawy, I. M. A. and Mohamed, N. E. (2018). Phenotypic and genotypic variability in a set of sesame (*Sesamum indicum* L.) genotypes. *Egypt. J. Agron, 40* (3), 193 - 205.

Bhardwaj, A., Sharma, A. and Lata, H. (2020). Genetic variability for pod yield and related traits in garden pea (*Pisum sativum* L.). *Electronic Journal of Plant Breeding, 11*(4), 1233-1238.

Chauhan, A., Sharma, A., Sharma, P., Katoch, V., Chadha, S. and Kumari, V. (2023). Genetic variability for pod yield and component traits in Sugar Snaps (*Pisum sativum* var. *saccharatum*). *Legume Research, 46*(5), 548-554.

El-Dakkak, A. A. A. (2016 a). Genetic improvement for yield and quality characters in Pea by using selection. *J. Plant Production, Mansoura Univ., 7*(8), 837 – 842.

El-Dakkak, A. A. A. (2016 b). Inheritance of seeds color and some economic characters in Pea (*Pisum sativum* L.). *J. Plant Production, Mansoura Univ., 7*(8), 829 – 835.

Falconer, D. S. (1985). Introduction to Quantitative Genetics (Hong Kong: Longman Science & Technical).

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. Curr. Microbiol. App. Sci, 6*(8), 2384-2391.

Harmankaya, M.,Özcan, M. M., Karada, S. S. and Ceyhan, E. (2010). Protein and mineral contents of pea (*Pisum sativum* L.) genotypes grown in central Anatolian

region of Turkey. South West. *J. Hortic. Biol. Environ, 1*, 159–165.

Jagadeesh, K., Mahto, C. S. and Kumar, N. (2023). Genetic variability studies in field pea (*Pisum sativum* L.) for yield and associated characters. *Environment Conservation Journal 24,* (2), 244-249.

Kalloo, G., Rai, M., Singh, J., Verma, M., Kumar, R. and Rai, G. K. Vishwanath (2005). Morphological and biochemical variability in pea (*Pisum sativum* L.). *Veg. Sci, 32,* 19-23.

Kumar, D., Malik, S., Singh, S. K. and Kumar, M. (2013). Genetic variability, heritability and genetic advance for seed yield and yield components in garden pea (*Pisum sativum* L.). *Vegetos-An Inter. J. Pt. Res, 26* (1), 182-184.

Lam, A. C. Y., Can Karaca, A., Tyler, R. T. and Nickerson, M. T. (2018). Pea protein isolates: Structure, extraction, and functionality. *Food Rev. Int, 34,* 126–147.

Pandey, P., Singh K. P., Tripathi, H., Singh, H. C., Saini, P. K. Rajiv, Singh, L. and Singh, P. K. (2023). Genetic variability and selection parameters for green pod yield in table Pea (*Pisum sativum* L. var. hortense).

Biological Forum – An International Journal, 15(4), 829-833.

Patil, M. K. and Lokesha, R. (2018). Estimation of genetic variability, heritability, genetic advance, correlations and path analysis in advanced mutant breeding lines of sesame (*Sesamum indicum* L.). *J. Pharmacog. Nat. Prod,* (4)1, 100-151.

Rashwan A. M. A. and El-Shaieny A. A. H. (2016). Pedigree selection in pea (*Pisum sativum* L.). *International Journal of Advanced Research, 4* (7), 1366-1371.

SAS Institute (2008) The SAS system for Windows, release 9.2. SAS Institute, Cary, N.C. USA.

Tasnim, S., Poly, N. Y., Jahan, N. and Khan, A. U. (2022). Relationship of quantitative traits in different morphological characters of pea (*Pisum sativum* L.) *Journal of Multidisciplinary Applied Natural Science, 2* (2), 103-114.

Vinayaka, N. G. R., Vilas, D. Gasti, K. H.,Yashavanthkumar, N., Thammaiah, M. H. Tatagar and Vijayakumar Rathod (2022). Variability, heritability and genetic advance among Garden Pea (*Pisum sativum* L.) genotypes at both genotypic and phenotypic levels. *Biological Forum – An International Journal, 14*(4), 572-578.