CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN FIELD PEA (*Pisum sativum* L.)

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BY

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CERTIFICATE

*This is to certify that the thesis entitled, "**CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS FOR YIELD AND YIELD CONTRIBUTING CHARACTERS IN FIELD 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 **Md Arifuzzaman ; Registration No. 10-03918,** under my supervision and guidance. No part of this thesis has been submitted for any other degree or diploma.*

I further certify that any help or sources of information, as has been availed of during the course of this investigation have been duly acknowledged.

Dated: June, 2016

_____
(Professor Dr. Mohammad Saiful Islam)
Supervisor

Dedicated to
The Farmers Who
Feed the Nation

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ABSTRACT

A field experiment was conducted during December 2016 to March 2017 to study the genetic variability, correlation, path coefficient analysis and genetic diversity for quantitative traits in pea (*Pisum sativum* L.) with twenty one genotypes in a field experiment conducted at the research farm of Sher-E-Bangla Agricultural University, Dhaka. Experiment showed significant differences among the genotypes. Phenotypic variance was higher than that of genotypic variance for all the characters. Phenotypic coefficients of variation (PCV) was also close to genotypic coefficients of variation (GCV) for all the characters indicating that environment had influence on the expression of these characters. The high heritability coupled with high genetic advance in percent of mean observed in plant height, primary branches per plant, leaf length, Leaf diameter, flower per plant, pods per plant, pod length, seeds per plant, seed diameter, 100 seed weight and seed yield which would be selected for future breeding program. High heritability coupled with low genetic advance in percent of mean was observed in germination percentage, days of 50% flowering and days to maturity. Plant height, leaf length, leaf diameter, pod length, seed diameter and hundred seed weight showed highly significant and positive correlation with seed yield at both genotypic and phenotypic levels revealed that selection based on these traits would ultimately improve the seed yield. Path coefficient analysis revealed that hundred seed weight had the highest positive direct effect on seed. Hence, thrust has to be given for this character in future breeding program to improve the yield in pea. Multivariate analysis based on 13 agronomic characters indicated that the twenty one genotypes were grouped into five distant clusters. The maximum contributions of characters towards diversity were plant height, leaf length, leaf diameter, pod length, seed diameter, and hundred seed weight. Thus, these traits may be given high emphasis for future hybridization program. The inter cluster distance was the maximum between cluster I and cluster V. The highest intra-cluster distance was found in cluster III. It was concluded G2 (BD-4151), G6 (BD-4171), G7 (BD-4172), G14 (BD-4190), G16 (BD-4205) could be included in the furthest study in view of seed yield for releasing as pea varities**.**

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SOME COMMONLY USED ABBREVIATION

Abbreviations		Full word
AEZ	=	Agro-Ecological Zone
Agric.	=	Agriculture
Agril.	=	Agricultural
Agron.	=	Agronomy
BARI	=	Bangladesh Agricultural Research Institute
BBS	=	Bangladesh Bureau of Statistics
BD	=	Bangladesh
Fig.	=	Figure
CV%	=	Percentage of Coefficient of Variation
cv.	=	Cultivar (s)
DAS	=	Days After Sowing
df	=	Degrees of Freedom
DM	=	Dry Matter
et al.	=	And others
etc.	=	Et cetera
MSS	=	Mean sum of square
g	=	Gram (s)
G	=	Genotype
GN.	=	Genotype Number
hr.	=	Hour (s)
δ^2_g	=	Genotypic variance
j.	=	Journal
δ^2_p	=	Phenotypic variance
m	=	Metre
M.P.	=	Muriate of Potash
m^2	=	Meter Square
PCV	=	Phenotypic co-efficient of variation
No.	=	Number
NS	=	Non Significant
GA	=	Genetic Advance
GCV	=	Genotypic co-efficient of variation
RCBD	=	Randomized Complete Block Design
Res.	=	Research
SAU	=	Sher-e-Bangla Agricultural University
Sci.	=	Science
SE	=	Standard Error
T.S.P.	=	Triple Super Phosphate
t/ha	=	Tonnes per hectare
Univ.	=	University
var.	=	Variety

CHAPTER I

INTRODUCTION

The Pea (*Pisum sativum* L.) is an annual herbaceous crop under subfamily Papilionace belonging to the family Leguminosae. Its chromosome number is 2n=2x=14. It is very nutritious and tasty vegetable in Bangladesh. The green seed and vegetative parts of this plant is used id food, where matured and ripe seeds are used as pulse and green plant parts are used as vegetables. It is also grown as fodder or green manuring crop as it fixes nitrogen from atmosphere. Seeds are little angular and rounded. Matured and dried seed contains 22.9% protein, 60.17% carbohydrate, 1.4% fat, 2.7% ash, 1.4% crude fiber, 10.2 % water and others 1.23%.

