# CHARACTER ASSOCIATION AND MULTI VARIATE ANALYSIS IN PEA ( *Pisum sativum* L.)

**UMMA SABIHA TASNIM ARIN**


**DEPARTMENT OF GENETICS AND PLANT BREEDING**
**SHER-E-BANGLA AGRICULTURAL UNIVERSITY**
**DHAKA- 1207**

**DECEMBER, 2014**

# CHARACTER ASSOCIATION AND MULTI VARIATE ANALYSIS IN PEA ( *Pisum sativum* L.)

**BY**

**UMMA SABIHA TASNIM ARIN**

**REGISTRATION NO. 08-03138**

**A Thesis**

submitted to the Dept. of Genetics & Plant Breeding , Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka-1207
in partial fulfillment of the requirements
for the degree of

**MASTER OF SCIENCE**
**IN**
**GENETICS AND PLANT BREEDING**

**SEMESTER: JULY-DECEMBER, 2014**

**Approved by:**

| | |
|---|---|
| **Professor Dr. Firoz Mahmud** | **Professor Dr. Md. Sarowar Hossain** |
| **Supervisor** | **Co-Supervisor** |

**Professor Dr. Md. Sarwar Hossain**
Chairman
Examination Committee

*Dr. Firoz Mahmud*
*Professor*
*Department Genetics and Plant Breeding*
*Sher-E-Bangla Agricultural University*
*Dhaka-1207, Bangladesh*

*Mob: +8801552432589*
*E-mail: fmahmud08@gmail.com*

## *CERTIFICATE*

*This is to certify that thesis entitled, "**CHARACTER ASSOCIATION AND MULTI VARIATE ANALYSIS IN PEA (Pisum sativum L.)** submitted to the Faculty of Agriculture, Sher-E-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,** embodies the result of a piece of bona fide research work carried out by **UMMA SABIHA TASNIM ARIN**, Registration No. **08-03138** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

*I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged*

.

***Dated: December, 2014***
***Place: Dhaka, Bangladesh***

***(Professor Dr. Firoz Mahmud)***
***Supervisor***

## *ACKNOWLEDGEMENTS*

*All praises and kind full trust on to the Almighty Allah for His never-ending blessing. It is a great pleasure to express profound thankfulness to her respected parents, who entitled much hardship inspiring for prosecuting her studies, thereby receiving proper education.*

*The author would to express her earnest respect, sincere appreciation and enormous indebtedness to her reverend supervisor, Prof. Dr. Firoz Mahmud, Department of Genetics and Plant Breeding, Sher-E-Bangla Agricultural University, Dhaka for his scholastic supervision, helpful commentary and unvarying inspiration throughout the research work and preparation of the thesis.*

*The author wishes to express her gratitude and best regards to her respected Co- supervisor, Prof. Dr. Mr. Sarowar Hossain, Chairman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his continuous direction, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis.*

*The author is also highly grateful to her honorable teachers Prof. Dr. Md. Shahidur Rashid Bhuiyan, Prof. Dr. Naheed Zeba, Department of Genetics Plant Breeding, Sher-E-Bangla Agricultural university, for their valuable teaching, direct and indirect advice and encouragement and cooperation during the whole study period.*

*The author feels to expresses her heartfelt thanks to other teachers of the Department of Genetics and Plant Breeding, Sher-E-Bangla Agricultural University, Dhaka for their valuable suggestions and encouragement during the period of her study.*

*The author thanks to her husband Dr. A M Anisul Islam for his help and inspiration in preparing of this thesis.*

*The author founds no words to thanks her parents, her two sisters Sadia Arefin Lupin and Saira Tahsad Polin for their unquantifiable love and continuous supports, their sacrifice never ending affection, immense strength and untiring efforts for bringing her dream to proper shape. They were constant source of inspiration, zeal and enthusiasm in the critical moment of her studies.*

*Dated December, 2014* *The Author*

# CHARACTER ASSOCIATION AND MULTI VARIATE ANALYSIS IN PEA (*Pisum sativum* L.)

**By**
**UMMA SABIHA TASNIM ARIN**

ABSTRACT

A field experiment was conducted during December 2013 to March 2014 to study the genetic variability, correlation, path coefficient analysis and genetic diversity for quantitative traits in pea (*Pisum sativum* L.) with forty five genotypes in randomized complete block design with three replications. The genotypes were sowing in a field experiment conducted at the research farm of Sher-E-Bangla Agricultural University, Dhaka. Analysis of variance for each trait showed significant differences among the genotypes. Phenotypic coefficients of variation (PCV) was also close to genotypic coefficients of variation (GCV) for all the characters except branches per plant, number of nodes per plant, pods per plant, seeds per pod and seed yield per plant indicating that environment had influence on the expression of these characters. High heritability associated with high genetic advance percent of mean was observed for pod length and hundred seed weight which indicated that selection for these characters would be effective. Seed yield per plant had highly significant positive genotypic and phenotypic association with pod length, hundred seed weight, pods per plant, and seeds per plant, revealing that selection based on these traits would ultimately improve the seed yield. Path coefficient analysis revealed that seeds per plant and hundred seed weight had the highest positive direct effect on seed. Hence, thrust has to be given for these characters in future breeding program to improve the yield in pea. Multivariate analysis based on 11 agronomic characters indicated that the forty five genotypes were grouped into five distant clusters. The maximum contribution of characters towards diversity was observed by days of 50% flowering, plant height and branches per plant. Thus, these traits may be given high emphasis while selecting the lines for hybridization. The inter cluster distance was maximum between cluster II and cluster V. The highest intra-cluster distance was found in cluster II. From the results it can be concluded that the following genotypes viz., BD-4142 (G7), BD-4243 (G8), BD-4141 (G6) and BD- 4145(G10) were identified as potential genotypes for higher seed yield in pea.

## TABLE OF CONTENTS

**TABLE OF CONTENTS (Cont'd.)**

**TABLE OF CONTENTS (Cont'd.)**

**TABLE OF CONTENTS (Cont'd.)**

**TABLE OF CONTENTS (Cont'd.)**

## TABLE OF TABLES

## LIST OF FIGURES



## LIST OF PLATS

## LIST OF APPENDICES

## LIST OF ABBREVIATED TERMS

| **Abbreviations** | **Full word** |
|---|---|
| AEZ | Agro-Ecological Zone |
| *et al.* | And others |
| ACC | Accessions |
| BARI | Bangladesh Agricultural Research Institute |
| BBS | Bangladesh Bureau of Statistics |
| Cm | Centimeter |
| CV | Co-efficient of Variation |
| etc. | Etcetera |
| Fig. | Figure |
| G | Genotype |
| GA | Genetic Advance |
| GCV | Genotypic Co-efficient of Variation |
| $\delta^2_g$ | Genotypic Variance |
| G | Gram |
| $h^2b$ | Heritability in broad sense |
| J. | Journal |
| Kg | Kilogram |
| M | Meter |

| | |
|---|---|
| MSS | Mean Sum of Square |
| Mm | Millimeter |
| MP | Muriate of Potash |
| No. | Number |
| % | Percent |
| PCV | Phenotypic Co-efficient of Variation |
| $\delta^2_p$ | Phenotypic variance |
| RCBD | Randomized Complete Block Design |
| R | Replication |
| Res. | Research |
| SAU | Sher-E-Bangla Agricultural University |
| SE | Standard Error |
| $m^2$ | Square meter |
| TSP | Triple Super Phosphate |

# CHAPTER I
# INTRODUCTION

The Pea *(Pisum sativum* L.*)* is a spreading, glabrous, herbaceous annual self pollinated grain legume. It is under subfamily Papilionaceae belonging to the family Leguminosae. Its chromosome number is 2n=2x=14. It is a very common nutritious vegetable grown in the cool season throughout the world. It can be grown in tropical areas at high altitudes of up to 2700m, and during cold winter months in the subtropics. The crop is reported to perform better in subtropical areas having a cold winter of five months duration. The major green pea producing countries of the world are India, China, USA, France, UK, Egypt, Hungary, Italy, Pakistan, Japan and Thailand. Now Bangladesh is producing a good amount of Peas. In Bangladesh Pea has great demand throughout the year but is available and cheaper during the winter season. In Bangladesh it is cultivated as winter vegetable. The major pea producing districts are Faridpur, Jessore, Kushtia, Rajshahi, Commilla and Pabna. The total area of pea cultivation is gradually decreased in which occupies on area of 15779 ha of land (2010-11) 16054 ha of land (2011-12) and 14928 ha of land (2012-13), respectively (BBS. 2013). Thus the average production of Pea was 6149 metric tons (2010-11) 6153 metric tons (2011-12) and 5721 metric tons (2012-13, respectively (BBS, 2013). The average yield being 766 kg/ha. Pea is highly nutritive containing high percentage of digestible protein along with carbohydrates and vitamins. It is also very rich in minerals. It is an excellent food for human consumption, taken either as a vegetable or in soup. Large proportion of peas are processed (canned, frozen or dehydrated) for consumption in the off season. Pea straw is a nutritious fodder. Due to rich in protein it is very valuable for the vegetarians.

Now a day the average production of field pea in Bangladesh has been drastically reduced due to introduction of HYV rice and wheat. Thus the scope of its production as field crop has already been limited. On the other hand there is a shortage of off-season vegetable in our country. Green pea can be considered as vegetable crop as it need smaller area of land and can also be grown without competition with cereal crops. Under frozen condition we can make the vegetable available throughout the year. Thus protein and vegetable deficiency can be overcome by developing high yielding vegetable pea in Bangladesh. Compared to other grain crops no attempt has

been made to develop improved cultivars of vegetable pea in this country. Moreover, the quality of green pea as vegetable depends largely on sugar contents in seed. So efforts should be given to develop high yielding vegetable pea having vegetable quality through hybridization.

Considering the potentiality of this crop, there is a need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific end use. A thorough knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement programme. With limited variability much can not be achieved and the breeder will have to enrich the germplasm or he can resort to create greater variability through hybridization, mutation and polyploidy breeding.

The phenotypic expression of the plant characters is mainly controlled by the genetic makeup of the plant and the environment, in which it is growing. Further, the genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epitasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. Further, genetic advance can be used to predict the efficiency of selection.

Yield is a complex character controlled by a large number of contributing characters and their interactions. A study of correlation between different quantitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield components. For any effective selection programme, it would be desirable to consider the relative magnitude of association of various characters with yield. The path coefficient technique developed by Wright (1921) helps in estimating direct and indirect contribution of various components in building up the total correlation towards yield. On the basis of these studies the quantum importance of individual characters is marked to facilitate the selection programme for better yield.

Commercial $F_1$ hybrids are common in pea and selection of new parents for high heterosis is a continuous process. Generally diverse plants are expected to give high hybrid vigor (Flarrington, 1940), Hence, it necessitates the study of genetic divergence among the existing varieties and germplasm collection for identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme. $D^2$ statistics developed by Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes under comparison. It considers the variation produced by any character and their consequent effect that it bears on other characters. The technique was first used by Mahalanobis in an anthropometric survey.

This technique has been applied in several crops to select genotypes for further breeding programmes. Grouping of genotypes based on $D^2$ analysis will be useful in choosing suitable parental lines for heterosis breeding. Such studies are also useful in selection of parents for hybridization to recover superior transgressive segregants and it can further result into release of improved open pollinated varieties for commercial cultivation.

Therefore, the present investigation on "Character Association and Multi Variate Analysis In Pea ( *Pisum sativum* L.)" was under taken involving popular varieties and freshly developed lines with the following objectives:

1. To asses genetic diversity among the genotypes,
2. To identify divergent parents for hybridization programme and
3. To know the association of traits with yield and yield contributing traits.

# CHAPTER II
# REVIEW OF LITERATURE

The Pea (*Pisum sativum* L.) is an annual herbaceous legume belonging to the family papilionaceae. The present research work has aimed to study the variability, heritability, genetic advance, genetic divergence, inter-relationship among different yield contributing characters and path analysis. Different workers in different institutes of the world have already performed related works. Some of the most relevant literatures are cited here on objective basis.

## 2.1 Variability, heritability and genetic advance

Genetic variability, heritability and genetic advance for 11 characters in 46 varieties of Pea (*Pisum sativum* L.) were studied. Wide range of variation exhibited for plant height, days to flowering, number of pods per plant, grain yield per plant, days to maturity and harvest index. Significant differences for all the characters except number of primary branches and highest GV and PCV was recorded, for grain yield per plant followed by number of pods per plant, number of seeds per pod and 100-grain weight. Heritability coupled with genetic advance was highest for grain yield per plant followed by number of seeds per pod, number of pods per plant, 100-grain weight and harvest index while genetic advance was maximum for grain yield per plant (Bhupendra, 2008).

Thirty-one advanced lines and 6 cultivars (control) of pea were studied for genetic variability, heritability, genetic advance for seed yield per plant and related attributes by Singh and Singh (2006). Variability was greatest for seed yield per plant, followed by number of pods per plant, plant height, number of branches per plant, and 100-seed weight. Estimates of heritability in the broad sense were high for all characters except number of days to flowering and pod length. High expected genetic advance coupled with high heritability estimates were predicted for seed yield per plant, number of pods per plant, and plant height, indicating the low variation due to the environment.

Gupta *et al*., (2006) studied on genetic variability and heritability for 18 yield characters in 83 indigenous and exotic genotypes of garden pea. Analysis of variance revealed highly significant differences for all characters studied. Coefficient of

variation ranged from 2.44% (days to seed maturity) to 16.93% (number of green pods per plant). Both phenotypic and genotypic coefficients of variation were highest for green pod yield. Heritability ranged from 36.05% for total soluble solids to 99.16% for early yield per plant. Genetic advance was highest for green pod yield per plant. High heritability coupled with high genetic advance was observed for days to first flowering nodes, plant height, number of first flowering nodes, dry matter weight per plant, green pod yield per plant and number of primary branches per plant, indicating the preponderance of additive gene effects and the potential of selection for these characters to improve garden pea yield.

Singh and Mir (2005) carried out an experiment on pea to assess the mean, variability, heritability and genetic advance among 18 pea genotypes. Of the 18 genotypes, VL-7 (17.59 q/ha), recorded highest seed yield followed by Arkel (16.33 q/ha), Azad-P-3 (16.33 q/ha) and Azad-P-1 (15.72 q/ha). High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for the number of branches per plant, number of pods per plant, seed yield (q/ha) and average seed yield per plot. High heritability was observed for seed yield (q/ha), average seed yield per plot, number of pods per plant and days to 50% flowering. When heritability and genetic gain were considered together, seed yield (q/ha), average seed yield per plot and number of pods per plant recorded the highest values; however, the number of branches per plant, pod length, plant height and pod diameter recorded moderate heritability with higher genetic gain.

A study was conducted to evaluate the extent of genetic variability in 53 diverse pea genotypes by Seema *et al*., (2005). Analysis of variance for all traits indicated significant differences among the genotypes. A wide range of variability for pod yield per plant (42.99-100.78 g) and plant height (42.83-131.23 cm) along with high estimates of phenotypic and genotypic coefficients of variation (PCV and GCV, respectively) indicated that these characters would respond to selection. However, low PCV and GCV were recorded for pod length and total soluble solids. A small difference between PCV and GCV was observed for node at which the first flower appear followed by the number of grains per pod and pod width, which indicated that these characters were least influenced by the environment. A high heritability along with high genetic gain for node at which first flower appears and the number of grains

per pod indicated an additive gene action, which suggested that selection may be effective for these traits.

Chaudhary and Sharma (2003) investigated genetic variation and correlation for yield and yield components i.e. number of days to first flowering, first flowering node, days to 50% flowering, days to first green pod harvest, pod length, number of grains per pod, pod yield per plant, plant height, shelling percentage, and 1000-seed weight in garden pea. Significant genetic variation observed among the F1 hybrids for all the characters. Plant height, number of pods per plant and first flowering node recorded the greatest phenotypic coefficient of variation. The estimates of heritability were the highest for plant height. Plant height and pod yield exhibited the greatest genetic gain. High heritability coupled with high genetic advance was observed for pod yield per plant, plant height, number of pods per plant and 1000-seed weight.

Sharma *et al.,* (2003) studied sixty-three genotypes of pea (*Pisum sativum* L) including indigenous and exotic cultivars for variability parameters and character association. All characters exhibited significant variability. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for seed yield per plant, followed by pods per plant and biological yield per plant. High heritability was observed for all characters, except for days to maturity.

Kumar and Jam (2003) conducted a field experiment during 1995 and 1996 in Ranchi, Bihar, India, to determine the variability, heritability, and genetic advance of 36 pea cultivars. The genotypic coefficient of variation was high for pod yield per plot, plant height, number of primary branches and pod weight. The highest phenotypic coefficient of variation was observed for grain yield per plot. The heritability estimates was highest for plant height. The genetic advance as percent of mean was highest for grain yield per plot.

Genetic variation analyses for 9 traits were conducted using 29 pea cultivars during the rabi season of 1997/98 by Pathak and Jamwal (2002). High heritability, coupled with high genetic advance (GA) and genotypic coefficient of variation (GCV), was recorded for pod yield per plant. Moderate GA along with moderate to high GCV were recorded for number of days to 50% flowering and plant height, indicating the role of additive gene action for the inheritance of these characters. High heritability

with low GA and GCV for number of days to first picking, pod length and average pod weight, and high heritability with low GA and high GCV for ascorbic acid content and number of plants per plant may be attributed to non-additive gene actions.

Tiwari *et al*., (2001) investigated thirty-four diverge genotypes of pea (*Pisum sativum* L.) for genetic variation, heritability, genetic advance, correlation. The highest variability was observed for seed yield per plant, number of pods per plant, plant height and number of primary branches per plant. Low to very high heritability coupled with low to moderate genetic advance was observed for most of the characters, indicating little scope for the selection of these characters due to the non-additive gene action.

Twenty four advanced lines with one check of field pea were assessed for variability for yield and its attributes in Keonjhar, Orissa, India, during 1993-94 by Mahanta *et al*., (2001) and revealed that DPFPD 8 was the highest yielder followed by KFPD 59 having moderately susceptibility to powdery mildew [Erysiphe pisi]. Similarity in phenotypic coefficient of variation and genotypic coefficient of variation of all traits showed low environmental influence. High heritability estimates were recorded for all characters. High heritability coupled with high genetic advance observed for yield/plant, pods/plant, plant height, seeds/pod and 100 seed weight indicate additive gene effect.

Seventy-three pea cultivars belonging to different eco-geographical regions of India were evaluated for genetic variability, heritability and genetic advance with respect to 13 quantitative and 2 qualitative traits by Shinde (2000). Significant differences were observed for all the characters among the genotypes. The results revealed that the characters weight of pod, yield/ha and yield/plant had high heritability values coupled with high percentage of genetic advance indicating additive gene effects and greater scope for selection.

Genetic variability, heritability and genetic advance were studied in a collection of 30 indigenous and exotic genotypes of garden pea. The experiment was conducted in India. During the rabi season of 1997-98. Considerable genetic variability for pod yield and its component characters were observed. High heritability in association with high genetic advance observed for plant height, length of internodes, pod

yield/plant, number of pods/plant, seed yield/plant, number of primary branches and 100-seed weight, indicating additive gene effects and emphasized the effectiveness of selection for these traits to improve economic yield (Sureja and Sharma, 2000).

Abdou *et al*., (1999) estimate heritability of four diverse pea (*Pisum sativum* L.) genotypes on growth and yield related traits and suggested that environmental influences had only a minor role in determining variability among cultivars. Expected selection gain for green pod yield was high (68%). It is suggested that days to harvesting of marketable green pods could be reduced by 25%. Pod length and number of pods per plant may be used as preliminary selection criteria for green pod yield. However, green pod yield was suggested to be the most efficient criterion for top score of cultivar productively. Records on stem length and pod filling should be considered independently in selecting among elite genotypes. An opportunity exists to obtain cultivars combining earliness and high pod yields.