Pea seeds contain some essential amino acids like tryptophan and lysine which are rarely found in other cereal crops. Thus it can be a great source of vegetable protein. It enriches the food quality, nutrition status and food value by supplying its nutritional properties. Further it can be used with low protein contained food as a supplement to maintain the balance of nutrients and nutritional properties.

Pea is grown everywhere in the world that remains cold weather and climate region. In tropical areas it can even be grow in 2700m altitude and cold regions in subtropical area. It is reported that pea performs better in subtropical areas which have consecutive five months of cold winter. The major pea producing countries are Thailand, China, UK, France, USA, Pakistan, Hungary, Italy, Egypt and Japan. Bangladesh is also in the way of producing good amount of peas. In Bangladesh it is cultivated in Rabi season which is from October to March of every year. The major pea growing areas of Bangladesh are Pabna, Comilla, Jessore, Rajshahi, Faridpur and Kushtia. But the cultivation and production of pea vegetable is decreasing day by day. According to statistics the occupying area of pea 15779 ha of land (2010-11), 16054 ha of land (2011-12), and 14928 ha of land (2012-13), 18870 ha of land (2013-14) and 18749 ha of land (2014-15) [BBS, 2016].The production of pea is increasing along with land. The production of pea was 6149 metric tons (2010-11), 6153 metric tons (2011-12), 5721 metric tons (2012-13), 6961 metric tons (2013-14), 7086 metric tons (2014-15) in respective years [BBS, 2016].

Presently the average production of pea in Bangladesh has been significantly reduced due to introduction of HYV rice and wheat varieties. Consequently the scope of its production

as field crop has already been restricted. However there's a scarcity of offseason vegetable in our country. Field pea can be taken into consideration as vegetable crop because it need small piece of land and can also be grown without competition with cereal crops. It can also be consumed all year round preserving it in frozen condition. Thus through developing high yielding pea we can meet the protein and vegetable requirement. The effort of developing new high yielding pea varieties is hardy found compared to other grain crops. Besides the pea quality depends on its sugar content in seed. Authorities should be care of developing high yielding pea varieties with proper sugar content in seed through hybridization and other improved breeding techniques.

Breeding attempts have added greatly to improve yield potential, regional adaptation through tolerance or resistance to biotic and abiotic stress, plant variety and feed traits. Quantum of genetic variability and the degree to which heritable and non hereditable variations are associated with the characters should be given priorities for the degree of genetic improvement.

Yield is a very complex character and it is managed with a large number of genes and significantly affected from the environment and quality traits influence the yield both directly and indirectly. These genetic traits are simply just inherited and less influenced by the environment in terms of yield. Thus assortment depending on these traits has greater possibility of success in comparison to selection for yield alone. Yield components and yield are usually linked mainly to linkage and pleiotropic effects of gene. The genotypic correlation indicates the extents to that the two characters are controlled by the exact same group of genes are experiencing the physiological basis of their expression. Information regarding direct and indirect effects which contribute in yield will be added advantages in improvement of the crop. Wright (1921) introduced path co efficient analysis technique through which it can be measured the direct and indirect role in various components which make the total correlation to yield. Depending on this study, the individual character is identified which help to facilitate in breeding program for better yield.

Selection of parents for heterosis and hybrid seed production is a common process. The divergent are the parents, the better it will yield. Divergent parents produce hybrid vigor seed (Harrington, 1940). That’s why it is very important to study the divergence among germplasm and existing varieties to identify the most divergent parents for better yield. The traits, considered to contribute towards greater yield and quality, are to be studied and their information of divergence is very important breeding planning and program. Mahalanobis (1936) developed D^2 statistics which provides a measure of degree of divergence between two genotypes which are under comparison. In an anthropometric

survey Mahalanobis used this at first. It considers any character which creates variation and subsequent effect on other characters.

This technique has been applied in various crops to choose genotypes for further breeding programs. Clustering of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding.These type of studies are also useful in parental selection 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 Diversity Analysis In Pea (*Pisum sativum* L.)" was under taken involving advanced breeding lines with the following objectives.

1. To assess genetic diversity among the genotypes.
2. To identify the distant parents for future improvement through hybridization
3. To know the association of traits with yield and yield contributing characters.
4. To know the degree and direction of relationship between the yield and yield contributing characters.
5. To know the direct and indirect contribution of yield contributing traits on yield.
6. To find out the superior genotypes for utilization in future breeding program and
7. To know the contribution of genetic and environmental factors on the phenotypic expression of the character as well as type of gene action involved,

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 5 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 6 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 7 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 8 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 10 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 11 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 F1 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 F1 and F2 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, F1s and F2s 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 appeared; 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 F1 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 16 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% 17 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 programs 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 18 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 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 (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 19 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 20 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 D2 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 21 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 22 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 D^2 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 23 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^2analysis. 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 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 D^2 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 D^2 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 2016 March 2017 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 2016 to March 2017.

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

The experimental area has subtropical climate, characterized by high temperature, high relative humidity 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 21 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 21 advanced lines 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.

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 , 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 21 genotypes were sown on 01 December 2016. The seedlings were em erged five to twelve days after sowing.

Table:1 Name of 21 Pea genotypes used in the study

Genotypic Code	Genotypic Name	Genotypic Code	Genotypic Name	Genotypic Code	Genotypic Name
G1	BD-4150	G8	BD-4176	G15	BD-4193
G2	BD-4151	G9	BD-4178	G16	BD-4205
G3	BD-4154	G10	BD-4182	G17	BD-4206
G4	BD-4157	G11	BD-4183	G18	BD-4207
G5	BD-4161	G12	BD-4186	G19	BD-4220
G6	BD-4171	G13	BD-4188	G20	BD-4222
G7	BD-4172	G14	BD-4190	G21	BD-4223

Source: Bangladesh Agricultural Research Institute (BARI)

3.10 Intercultural operation

Four weeding and thinning were done on same date, which were 23, 35,50and 60 days after sowing. Other intercultural operations were done as per need.

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 2 times at an interval of 12 days from 22 December to 16 January 2017. 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 late 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 Germination percentage

The numbers of germinated seedlings were recorded in each plot and percentage was calculated.

3.13.2 Days to 50% flowering

The days determined as the days required from sowing to 50% anthesis**.**

Plate1: Plants in experimental plot

Plate 2: Experimental Site with Supervisor

Plate 3: A pea plant with pod, leaf and stem

Plate 4: Replication view of the experimental plot

3.13.4 Primary branches per plant

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

3.13.5 Length of Leaves (cm)

The lengths of leaves from ten randomly selected plants were measured.

3.13.6 Diameter of Leaves (cm)

The diameters of leaves ten randomly selected plants were measured.

3.13.7 Flowers per plant

The numbers of flowers ten randomly selected plants were measured.

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

3.13.8 Pods per plant

The mean numbers of pods from ten randomly selected plants.

3.13.9 Pod length (cm)

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

3.13. 10 Seeds per pod

The average numbers of seeds from ten randomly selected pods were counted.

3.13.11 Diameter of Seeds (mm)

The mean diameters (mm) of pods from ten randomly selected plants were recorded.

3.13.12 Seeds per plant

The mean numbers of seeds from ten randomly selected plants were calculated.

3.13.13Hundred seed weight (g)

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

3.13.14 Days to plant maturity

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

3.13.15 Seed yield (ton/ha)

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 program. 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 2007 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). Genotypic variances (σ^2_g) were obtained by subtracting Error MS from Genotypic MS and dividing by the number of replications as shown below:

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

The phenotypic variance (σ^2_p) were derived by adding genotypic variance (σ^2_g) with error variance (σ^2_e) as given by following formula-

Phenotypic variance (σ^2_p)=$\sigma^2_g + \sigma^2_e$

Where,

σ^2_g = Genotypic variance

σ^2_e = Error variance

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 %) = $\frac{\sigma_g}{\bar{X}} \times 100$

Where,

σ_g = Genotypic standard deviation

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula-

Phenotypic co-efficient variation (PCV) = $\frac{\sigma_P}{\bar{X}} \times 100$

Where,

σ_p = Phenotypic standard deviation

$\bar{x}$ = 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).