Vikas and Singh (1999) evaluated six pea crosses and their parents for variability. High estimates of genotypic and phenotypic coefficients of variation, heritability and genetic advance were recorded for plant height, pods per plant, seed yield per plant and biological yield in most of the crosses. Phenotypic correlations were estimated in parents and each cross separately for seed yield and its component characters.

Devendra *et al*., (1998) assessed genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, genetic advance and correlations from 11 yield related traits in 31 tall genotypes of pea (*Pisum sativum* L.). There were significant differences among the genotypes for all characters studied. Significant differences were also observed when analysis was carried out separately on tall and dwarf genotypes. Genotypic and phenotypic coefficients of variation, heritability and genetic advance were higher in the traits plant height, biological, seed yield, number of pods per plant and partitioning index.

Gupta *et al*. (1998) estimated heritability and genetic advance is derived from data on seven yield related traits in 40 pea genotypes. Result show that the phenotypic correlation was lower than its genotypic counterpart for most of the characters. Days to 50% flowering, pod weight per plant, 100-seed weight and protein content exhibited high estimates of heritability.

## 2.2 Correlation coefficient

Association studies indicated that pods per plant, clusters per plant, seeds per pod and days to 50% flowering were significantly correlated with grain yield (Inderjit *et al*., 2007).

The present investigations were conducted on 35 advance generation lines of pea. Highly significant and positive correlation was observed between green pod yield per plant and number of pods per plant, number of seeds per pod, total phenol content, pod length, crude protein content, days taken to flower initiation, number of branches and shelling percentage, suggesting that these are the major yield contributing characters (Harpreet *et al*., 2007).

Correlation studies showed that the pod yield was significant positive correlated with pods per plant and hundred seed weight (Avc and Ceyhan, 2006).

Seed yield per plant had significant and positive association with number of pods per plant, plant height, harvest index, and number of grains per pod (Singh and Singh, 2006).

Singh and Yadav (2005) estimated correlation between seed yield and yield contributing characters for 18 genotypes of peas. Seed yield had strong positive genotypic and phenotypic correlation with number of pods per plant, number of branches per plant, number of seeds per pod, pod length and pod diameter. The number of days to 50% flowering exhibited significant negative genotypic and phenotypic correlation with seed yield, number of pods per plant, and number of branches per plant.

Mohan *et al*., (2005) studied in thirty-nine advance generation lines of garden pea, grown in Ludhiana, Punjab, India, were subjected to correlation at both phenotypic and genotypic levels. It revealed that fruit yield per plant was positively correlated with number of pods per plant, number of seeds per pod, shelling percentage and number of days taken from sowing to marketable maturity.

Seema *et al*., (2005) reported on correlation of 10 characters in 53 genetically diverse pea genotypes were conducted during winter 1998/99 in India. Significant differences

were observed for all the characters under study. Green pod yield had significant and positive association with number of green pods per plant, number of grains per pod, shelling percentage and pod length.

Mahak *et al*., (2004) stidied the character association in field pea for estimation of phenotypic, genotypic and environmental correlation coefficients. In general, the estimated value of genotypic correlation coefficients was higher in magnitude than that of phenotypic correlation coefficients. The nature and magnitude of relationship between yield and yield contributing characters and among the characters themselves were also determined. Grain yield per plant exhibited significant and positive association with length of pod, number of pods per plant, number of seeds per pod, number of branches per plant, 100-grain weight and harvest Index. The characters days to maturity, length of pod, number of pods per plant, number of seeds per pod, number of branches per plant, 100-grain weight and harvest index were the major yield-contributing characters in field pea.

Satyawan *et al*., (2004) were estimated correlation in 36 elite genotypes of pea. Grain yield was significantly and positively correlated with number of nodes, height at which the first pod appears, plant height, number of primary branches per plant, pod length, and 100 seed weight. These characters were also positively correlated with each other.

The genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Pod yield per plant showed positive phenotypic correlation with pod length, number of grains per pod, number of pods per plant and shelling percentage described by Chaudhary and Sharma (2003).

Kumar and Jam (2003) studied on correlation for yield and yield components of pea. The genotypic correlation was greater than the corresponding phenotypic correlation. Yield per plant was positively associated with number of pods per plant, number of primary branches per plant, plant height, pod length and number of seeds. Per pod at the genotypic level. The Number of days to flowering showed a positive association with number of days to maturity and number of seeds per pod. Plant height showed a positive correlation with number of secondary branches, number of pods per plant and harvest index. The Number of primary branches was positively associated with the

number of secondary branches, number of days to maturity, number of pods per plant, number of seeds per plant, pod length, and 100-grain weight. The number of secondary branches was positively correlated with pod length and number of pods per plant. The number of days to maturity showed a significant association with 100-grain weight and number of seeds per pod. The number of pods per plant and number of seeds per pod were positively correlated with pod length.

Manoj *et al*., (2003) conducted correlation analysis for yield and yield components in pea using 40 $F_1$ hybrids and 14 parents. The estimates of genotypic correlation coefficients were higher than those of phenotypic correlation coefficients. Pod yield per plant exhibited a significant and positive correlation with number of pods per plant, mean pod weight, weight of edible grains per pod, number of days to first picking, number of edible grains per pod. Pod length, internodes length, shelling percentage and number of branches per plant.

Character association studies conducted by Sharma *et al*., (2003) and indicated that positive and significant association of seed yield per plant with biological yield per plant, pods per plant and pod length. Significant negative correlation of harvest index was observed with plant height. It can be predicted that selection for pods per plant, pod length and biological yield per. plant would improve seed yield per plant. Recombination breeding may be suggested for simultaneous improvement of biological yield per plant and harvest index.

Correlation and path analyses were performed in thirty six genotypes of garden pea (*Pisum sativum* L) and found pod weight per plant had strong positive association with number of pods per plant, number of grains per pod, mean pod weight, pod length, plant height and grain weight per pod (Ramesh and Tewatia, 2002).

Correlation among the parents $F_1$ and $F_2$ of 10x10 diallel cross and the path coefficient analysis were studied in pea (*Pisum sativum* L). The seed yield per plant was positively and significantly associated with pods per plant, harvest index and primary branches per plant. Pods per plant had the highest direct effect followed by harvest index on seed yield. The selection criteria based on pods per plant, harvest index and primary branches per plant will give fruitful results for yield improvement in pea (Dharmendra and Mishra, 2002).

Pathak and Jamwal (2002) carried out experiment with pea and revealed that the genotypic correlation coefficients were generally higher than the corresponding phenotypic correlation coefficients. At the phenotypic level, pod yield per plant was positively correlated with number of pods per plant, plant height and average pod weight. Positive associations were also observed between number of days to 50% flowering and number of days to first picking, number of pods per plant and plant height, pod length and number of seeds per pod and average pod weight, and number of seeds per pod and average pod weight. Thus, high- yielding cultivars may be developed via selection for greater number of pods per plant, plant height, average pod weight, pod length and number of seeds per pod.

Dharmendra and Mishra (2002) studied correlation among the parents, $F_1$s and $F_2$s of 10x10 diallel cross and the path coefficient analysis were studied in pea (*Pisum sativum* L.). The seed yield per plant was positively and significantly associated with pods per plant, harvest index and primary branches per plant. Pods per plant had the highest direct effect followed by harvest index on seed yield. The selection criteria based on pods per plant, harvest index and primary branches per plant will give fruitful results for yield improvement in pea.

Ramesh *et al*., (2002) performed correlation in thirty-six genotypes of garden pea (*Pisum sativum* L.). Pod weight per plant had strong positive association with number of pods per plant, number of grains per pod, mean pod weight, pod length, plant height and grain weight per pod.

Devendra *et al*., (2001) evaluated yield and yield components (number of nodes, bearing first flower, height of nodes bearing first flower, plant height, pods per plant, seeds per plant, seeds per pod and 100-seed weight) of pea. Highly significant and positive correlations in both field and vegetable peas were observed for days to first flower and number of nodes bearing the first flower, height of node bearing the first flower and plant height, pods and seeds per plant, pods and yield per plant, seeds and yield per plant, and 100-seed weight and yield per plant.

Seed yield per plant exhibited a significant and positive correlation with plant height, number of pods per plant, 1000-seed weight, number of grains per pod and harvest index (Tiwari *et al*., 2001).

Raj *et al*., (2000) conducted experiment in India, with seven genotypes of peas during the rabi season of 1996-97, revealed that the number of pods per plant and pod girth exhibited significant association with pod yield per plant.

Fifteen genetically diverse genotypes of garden pea were grown at Solan during the winter (rabi) seasons of 1993-94 and 1994-95 to study the correlation coefficients among 10 characters. Significant differences were observed for all the 10 characters. Yield had significant and positive associations with node number bearing first flower, days to 50% flowering, shelling percentage and number of pods per plant (Bhardwaj and Kohli, 1999).

Vikas and Singh (1999) evaluated six pea crosses and their parents for correlation. Seed yield per plant had positive correlations with pods per plant, biological yield (in parents and all 6 crosses), seeds per pod (in three crosses), 100-seed weight (in parents and three crosses) and harvest index (in parents and two crosses). Therefore, these characters should be taken into consideration for improving seed yield in pea.

Significant positive correlations of seed yield with plant height, pod length, number of pods per plant and straw yield per plant were reported (Devendra *et al*., (1998).

Gupta *et al*., (1998) estimated correlation is derived from data on seven yield related traits in 40 pea genotypes. Days to 50% flowering exhibited significant and positive phenotypic association with pods per plant, number of seeds per plant, pod weight per plant and 100- seed weight. Number of pods per plant was positively and significantly correlated with pod weight per plant, and negatively correlated with pod length, 100-seed weight and protein content. Number of seeds per pod and pod weight per plant showed significant negative association with protein content while 100-seed weight expressed positive and significant association with protein content.

### 2.3 Path Co-efficient

Pods per plant, 100-seed weight, seeds per pod and days to maturity had positive direct effect on grain yield, while plant height, pods per cluster and pod length had negative direct effect on grain yield (Inderjit *et al*., 2007).

The results of path analysis revealed that direct effects were highest for number of pods per plant, node at which first fertile pod develops, number of branches, number of seeds per pod and pod length which can serve as reliable variable for selection (Harpreet *et al*., 2007).

Pods per plant, 100-seed weight, seeds per pod and days to maturity had positive direct effect on grain yield, while plant height, pods per cluster and pod length had negative direct effect on grain yield (Singh and Singh, 2006).

Path coefficient analysis revealed that number of pods per plant and shelling percentage had the maximum direct effect on green pod yield. Thus, due importance should be given to these characters for improvement of yield (Mohan *et al*., 2005).

The number of seeds per pod exhibited highest (3.55 8) direct effects towards seed yield at genotypic level. Hence, maximum weightage should be given to number of seeds per pod during selection programme for yield improvement in pea (Shinde, 2000).

The highest direct effect was exhibited by pods per plant, indirect effects, especially through the seeds per pod in pea (Avc and Ceyhan, 2006).

Singh and Yadav (2005) estimated path analyses of seed yield and yield related characters for 18 genotypes of peas. Path analysis revealed that the number of pods per plant had the greatest direct genotypic and phenotypic effects on seed yield, followed by pod length. These traits should be considered important in any selection programmed for the improvement of pea yield.

Path analysis indicated that the number of pods per plant and pod length exerted high direct effect on pod yield per plant. Therefore, these characters require the highest consideration while selecting high yielding genotypes of pea (Seema *et al*., (2005).

Satyawan *et al*., (2004) were estimated path coefficient analyses in 36 elite genotypes of pea and confirmed that the major yield components were number of nodes and height at which the first pod appears, number of primary branches per plant, and 100-seed weight, although the direct effect of 100-seed weight was negative. The number of pods per plant had the greatest direct effect on seed yield, followed by height at

which the first pod appears, plant height, node number at which the first pod appears, and number of primary branches per plant.

Chaudhary and Sharma (2003) investigate path analyses for yield and yield components (number of days to first flowering, first flowering node, number of days to 50% flowering, number of days to first green pod harvest, pod length, number of grains per pod, pod yield per plant, plant height, shelling percentage, and 1000-seed weight) in pea. It revealed that the number of grains per pod, pod length, number of pods per plant, and 1000-seed weight had the greatest direct effect on pod yield per plant. The greatest negative direct effects on pod yield were exhibited by number of days to 50% flowering. The number of pods per plant and number of grains per pod appeared to be the most important selection indices for green pod yield.

Kumar *et al.,* (2003) estimated path coefficient analysis which revealed that the number of pods per plant had the greatest direct effect on yield per plant in pea. The number of days to flowering, number of primary and secondary branches, and number of days to maturity exhibited a negative direct effect on grain yield. The number of pods per plant, number of seeds per pod, plant height, and pod length were the major yield components.

Manoj *et al.*, (2003) conducted path coefficient analysis for yield and yield components in pea using 40 $F_1$ hybrids and 14 parents. Path coefficient analysis revealed that the number of pods per plant had the greatest positive direct effect on pod yield per plant, followed by mean pod weight and number of edible grains per pod. The number of pods per plant had an indirect effect on pod yield per plant through internodes length, plant height, number of days to 50% flowering, number of branches per plant, number of days to first picking, shelling percentage and node at which the first pod appears. Plant height had the greatest negative direct on pod yield per plant, followed by number of days to first picking and number of days to 50% flowering. The number of pods per plant, mean pod weight and number of edible grains per pod were the major components of pod yield per plant in pea.

Dharmendra and Mishra (2008) studied the path coefficient analysis in pea (*Pisum sativum* L.). Pods per plant had the highest direct effect followed by harvest index on

seed yield. The selection criteria based on pods per plant, harvest index and primary branches per plant will give fruitful results for yield improvement in pea.

Ramesh and Tewatia (2002) studied in garden pea for path analysis and revealed that number of pods per plant had maximum direct genotypic effect on pod weight per plant, followed by mean pod weight, total sugars in edible grain, number of nodes on main stem per plant, days to first picking and grain weight per pod. These traits should be considered important in any selection programme for the yield improvement in garden pea.

Ramesh *et al*., (2002) performed path analyses in thirty-six genotypes of garden pea (*Pisum sativum* L.). It revealed that number of pods per plant had maximum direct genotypic effect on pod weight per plant, followed by mean pod weight, total sugars in edible grain, number of nodes on main stem per plant, days to first picking and grain weight per pod. These traits should be considered important in any selection programme for the yield improvement in garden pea.

Tiwari *et al*., (2001) investigated thirty-four divergent genotypes of pea (*Pisum sativum* L.) for path analysis and it revealed that pods per plant, pod length, 1000-seed weight and number of grains per pod had moderate to high positive direct effects on seed yield per plant.

Bhardwaj and Kohil (1999) studied the path coefficient analysis among 10 characters in garden pea. It indicated that number of pods per plant and shelling percentage had high direct effects on yield, showing that these characters were the main yield determinants and could be taken as an index to improve the seed yield through selection.

Jamwal *et al*., (1999) reported with twenty-nine powdery mildew-resistant cultivars of garden pea (*Pisum sativum* L.) were evaluated in a field experiment conducted in Palampur, Himachal Pradesh, India from 1997 to 1998 to determine the direct and indirect effects of yield components on yield through path coefficient analysis. The number of pods per plant had the highest positive direct effect on pod yield per plant, followed by days to first picking, number of seeds per pod and average pod weight. Negative direct effects were determined in shelling percentage, days to 50%

flowering, powdery mildew intensity, pod length, protein content, plant height and total soluble solids.

Sharma and Mishra (1997) assessed the path coefficient analysis in 32 pea genotypes. The results revealed that the selection for green pod yield should be based upon pods per plant and pod breadth. However pod length had indirect effects on green pod yield via pod breadth. Significant positive associations between pods per plant and plant height, shelling percentage and grains per pod and pod length and pod breadth were also observed.

Sarnaik *et al*., (1990) investigated path analysis of green pod yield components in pea and showed number of green pods per plant had the highest positive direct effect on green pod yield. Path analysis in pea showed that number of green pods per plant had the highest positive direct effect on green pod yield.

**2.4 Genetic diversity**

The genetic divergence using Mahalanobis $D^2$ statistic was studied in 21 genetically diverse pea genotypes for days to flowering, plant height, pods per plant, seeds per pod, pod weight per plant and 1000-seed weight. The genotypes were grouped into 6 dusters. Cluster I was the biggest with 11 genotypes followed by clusters II and III with 4 and 3 genotypes, respectively. Cluster IV, V and VI were unique since they had only one genotype. The maximum inter-cluster distance was observed between dusters II and VI and was followed by dusters II and V, and dusters III and VI indicating wide divergence among these dusters, which also suggested that the genetic architecture of the genotypes in one duster differed entirely from those included in other clusters. The diversity among the genotypes measured by inter-duster distance (D value) was adequate for improvement of pea by hybridization and selection. The genotypes included in the diverse clusters can be used as promising parents for hybridization programmes for obtaining high heterotic response and thus better segregants in pea (Dharmendra and Mishra, 2008).

One hundred twenty genotypes were evaluated for 10 characters to study genetic diversity and association between yield and its components. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes

were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters (Inderjit *et al*. 2007).

Singh *et al*., (2007) evaluated one hundred twenty genotypes for 10 characters to study genetic diversity and association between yield and its components. The study indicated presence of considerable genetic divergence among the genotypes. The genotypes were grouped into six clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, Cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters.

Thirty-one advanced genotypes of pea (6 cultivars and 25 promising genotypes) were evaluated in Kanpur, Uttar Pradesh, India, during 2000-01 for genetic divergence for grain yield and yield components (number of days to flowering, number of days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, 100-seed weight, number of grains per pod and harvest index). The genotypes significantly varied for all traits. The genotypes were grouped into 6 clusters based on D2 values. Cluster I, which had the advanced genotype KPMR632, was more divergent and mono genotypic. Cluster VI was the largest, with 8 genotypes. The inter cluster distance was lowest (12.04) between clusters III and VI, and greatest (41.35) between clusters I and II, closely followed by clusters I and IV. The inter mating among the genotypes from clusters I, II and III may be used to improve the grain yield of pea (Singh and Singh, 2006).

Kumar *et al*., (2006) evaluated genetic divergence ($D^2$ statistics) analysis among 100 pea genotypes. These genotypes were grouped into 8 clusters. The cluster I was the largest and consisted of 32 genotypes, followed by cluster II with 20 genotypes and cluster VIII was the smallest with 3 genotypes. Intra-cluster $D^2$ values revealed that cluster VIII was the most diverse (13.49), followed by cluster VII (8.37) and cluster VI (8.16). Highest inter-cluster $D^2$ values were observed between clusters V and VII (23.15) followed by clusters VI and VII indicating that genotypes included in these clusters had maximum divergence. There was no parallelism between genetic and geographic diversity. The genotypes 02/1119 and PH-I (cluster V), HFP-2005 and HFP-9907A (cluster VI), HFP-9937 and MP-Arkel (cluster VII) and 02/1090 (cluster

VIII) might be used as promising parents for yield and quality attributes in hybridization for pea improvement programmer.

Gupta and Singh (2006) determined genetic divergence in 83 garden pea genotypes. Mahalanobi's $D^2$ statistical analysis grouped the genotypes into 27 clusters. Cluster I had the highest number of genotypes (17). Inter cluster variation was highest between clusters VI and XXIV (2127.75) and lowest between clusters XVII and XXVII (0). Cluster XII had the highest mean for green pod yield per plant (81.6 g), whereas cluster XXIV had the highest mean for earliness (89.6), number of first flowering nodes (20.4), number of days to first green pod picking (103.0) and shelling percentage (51.5). Cluster XXII had the highest mean for pod length (9.2) and 100-green pod weight (776.9). Cluster XIX recorded the highest mean for number of seeds (9), number of green pods (20.1) and number of days to maturity. Early yield per plant had the highest contribution to the genetic divergence among the genotypes tested.