Heritability (H_b %) = $\frac{\sigma^2_g}{\sigma^2_p} \times 100$

Where,

H_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = 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 $\times \frac{\sigma^2_g}{\sigma^2_p} \times \sigma_p$

Where,

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

σ_p =Phenotypic standard deviation

σ^2_g = Genotypic variance

σ^2_p = 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 (1955).

$$\text{Genetic advance (\% mean)} = \frac{\text{Genetic Advance}}{\text{Population mean}} \times 100$$

3.14.6 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) and Johnson *et al.*, (1955) were adopted.

The genotypic co-variance component between two traits and have the phenotypic co-variance 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 pair of characters, are presented as follows:

$$\text{Genotypic correlation } (r_{gxy}) = \frac{\sigma^2_{gxy}}{\sqrt{\left(\sigma^2_{gx} \times \sigma^2_{gy}\right)}}$$

Where,

σ_{gxy} =Genotypic co-variance between the traits x and y

σ^2_{gx} =Genotypic variance of the trait x

σ^2_{gy} =Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{\sigma^2_{pxy}}{\sqrt{\left(\sigma^2_{px} \times \sigma^2_{py}\right)}}$$

Where,

σ_{pxy} =Phenotypic covariance between the traits x and y

σ^2_{px} =Phenotypic variance of the trait x

σ^2_{py} =Phenotypic variance of the trait y

3.14.7 Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yx1} = p_{yx1} + p_{yx2}\, r_{x1x2} + P_{yx3}\, r_{x1x3}$

$r_{yx2} = p_{yx1} r_{x1x2} + p_{yx2} + p_{yx3}\, r_{x2x3}$

$r_{yx3} = p_{yx1} r_{x1x3} + p_{yx2}\, r_{x2x3} + p_{yx3}$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

p_{yx1} = The direct effect of x_1 on y.

$p_{yx2}\, r_{x1x2}$ = The indirect effect of x_1 via x_2 on y

$p_{yx3}\, r_{x1x3}$ = The indirect effect of $x_1$via x_3 on y

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):

$P^2_{RY} = 1 - \sum p_{iy} \cdot r_{iy}$

Where,

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

p_{iy} = Direct effect of the character on yield

r_{iy} = Correlation of the character with yield

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 parent's 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.

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 (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

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).

Average intra-cluster distance= $\frac{\sum D_i^2}{n}$

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= $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible Combinations of the populations in cluster i and j

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

3.15.8 Cluster diagram

Using the values of intra and inter-cluster distances (D = $\sqrt{D^2}$), 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.

CHAPTER IV

RESULTS AND DISCUSSION

The results found from the experiment are discussed and presented in this section. The data collected for 21 field pea genotypes as well as yield and yield contributing characters are calculated and analyzed statistically and the result of the experiment of character association for yield and yield contributing characters and multivariate analysis in pea (*Pisum sativum* L.) which was carried out during Rabi season in 2016-17 are presented in the following headings:

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 of this experimental data shows significantly differences in all the characters under study *viz*., germination percentage, Plant height, days of 50% flowering, primary branches per plant, length of leaves, diameter of leaves, flowers per plant, pods per plant, pod length, number of seeds per pod, diameter of seeds , number of seeds per plant, hundred seed weight, days to plant maturity and seed yield .The analysis shows that there is great extent of variability among the genotypes regarding yield and yield components. So it is clear that, selection for all the traits among genotypes have a great impact and good scope of improvement. The analysis of variances , means of all 14 characters are presented in Appendix VIII

4.2 GENETIC VARIABILITY , HERETIBILITY AND GENETIC ADVANCE

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 carried out during Rabi 2013-14 are presented in the following sections

The achievement of crop improvement program relies on the amount of genetic variability present in germplasm or in the population. The extent of genetic variability can determine the pace and quantum of genetic improvement through hybridization followed by selection or through selection. Phenotypic variance indicates the degree of variation in phenotypic values whereas genotypic variance indicates variation created in genotypic values. Heritability indicates target in determining the relative amount of portion of variation which are heritable.

The presence of little gap between GCV and PCV for all the characters under study, suggested that traits which are being studied have low environmental effect. The estimates of heritability alone fail to estimate the response to selection (Johnson *et al.*, 1955). Therefore, the heritability estimates seems to be more significant when accompanied by estimates of genetic advance. The genetic advances as per cent mean (GAM) was also estimated.

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

4.2.1 Germination percentage

The mean of germination percentage of 21 genotypes was 89.21. Significant differences were found among the genotypes with respect to germination percentage (Table 2). The values were ranged from 82.33% to 96.97% , in the genotype "BD- 4188"and "BD-4207" respectively. The genotypic variance was found 14.32 and phenotypic variance was found 16.97. From the analysis it is found that phenotypic variances(16.97) was higher than genotypic variances(14.32). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 4.24 and phenotypic co-efficient of variation was found 4.62. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation found very low which indicates less environmental effect on this character. The estimation of heritability (84.4%)for this trait was moderately high, genetic advance was found 7.16 and genetic advance over percentage of mean was found 8.03 which is low indicates non- additive genes controlled the trait.

4.2.2 Days to 50% flowering

The mean number of days to 50% flowering was 42.32. Significant differences were found among the genotypes with respect to days to 50% flowering (Table 2). The values were ranged from 39.67 to 48.67, in the genotype "BD- 4188"and "BD-4172" respectively. The genotypic variance was found 3.95 and phenotypic variance was found 6.08. From the analysis it is found that phenotypic variance (6.08) was higher than genotypic variances (3.95). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 4.7 and phenotypic co-efficient of variation was found 5.83. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation found very low which indicates less environmental effect on this character. The estimation of heritability (65%) for this trait was moderately high, genetic advance was