Singh and Singh (2006) evaluated thirty-one advanced genotypes of pea for genetic divergence for grain yield and yield components (number of days to flowering, number of days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, 100-seed weight, number of grains per pod and harvest index). The genotypes significantly varied for all traits. The genotypes were grouped into 6 clusters based on $D^2$ values. Cluster I, which had the advanced genotype KPMR632, was more divergent and mono genotypic. Cluster VI was the largest, with 8 genotypes. The inter cluster distance was lowest (12.04) between clusters III and VI, and greatest (41.35) between clusters I and II, closely followed by clusters I and IV. The inter mating among the genotypes from clusters I, II and III may be used to improve the grain yield of pea.

Mahamad *et al*., (2006) evaluated forty-nine genotypes of vegetable pea grown for genetic diversity for 14 traits. There was no definite relationship between genetic diversity and geographical origin. Intra cluster $D^2$ values ranged from 0 (solitary cluster) to 57.08 (cluster II), whereas the inter cluster $D^2$ values ranged from 34.46 (clusters VI and VII) to 259.13 (clusters IV and XIII). The number of branches per plant, number of pods per plant, grain seed yield per plant, number of seeds per pod, number of days to 50% flowering, number of days to first picking, and number of days to second picking had the greatest contribution to the total divergence. The

accessions under cluster IV recorded high values for number of branches per plant, green seed yield per plant, 100-green-seed volume, number of seeds per pod, green pod length, and green pod width (cluster IV), whereas those under cluster XIII were characterized by early flowering and maturity, dwarf plant types, and early picking. Hybridization between these accessions may yield desirable segregants.

An experiment was conducted on 25 genotypes of pea to measure genetic distances among genotypes using $D^2$ statistics for yield and its component characters. The cultivars were grouped into seven clusters. The maximum number of genotypes was found in clusters I and V each having five genotypes, while, minimum two genotypes in each clusters IV and VII. Maximum genetic distance was recorded between cluster III and VII (6.179) followed by IV and VII (5.535) suggesting wide diversity among these groups. Considering cultivars of I (UDR-59, DDR-44, DDR-63, PUSA-l0) and VII (PC-99, DDR-55) are likely to recombine genes for higher yield (Sirohi *et al*., 2006).

Gohil (2006) conducted an experiment to study the genetic diversity among 39 pea cultivars. Data were recorded on grain yield per plant, days to 50% flowering, days to maturity, number of pods per cluster, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, harvest index, plant height and protein content. The cultivars were grouped into 5 clusters, which indicated the presence of a large amount of diversity in the population. A total of 35 genotypes were grouped in cluster I while the remaining clusters contained a single genotype. The value of intra cluster distance for cluster I was 39.98. The maximum inter cluster distance was between clusters I and IV followed by that between cluster IV and II. There was a minimum distance between cluster II and III.

Satyawan *et al*., (2004) were evaluated genetic divergence among 36 elite genotypes of field pea (*Pisum sativum* L.) with regard to seed yield and eight morphological characters (node number at which the first pod appeared, height of plant at which the first pod appeared, plant height, number of primary branches, number of pods per plant, number of seeds per pod, pod length, and 100-seed weight). The genotypes were grouped into nine clusters. Cluster I had the highest number of genotypes (16), whereas clusters VII, VIII and IX had only one genotype each. The inter-cluster

distance was the greatest between clusters I and IX (1116.13), followed by III and IX (979.25), I and VI (932.69), and I and V (854.74). The higher inter-cluster distance, the greater the diversity between genotypes and vice versa. It is expected that crosses between genotypes from distant clusters will give better transgressive segregants. The mean value for all the characters varied in different clusters.

Yadav *et al*., (2004) conducted an experiment to study the genetic divergence of on 45 pea lines was carried out in a field experiment conducted in Hisar, Haryana, India during the rabi season of 2000-01. The lines were clustered into 15 groups, with 25 genotypes clustering into 5 groups and the remaining 20 lines clustering into 10 groups. Intra cluster divergence was low for clusters V, VII, VIII and IX. Genetic divergence was lowest between Rachna and Pb-88-2C and highest between LMR-400 and Pb-29(b)-14. Genotypes SN-32, Sn-44 and Pb-88-2c flowered the earliest and recorded the highest green pod yield and shelling percentage, whereas SN-32 and Pb-29(b)-14 recorded the highest protein and sugar content. The genetic constitution rather than the geographical placement played a major role in the clustering pattern of the genotypes.

Singh and Singh (2003) studied genetic divergence for 10 traits (number of days to 50% flowering, number of days to maturity, plant height, pod length, number of pods per plant. number of seeds per pod, 100-seed weight, biological yield, seed yield per plant, and harvest index) of pea. The genotypes were grouped into 11 clusters based on multivariate analysis using Mahalanobis $D^2$ statistics. Cluster XI was the largest (9 genotypes), followed by cluster 11(8), cluster VI (7), cluster I (5), cluster V (5), cluster X (5), cluster VIII (4), cluster IV (3), cluster IX (2), cluster III (1) and cluster VII (1). The highest intra cluster $D^2$ values were recorded for cluster IX (2.47), whereas the highest inter cluster $D^2$ value was observed between cluster III and IX. Cluster means for the 10 traits indicated that the genotypes included in cluster IX gave the highest seed yield per plant, biological yield, number of pods per plant, and pod length, whereas those included in cluster X had the highest number of seeds per pod and pod length, and average 100-seed weight and number of pods per plant. The genotypes in cluster VIII had high 100-seed weight and average seed yield per plant, whereas those in cluster III had the highest harvest index, and average 100- seed

weight and seed yield per plant. The results suggest that the genotypes under these diverse clusters had good potential as parents for hybridization studies in pea.

Dixit *et al*., (2002) used fifty-three genotypes of field pea (*Pisum sativum* L.) to study genetic divergences following D2 Genotypes were grouped into 11 different clusters. Clusters I and II consisted of 15 genotypes each. Plant height contributed maximum to the genetic diversity. Intra cluster distance was highest in cluster III followed by clusters I and II. Inter cluster distances were maximum between clusters IV and X followed by clusters IV and XI. Inter cluster distances were minimum between clusters X and XI, IV and VIII and III and IV. The study indicated lack of parallelism between genetic and geographic diversity. The genotypes included in the diverse clusters can be used as promising parents for hybridization to obtain higher heterotic response and thus better segrenants in field pea.

Rudnicki and Wenda (2002) conducted a field experiment on 16 pea cultivars in mixed cropping with spring triticale. Multivariate analysis of usefulness of pea cultivars for mixture cropping with spring triticale was based on the six following multiple cropping characteristic: mixture yield, stability of mixture yield, yield of pea variety in mixture, stability of pea yield, lodging resistance and uniformity of maturation of pea and triticale in mixture. Tested pea cultivars as components of triticale in mixed cropping revealed both positive and negative features. Multivariate analysis showed small differences among pea cultivars in terms of usefulness in mixed cropping.

Sureja and Sharma (2001) evaluated genetic divergence for 16 quantitative traits in 30 indigenous and exotic genotypes of garden pea grown India. Analysis of variance showed highly significant differences among genotypes for all traits. Mahanalobis $D^2$ analysis grouped the genotypes into four clusters, with I, II and III each comprising six genotypes and IV comprising 12 genotypes. The grouping pattern of the genotypes was random, indicating that geographical diversity and genetic divergence were unrelated. Therefore, selection of genotypes for hybridization should be based on genetic divergence rather than geographical diversity.

Backiyarani *et al*., (2000) conducted a study to evaluate genetic divergence among 32 genotypes of cowpea based on seven physiological traits viz., plant height, primary

leaf area, days to 50% flowering, total chlorophyll content, leaf area index, harvest index and single plant yield. Mahalanobis' $D^2$ analysis revealed considerable diversity in the material studied, which was grouped into six clusters. Geographic diversity was not related to genetic diversity. Single plant yield, harvest index and earliness in flowering together accounted for 80% of the total genetic divergence.

Ushakumari *et al*., (2000) assessed genetic diversity in cowpea ( *Vigna unguiculata* L) based on traits. Fifty genotypes of cowpea were grouped into 13 clusters by Mahalanobis' $D^2$ analysis. The highest contributions towards divergence were recorded for plant height (22.69%), seeds per pod (17.63%), number of branches per plant (16.82%), number of pods per cluster (15.27%) and pod length (13.47%).

Manikannan *et al*., (2000) estimated the genetic divergence among 31 genotypes of black gram (*Vigna mungo* L.) with diverse geographic origin. Analysis of variance showed significant differences between genotypes for all the 10 characters studied. The values of $D^2$ corresponding to 465 pairs of possible combinations ranged from 2.69 to 78.80 indicating high divergence among the genotypes. Clusters I and II were the largest with 9 genotypes each, followed by cluster I, five genotypes, and cluster IV with four genotypes. Clusters I and II were the largest with nine genotypes each, followed by cluster II, five genotypes, and cluster IV with four genotypes. Clusters V and VI were the smallest and had two genotypes each. The clustering pattern showed that the genotypes for the 10 characters studied had 2 genotypes each. The clustering pattern showed that the genotypes for the 10 characters studied had considerable genetic differences between groups. The contribution towards genetic divergence indicated that the photosynthetic rate (47.83%), 100 seed weight (11.83%) contributed more to the total genetic divergence in the 31 genotypes of black gram.

Manivannan *et al*., (1999) measured genetic diversity of thirty mungbean ( *Vigna mungo* L.) genotypes by grouping them into six clusters. The pattern of $D^2$ clusters demonstrated that geographical distribution in mungbean was not related to genetic diversity. Among the characters, number of pods per cluster, number of pods per plant and number of clusters per plant contributed maximum towards the genetic divergence.

Vikas *et al*., (1999) found genetic divergence ($D^2$ statistics) among 45 pea (*Pisum sativum* L.) genotypes indicated the existence of considerable diversity. Maximum inter-cluster $D^2$ values were observed between cluster III & IV (Environment 1), cluster V & IX (Environment 2) and cluster IV & V (pooled), indicating that the genotypes included in these clusters had maximum divergence. The diversity among the genotypes measured by inter- cluster distance was adequate for improvement of pea by hybridization and selection. The genotypes included in the diverse clusters may be used as promising parents for hybridization for obtaining better segregants in pea.

Aher *et al*., (1998) evaluated fifty four genotypes of early pigeon pea (*Cajanus cajan* L.) for 10 yield related traits. The genotypes were grouped into 12 clusters on the basis of D2 analysis of the data obtained. They found that genetic diversity was not correlated with geographical diversity.

Santos *et al*., (1997) estimated genetic divergence of 10 yield related characters in 50 *Vigna unguiculata* L. genotypes grown in irrigated and rain fed conditions. The genotypes were grouped into 9 and 12 clusters during irrigated and rain fed conditions, respectively. The constituents of each cluster were not same, except for cluster IV. Length of the main branch, 100-seed weight and pod length were the most important characters to affect divergence.

Tripathi (1997) examined 100 genotypes of chickpea (*Cicer arietinum*) from several worldwide locations for 13 agronomic characters to study patterns of genetic divergence using multivariate $D^2$ (Mahalanobis') analysis. The genotypes were grouped into 12 clusters on the basis of yield and yield components. Hybridization among genotypes from the diverse clusters identified will aid breeding for higher yields of chickpea.

Multivariate analysis of divergence among 60 entries of chickpea for seven developmental characters led to their grouping into five clusters. Grouping of entries ion different clusters was not related to their geographic origin. The inter cluster $D^2$ values ranged from 8.0 to 38.2. Based on mean performance, genetic distance and clustering pattern, hybridization involving parents from clusters II and V may give higher yielding varieties (Narendra and Kumar, 1997).

Thirty strains of black gram (*Vigna mungo* L.) were evaluated for genetic divergence on the basis of D2 analysis of eight yield-related traits. The strains were grouped into eight clusters, with the clustering pattern being independent of geographic distribution. Pod yield and seeds per pod were important contributors to genetic divergence (*Ram et al*., 1997).

Genetic divergence measured by Mahalanobis' $D^2$ statistic was derived from data recorded on days to 50% flowering, days to 50%pod formation, days to 50% pod maturity, pods per peduncle,. seeds per pod, plant height, seed yield per plant and harvest index in 42 indigenous and exotic strains of cowpea (*Vigna unguiculata* L.). The strains were grouped into six different clusters. Days to 50% flowering, plant height, pods per peduncle and harvest index contributed the most towards genetic divergence. Seed yield had a high positive phenotypic correlation with pods per peduncle, number of seeds per pod and harvest index (Sharma and Mishra, 1997).

Singh and Gumber (1996) assed genetic diversity on yield related characters of 36 pigeon pea (*Cajanus cajan* L.) genotypes by multivariate analysis. Based on Mahalanobis' $D^2$ statistic, the genotypes were grouped into 13 clusters with 100-seed weight showing the highest contribution to total divergence (41.6%), followed by number of days to maturity (24.9%) and biological yield (12.5%). Crossing of genotypes from cluster V (characterized by high seed yield and number of pods per plant) and cluster VII (characterized by high seed yield and long duration) with cluster II (characterized by low yields and short-duration) is suggested to obtain a high yielding, short-duration genotype of short stature.

# CHAPTER III

# MATERIALS AND METHODS

An experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka- 1207, Bangladesh during the period from December 2013 March 2014 to study on the genetic diversity, correlation and path coefficient analysis in Pea (*Pisum sativum* L). A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc., which are presented as follows:

## 3.1 Experimental site

The research work relating to determine the genetic diversity of pea was conducted at the Sher-E-Bangla Agricultural University Farm, Dhaka-1207 during December 2013 to March 2014.

## 3.2 Geographical location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level (Anon., 2004).The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as 'islands' surrounded by floodplain (Anon., 1988b). The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

## 3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty rainfall associated with moderately low temperature during the Rabi season (October-March). Weather information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

### 3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

### 3.5 Planting materials

The material comprised of 45 genotypes of pea. The genetically pure and physically healthy seeds of these genotypes were obtained from the Germplsam Bank of Bangladesh Agricultural Research Institute (BARI), Gazipur. There were 44 lines and one variety (BARI Motor-1) used for this experiment. List of the genotypes are given in Table 1

### 3.6 Design and layout of the experiment

The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. The units plot size was six meter square. Spaces between and within row were 30 cm and 15 cm, respectively. The genotype was randomly assigned to each plot within each replication.

**Table 1. Name and origin of forty-six pea genotypes used in the present study**

| Genotypic Code | Genotypic Name | Genotypic Code | Genotypic Name |
|---|---|---|---|
| G1 | BD-4135 | G23 | BD-4164 |
| G2 | BD-4136 | G24 | BD-4165 |
| G3 | BD-4137 | G25 | BD-4166 |
| G4 | BD-4138 | G26 | BD-4167 |
| G5 | BD-4139 | G27 | BD-4168 |
| G6 | BD-4141 | G28 | BD-4159 |
| G7 | BD-4142 | G29 | BD-4170 |
| G8 | BD-4143 | G30 | BD-4171 |
| G9 | BD-4144 | G31 | BD-4173 |
| G10 | BD-4145 | G32 | BD-4174 |
| G11 | BD-4146 | G33 | BD-4175 |
| G12 | BD-4147 | G34 | BD-4176 |
| G13 | BD-4149 | G35 | BD-4177 |
| G14 | BD-4150 | G36 | BD-4178 |
| G15 | BD-4151 | G37 | BD-4191 |
| G16 | BD-4152 | G38 | BD-4192 |
| G17 | BD-4153 | G39 | BD-4492 |
| G18 | BD-4156 | G40 | BD-6944 |
| G19 | BD-4160 | G41 | BD-7215 |
| G20 | BD-4161 | G42 | BD-7217 |
| G21 | BD-4162 | G43 | BD-7217 |
| G22 | BD-4163 | G44 | BD-7218 |
| | | G45 | BARI Motor-1 |

Source: Bangladesh Agricultural Research Institute (BARI)

**Plate -1 Replication view of the experimental field.**

**Plate -2 The experimental site at harvesting stage**

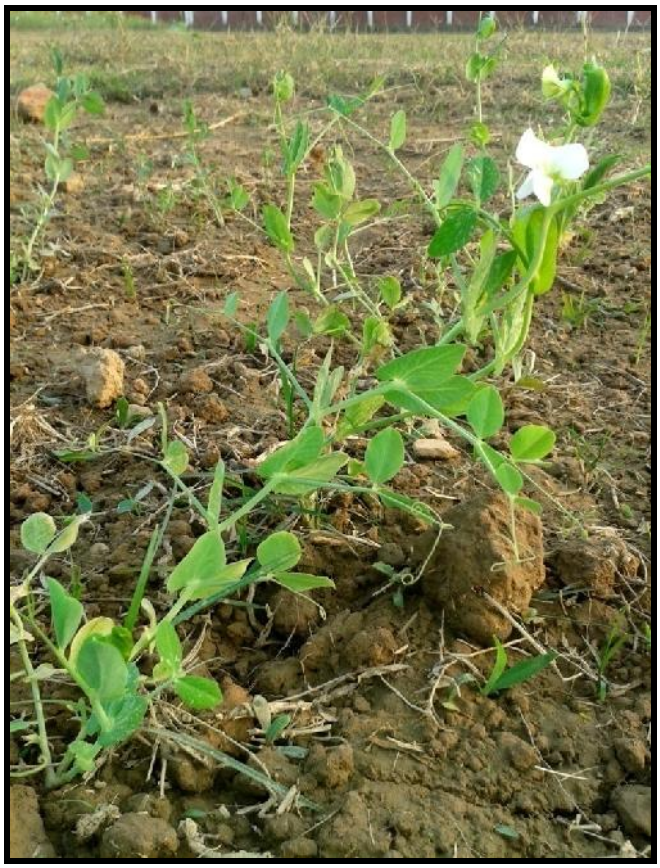

**Plate -3 A pea plant with flower.**

### 3.7 Land preparation

The experimental plot was prepared by deep ploughing followed by harrowing and laddering. Weeds and stables were removed during final ploughing.

### 3.8 Manure and fertilizer application

The plots were fertilized with cow dung, urea, TSP and MP @ 10 t, 45 kg, 62.5 kg, 50 kg per ha, respectively. The entire cow dung, TSP, MP and half of the urea were applied at the time of final land preparation. The remaining half of urea was applied as top dressing in two installments, first after 21 days and second after 42 days of sowing.

### 3.9 Seed sowing

Seeds of the 45 genotypes were sown on 05 December 2013. The seedlings were emerged five to twelve days after sowing.

### 3.10 Intercultural operation

Intercultural operations were done as and when necessary.

### 3.11 Pesticide application

During the cropping period, since there was no significant pest infestation in the field, hence no control measure was undertaken. In order to prevent disease infestation,' Ripcord’ was used for 6 times at an interval of 7 days from 22 December to 1 January 2014. There were different types of weeds which were controlled effectively by hand weeding.

### 3.12 Harvesting

Pods were picked on the basis of horticultural maturity, size, color and age being determined for the purpose of consumption throughout the harvesting period. Harvesting was done in February.

### 3.13. Data recording

Ten plants in each entry were selected randomly and were tagged. These tagged plants were used for recording observations for the following characters.

#### 3.13.1 Days to 50% flowering

Determined as the days required from sowing to 50% anthesis.

#### 3.13.2 Plant height (cm)

The average height (cm) of the main stem from the ground level to the tip measured at time of harvesting.

#### 3.13.3 Primary branches per plant

Mean number of primary branches per plant counted from ten sample plant after harvest.

#### 3.13.4 Secondary branches per plant

Mean number of secondary branches per plant counted from ten sample plant after harvest.

#### 3.13.5 Pod length (cm)

Mean length (cm) of pods excluding peduncle from ten randomly selected plants.

#### 3. 13.6 Hundred seed weight (g)

Weight of 100 seeds selected at random from each plant was expressed in grams.

#### 3.13.7 Pods per plant

Mean number of pods from ten randomly selected plants.

#### 3.13.8 Number of seeds per pod

Average number of seeds from ten randomly selected pods.

### 3.13.9 Seeds per plant

Mean number of seeds from ten randomly selected plants.