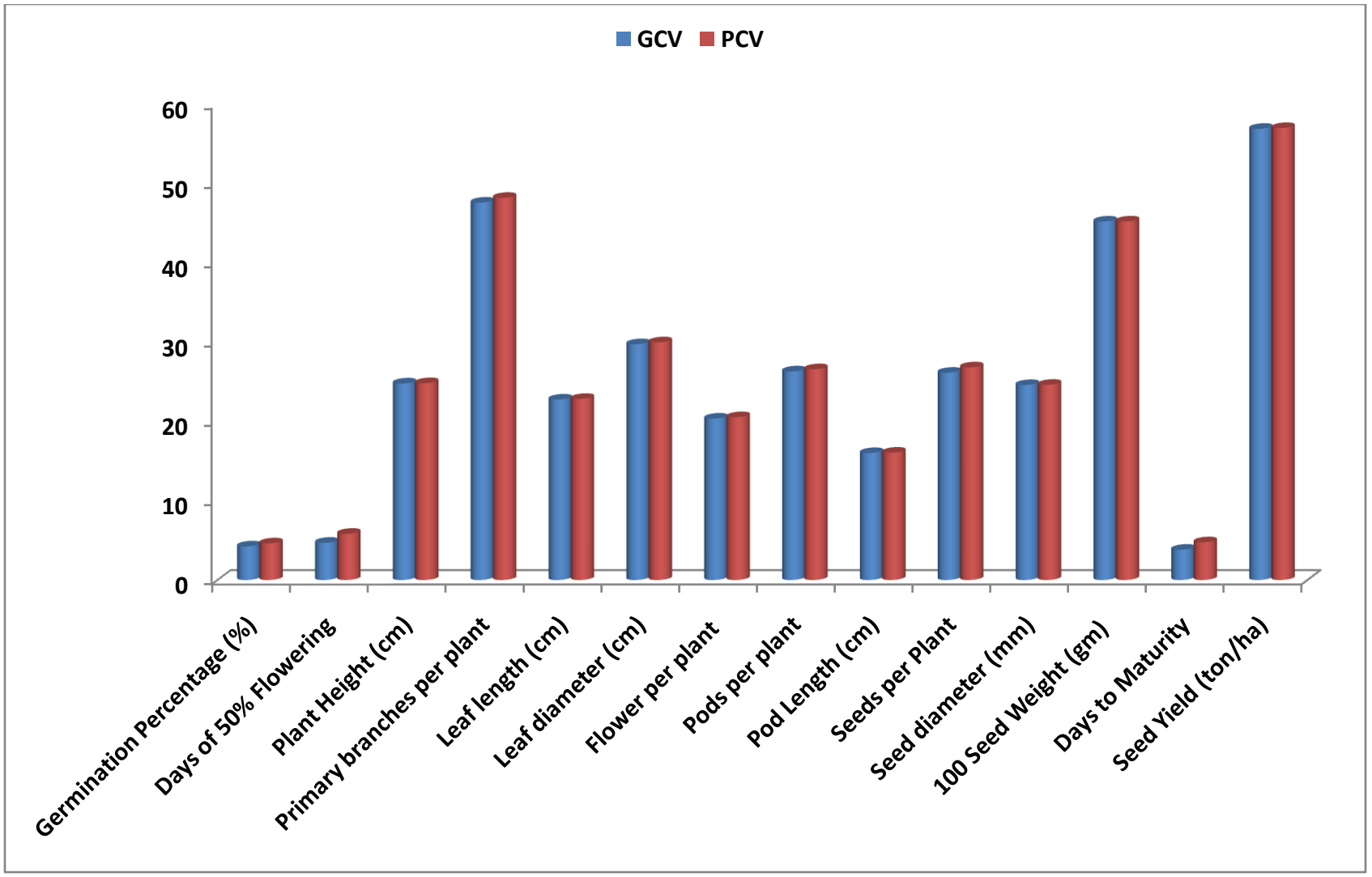

Figure 1: Genotypic and phenotypic variability in pea

Table 2. Range, mean, CV (%) and standard deviation of 21 pea genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Germination Percentage %	82.33	96.67	89.21	1.82	1.82	1.63
Days of 50% Flowering	39.67	48.67	42.32	3.45	3.45	1.46
Plant Height (cm)	52.00	123.00	77.33	1.19	1.19	0.92
Primary branches per plant	3.00	17.00	10.10	7.58	7.58	0.77
Leaf length (cm)	2.07	4.47	3.10	1.80	1.80	0.06
Leaf diameter (cm)	0.97	2.33	1.59	3.84	3.84	0.06
Flower per plant	71.00	155.67	110.67	2.64	2.64	2.92
Pods per plant	57.67	145.67	88.54	3.79	3.79	3.35
Pod Length (cm)	3.93	6.38	4.95	1.22	1.22	0.06
Seeds per Plant	227.33	631.67	378.63	5.98	5.98	22.66
Seed diameter (mm)	3.93	7.90	5.07	1.26	1.26	0.06
100 Seed Weight (gm)	4.93	18.23	9.07	0.60	0.60	0.05
Days to Maturity	79.33	90.67	84.10	2.85	2.85	2.40
Seed Yield (tn/ha)	0.59	2.71	1.27	3.24	189.32	2.40

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error

Table 3. Estimation of genetic parameters in fourteen characters of 21pea genotypes

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Germination Percentage (%)	16.97	14.32	2.65	4.62	4.24	1.82	84.40	7.16	8.03
Days of 50% Flowering	6.08	3.95	2.13	5.83	4.70	3.45	65.00	3.30	7.80
Plant Height (cm)	368.27	367.43	0.85	24.82	24.79	1.19	92.77	39.44	51.00
Primary branches per plant	23.68	23.10	0.59	48.20	47.60	7.58	95.53	9.78	96.84
Leaf length (cm)	0.52	0.50	0.02	22.84	22.76	1.80	94.38	1.45	46.75
Leaf diameter (cm)	0.23	0.22	0.01	29.98	29.74	3.84	91.36	0.96	60.75
Flower per plant	516.00	507.46	8.54	20.53	20.36	2.64	92.34	46.02	41.58
Pods per plant	553.88	542.64	11.24	26.58	26.31	3.79	94.97	47.50	53.65
Pod Length (cm)	0.63	0.63	0.00	16.06	16.01	1.22	92.42	1.63	32.88
Seeds per Plant	10308.96	9795.64	513.32	26.82	26.14	5.98	95.02	198.74	52.49
Seed diameter (mm)	1.56	1.55	0.00	24.62	24.59	1.26	97.74	2.56	50.58
100 Seed Weight (gm)	16.80	16.80	0.00	45.22	45.21	0.60	98.98	8.44	93.13
Days to Maturity	16.06	10.31	5.75	4.76	3.82	2.85	64.20	5.30	6.30
Seed Yield (ton/ha)	0.52	0.52	0.00	57.00	56.90	3.24	98.68	1.48	117.03