### 3.13.10 Plant maturity

Number of days taken from sowing to 80 per cent of the green pods to dry was taken as days to maturity.

### 3.13.11 Seed yield per plant (g)

Average seed yield from ten randomly selected plants was recorded in grams.

### 3.14 Statistical analysis:

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Coordinate Analysis (PCO), Cluster Analysis (CVA).

### 3.14.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al*., (1955).

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

Where,

GMS = Genotypic mean sum of squares
EMS = Error mean sum of square
r = number of replications

Phenotypic variance ($\sigma^2_{ph}$) = $\sigma^2_g$+ EMS

Where,

$\sigma^2_g$= Genotypic variance

EMS = Error mean sum of square

**3.14.2 Estimation of genotypic and phenotypic co-efficient of variation**

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation (GCV %) $= \frac{\sqrt{\sigma^2 g}}{x} \times 100$

Where,

$\sigma^2_g$+ = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) $= \frac{\sqrt{\sigma^2 ph}}{x} \times 100$

Where,

$\sigma^2_{ph}$= Phenotypic variance

$\bar{x}$ = Population mean

**3.14.3 Estimation of heritability**

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.*, (1955).

$$H^2_b\% = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where,

$h^2_b$ = Heritability in broad sense

$\sigma^2_g$ Genotypic variance

$\sigma^2_{ph}$ = Phenotypic variance

### 3.14.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance (GA) = K. $h^2$. $\sigma_{ph}$

$$GA = K. \frac{\sigma^2_g}{\sigma^2_{ph}} . \sigma_{ph}$$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

$\sigma_{ph}$ = Phenotypic standard deviation

$h^2_b$ = Heritability in broad sense

$\sigma^2_g$ = Genotypic variance

$\sigma^2_{ph}$= Phenotypic variance

### 3.14.5 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1922):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean } (\bar{x})} \text{ X } 100$$

### 3.14.6 Estimation of simple correlation co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{[\{\sum x^2 - \frac{(\sum x)^2}{N}\}\{\sum y^2 - \frac{(\sum y)^2}{N}\}]}}$$

Where, $\sum$ = Summation

x and y are the two variables correlated

N= Number of observations

### 3.14 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.*, (1958), Johnson *et al*., (1955) and Hanson *et al*., (1956) were adopted.

The genotypic co-variance component between two traits and have the phenotypic covariance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic correlation ($r_{g\times y}$) = $\frac{GCOVxy}{\sqrt{GVx \cdot GVy}} = \frac{\sigma_{g\times y}}{\sqrt{(\sigma_{g\times} . \sigma^2_{gy})}}$

Where,

$\sigma_{gxy}$ = Genotypic co-variance between the traits x and y

$\sigma^2_{gx}$ = Genotypic variance of the trait x

$\sigma^2_{py}$ = Genotypic variance of the trait y

Phenotypic correlation ($r_{pxy}$) = $\frac{PCOVxy}{\sqrt{PVx \cdot PVy}} = \frac{\sigma_{p\times y}}{\sqrt{(\sigma_{p\times} . \sigma^2_{py})}}$

Where,

$\sigma^2_{pxy}$ = Phenotypic covariance between the traits x and y

$\sigma^2_{px}$ = Phenotypic variance of the trait x

$\sigma^2_{px}$ = Phenotypic variance of the trait y

### 3.14.8 Path coefficient analysis

Path coefficient is a standardized partial regression coefficient and as such it is a measure of direct and indirect effect of set variables (component characters) as a dependent variable such as fruit yield. Direct and indirect effect of component characters on fruit yield were computed using appropriate correlation coefficient of different component characters as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1955) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on seed yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3..... and ,11 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$r_{1.y} = P_{1.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y} + r_{1.9} P_{9.y} + r_{1.10} P_{10.y} + r_{1.11} P_{11.y})$

$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y} + r_{2.9} P_{9.y} + r_{2.10} P_{10.y} + r_{2.11} P_{11.y})$

$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y} + r_{3.9} P_{9.y} + r_{3.10} P_{10.y} + r_{3.11} P_{11.y})$

$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r_{4.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y} + r_{4.9} P_{9.y} + r_{4.10} P_{10.y} + r_{4.11} P_{11.y})$

$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y} + r_{5.9} P_{9.y} + r_{5.10} P_{10.y} + r_{5.11} P_{11.y})$

$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y} + r_{6.9} P_{9.y} + r_{6.10} P_{10.y} + r_{6.11} P_{11.y})$

$r_{7.y} = r_{1.7} P_{1.y} + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.y} + r_{7.9} P_{9.y} + r_{7.10} P_{10.y} + r_{7.11} P_{11.y})$

$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y} + r_{8.9} P_{9.y} + r_{8.10} P_{10.y} + r_{8.11} P_{11.y})$

$r_{9.y} = r_{1.9} P_{1.y} + r_{2.9} P_{2.y} + r_{3.9} P_{3.y} + r_{4.9} P_{4.y} + r_{5.9} P_{5.y} + r_{6.9} P_{6.y} + r_{7.9} P_{7.y} + r_{8.9} P_{8.y} + P_{9.y} + r_{9.10} P_{10.y} + r_{9.11} P_{11.y})$

$r_{10.y} = r_{1.10} P_{1.y} + r_{2.10} P_{2.y} + r_{3.10} P_{3.y} + r_{4.10} P_{4.y} + r_{5.10} P_{5.y} + r_{6.10} P_{6.y} + r_{7.10} P_{7.y} + r_{8.10} P_{8.y} + r_{9.10} P_{9.y} + P_{10.y} + r_{10.11} P_{11.y})$

$r_{11.y} = r_{1.11} P_{1.y} + r_{2.11} P_{2.y} + r_{3.11} P_{3.y} + r_{4.11} P_{4.y} + r_{5.11} P_{5.y} + r_{6.11} P_{6.y} + r_{7.11} P_{7.y} + r_{8.11} P_{8.y} + r_{9.11} P_{9.y} + r_{10.11} P_{10.y} + P_{11.y})$

Where,

$r_{iy}$ = Genotypic correlation coefficients between y and i th character (y= Grain yield)

$P_{iy}$ = Path coefficient due to i th character (i=1, 2, 3.....11

1 = Plant height (cm)

2 = Days to 50% flowering.

3 = Primary branches per plant

4 = Secondary branches per plant

5 = Pod length (cm)

6 = Plant maturity

7 =Pods per Plant

8 = Number of Seeds per Pod

9 = Seeds per plant

10 = Hundred seed weight (g)

11 = Seed yield per plant (g)

**Total correlation, say between 1 and y i.e., $r_{1y}$ is thus partitioned as follows:**

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2}$ $P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3}$ $P_{3.y}$ = indirect effect of I via 3 on y

$r_{1.4}$ $P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5}$ $P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6}$ $P_{6.y}$ = indirect effect of I via 6 on y

$r_{1.7}$ $P_{7.y}$ = indirect effect of I via 7 on y

$r_{1.8}$ $P_{8.y}$ = indirect effect of 1 via 8 on y

$r_{1.9}$ $P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10}$ $P_{10.y}$ = indirect effect of I via 10 on y

$r_{1.11}$ $P_{11.y}$ = indirect effect of 1 via 11 on y

Where,

$P_{1.y}$, $P_{2.y}$, $P_{3.y}$..... $P_{8.y}$ = Path coefficient of the independent variables 1, 2,

3,.....11 on the dependent variable y, respectively.

$r_{1.y,}$ $r_{2.y,}$ $r_{3.y,}$..... $r_{11.y}$ = Correlation coefficient of 1,2,3,.....11 with y, respectively.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985)

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y}..... + r_{11.y} P_{11.y})$

Where,

$P^2_{RY} = R^2$

And hence residual effect, $R = (P^2_{RY} = R^2)^{1/2}$

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y.

### 3.15 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance ($D^2$) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's $D^2$ statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

#### 3.15.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

### 3.15.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al*., 1989).

### 3.15.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

Average intra-cluster distance = $\frac{\sum Di2}{n}$

Where,

$D_i^2$= the sum of distances between all possible combinations (n) of genotypes included in a cluster.

n = Number of all possible combinations between the populations in cluster.

### 3.15.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

Average inter-cluster distance = $\frac{\sum Dij2}{ni \times nj}$

Where,

$\sum D\,ij2$ =The sum of distances between all possible combinations of the populations in cluster i and j.

= Number of populations in cluster i. n Number of populations in cluster j.

3.15.8 Cluster diagram

Using the values of intra and inter-cluster distances (D a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster

**3.15.4 Canonical Vector analysis (CVA)**

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

**3.15.5 Calculation of $D^2$ values**

The Mahalanobis's distance (D2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D2 values were estimated for all possible combinations between genotypes. In simpler form D2 statistic is defined by the formula

D2= d,2=(Y'—Y) (jk)

Where,

Y = Uncorrelated variable (character) which varies from i = 1------ to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

### 3.15.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

### 3.15.9 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those which fall into different clusters. Clusters separated by largest statistical distance ($D^2$) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

i. Choice of cluster from which genotypes are selected for use as parent (s)

ii. Selection of particular genotype(s) from the selected cluster(s)

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes performance

# CHAPTER IV

# RESULTS AND DISCUSSION

The results obtained from the study are presented and discussed in this chapter. The data pertaining to forty five pea genotypes as well as yield and its contributing characters were computed and statistically analyzed and the result of the present investigation of characters association and multivariate analysis in pea (*Pisum sativum* L.) carried out during Rabi 2013-14 are presented in the following sections.

4.1 Genetic parameters

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation co-efficient

4.4 Path co-efficient analysis

4.5 Multivariate analysis

## 4.1 Genetic parameters

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied viz., days to 50% flowering,80% maturity, plant height, primary branches per plans, second branches per plant, pod length, hundred seed weight, pods per plant, number of seeds per pod, seeds per plant, seed yield per plant. The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore there is a lot of scope for selection for majority of the traits in the genotypes. The mean sum of squares of all the 11 characters is presented in Appendices V.

## 4.2 Genetic variability, heritability and genetic advance

The success of crop improvement program depends on the extent of genetic variability existing in the population or germplasm. The magnitude of genetic variability can determine the pace and quantum of genetic improvement through selection or through hybridization followed by selection. Phenotypic variance

measures the magnitude of variation arising out of differences in phenotypic values while the genotypic variance measures the magnitude of variation due to difference within the genotypic values. Heritability estimates aim in determining the relative amount of heritable portion of variation.

The presence of narrow gap between PCV and GCV for all the characters under study, suggested that these traits studied has low environmental influence. The estimates of heritability alone fail to indicate the response to selection (Johnson *et al*., 1955). Therefore, the heritability estimates appears to be more meaningful when accompanied by estimates of genetic advance. The genetic advances as per cent mean (GAM) was also estimated.

The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent mean for all the characters were studied and the results are presented in Table 2 and depicted in Fig. 1 and Fig 2. The mean performance of pea genotypes for various growth characters and yield components are presented in Appendix V.

### 4.2.1 Days to 50% flowering

Significant differences were recorded among the entries with respect to days to 50% flowering (Table 2). The value ranged from 29.67 to 43.00 days, in the genotype 'BD-7215'and 'BD-4143' respectively. The Genotypic and phenotypic variances observed were 10.32 and 11.58 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The difference between the genotypic co-efficient of variation (8.91) and phenotypic co-efficient of variation (9.44) were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (89.10%) estimates for this trait was moderately high, genetic advance (6.25) and genetic advance over percentage of mean (17.32) were found low (Table 2) indicated that this trait was controlled by non-additive gene.

### 4.2.2 Plant height (cm)

The grand mean of plant height was recorded 74.51 cm. It ranged from 31.04 cm to 95.50 cm. The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (95.50 cm) was recorded by the genotype 'BD-4162' and the lowest plant height (31.04 cm) was recorded by 'BARI Motor-1'. Highest genotypic and phenotypic variance was observed 191.67 and 221.86, respectively for plant height with large environmental influence. The phenotypic coefficient of variation (11.95) was higher than the genotypic co-efficient of variation (18.58), which indicated presence of considerable variability among the genotypes for this trait. The heritability (86.39%) estimates for this trait was moderately high, genetic advance (26.51) was moderately high and genetic advance in per cent of mean (35.57) was found low (Table 2) revealed that this trait was governed by non-additive gene.

### 4.2.3 Primary branches per plant

It ranged from 4.00 to 38.27 with a mean value of 20.95. The maximum number of branches was recorded in 'BD-4142' and 'BARI Motor-1' genotype showed the minimum number of branches. The phenotypic variance (67.77) appeared to be higher than the genotypic variance (61.84) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic coefficient of variation was 37.54 and 39.30, respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (91.24%) estimates for this trait was moderately high, genetic advance (15.47) was low and genetic advance in per cent of mean (73.86) were found moderately high (Table 2) revealed that this trait was governed by non-additive gene.

### 4.2.4 Number of secondary braches per plant

The no. of secondary branches per plants was ranged from 0.00 to 1.90 with a mean of 0.74. Maximum no. of secondary branches was recorded in genotype BD-4138 and no secondary branch was in BD-4173. The phenotypic variance (0.18) appeared to be higher than the genotypic variance (0.17) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-

efficient of variation and phenotypic co-efficient of variation were 57.03 and 57.25 respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (97.20%) estimates for this trait was high, genetic advance (0.85) was low and genetic advance in per cent of mean (114.2) was found moderately high (Table 2) revealed that this trait was governed by non-additive gene.

### 4.2.5 Pods per plant

It ranged from 31.08 to 89.00 with a mean value of 62.50. The maximum number of pod was recorded in 'BD-7215' and 'BARI Motor-1' genotype showed the minimum number of pod. The phenotypic variance (181.37) appeared to be higher than the genotypic variance (167.35) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 20.7 and 21.60 respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (92.27%) estimates for this trait was moderately high, genetic advance (25.60) was low and genetic advance in per cent of mean (40.90) were found moderately high (Table 2) revealed that this trait was governed by non-additive.

### 4.2.6 Pod length (cm)

It ranged from 3.42 to 6.31 cm with a mean of 4.06 cm. The minimum pod length was recorded by the accession 'BD- 4169' and accession 'BARI Motor-1' showed the maximum pod length. The phenotypic variance (0.34) appeared to be higher than the genotypic variance (0.26) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 14.29 and 12.45 respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (75.92%) estimates for this trait was high, genetic advance (0.91) was low and genetic advance in per cent of mean (22.34) was found moderately high (Table 2) revealed that this trait was governed by non-additive gene.

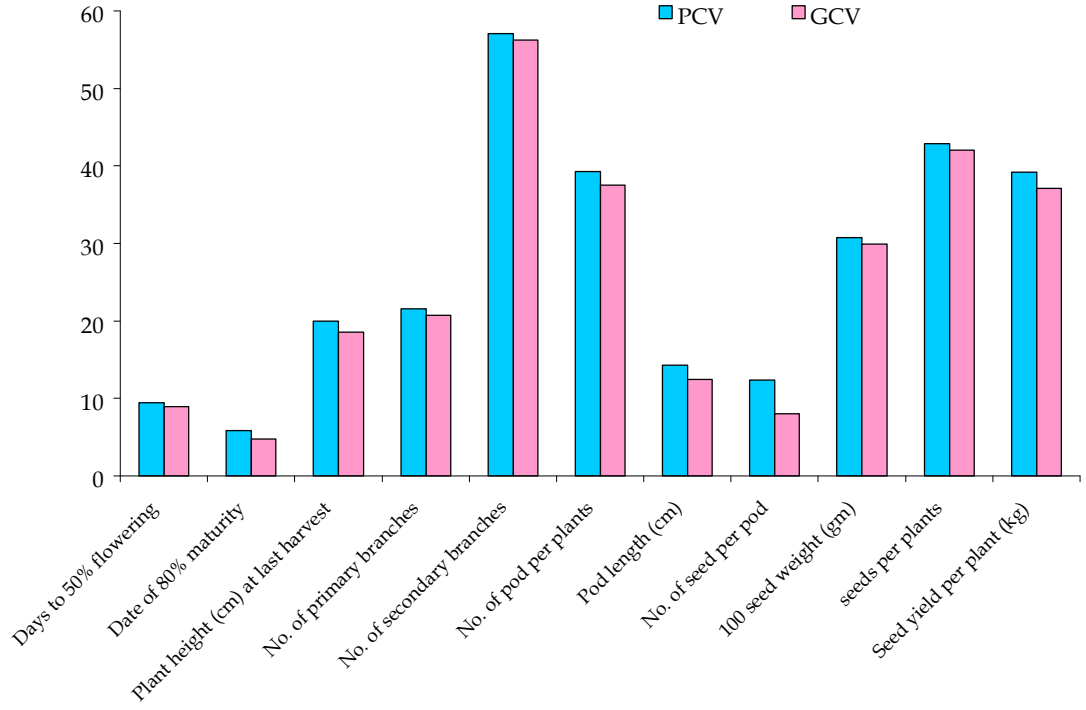


**Fig1: Genotypic & phenotypic variability in Pea**

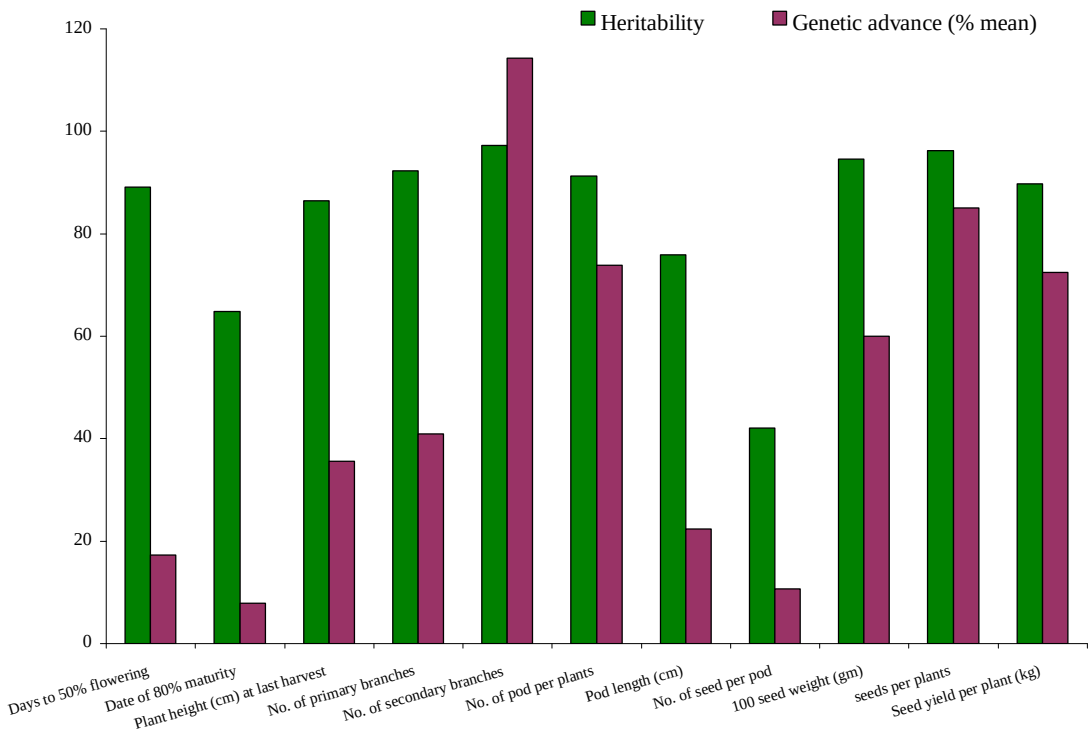


**Fig2: Heritability & genetic advance over mean in Pea**

### 4.2.8 Hundred seed weight (g)

The mean hundred seed weight noticed was 7.55 g with a range of 5.13 g to 21.40 g. The line ‘BD-4137’ showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession ‘BARI Motor-1’. The phenotypic variance (5.40) appeared to be higher than the genotypic variance (5.1) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 30.79 and 29.94, respectively which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The heritability (94.59%) estimates for this trait was very high, genetic advance (4.53) was moderately high and genetic advance in per cent of mean (59.99) was found high (Table 2), revealed that this trait was governed by additive gene.