$\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

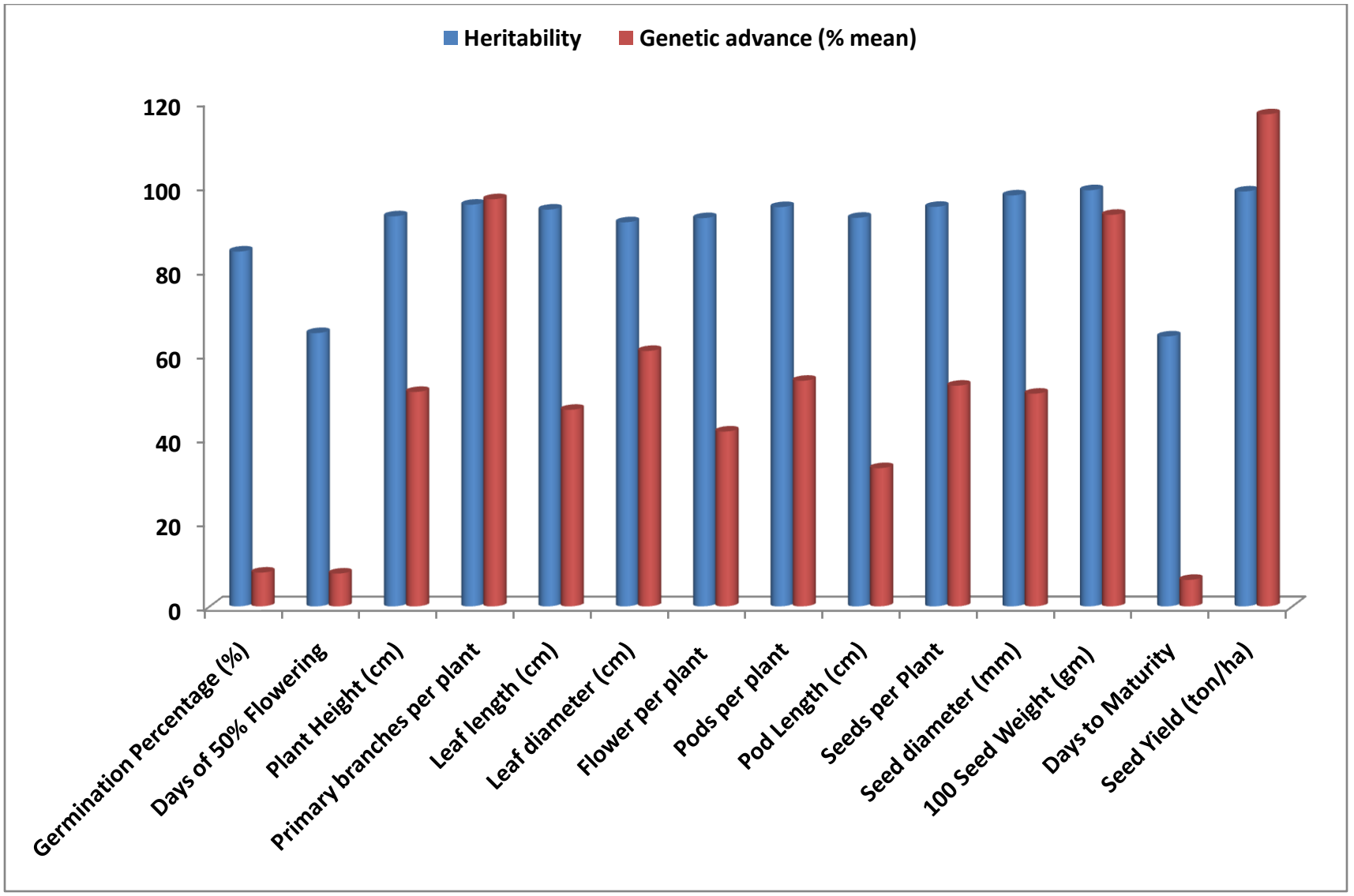

Figure 2. Heritability and genetic advance over mean in pea

found 3.3 and genetic advance over percentage of mean was found 7.8 which is low indicating non- additive genes controlled the trait.

4.2.3 Plant height (cm)

The mean number of plant height was 77.33. Significant differences were found among the genotypes with respect to plant height (Table 2). The values were ranged from 52 cm to 123 cm, in the genotype "BD- 4157"and "BD-4222" respectively. The genotypic variance was found 367.43 and phenotypic variance was found 368.27. From the analysis it is found that phenotypic variance (368.27) was higher than genotypic variances (367.43). It indicates that influence of environment on the expression of trait controlling genes was little bit higher but not considerable because their gap is very little. The genotypic co-efficient of variation was found 24.79 and phenotypic co-efficient of variation was found 24.82. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (92.77%)for this trait was high, genetic advance was found 39.44 which was medium and genetic advance over percentage of mean was found 51.00 which is medium indicating both additive and non- additive genes controlled the trait.