### 4.2.9 Pods per plant

The number of pods per plant was ranged from 31.08 to 89.00 with mean of 62.50.The minimum number of pods per plant was observed in accession ‘BARI Motor-1’ while maximum number of pods per plant was found in the genotype ‘BD-7215’. The phenotypic variance (181.37) appeared to be higher than the genotypic variance (167.35) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 20.7 and 21.55 respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (92.27%) estimates for this trait was low, genetic advance (7.58) was moderately high and genetic advance in per cent of mean (40.90) was found low (Table 2) revealed that this trait was governed by non-additive gene. Genotypic and phenotypic coefficients of variation were higher reported by Devendra *et al.,* (1998) and Vikas *et al.,* (1999).

### 4.2.10 Number of seeds per pod

The genotypes stations differed significantly for this character. The values ranged from 3.35 to 5.17 with a mean of 4.14. The genotype 'BARI Motor-1' had the highest number of seeds per pod while it was lowest in the genotype 'BD-4173'.The phenotypic variance (0.26) appeared to be higher than the genotypic variance (0.11) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 12.37 and 8.03 respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (42.13%) estimates for this trait was low, genetic advance (0.44) and genetic advance in per cent of mean (10.74) was found low (Table 2) revealed that this trait was governed by non-additive gene.

**4.2.11 Seeds per plant**

It ranged from 12.67 to 178.00 with a mean of 86.00. Highest seeds per plant were recorded by the accession 'BD-4142 while accession 'BARI Motor-I' showed the lowest seeds per plant. The phenotypic variance (1359.10) appeared to be higher than the genotypic variance (1307.89) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 29.94 and 30.79 respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability (96.23%) estimates for this trait was low, genetic advance (73.08) was very high and genetic advance in per cent of mean (84.98) was found low (Table 2), revealed that this trait was governed by non-additive gene.

**4.2.12 Plant maturity**

The value ranged from 55.0 to 68.33 with a mean of 61.26. The genotype 'BD-4150' had highest and lowest in the genotype BD-4162. The phenotypic variance (12.99) appeared to be higher than the genotypic variance (8.41) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 4.78 and 5.88, respectively (Table 2) which were close to each other (Table 2). There was a very little difference between phenotypic and genotypic co-efficient of variation,

Indicating minor environmental influence on this character. The heritability (64.79%) estimates for this trait was low, genetic advance (4.81) and genetic advance in per cent of mean (7.85) was found low (Table 2) revealed that this trait was governed by non-additive gene. The low GCV and PCV was also observed by Gupta *et al*. (2006) supported this findings.

**4.2.13 Seed yield per plant (g)**

The mean seed yield per plant noticed was 6.40 g with a range of 2.74 g to 6.28g in the genotype 'BD-4174' and 'BD-4142' respectively. The phenotypic variance (6.28) appeared to be higher than the genotypic variance (5.64) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 37.12 and 39.19, respectively (Table 2) which indicated presence of considerable variability among the genotypes. The heritability 89.69%) estimates for this trait was low, genetic advance (4.63) and genetic advance in per cent of mean (72.41) was found low (Table 2), revealed that this trait was governed by non-additive gene. The high genotypic and phenotypic coefficient of variability were exhibited by fruit yield per plant, these findings are similar with earlier reports of Bhupendra (2008), and Pathak and Jamwal (2002). Tiwari *et al*. (2001) suggested the findings as moderate heritability coupled with moderate genetic advance attributed to non-additive gene actions.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was observed for number of branches, plant height, and number of pod per plant. These traits were most probably controlled by additive gene action which is very useful in selection.

The highest heritability and low genetic advance recorded for no. of secondary branches per plant revealed the major role of non-additive gene action in the transmission of these characters from parents to off springs.

**4.3 CORRELATION CO-EFFICIENT**

Grafius (1964) pointed out that the structure of yield proved through its components rather than directly would be more efficient. The study of yield components and their inter relationship along with yield and their direct and indirect contribution to yield is

of immense importance. Falconer (1981) said that the help to base selection procedure is to strike a balance when two opposite desirable characters affecting the principal characters are being selected. It also helps to improve different characters simultaneously.

Yield is the resultant of combined effect of several component characters and environment. Understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Correlation studies provide information on the nature and extent of association between only two pairs of metric characters. From this it would be possible to bring about genetic up gradation in one character by selection of the other of a pair obviously; knowledge about character associations will surely help to identify the characters to make selection for higher yield with a view to determine the extent and nature of relationship prevailing among yield contributing characters. Hence, an attempt has been made to study the character association in the pea accessions at both the levels.

For clear understanding correlation coefficients were separated into genotypic and phenotypic level in Table 3. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. In some cases phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level.

**4.3.2 Days to 50 per cent flowering:**

The correlation of days to 50 per cent flowering with number of secondary branches per plant (0.403) and plant height (0.367) was positive and highly significant at genotypic level.

**4.3.3 Plant height:**

Plant height had highly significant and positive correlation with no. of secondary branches per plant (0.604 and 0.608), pod per plant (0.563 and 0.573), seeds per pod (0.500 and 0.503) and seed yield per plant (0.594 and 0.603) at both the levels. A significant negative correlation of plant height with pod length (-0.306 and -0.315) and hundred seed weight (-0.384 and -0.391) at both levels (Table 3).

**4.3.4 Number of Primary branches per plant:**

The number of primary branches per plant had positive and highly significant correlation with seeds yield per plant (0.315 and 0.324) both at genotypic and phenotypic level and with internodes length (0.303) and no. of seeds per pod (0.330) at only genotypic level(Table 3). It had a negative and significant association with hundred seed weight (-0.331 and -0.192) at both the levels.

**4.3.10 Number of seeds per pod:**

Number of seeds per pod showed positive and highly significant correlation with seeds yield per plant (0.341 and 0.335) (Table 3).

### 4.3.11 Seeds per plant:

Seeds per plant had significant positive association with seed yield per plant (0.887) at both level (Table 3).

### 4.3.12 Plant Maturity:

Plant maturity had significant positive association with 100 seed weight (0.866 and 0.988) and no. of secondary branches per plant (0.616 and 0.718) at both level. It also had significant negative association with no. of seed per pod (-0.619 and -.0.685) at both level (Table 3).

### 4.3.13 Seed yield per Plant:

A highly significant and positive association of seed yield per plant at both the genotypic and phenotypic levels was observed with pod per plant (0.872 and 0.872), seed per plant (0.887 and 0.887), plant height (0.593 and 0.603) and seeds per pod (0.341 and 0.335), secondary branches per plant (0.513 and 0.519) and primary branches per plant (0.315 and 0.324) had shown significant positive association with fruit yield per plant at both the levels (Table 3).

Inderjit *et al.*, (2007) reported that significant positive correlation of seed yield with pods per plant, clusters per plant and seeds per pod. Highly significant and positive correlation was observed between seed yield per plant and number of pods per plant, number of seeds per pod, pod length suggesting that these were the major yield contributing characters (Harpreet *et al*., 2007).

In the present study, yield and yield components were investigated and their relationship with fruit yield per plant as well as among themselves was determined using correlation analysis. The character, number of fruits per plant had highly positive and significant correlation with fruit yield per plant respectively at both genotypic and phenotypic levels. Direct selection of genotype based on such characters in different. Therefore, selection for any of these highly associated characters with fruit yield per plant will indirectly help in selecting the plants with high

yield. Hence, it is worthwhile to have genotypes with higher number of fruits per plant to get higher yields. Similar result was observed by Das *et al.*, (1998), Raijadhav *et al.*, (1996), Singh *et al*., (1997) and Aravindakumar and Malge (2002), who also noticed positive association of number of fruits per plant with fruit yield per plant.

Hence, selection for any of these traits would improve the other traits.

These results were in conformity with the findings of Anandagouda (1997) and Patil (1998). These results suggested that the number of branches can advantageously can be used as criteria for selection.

**4.4 Path coefficient analysis**

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder too specifically

**G12** **G25**

**Plate-4. Two different color of flower in two genotypes**

**G21** **G45**

**Plate-5. Two different plant types in two genotypes**

identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

In path coefficient analysis the direct effect of a trait on fruit yield per plant and its indirect effect through other characters were computed and the results are presented in Table 4.

### 4.4.1 Direct effect

Six out of eleven characters had positive direct effect on seed yield per plant. The characters which had positive direct effect are plant height (0.251), days to 80% maturity (0.0427), pod per plant (0.6719), hundred seed weight (0.2392), number of seeds per pod (0.2321) and seeds per plant (0.2778) (Table 4). However, character viz., days to 50% flowering (-0.0918), primary branches per plant (-0.0175), secondary branches per plant (-0.1711), pod length (-0.0396) had negative direct effect on seed yield.

Path coefficient analysis revealed that seed yield per plant was directly influenced by seeds per plant, hundred seed weight and internodes length. Hence, selection for any of these independent traits leads to improving the genotypes for seed yield per plant.

### 4.4.2 Indirect effects

#### 4.4.2.2 Days to 50 per cent flowering:

Days to 50 per cent flowering showed positive indirect effect to seed yield per plant via plant height (0.0879). It had a negative indirect effect through secondary branches (-0.0679) (Table 4).

#### 4.4.2.3 Plant height:

The indirect and positive effect on seed yield per plant exhibited by plant height via pod per plant (0.3783), pod length (0.0121) and seeds per plant (0.0462), whereas, It had a negative indirect effect through seeds per plant (-0.1389) and no, of secondary branches per plant (-0.1033) (Table 4).

**4.4.2.4 Primary Branches per plant:**

Branches per plant had negative indirect effect through hundred seed weight (-0.0779) (Table 4). However, its indirect effects through pod per plant (0.1881) and seeds per pod (0.083) leading to positive association.

**4.4.2.5 Number of Secondary branches per plant:**

Number of secondary branches showed indirect positive effects on seed yield per plant by pod per plant (.03917). It showed negative indirect effects towards yield through hundred seed weight (-0.0459) (Table 4).

**4.4.2.6 Pod length (cm):**

Pod length showed indirect positive effects on seed yield per plant by hundred seed weight (0.1579), number of seeds per pod (0.0269) and secondary branches per plant (0.011). It showed indirect negative effect on seed yield per plant through seeds per plant (-0.0702) and no. of pod per plant (-0.2156). Pod length had negative direct effect on seed yield per plant. Further, it showed positive indirect effects towards yield through hundred seed weight.

**4.4.2.7 Hundred seed weight (g):**

Hundred seed weight had positive indirect effect through plant maturity (0.0369), primary branches per plant (0.057) and secondary branches per plant (0.0328) to seed yield. This trait showed negative indirect effect via seeds per plant (-0.1052), pod length (-0.0261) and pod per plant (-0.278).

**4.4.2.9 Pods per plant:**

Pods per plant showed positive indirect effect through seeds per plant (0.2519), plant height (0.1414) and seeds per pod (0.0274). This trait showed the negative indirect effect with hundred seed weight (-0.099) and branches per plant (-0.0049) to the seed yield. Pods per plant had negative direct effect on fruit yield per plant and it showed positive indirect contribution towards yield through seeds per plant and pod length.

**4.4.2.10 Number of seeds per pod:**

Number of seeds per pod had positive and indirect influence on seed yield per plant through seed per plant (0.789) pods per plant (0.0793) plant height (0.0499). However, this trait showed the negative indirect effect for 50% flowering (0.0197) and 80% maturity (0.0264).

**4.4.2.11 Seeds per plant:**

Seeds per plant had positive influence via plant height (0.1256), pod per plant (0.6094) and seeds per pod (0.0659). It influenced the seed yield per plant negatively through hundred seed weight 0.0906).

**4.4.2.12 Plant maturity:**

Plant maturity showed positive influenced for seeds per plant (0.050) and 100 seed weight (0.2071), it influenced the seed yield per plant in negative direction through hundred seed weight (-0.1436) and secondary branches per plant (-0.1054).

From the present path analysis study in pea, it may be concluded that improvement in seed yield per plant could be brought by selection for component characters like seeds per plant, hundred seed weight and internodes length.

**4.5 MULTVARIATE ANALYSIS**

### 4.5.1 Principal component analysis (PCA):

Analysis yielded Eigen values of each principal component axes of coordination of genotypes in which the first axes accounted 39.806% of the total variation among the genotypes, while 10 of these with Eigen values above unity accounted for 99.55% presented in Table 5. Based on principal component scores I and II obtained from the principal component analysis, a two dimensional scatter diagram ($Z_1$-$Z_2$) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in Fig 3. The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes.

**Table 5. Eigen value, % variance and cumulative (%) total variance of the principal components**

| Principal component axes | Eigen value | % Variance | Cumulative (%) total variance |
|---|---|---|---|
| I | 4.379 | 39.806 | 39.81 |
| II | 1.624 | 14.767 | 54.57 |
| III | 1.253 | 11.389 | 65.96 |
| IV | 1.051 | 9.555 | 75.52 |
| V | 0.891 | 8.100 | 83.62 |
| VI | 0.580 | 5.270 | 88.89 |
| VII | 0.492 | 4.469 | 93.36 |
| VIII | 0.326 | 2.965 | 96.32 |
| IX | 0.287 | 2.612 | 98.93 |
| X | 0.068 | 0.619 | 99.55 |
| XI | 0.049 | 0.449 | 100.00 |

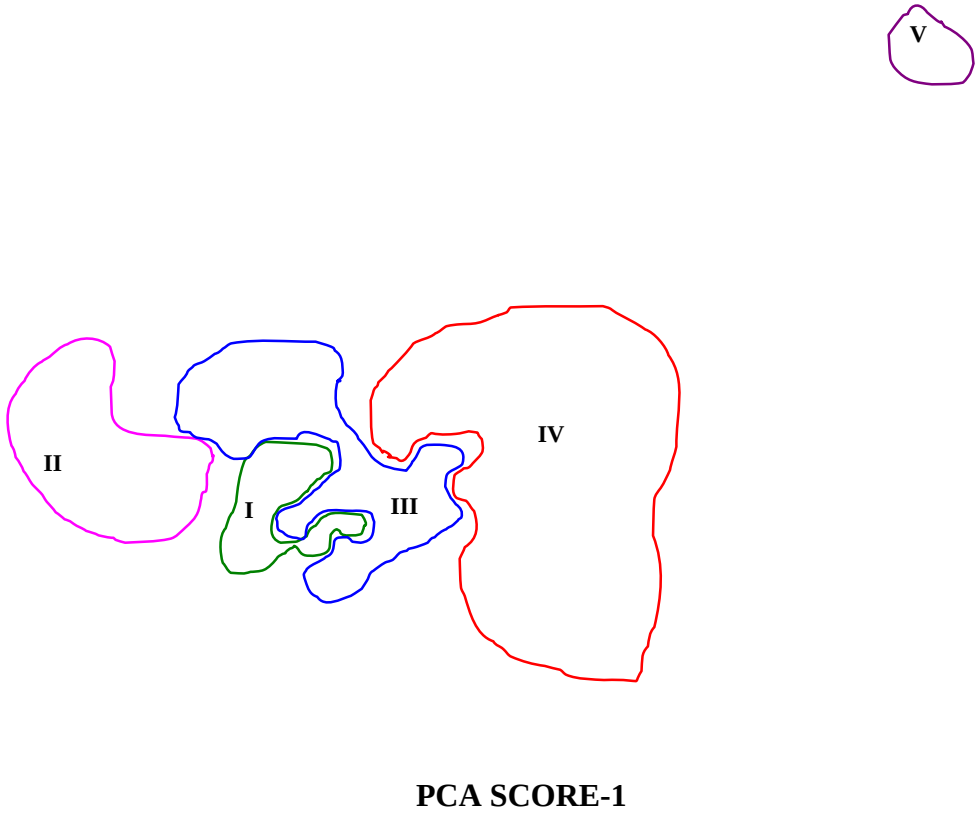


**Fig .3 Scatter diagram of 45 genotypes of based on their principal component scores**

### 4.5.2 Nonhierarchical clustering

With the application of co variance matrix for non hierarchical clustering, 45 pea genotypes were grouped into five different clusters. From Table 6, cluster III had the maximum 14 genotypes (BD-4147, BD-4151, BD-4152, BD-4153, BD-4160, BD-4161, BD-4162,BD-4163, BD-4164, BD-4165, BD-4166,BD-4167,BD-4192, BD-4492) followed by cluster IV (BD-4169, BD4170, BD-4171,BD-4173, BD-4174, BD-4175,BD-4176, BD-4177, BD-4178, BD4191,BD-4492, BD-7216 and BD-7218), cluster II (BD-4137, BD-4138, BD-4139, BD-4142, BD-4143, BD-4144, BD-4145, BD-4146, BD-7215 and BD-7217) and cluster I (BD-4135, BD-4136, BD-4141, BD-4149, BD4150, BD-4156 and BD-4168). Cluster V comprised with a single genotype BARI Motor-I. Satyawan *et al*., (2004) reported nine clustering in field pea, Singh and Singh (2003) studied genetic divergence for 13 traits and had six clusters and Vikas and Singh (1999) had nine clusters for 45 pea genotypes.

The results confirmed the clustering pattern of the genotype according to the principal component analysis. Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 6. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. For that reason it could be said that the results obtained through PCA were established by non-hierarchical clustering.

**Table.6 Number, percent and name of genotypes in different cluster**

| Cluster number | Number of genotypes | Percent (%) | Name of genotypes |
|---|---|---|---|
| I | 7 | 15.56 | $G_1$, $G_2$, $G_6$, $G_{13}$, $G_{14}$, $G_{18}$ and $G_{27}$ |
| II | 10 | 22.22 | $G_3$, $G_4$, $G_5$, $G_7$, $G_8$, $G_9$, $G_{10}$, $G_{11}$, $G_{41}$ and $G_{43}$ |
| III | 14 | 31.11 | $G_{12}$, $G_{15}$, $G_{16}$, $G_{17}$, $G_{19}$, $G_{20}$, $G_{21}$, $G_{22}$, $G_{23}$, $G_{24}$, $G_{25}$, $G_{26}$, $G_{38}$ and $G_{40}$ |
| IV | 13 | 28.89 | $G_{28}$, $G_{29}$, $G_{30}$, $G_{31}$, $G_{32}$, $G_{33}$, $G_{34}$, $G_{35}$, $G_{36}$, $G_{37}$, $G_{39}$, $G_{42}$ and $G_{44}$ |
| V | 1 | 2.22 | $G_{45}$ |

### 4.5.3 Canonical variate analysis

The inter cluster $D^2$ values are given in Table 7 and the nearest cluster from each cluster based on $D^2$ values are given in Table 7. The inter cluster $D^2$ values were the maximum (39.58) between the cluster II and cluster V, flowed by II and V (36.12) and II and IV (35.07) and I II and V (34.53). The higher inter cluster distance between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between the cluster II and cluster V indicate the genotype of these clusters were diverse then those clusters.

The minimum distance was observed between the cluster I and cluster III (14.33) indicate the genotype of these clusters were closely related with those clusters.

The intra cluster $D^2$ values are given in Table 7. The intra cluster distance was observed in the clusters I, II,III, IV. The intra cluster $D^2$ values were the maximum (23.65) in the cluster II , flowed by III(15.62) and I (12.22). The inter cluster distance was higher than intra cluster distance indicate the genotype of same clusters were closely related with each other, where largely distance indicate genetic diversity among the genotype of different groups.

**Table: 7 Intra-Inter cluster distance for 45 genotype**

| Characters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V |
|---|---|---|---|---|---|
| I | 149.37<br>(12.22) | 464.40<br>(21.55) | 205.33<br>(14.33) | 503.63<br>(22.44) | 1059.40<br>(32.55) |
| II | | 559.20<br>(23.65) | 616.71<br>(24.83) | 1230.04<br>(35.07) | 1566.56<br>(39.58) |
| III | | | 243.84<br>(15.62) | 418.45<br>(20.46) | 1192.53<br>(34.53) |
| IV | | | | 122.55<br>(11.07) | 1304.84<br>(36.12) |
| V | | | | | 0.000 |

**Table: 8 The nearest & farthest clusters from each clusters between $D^2$ value**

| Sl. No | Clusters | Nearest clusters with $D^2$ value | Farthest clusters with $D^2$ value |
|---|---|---|---|
| 1. | I | III (14.33) | V(32.55) |
| 2. | II | III (24.83) | V (39.58) |
| 3. | III | IV (20.46) | V(34.53) |
| 4. | IV | v (36.12) | |

### 4.5.4 Principal co-ordinate analysis (PCO)

Inter genotypic distances ($D^2$) as obtained by principal coordinate analysis (PCO) for all possible combinations between the pairs of genotypes. Inter genotypic distances as obtained from principal coordinate analysis showed that the highest distance was observed between the genotype 10 and 33 (Table 9). The lowest distance was observed between genotypes 32 and 35. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 45 genotypes of pea studied.

**Table.9 Ten highest and lowest distances among 45 genotypes**

| **Highest Distance** | | | | **Lowest Distance** | | | |
|---|---|---|---|---|---|---|---|
| Sl. No | Genotype | | Distance | Sl. No | Genotype | | Distance |
| 1. | G10 | G33 | 3453.67 | 1. | G32 | G34 | 11.11 |
| 2. | G10 | G31 | 3313.45 | 2. | G30 | G35 | 12.34 |
| 3. | G10 | G39 | 3293.02 | 3. | G35 | G36 | 15.36 |
| 4. | G4 | G39 | 3172.58 | 4. | G30 | G36 | 19.39 |
| 5. | G4 | G36 | 3030.51 | 5. | G33 | G39 | 19.49 |
| 6. | G10 | G30 | 2201.81 | 6. | G33 | G36 | 20.29 |
| 7. | G10 | G28 | 2877.62 | 7. | G31 | G33 | 22.65 |
| 8. | G10 | G34 | 2843.56 | 8. | G33 | G35 | 27.35 |
| 9. | G10 | G33 | 2435.24 | 9. | G34 | G35 | 28.66 |
| 10. | G10 | G11 | 2368.62 | 10. | G34 | G36 | 28.77 |

### 4.5.5 Cluster mean analysis

The cluster means of 11 different characters (Table 10) were compared and indicated considerable differences between clusters for all the characters studied .Maximum (38.00) and minimum (33.94) days to 50 per cent flowering were observed in cluster V and IV respectively. Genotypes in cluster V showed the lowest plant height (31.04) and that in cluster III had the highest mean (84.61) plant height. Maximum (31.13) and minimum (4.00) number of primary branches were observed in cluster II and V respectively. Maximum number of secondary branches per plant was observed in cluster II (1.11); whereas minimum number was observed in cluster IV. The maximum pod Length (6.31) was observed in the cluster V where as minimum pod Length (3.74) was observed in cluster I.

100 Seed Weight was the least in cluster II with a mean value of (6.71) and it was highest in genotypes belongs to the cluster V (21.4). Least pods per plant were recorded by the cluster V (31.4) while cluster II (72.32) showed the highest pods per plant. The minimum number of seed per pod was observed in cluster I (3.86); whereas maximum number of seed per Pod was observed in cluster III (4.42).

A least seed per plant was recorded by the genotype making up cluster V (12.67) while cluster II showed the highest seeds (137.53) per plant. Cluster V composed of genotypes showing the highest plant maturity (65.5) and the lowest in the cluster II (58.33). The minimum seed yield per plant (2.75 g) was observed in the cluster V, whereas the maximum (9.24) was in the cluster II.

Cluster V mainly had a late flowering genotype, maximum pod length & 100 seed weight where as it produced the lowest mean values for plant height, no. of primary branches, no. of pod per plant, seed per pod & seed yield per plant. Cluster II had the lowest pod length, 100 seed weight, highest primary branches per plant, secondary branches, pods per plant, seed per pod, seeds per plant, seed yield per plant & least pod length, 100 seed weight. Again cluster IV had the minimum days to 50% flowering &no. of secondary branches. The genotypes belonging to the cluster V were low yielder because they possessed the lowest number of seeds per pod and lowest seed yield per plant later flowering i.e. they need maximum days to 50% flowering. They were short i.e. possessed the lowest mean values for plant height and number of primary branches per plant. The genotypes of the cluster II were more yielder because of maximum pods per plant, seeds per plant and seed yield per plant. They also had least pod length and 100 seed weight and more branches per plant. To develop high yielding varieties these groups can be used in hybridization program.

**Table. 10 Cluster mean for twelve yield and yield characters of 45 genotypes**

| Characters | Cluster I | Cluster II | Cluster II | Cluster IV | Cluster V |
|---|---|---|---|---|---|
| Days to 50% flowering | 37.62 | 37.13 | 36.33 | 33.97 | 38.00 |
| Date of 80% maturity | 65.05 | 62.80 | 58.33 | 61.20 | 61.00 |
| Plant height (cm) at last harvest | 79.40 | 80.84 | 84.61 | 59.48 | 31.04 |
| No. of primary branches | 58.46 | 72.32 | 62.31 | 59.73 | 31.04 |
| No. of secondary branches | 0.79 | 1.11 | 0.87 | 0.32 | 0.43 |
| No. of pod per plants | 23.93 | 31.16 | 21.07 | 12.67 | 4.00 |
| Pod length (cm) | 3.87 | 3.97 | 4.03 | 4.08 | 6.31 |
| No. of seed per pod | 3.86 | 4.42 | 4.15 | 4.08 | 4.01 |
| 100 seed weight (gm) | 7.08 | 6.71 | 7.57 | 7.35 | 21.40 |
| seeds per plants | 92.10 | 137.53 | 83.25 | 51.69 | 12.67 |

| | | | | | |
|---|---|---|---|---|---|
| Seed yield per plant (kg) | 6.88 | 9.24 | 6.77 | 3.83 | 2.75 |

### 4.5.6 Cluster diagram

With the help of $D^2$ values within and between clusters, an arbitrary cluster diagram (Fig 4) was constructed, which showed the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the (Fig 4) that the genotypes included in the cluster II was far diverse from the genotypes of the cluster V and where the genotypes belonging to III- IV were the least diverse. Genotypes of cluster I and II and I-IV were moderately diverse from each other. The similar diverse genotypes were included between the cluster IV-V and II- IV.

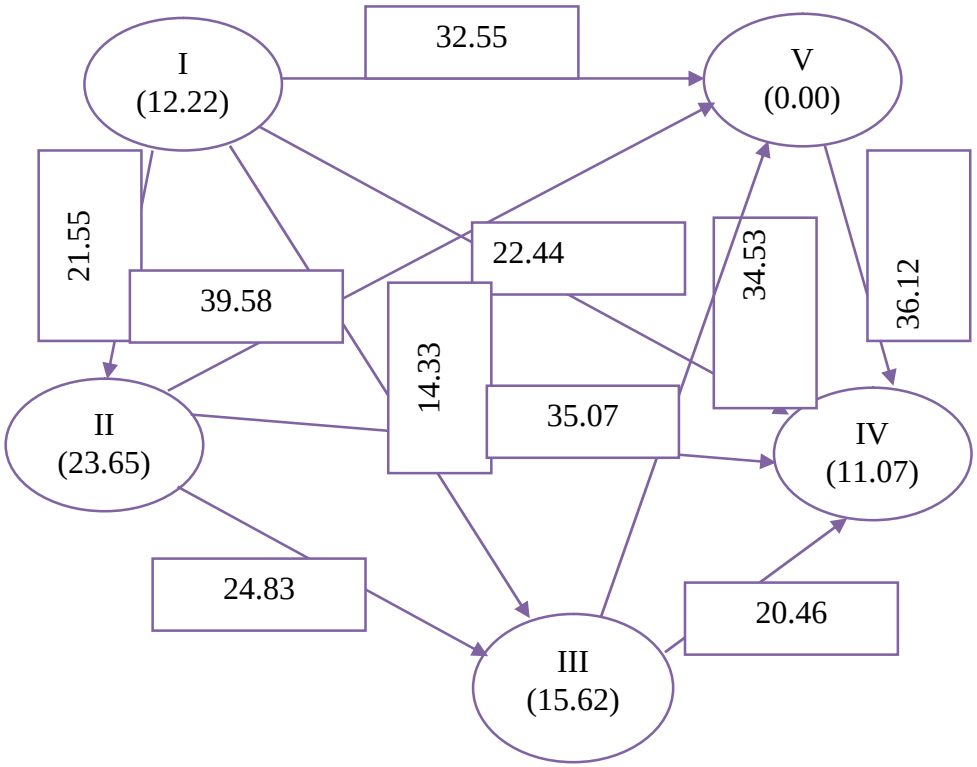


**Fig. 4. Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$ Values) of 45 genotypes.**

**4.5.7 Selection of genotypes as parent for hybridization programme:**

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distance parents, (Falconer, 1960; Moll et *al*., 1962; 1962 Ramanujan *et al*., 1974; Ghaderi *et al.*, 1984). Considering the magnitude of cluster mean and agronomic performance the genotype G 41(BD-715) for minimum days to 50% flowering from cluster II; G45 (BARI Motor-I) for maximum seed size and maximum pod length from cluster II; G21 (BD-4162) for maximum plant height from cluster III were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G10 (BD-4145) and G33 (BD-4174); G10 (BD-4145) and G31 (4173); G10 (BD4145) and G39 (BD-4492); G10 (BD-4174) and G28 (BD-4169); G4 (BD-4138) and G39 (BD-4492) may be suggested for future hybridization program.

# CHAPTER V

## SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify divergent parents for hybridization programme, identify the characters contributing to genetic diversity, asses the magnitude of genetic divergence in genotypes and determine the variability in respect of yield and some yield contributing characters, the degrees of association among the characters and their direct and indirect effects of 45 genotypes of *Pisum sativum* L. at the experimental farm of Sher-E-Bangla Agricultural University, Dhaka, during December 2013 to March 2014. The salient findings of the present study have been summarized on the basis of the characters studied.

The analysis of variance showed significant differences among the genotypes for all the characters. The accession BD-7215 was the earliest to first flower of 26.64 days while BD-4143 was late to first flower for 40.00 days. The maximum plant height (95.50 cm) was recorded by the genotype BD-4162 and the lowest plant height (30.14 cm) was recorded by BARI Motor-I. The maximum number of branches per plant was recorded in BD-4142 and BARI Motor-I genotype showed the minimum number of branches per plant. The maximum number of secondary branches per plant was recorded in the genotype BD-4144 and the minimum in the genotype BD- 4173. The minimum pod length was recorded by the accession BD- 4169 and accession BARI Motor-1 showed the maximum pod length. The line BD-4137 showed the minimum hundred seed weight and the maximum hundred seed weight was recorded in the accession BARI Motor-1. The minimum number of pods per plant was observed in accession BARI Motor-1 while maximum number of pods per plant was found in the genotype BD-7215. The genotype BARI Motor-1 had highest number of seeds per pod while it was the lowest in the genotype BD-4142. Highest seeds per plant were recorded by the accession BD-4142 while accession BARI Motor-1 showed the lowest seeds per plant. The genotype BD-4173 had highest plant maturity and. lowest in the genotype BARI Motor-1. Genotype BD-4150 and BD-4l62 were the lowest and the highest for seed yield per plant, respectively. The phenotypic variance was higher than genotypic variance in all the characters studied. The phenotypic coefficients of variation were also higher than genotypic coefficients of variation in all the characters studied. Phenotypic coefficients of variation were also close to genotypic

coefficients of variation for most of the characters except plant height, branches per plant, pods per plant and seeds per plant. High heritability (> 60%) was observed for the characters like days to first flowering, pod length and hundred seed weight. The high heritability coupled with high genetic advance in percent of mean observed in pod length and hundred seed weight suggested that effective selection may be done for these characters. Low heritability coupled with low genetic advance in percent of mean was observed nodes per plant, pods per plant and number of seeds per pod.

Pod length, hundred seed weight, pods per plant, and seeds per plant showed significant and positive correlation with seed yield per plant at both genotypic and phenotypic levels. Significant and positive genotypic and phenotypic correlation was observed between days to first flowering and days to 50% flowering. Plant height was positively and significantly correlated with branches per plant, nodes per plant, internode length, pods per plant and seeds per plant at both levels. Significant and positive correlation was observed between branches plant and pods per plant and seeds per plant. Nodes per plant were significantly and positively correlate with internode length. Significant positive genotypic and phenotypic correlation was observed by pod length with hundred seed weight and number of seeds per pod. Pods per plant were positively and significantly correlated with seeds per plant.

Seeds per plant showed the highest positive direct effect (0.6719) with seed yield per plant. On the other hand negative direct effect on seed yield per plant showed by days to first and 50% flowering, branches per plant, nodes per plant, pod length, pods per plant and plant maturity. Plant height, internode length, hundred seed weight and number of seeds per pod also showed positive direct effect on seed yield. The highest indirect effect of pods per plant observed with seeds per pod. Seeds per pod showed high direct effect on seed yield indicated that direct selection for this trait might be effective and there is a possibility of improving seed yield per plant through selection based on those characters.

Genetic diversity of forty five pea genotypes based on thirteen characters was measured through multivariate analysis. The 45 genotypes fell into five distant clusters. The cluster III comprised the maximum number 14 of genotypes followed by cluster IV 13. The cluster I, II and V comprised 7, 10 and 1 genotypes, respectively. The highest inter-cluster distance (39.58) was observed between the cluster II and V and the

highest distant genotypes were G10 (BD-4145) and G33 (BD-4175). The lowest inter-cluster distance (14.33) was observed between the cluster I and III and the lowest distance genotypes were G32 (BD-4175) and G34 (BD-4176).

The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire five clusters was more or less low indicating that the genotypes within the same cluster were closely related. Days of 50% Flowering, Plant Height and Branches per plant were the important component characters having higher contribution to the genetic divergence.

The result of the present study revealed that a wide variability exists among the collected pea genotypes. In addition, there was also genotype of different yield contributing characters with yield of pea. From the findings of the present study, the following conclusions could be drawn:

1. Wide range of genetic diversity existed among the pea genotypes. Wide genetic diversity was observed in 45 genotypes of pea, which were grouped into five clusters and most diverse genotypes were G33 and G10. That variability could be used for future breeding programme of pea in Bangladesh.

2. High heritability coupled with high genetic advance in percent of mean was observed in pod length and hundred seed weight. Hence, yield improvement in pea would be achieved though selection of these characters.

3. The characters of Pod length, hundred seed weight, pods per plant, and seeds per plant showed significant and positive correlation with seed yield per plant at both genotypic and phenotypic levels. This results suggested that seed yield per plant can be increased by improving these characters.

4. Plant height, internode length, hundred seed weight, number of seeds per pod and seeds per plant showed positive direct effect on yield. So yield improvement was associated with these characters.

5. The genotypes of clusters II were more diverse from the genotypes of cluster V.

6. Pod length and pods per plant were found responsible for the maximum diversity. On the other hand, number of seed per Pod and days of first flowering have the least responsibility of both the primary and secondary differentiation of genotypes.

7. Further collection of pea germplasms would be continued for getting more variability and desired traits in pea.

**Based on the results of the study, the following recommendations may be drawn:**

1. Genotypes G7 (BD-4142), G8 (BD-4243), G6 (BD-4141), G10 (BD-4145), G34(BD-4175) could be included in the furthest study in view of seed yield for releasing as pea verities.

2. The maximum variability found for pod length, seeds per pod and hundred seed weight. So selection based on these characters could be effective for the improvement of pea yield.

3. The genotypes of cluster II and V could be used as parents for future breeding programme to developed pea variety.

## REFERENCES


Abdou, A.B.A., Mohamed, M.F. and Kandeel, N.M. (1999). Breeding implications on cultivar selection in garden pea *(Pisum sativum* L.*)* towards enhancing earliness and pod yield. AsianJ. *Agril. Sd., **30**(3): 117-132.*

Aher, R.P., Salunke, J.S., Shinde, GC. and Kute, N. S. (1998). Genetic diversity in early pigeon *pea. Indian J. Pulse Res.* **11**(1): 68-71.

AI-Jibouri, H.A., Miller, P.A. and Robinson, H.V., (1958). Genotypic and environmental variances and co-variances in an upland cotton cross of inter specific origin. *Agron.1, **50**:633-636.*

Avc, M.A. and Ceyhan, E. (2006). Correlations and genetic analysis of pod characteristics in pea (*Pisum sativum* L.*). Asian 1 P1. Sd., 5(1): 1-4.*

Backiyarani, Nadarajan, S. N., Rajendra, C. and Shanti, S. (2000). Genetic divergence for physiological traits in cowpea ( *Vinga unguiculata* L.). *Legume Res.* **23**(2): 114-117.

BBS. (2013). Year Book of Agricultural Statistics of Bangladesh. Bangladesh Bureau of Statistics, Planning Division, Ministry of Planning, Govt. of the Peoples Republic of Bangladesh, Dhaka. p. 110.

Bhardwaj, R.K. and Kohli, U.K. (1999). Association and path analysis in garden pea *(Pisum sativum* L.*). Hort. J.,* **12**(2): 6 1-65.

Bhupendra K. (2008). Variability, heritability and genetic advance in pea *(Pisum sativum* L.*). Intl. I Fl. Sd.*, **3**(1): 211-212.

Blixt, S. (1970). *Pisum*. In genetic resources in plant-Their Exploration and Conservation. 0. H. Frankel and E. Bennet *(eds.). lnt. Biol. Prog.,* Blackwell Sci. Publ. Oxford., pp: 31-326.

Burton, G.W., (1952., Quantitative interaction in grasses. In : *Proc.* 6th Inter Grassland Congr., **1**: 277-283.

Chaudhary, D.K. and Sharma R.R.. (2003). Genetic variability, correlation and path analysis for green pod yield and its components in garden pea. *Indian I Hort.,* **60** (3): 251-256.

Cooper, D.C. (1938). Embryology of *Pisum sativum* L. *Bot Got. Gaz.,***100**: 123-132.

Devendra, K., B.P.S. Malik R. Lekh, Kumar D.and Raj, L. (1998). Genetic variability and correlation studies in field pea *(Pisum sativum* L.*). Legume Res.,* **21**(l): 23-29.

Devendra, K., B.P.S. Malik, R. Lekh, D. Kumar and Raj L. (1998). Genetic variability and correlation studies in field pea *(Pisum sativum* L.*). Legume Res.,* **21**(1): 23-29.

Devendra, P., Singh D.P. and Singh. B.B. (2001). Evaluation of pea germpasm for yield and yield components. IndianJ. Pulses Res., **14**(2): 148-149.

Deway, D.R. and Lu, K.N.,( 1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. 1, **51**:515-518.*

Dharmendra S. and Mishra,V.K. (2008). Studies on genetic divergence in pea *(Pisum sativum* L.*). Agric. Sci. Digest,* **28**(1): 77-78.

Dharmenda, S. and Mishra,V.K. (2002). Correlation and path analysis in a diallel cross of pea. *Legume Res.,* **25**(1): 44-46.

Digby, P.N. Gaiway and Lane. P. (1989). Genstat 5, A second course. *Oxford Sd. Pubi., Oxford.* pp 103-108.

Dixit, G.P., Singh, I.P and Khare, A.P. (2002). Genetic divergence study in field pea. *Legume Res*., **25**(3): 199-201.

Gohil, R.H. (2006). Genetic divergence in pigeon pea *(Cal anus cajan* L.*). Res. on Crops.* **7** (3):748-750.

Gritton E,T and Wierzbicka, B. (1975). An embryological study of a Pisum sativum *X Vicia faba crosses. Euphytica.* **24:** 277-284.

Gritton, E.T.K. (1986). Pea Breeding, In M.J. Bassett (ed.), Breeding Veg. crops. AVI Pubi. Co. Westport. pp. 283-319.

Gupta, A.J. and Singh, Y.V. (2006). Genetic divergence in garden pea *(Pisum sativum* L. *). Indian I Genet. P1. Breed.* **66** (4): 34 1-342.

Gupta, A.J. Singh, Y.V. and Verma, T.S. (2006). Genetic variability and heritability in garden pea *(Pisum sativum* L.*). Indian I Hort*., **63**(3): 332-334.

Gupta, M.K., Singh J.P. and V.K. Mishra. (1998). Heritability, genetic advance and correlation analysis in pea *(Pisum sativum* L.*). Hisar. Crop Res*. **16** (2): 202-204.

Harland, S.C. (1984). Inheritance of immunity to mildew in Peruvian forms of *Pisum sativum* L. *Heredity*, **2**: 263-269.

Harpreet, K, Mohan S. and Brar,P.S. (2007). Correlation and path analysis in garden pea (*Pisum sativum* L.). Crop Improv., **34**(2): 186-191.

Harrington, J.B., (1940). Yielding capacity of wheat crosses as indicated by hybrid tests. Candiani. Res., **18** :5-584.

Inderjit S., Pritpal S. and Sandhu, J.S. (2007). Genetic divergence and association studies in field pea *(Pisum sativum* L.*). Crop Improv.*, ***34***(2): 179-182.

Jager, M.1., Gerethojones D. and Griffiths E. (1983). Component of partial resistant of wheat seedlings to *Seporia nodrom. Euphytica*. **32**: 575-5 85.

Jamwal, R.S., Sanjeev P. and Pritam K. (1999). Path analysis in powdery mildew resistant genotypes of garden pea *(Pisum sativum* L.*). South Indian Hort*., **47**(1-6): 313-314.

Johnson, H.W., Robinson, H.F. and Comstock, R.E., (1955). Estimation of genetic and environmental variability in soybean. *Agron.J.*, **47** : 477-483.

Kumar A and Jam B.P.. (2003). Genetic variability in pea *(Pisum sativum* L.*). J. Res. Birsa Agric. Univ*., **15**(1): 55-59.

Kumar, B.L. Ram, J.D. Singh and B. Singh. (2003). Correlation and path coefficient analysis in pea *(Pisum sativum* L.*). Frog. Agric.* **3** (12): 141-142.

Kumar, R., Dhari, R and Kumar, K. (2006). Divergence studies in pea germplasm (*Pisum sativum* L.). Nationali Fl. Improv., **8** (2): 122-124.

Mahak, S., Singh S.P., Singh B.and Kumar, P. (2004). Character association in filed pea *(Pisum sativum* L.*). Frog. Agric*. **4** (1): 41-43.

Mahalanobis, P.C., (1936). On the generalized distance in statistics. Proceedings of *National academic Sd. (India), **2*** : 79-85.

Mahamad, F., Gowda M.B and Girish, G. (2006). Assessment of genetic divergence in vegetable pigeon pea germplasm. Environ. *Eco.*, **24**S *(Special 4):* 1135-1139.

Mahanta, 1. C., Senapati, N., Samal,K.M and DhaI, A. (2001). Genetic variability performance character association and coheritability in field pea *(Pisum sativum* L.*). Legume Res.***24**(2): 92- 96.

Manikannan, C., Jebaraj S.and Ashok, S. (2000). Genetic divergence in black gram *(Vinga mungo* L.*). Madras Agril. J*. **87** (7-9): 520-523.

Manivannan, N., Murugan, E.P. Viswanathan, K. Sethuraman and Dhanakodi, C. V. (1999). Genetic divergence in mungbean. *Indian I Pulses Res.*, **12** (1): 25-29.

Manoj, K., Tewatia A.S. and Sharma. N.K. (2003). Correlation and path analysis in pea *(Pisum sativum* L.*). Haryanai. Hort. Sci.*, **32**(12): 104-107.

Mohan, S.,Yuvinder, K., Harinder, S. and Brar, P.S. (2005). Correlation and path coefficient analysis in garden pea *(Pisum sativum* L.*). Environ. Eco.*, **23**(2): 3 1 5-318.

Narendra, K. and Kumar N.. (1997). Genetic diversity among chickpea accessions. *Indian I Genetics P1. Breed.*, **57** (1): 87-90.

Pathak, S. and Jamwal, R.S. (2002). Variability and correlations for economic traits in powdery mildew resistant genotypes of garden pea *(Pisum sativum* L.*). Himachal I Agric. Res.*,**28**(1/2): 34-39.

Raj, N., Rastogi,K.B., Sharma, D.K., Sumati, N. and Kanaujia, S. P. (2000). Association of characters in pea *(Pisum sativum* L.*). Haryanal Hort. Sd*., **29**(1-2): 94-95.

Ram, S. G., Gomathinayagam P.and Rathnaswamy R.. (1997). Genetic divergence in black gram. *Madras Agril. .1*, **84** (3): 160-162.

Ramesh, C. and Tewatia, A.S. (2002). Character association and path analysis studies in garden pea *(Pisum sativum* L.*). Haryana I Hort. Sd.,* **31**(1/2): 94-97.

Ramesh, C., Tewatia A.S. and Dahiya M.S. (2002). Genetic variability and heritability studies in garden peas *(Pisum sativum* L.*). Haryana I Hort. Sd.* **31**(3-4): 250-252.

Robinson, H.F., Comstock, R.E. and Harvey, V.H. (1949). Estimates of heritability and degree of dominance in corn. *Agron.* 1, **41** : 353-359.

Rudnicki and Wenda, A.P. (2002). Usefulness of pea cultivars for mixtures with spring cereals cultivated on wheat soil complex. *Roslin.,* **221** (6): 1 99-206.

Santos, C.A.F., Menzes E.A. and *Araujo.* F.P. (1997). Genetic diversity in genotypes of cowpea under two different environments. Revista Ceres., **44** (251): 35-42.

Sarnaike, D.A., Singh, C.B. Hasija and Rao, S.K. (1990). Path analysis of green pod yield components in pea. Res. *Devel. Reporter.,* **7** (1-2): 111-114.

Satyawan, A., Malik B.P.S. and Kumar R. (2004). Variability, correlation and path analysis in field pea *(Pisum sativum* L.*). HaryanaAgril. Univ. J. Res.*, **34**(2): 149-153.

Seema, M., Kohli, U.K., Devinder, M. and Dharminder, K. (2005). Genetic variability studies in pea *(Pisum sativum* L.*). Haryanal Hort. Sci*.,**34**(12): 140-14 1.

Sharma, A.K., Singh S.P. and Sharma, M.K.. (2003). Genetic variability, heritability and character association in pea *(Pisum sativum* L.*). Crop. Res. Hisar.,* **26** (1): 135-139.'

Sharma, T.R. and Mishra S.N.. (1997). Genetic divergence and character association studies in cowpea. *Corp Res. Hisar.,* **13**(1): 109-114.

Shinde, K.G. (2000). Genetic parameters for some quantitative and qualitative traits in pea *(Pisum sativum* L.*). Orissa .1 Hort.,* **28**(1): 21-24

Shivasubramanjan, S. and Menon, N., (1973), Heterosis and inbreeding depression in rice. Madras *AgriL* 1, **60**: 1139-1144.

Singh, A.K. and Mir, M.S.( 2005). Genetic variability, heritability and genetic advance in pea *(Pisum sativum* L.*)* under cold arid region of Ladakh. Environ. Eco., 23S(Special 3):445- 49.

Singh, A.K. and Yadav, V.K.(2005). Character association and path coefficient analysis studies for certain metric traits in pea *(Pisum sativum* L.*)* under cold arid region of Ladakh. Hort. 1, **18**(1): 35-38.

Singh, G and Singh, S.P. (2003). Genetic divergence in pea *(Pisum sativum* L.*). Legum* Res., 26 2): 13 1-133.

Singh, I., Singh, P. and Sandhu, J. S. (2007). Genetic divergence and association studies in field pea *(Pisum sativum* L.*).* Crop Improv., **34**(2): 179-182.

Singh, J. D. and Singh, I. P. (2006). Genetic divergence in advanced genotypes for grain yield in field pea *(Pisum sativum* L.*). Legume Res.* **29** (4): 301-303.

Singh, J.D. and Singh, I.P. (2006). Genetic variability, heritability, expected genetic advance and character association in field pea *(Pisum sativum* L.). Legume Res. **29**(1): 65-67.

Singh, J. D. and Singh, I.P. (2006). Genetic divergence in advanced genotypes for grain yield in field pea *(Pisum sativum* L.*). Legume Res*., **29**(4): 30 1-303.

Singh, S. and R.K. Gumber. (1996). Assessment of genetic diversity in basic generations of pigeon pea. Intl. *Chickpea Pigeon pea Newsi.,* **3**: 62-64.

Sirohi, S.P.S., Yadav R. and Malik. S. (2006). Genetic variability, correlations and path coefficient analysis for seed yield and its component characters in peas *(Pisum sativuni* L.*). Fl. Arc.* **6** (2): 737-740.

Sureja, A.K and Sharma,R.R. (2001). Genetic divergence in garden pea (*Pisum sativum* L. sub. sp. *Hortense Asch and Graebn). Veg. Sci.,* **28**(1): 63-64.

Sureja, A.K. and Sharma, R.R. (2000). Genetic variability and heritability studies in garden *pea (Pisum sativum* L.*). Indian J. Hort.,* **57**(3): 243-247.

Tiwari, S.K., Singh, H.L.. Kumar R and Nigam. H.K. (2001). A postmortem of selection parameters in pea *(Pisum sativum* L.*). Crop Res*., **2** (2): 237-242.

Tripathi, A.K. (1997). Genetic divergence in chickpea. *Advance in P1. Sci.* **10** (2): 103-105.

Ushakumari, R.,S. Backiyarani and Dhanakodi, C.V. (2000). Character contribution to diversity in cowpea. *Legume Res.* **23**(2): 122-125.

Vavilov, N.1. (1926). Studies on the origin of cultivated plants. *Bull. Appl. Rot. Fl. Breed.* **16**:139-248.

Vikas, K.M. and Singh, S.P. (1999). Genetic divergence over environments in pea *(Pisurn sativum* L.*). Legume Res.* **22** (2): 104-108.

Weber, C.R. and Moot-thy, H.R. (1952). Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F2 generation of soybean crosses. *Agron.J,* **44**: 202-209.

White, 0. (1917). Studies of inheritance in *Pisum,* II. The present state of knowledge of heredity and variation in peas. *Proc. Am. Phil. Soc*. **56** : 487-5 88.

Wright, S. (1921).Correlation and Causation. *J Agric. Res.,* **20** : 202-209.

Yadav, P.K., Partap, P.S., Rana, M.K. and Tewatia, A.S. (2004). Genetic divergence studies in garden pea. *Haryana J. Hort. Sci.,* **33**(1/2): 102-105.

Yarnell, S.H. (1962). Cytogenetics of vegetable crops. III. Legumes-Garden Peas, (*Pisum sativum* L). *Bot. Rev*., **28**: 463-537.

## APPENDICES

**Appendix I. Experimental site at Sher-e-Bangla Agricultural University, Dhaka-1207**

**Appendix** II. **(A) Records of meteorological information (monthly) during the period from October 2013 to March 2014**

| Name of Months | Air temperature ($^0$C) | | Relative humidity | Rainfall (mm) |
|---|---|---|---|---|
| | Maximum | Minimum | | |
| October, 2013 | 30 | 18 | 81 | 37 |
| November, 2013 | 25 | 16 | 78 | 0 |
| December, 2013 | 22 | 14 | 74 | 0 |
| January, 2014 | 24 | 12 | 68 | 0 |
| February, 2014 | 27 | 17 | 67 | 3 |
| March, 2014 | 31 | 19 | 56 | 11 |

Source: Bangladesh Meteorological Department (Climate and weather division) Agargaon, Dhaka

**Appendix III: Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site**

**A. Physical composition of the soil**

| Soil separates | % | Methods employed |
|---|---|---|
| Sand | 36.90 | Hydrometer method (Day, 1915) |
| Silt | 26.40 | Do |
| Clay | 36.66 | Do |
| Texture class | Clay loam | Do |

**B. Chemical composition of the soil**

| Sl. No. | Soil characteristics | Analytical data | Methods employed |
|---|---|---|---|
| 1 | Organic carbon (%) | 0.82 | Walkley and Black, 1947 |
| 2 | Total N (kg/ha) | 1790.00 | Bremner and Mulvaney, 1965 |
| 3 | Total S (ppm) | 225.00 | Bardsley and Lanester, 1965 |
| 4 | Total P (ppm) | 840.00 | Olsen and Sommers, 1982 |
| 5 | Available N (kg/ha) | 54.00 | Bremner, 1965 |
| 6 | Available P (kg/ha) | 69.00 | Olsen and Dean, 1965 |
| 7 | Exchangeable K (kg/ha) | 89.50 | Pratt, 1965 |

| | | | |
|---|---|---|---|
| 8 | Available S (ppm) | 16.00 | Hunter, 1984 |
| 9 | pH (1:2.5 soil to water) | 5.55 | Jackson, 1958 |
| 10 | CEC | 11.23 | Chapman, 1965 |

**Source:** Central library, Sher-e-Bangla Agricultural University, Dhaka.

**Appendix IV: Analysis of variance for different morphological plant characters of 45 genotypes**

| Characters | d.f | Days to 50% flowering | Date of 80% maturity | Plant height (cm) at last harvest | No. of primary branches | No. of secondary branches | No. of pod per plants | Pod length (cm) | No. of seed per pod | 100 seed weight (gm) | seeds per plants | Seed yield per plant (kg) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 1.075 | 4.069 | 37.39 | 15.16 | 0.004 | 28.35 | 0.060 | 0.239 | 0.643 | 258.89 | 0.639 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotypes | 44 | 32.221** | 29.816** | 605.19** | 516.06** | 0.526** | 191.45** | 0.847** | 0.484** | 15.605** | 3974.87** | 17.558** |
| Error | 88 | 1.263 | 4.572 | 30.19 | 14.02 | 0.005 | 5.93 | 0.081 | 0.152 | 0.292 | 51.20 | 0.648 |

** indicates significant at 0.01 probability level.

**Appendix V: Mean performance of 45 genotypes based on different morphological traits related to yield**

| Genotypes | Days to 50% flowering | Date of 80% maturity | Plant height (cm) at last harvest | No. of pod per plants |
|---|---|---|---|---|
| $G_1$ | 35.67 ghijk | 66.00 abc | 77.73 fghijkl | 55.60 mnopqr |
| $G_2$ | 35.67 ghijk | 66.00 abc | 84.00 bcdefgh | 62.50 ijklmn |
| $G_3$ | 36.33 fghi | 65.33 abcde | 83.97 bcdefgh | 60.60 jklmno |
| $G_4$ | 37.00 efg | 62.67 cdefgh | 79.80 efghijk | 64.20 hijkl |
| $G_5$ | 40.67 bc | 61.33 efghijkl | 86.20 abcdef | 82.50 bc |
| $G_6$ | 36.00 fghij | 62.00 cdefghij | 72.17 ijklmno | 58.90 klmnop |
| $G_7$ | 36.00 fghij | 63.00 bcdefgh | 71.77 jklmno | 60.20 klmno |
| $G_8$ | 43.00 a | 64.00 bcdefg | 74.27 hijklm | 52.01 pqrs |
| $G_9$ | 41.67 ab | 65.67 abcd | 82.51 cdefghi | 78.20 cde |
| $G_{10}$ | 36.33 fghi | 61.00 fghijklm | 71.57 jklmno | 80.40 cd |
| $G_{11}$ | 36.33 fghi | 60.00 hijklmno | 83.07 cdefgh | 68.40 fghi |
| $G_{12}$ | 35.33 ghijkl | 59.33 hijklmnop | 74.62 ghijklm | 60.50 jklmno |
| $G_{13}$ | 36.00 fghij | 64.33 abcdef | 74.38 hijklm | 45.90 st |
| $G_{14}$ | 42.00 ab | 68.33 a | 82.87 cdefgh | 50.20 rs |
| $G_{15}$ | 36.00 fghij | 58.33 ijklmnopq | 85.20 abcdefg | 55.30 nopqr |
| $G_{16}$ | 36.00 fghij | 61.00 fghijklm | 70.17 klmnop | 80.33 cd |
| $G_{17}$ | 38.00 ef | 57.00 mnopq | 91.67 abcd | 41.87 t |
| $G_{18}$ | 41.67 ab | 63.00 bcdefgh | 91.40 abcd | 62.80 lm |
| $G_{19}$ | 37.33 efg | 61.67 defghijk | 92.97 abc | 64.01 hijkl |
| $G_{20}$ | 40.00 bcd | 60.67 fghijklm | 94.00 ab | 75.00 def |
| $G_{21}$ | 38.00 def | 55.00 q | 95.50 a | 69.50 fghi |
| $G_{22}$ | 38.00 def | 57.33 lmnopq | 91.80 abcd | 61.00 jklmno |
| $G_{23}$ | 37.33 efg | 56.00 opq | 85.17 abcdefg | 33.03 u |
| $G_{24}$ | 34.67 hijklm | 56.33 nopq | 89.03 abcde | 61.02 jklmno |
| $G_{25}$ | 36.33 fghi | 62.00 cdefghij | 85.41 abcdef | 41.73 t |
| $G_{26}$ | 36.67 fgh | 55.67 pq | 78.53 efghijkl | 78.73 cde |
| $G_{27}$ | 36.33 fghi | 65.67 abcd | 73.27 hijklmn | 73.33 efg |
| $G_{28}$ | 39.00 cde | 61.00 fghijklm | 57.47 rstuv | 57.47 lmnopq |
| $G_{29}$ | 42.00 ab | 61.00 fghijklm | 66.33 mnopqr | 67.80 ghij |
| $G_{30}$ | 32.00 nopq | 62.33 cdefghi | 51.20 v | 51.20 qrs |
| $G_{31}$ | 31.33 opqr | 62.00 cdefghij | 65.47 mnopqrs | 65.47 hijk |
| $G_{32}$ | 32.67 mnopq | 61.33 efghijkl | 61.07 pqrstuv | 62.40 ijklmn |
| $G_{33}$ | 32.00 nopq | 64.00 bcdefg | 55.27 stuv | 55.27 nopqr |
| $G_{34}$ | 30.67 qr | 60.33 fghijklmn | 63.33 nopqrst | 63.73 hijkl |
| $G_{35}$ | 33.33 lmno | 61.33 efghijkl | 52.53 uv | 52.53 pqrs |
| $G_{36}$ | 33.67 klmn | 62.00 cdefghij | 54.33 uv | 54.33 opqr |
| $G_{37}$ | 34.00 jklmn | 62.00 cdefghij | 58.77 qrstuv | 58.8 klmnop |
| $G_{38}$ | 34.00 jklmn | 59.00 hijklmnopq | 68.93 lmnopq | 68.87 fghi |
| $G_{39}$ | 33.00 mnop | 57.67 klmnopq | 54.87 tuv | 54.87 opqr |
| $G_{40}$ | 31.00 pqr | 57.33 lmnopq | 81.56 defghij | 81.46 bcd |
| $G_{41}$ | 29.67 r | 58.00 jklmnopq | 87.55 abcdef | 89.00 a |
| $G_{42}$ | 31.00 pqr | 60.00 ghijklmno | 62.59 opqrstu | 62.61 ijklmn |
| $G_{43}$ | 34.33 ijklm | 67.00 ab | 87.71 abcdef | 87.71 ab |
| $G_{44}$ | 37.00 efg | 60.67 fghijklm | 70.04 klmnop | 70.03 fgh |
| $G_{45}$ | 38.00 ef | 61.00 fghijklm | 31.04 w | 31.04 u |
| $LSD_{(0.05)}$ | 1.82 | 3.47 | 8.91 | 6.07 |
| SE (±) | 0.49 | 0.47 | 2.12 | 1.96 |
| SD | 3.28 | 3.15 | 14.20 | 13.12 |
| Mean | 36.07 | 61.26 | 74.51 | 62.50 |
| Minimum | 29.67 | 55.00 | 31.04 | 31.04 |
| Maximum | 43.00 | 68.33 | 95.50 | 89.00 |
| CV (%) | **3.12** | **3.49** | **7.37** | **5.99** |

Genotypes with the different letter (s) are significantly different.

## Appendix V: Continued

| Genotypes | No. of secondary branches | | No. of primary branches | | Pod length (cm) | | No. of seed per pod | |
|---|---|---|---|---|---|---|---|---|
| **$G_1$** | 0.7000 | klmno | 22.07 | klm | 4.070 | cdefg | 3.913 | cdefghijkl |
| **$G_2$** | 1.070 | fg | 24.00 | hijk | 3.953 | cdefgh | 4.027 | bcdefghijkl |
| **$G_3$** | 1.230 | cd | 31.80 | bcde | 3.860 | cdefgh | 4.207 | bcdefghij |
| **$G_4$** | 1.900 | a | 30.20 | cdef | 3.853 | cdefgh | 3.953 | bcdefghijkl |
| **$G_5$** | 0.7900 | jkl | 34.99 | ab | 4.043 | cdefg | 4.053 | bcdefghijkl |
| **$G_6$** | 0.6333 | nopqr | 30.23 | cdef | 3.653 | fgh | 3.440 | jkl |
| **$G_7$** | 0.8700 | hij | 38.27 | a | 4.140 | bcdef | 4.637 | abcde |
| **$G_8$** | 0.9700 | gh | 34.40 | abc | 3.513 | gh | 4.373 | bcdefghi |
| **$G_9$** | 1.110 | ef | 26.69 | fghij | 4.290 | bcde | 5.173 | a |
| **$G_{10}$** | 1.870 | a | 29.78 | def | 3.970 | cdefgh | 4.697 | abc |
| **$G_{11}$** | 0.5000 | rstu | 33.37 | bcd | 3.863 | cdefgh | 4.247 | bcdefghi |
| **$G_{12}$** | 0.6833 | lmno | 24.76 | ghijk | 3.647 | fgh | 3.930 | cdefghijkl |
| **$G_{13}$** | 0.6467 | mnopq | 28.67 | efg | 3.733 | efgh | 3.843 | fghijkl |
| **$G_{14}$** | 0.8667 | hij | 24.07 | hijk | 3.873 | cdefgh | 3.640 | ijkl |
| **$G_{15}$** | 0.8700 | hij | 21.07 | klmn | 4.320 | bcd | 3.777 | ghijkl |
| **$G_{16}$** | 0.5333 | pqrst | 22.77 | jkl | 3.637 | fgh | 3.887 | defghijkl |
| **$G_{17}$** | 1.067 | fg | 22.00 | klm | 3.767 | defgh | 3.387 | kl |
| **$G_{18}$** | 1.100 | ef | 18.33 | lmnopq | 3.940 | cdefgh | 3.800 | fghijkl |
| **$G_{19}$** | 0.9300 | hi | 21.92 | klm | 4.290 | bcde | 4.530 | abcdefg |
| **$G_{20}$** | 0.7700 | jklm | 16.93 | nopqr | 3.640 | fgh | 4.700 | abc |
| **$G_{21}$** | 0.8300 | ijk | 20.00 | klmnop | 3.830 | cdefgh | 4.653 | abcd |
| **$G_{22}$** | 1.430 | B | 28.20 | efgh | 4.040 | cdefg | 4.540 | abcdefg |
| **$G_{23}$** | 0.7300 | klmn | 21.70 | klm | 4.403 | bc | 4.367 | bcdefghi |
| **$G_{24}$** | 0.8300 | ijk | 23.20 | ijk | 4.080 | bcdefg | 4.513 | abcdefgh |
| **$G_{25}$** | 1.200 | cde | 12.20 | stu | 4.193 | bcdef | 4.200 | bcdefghij |
| **$G_{26}$** | 0.7300 | klmn | 20.93 | klmno | 4.023 | cdefg | 3.760 | ghijkl |
| **$G_{27}$** | 0.5300 | qrst | 20.13 | klmnop | 3.880 | cdefgh | 4.347 | bcdefghi |
| **$G_{28}$** | 0.4000 | uv | 12.93 | rst | 4.137 | bcdef | 4.177 | bcdefghij |
| **$G_{29}$** | 0.6000 | nopqr | 14.40 | qrst | 4.063 | cdefg | 4.347 | bcdefghi |
| **$G_{30}$** | 0.2000 | xy | 12.40 | rstu | 3.783 | defgh | 3.720 | hijkl |
| **$G_{31}$** | 0.0000 | z | 13.33 | rst | 3.423 | h | 3.350 | i |
| **$G_{32}$** | 0.3300 | vw | 8.200 | u | 4.047 | cdefg | 4.733 | ab |
| **$G_{33}$** | 0.0000 | z | 13.00 | rst | 3.660 | fgh | 4.120 | bcdefghijkl |
| **$G_{34}$** | 0.2700 | wx | 10.07 | tu | 3.897 | cdefgh | 3.943 | bcdefghijkl |
| **$G_{35}$** | 0.2700 | wx | 13.20 | rst | 3.960 | cdefgh | 3.757 | ghijkl |
| **$G_{36}$** | 0.1300 | y | 10.67 | tu | 4.140 | bcdef | 4.637 | abcde |
| **$G_{37}$** | 0.6000 | nopqr | 16.13 | pqrs | 3.893 | cdefgh | 3.860 | efghijkl |
| **$G_{38}$** | 0.9333 | hi | 21.33 | klmn | 3.950 | cdefgh | 4.083 | bcdefghijkl |
| **$G_{39}$** | 0.2000 | xy | 16.47 | opqrs | 3.967 | cdefgh | 3.820 | fghijkl |
| **$G_{40}$** | 0.5833 | opqrs | 17.94 | mnopq | 4.630 | b | 3.770 | ghijkl |
| **$G_{41}$** | 1.270 | c | 27.72 | efghi | 4.110 | bcdef | 4.313 | bcdefghi |
| **$G_{42}$** | 0.4600 | stu | 14.09 | qrst | 6.180 | a | 4.160 | bcdefghijk |
| **$G_{43}$** | 0.6067 | nopqr | 24.37 | ghijk | 4.100 | bcdef | 4.590 | abcdef |
| **$G_{44}$** | 0.6667 | lmnop | 9.823 | tu | 3.923 | cdefgh | 4.413 | bcdefghi |
| **$G_{45}$** | 0.4300 | tuv | 4.000 | v | 6.310 | a | 4.007 | bcdefghijkl |
| $LSD_{(0.05)}$ | 0.115 | | 3.96 | | 0.462 | | 0.632 | |
| SE (±) | 0.06 | | 1.19 | | 0.08 | | 0.06 | |
| SD | 0.42 | | 7.99 | | 0.53 | | 0.40 | |
| Mean | 0.74 | | 20.95 | | 4.06 | | 4.14 | |
| Minimum | 0.00 | | 4.00 | | 3.42 | | 3.35 | |
| Maximum | 1.90 | | 38.27 | | 6.31 | | 5.17 | |
| CV (%) | **9.74** | | **11.63** | | **7.00** | | **9.41** | |

Genotypes with the different letter (s) are significantly different.

**Appendix V: Continued**

| Genotypes | 100 seed weight (gm) | seeds per plants | Seed yield per plant (g) |
|---|---|---|---|
| **$G_1$** | 6.767 Hijklm | 87.33 klmn | 5.973 hijklm |
| **$G_2$** | 5.767 Mno | 95.67 jk | 5.447 jklmn |
| **$G_3$** | 5.133 O | 134.3 cde | 6.860 efghij |
| **$G_4$** | 5.633 No | 120.0 fg | 7.520 defg |
| **$G_5$** | 6.467 Jklmn | 142.3 bc | 9.121 bc |
| **$G_6$** | 6.433 Jklmn | 105.0 hij | 9.362 bc |
| **$G_7$** | 6.400 Jklmn | 178.0 a | 11.39 a |
| **$G_8$** | 6.900 Ghijkl | 149.0 b | 10.29 ab |
| **$G_9$** | 7.067 Fghijkl | 131.0 cdef | 9.250 bc |
| **$G_{10}$** | 6.567 Ijklmn | 141.0 bcd | 9.320 bc |
| **$G_{11}$** | 6.167 Lmn | 141.3 bcd | 8.781 bcd |
| **$G_{12}$** | 7.167 Efghijkl | 97.67 jk | 7.040 efghi |
| **$G_{13}$** | 8.200 Bcde | 111.0 ghi | 9.120 bc |
| **$G_{14}$** | 8.167 Bcde | 89.00 klm | 7.237 efgh |
| **$G_{15}$** | 6.963 Ghijkl | 80.00 mnop | 6.467 ghijkl |
| **$G_{16}$** | 6.767 Hijklm | 89.33 klm | 6.107 ghijklm |
| **$G_{17}$** | 7.180 Efghijkl | 74.67 nopq | 5.357 jklmn |
| **$G_{18}$** | 7.680 Bcdefgh | 69.67 opqr | 5.277 klmno |
| **$G_{19}$** | 8.230 Bcde | 100.0 ijk | 8.190 cdef |
| **$G_{20}$** | 8.300 Bcd | 82.00 lmno | 6.750 fghijk |
| **$G_{21}$** | 7.667 Bcdefgh | 87.67 klmn | 9.721 bc |
| **$G_{22}$** | 7.567 Bcdefghi | 41.50 vw | 6.790 fghijk |
| **$G_{23}$** | 8.267 Bcd | 128.7 def | 8.330 cde |
| **$G_{24}$** | 8.433 B | 95.33 jkl | 8.850 bcd |
| **$G_{25}$** | 6.933 Ghijkl | 51.33 tuvw | 3.567 pqr |
| **$G_{26}$** | 6.333 Jklmn | 81.00 mnop | 4.990 lmnopq |
| **$G_{27}$** | 6.567 Ijklmn | 87.00 klmn | 5.720 hijklm |
| **$G_{28}$** | 6.533 Ijklmn | 55.00 tuv | 3.573 pqr |
| **$G_{29}$** | 7.400 Bcdefghij | 63.00 qrst | 4.653 mnopq |
| **$G_{30}$** | 7.300 Cdefghijk | 47.00 uvw | 3.450 qr |
| **$G_{31}$** | 8.467 B | 44.67 vw | 3.763 opqr |
| **$G_{32}$** | 6.933 Ghijkl | 39.00 w | 2.740 r |
| **$G_{33}$** | 6.767 Hijklm | 55.00 stuv | 3.723 pqr |
| **$G_{34}$** | 7.233 Defghijkl | 41.00 w | 2.860 r |
| **$G_{35}$** | 6.233 Klmn | 49.67 tuvw | 3.590 pqr |
| **$G_{36}$** | 8.033 Bcdef | 50.00 tuvw | 4.013 nopqr |
| **$G_{37}$** | 6.400 Jklmn | 62.67 qrst | 4.007 nopqr |
| **$G_{38}$** | 7.867 Bcdefg | 88.00 klmn | 7.033 efghi |
| **$G_{39}$** | 7.900 Bcdefg | 62.33 qrst | 5.043 lmnop |
| **$G_{40}$** | 8.233 Bcde | 68.33 pqrs | 5.610 ijklm |
| **$G_{41}$** | 8.367 Bc | 123.0 efg | 10.21 |
| **$G_{42}$** | 8.100 Bcdef | 59.33 rstu | 4.800 mnopq |
| **$G_{43}$** | 8.433 B | 115.3 gh | 9.620 bc |
| **$G_{44}$** | 8.233 Bcde | 43.33 vw | 3.567 pqr |
| **$G_{45}$** | 21.40 | 12.67 x | 2.750 r |
| $LSD_{(0.05)}$ | 0.876 | 11.61 | 1.31 |
| SE (±) | 0.34 | 5.43 | 0.36 |
| SD | 2.28 | 36.40 | 2.42 |
| Mean | 7.55 | 86.00 | 6.40 |
| Minimum | 5.13 | 12.67 | 2.74 |
| Maximum | 21.40 | 178.00 | 11.39 |
| CV (%) | **7.16** | **8.32** | **12.58** |

Genotypes with the different letter (s) are significantly different

**Table 2: Estimation of genetic parameters for morphological characters related to yield**

| SL. No. | Characters | Phenotypic variance ($¢^2p$) | Genotypic variance ($¢^2g$) | Grand mean | PCV (%) | GCV (%) | Heritability (%) | GA | GA (%) |
|---|---|---|---|---|---|---|---|---|---|
| **1** | Days to 50% flowering | 11.58 | 10.32 | 36.07 | 9.44 | 8.91 | 89.10 | 6.25 | 17.32 |
| **2** | Date of 80% maturity | 12.99 | 8.41 | 61.26 | 5.88 | 4.74 | 64.79 | 4.81 | 7.85 |
| **3** | Plant height (cm) at last harvest | 221.86 | 191.67 | 74.51 | 19.99 | 18.58 | 86.39 | 26.51 | 35.57 |
| **4** | No. of pod per plants | 181.37 | 167.35 | 62.50 | 21.55 | 20.70 | 92.27 | 25.60 | 40.96 |
| **5** | No. of secondary branches | 0.18 | 0.17 | 0.74 | 57.05 | 56.25 | 97.20 | 0.85 | 114.24 |
| **6** | No. of primary branches | 67.77 | 61.84 | 20.95 | 39.30 | 37.54 | 91.24 | 15.47 | 73.86 |
| **7** | Pod length (cm) | 0.34 | 0.26 | 4.06 | 14.29 | 12.45 | 75.92 | 0.91 | 22.34 |
| **8** | No. of seed per pod | 0.26 | 0.11 | 4.14 | 12.37 | 8.03 | 42.13 | 0.44 | 10.74 |
| **9** | 100 seed weight (gm) | 5.40 | 5.10 | 7.55 | 30.79 | 29.94 | 94.59 | 4.53 | 59.99 |
| **10** | seeds per plants | 1359.10 | 1307.89 | 86.00 | 42.87 | 42.05 | 96.23 | 73.08 | 84.98 |
| **11** | Seed yield per plant (kg) | 6.28 | 5.64 | 6.40 | 39.19 | 37.12 | 89.69 | 4.63 | 72.41 |

**Table 3.Coefficients of phenotypic and genotypic correlation among different yield components**

| Characters | correlation | Date of 80% maturity | Plant height (cm) at last harvest | No. of primary branches | No. of secondary branches | No. of pod per plants | Pod length (cm) | No. of seed per pod | 100 seed weight (gm) | Seeds per plants | Seed yield per plant (kg) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | $r_p$ | 0.210 | 0.350* | -0.098 | 0.397** | 0.320* | -0.108 | 0.215 | 0.030 | 0.298 | 0.298 |
| | $r_g$ | 0.193 | 0.367* | -0.098 | 0.403** | 0.321* | -0.113 | 0.219 | 0.023 | 0.302 | 0.309* |
| Date of 80% maturity | $r_p$ | | -0.013 | -0.0001 | 0.616** | -0.009 | 0.030 | -0.619** | 0.866** | 0.180 | 0.021 |
| | $r_g$ | | -0.007 | 0.00004 | 0.718** | -0.009 | 0.031 | -0.685** | 0.988** | 0.187 | 0.029 |
| Plant height (cm) at last harvest | $r_p$ | | | 0.333* | 0.604** | 0.563** | -0.306* | 0.199 | -0.384* | 0.500** | 0.593** |
| | $r_g$ | | | 0.317* | 0.608** | 0.573** | -0.315* | 0.234 | -0.391* | 0.503** | 0.603** |
| No. of primary branches | $r_p$ | | | | 0.182 | 0.280 | -0.206 | 0.300 | -0.326* | 0.299 | 0.315* |
| | $r_g$ | | | | 0.184 | 0.287 | -0.209 | 0.330* | -0.331* | 0.299 | 0.324* |
| No. of secondary branches | $r_p$ | | | | | 0.583** | -0.065 | 0.247 | -0.192 | 0.504** | 0.513** |
| | $r_g$ | | | | | 0.588** | -0.067 | 0.266 | -0.191 | 0.506** | 0.519** |
| No. of pod per plants | $r_p$ | | | | | | -0.321* | 0.118 | -0.414** | 0.907** | 0.872** |
| | $r_g$ | | | | | | -0.333* | 0.113 | -0.417** | 0.911** | 0.872** |
| Pod length (cm) | $r_p$ | | | | | | | 0.116 | 0.659** | -0.253 | -0.192 |
| | $r_g$ | | | | | | | 0.105 | 0.673** | -0.258 | -0.200 |
| No. of seed per pod | $r_p$ | | | | | | | | -0.004 | 0.284 | 0.341* |
| | $r_g$ | | | | | | | | -0.012 | 0.286 | 0.335* |
| 100 seed weight (gm) | $r_p$ | | | | | | | | | -0.379* | -0.195 |
| | $r_g$ | | | | | | | | | -0.381* | -0.201 |
| Seeds per plants | $r_p$ | | | | | | | | | | 0.887** |
| | $r_g$ | | | | | | | | | | 0.887** |

* and ** indicate significant at 5% and 1% level of probability, respectability.

**Table 4. Partitioning of phenotypic into direct and indirect effects of morphological characters of 45 pea genotypes by path coefficient analysis**

| Characters | Days to 50% flowering | Date of 80% maturity | Plant height (cm) at last harvest | No. of primary branches | No. of secondary branches | No. of pod per plants | Pod length (cm) | No. of seed per pod | 100 seed weight (gm) | Seeds per plants | Seed yield per plant (kg) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% flowering | **-0.0918** | 0.0089 | 0.0879 | 0.00171 | -0.0679 | 0.215 | 0.0043 | 0.0498 | 0.0071 | 0.0827 | 0.298 |
| Date of 80% maturity | -0.0192 | **0.0427** | -0.0033 | 0.0000018 | -0.1054 | -0.0060 | -0.0012 | -0.1436 | 0.2071 | 0.0500 | 0.021 |
| Plant height (cm) at last harvest | -0.0321 | -0.00056 | **0.251** | -0.0058 | -0.1033 | 0.3783 | 0.0121 | 0.0462 | -0.0918 | 0.1389 | 0.593** |
| No. of primary branches | 0.0090 | -0.000004 | 0.0836 | **-0.0175** | -0.0311 | 0.1881 | 0.0082 | 0.0696 | -0.0779 | 0.0830 | 0.315* |
| No. of secondary branches | -0.0365 | 0.0263 | 0.1517 | -0.0032 | **-0.1711** | 0.3917 | 0.0026 | 0.0573 | -0.0459 | 0.1400 | 0.513** |
| No. of pod per plants | -0.0294 | -0.00038 | 0.1414 | -0.0049 | -0.0997 | **0.6719** | 0.0127 | 0.0274 | -0.0990 | 0.2519 | 0.872** |
| Pod length (cm) | 0.0099 | 0.0013 | -0.0768 | 0.0036 | 0.0111 | -0.2156 | **-0.0396** | 0.0269 | 0.1576 | -0.0702 | -0.192 |
| No. of seed per pod | -0.0197 | -0.0264 | 0.0499 | -0.0053 | -0.0422 | 0.0793 | -0.0045 | **0.2321** | -0.0009 | 0.0789 | 0.341* |
| 100 seed weight (gm) | -0.0027 | 0.0369 | -0.0964 | 0.0057 | 0.0328 | -0.278 | -0.0261 | -0.00093 | **0.2392** | -0.1052 | -0.195 |
| seeds per plants | -0.0274 | 0.0076 | 0.1256 | -0.0052 | -0.0863 | 0.6094 | 0.01002 | 0.0659 | -0.0906 | **0.2778** | 0.887** |
| Diagonally bold figures indicate the direct effect | | | | | | | | | | | Residual effect = 0.09833 |