4.2.4 Primary branches per plant

The mean number of primary branches per plant was 10.10. Significant differences were found among the genotypes with respect to primary branches per plant (Table 2). The values were ranged from 3 to 17, in the genotype "BD- 4207"and "BD-4190" respectively. The genotypic variance was found 23.10 and phenotypic variance was found 23.68. From the analysis it is found that phenotypic variances (23.68) were higher than genotypic variances (23.10). It indicates that influence of environment on the expression of trait controlling genes was higher but not considerable because their gap is very little. The genotypic co-efficient of variation was found 47.60 and phenotypic co-efficient of variation was found 48.20. The difference between phenotypic co-efficient of

variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (95.53%)for this trait was high, genetic advance was found 9.78 and genetic advance over percentage of mean was found 96.84 which is low indicating additive genes controlled the trait.

4.2.5 Length of leaves (cm)

The mean number of length of leaves was 42.32. Significant differences were found among the genotypes with respect to length of leaves (Table 2). The values were ranged from 2.07cm to 4.47cm, in the genotype "BD- 4152"and "BD-4220" respectively. The genotypic variance was found 0.50 and phenotypic variance was found 0.52. From the analysis it is found that phenotypic variance (0.5) was higher than genotypic variances (0.50). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 22.76 and phenotypic co-efficient of variation was found 22.84. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (94.38%)for this trait was high, genetic advance was found 1.45 and genetic advance over percentage of mean was found 46.75 which is medium indicating both additive and non- additive gene controlled the trait.

4.2.6 Diameter of leaves (cm)

The mean diameter of leaves was 1.59 cm. Significant differences were found among the genotypes with respect to diameter of leaves (Table 2). The values were ranged from 0.97cm to 2.33cm, in the genotype "BD- 4150"and "BD-4223" respectively. The genotypic variance was found 0.22 and phenotypic variance was found 0.23. From the analysis it is found that phenotypic variance (0.23) was higher than genotypic variances (0.22). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 29.74 and phenotypic co-efficient of variation was found 29.98. The difference between

phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (91.36%)for this trait was high, genetic advance was found .97 and genetic advance over percentage of mean was found 60.75 which is high indicating additive genes controlled the trait.

4.2.7 Number of flowers per plant

The mean diameter of number flowers per plant was 110.67. Significant differences were found among the genotypes with respect to number flowers per plant (Table 2). The values were ranged from 71 to155.67, in the genotype "BD- 4171"and "BD-4190" respectively. The genotypic variance was found 507.46 and phenotypic variance was found 516. From the analysis it is found that phenotypic variance (516) was higher than genotypic variances (507.46). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 20.36 and phenotypic co-efficient of variation was found 20.53. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (92.34%)for this trait was high, genetic advance was found 46.02 and genetic advance over percentage of mean was found 41.58 which is medium indicating both additive and non- additive genes controlled the trait.

4.2.8 Pods per plant

The mean of number of pods per plant was 88.54. Significant differences were found among the genotypes with respect to number pods per plant (Table 2). The values were ranged from 57.67 to145.67, in the genotype "BD- 4171"and "BD-4190" respectively. The genotypic variance was found 542.64 and phenotypic variance was found 553.88. From the analysis it is found that phenotypic variance (553.88) was higher than genotypic variances (542.64). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation

was found 26.31 and phenotypic co-efficient of variation was found 26.58. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (94.97%) for this trait was high, genetic advance was found 47.50 and genetic advance over percentage of mean was found 53.65 which is medium indicating both additive and non- additive genes controlled the trait.

4.2.9 Pods length (cm)

The mean diameter of number pods length was 4.95cm. Significant differences were found among the genotypes with respect to pods length (Table 2). The values were ranged from 3.93cm to 6.38 cm, in the genotype "BD- 4190"and "BD-4223" respectively. The genotypic variance was found 0.63 and phenotypic variance was found 0.64. From the analysis it is found that phenotypic variance (0.64) was higher than genotypic variances (0.63). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 16.01 and phenotypic co-efficient of variation was found 16.06. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (92.42%) for this trait was high, genetic advance was found 1.63 and genetic advance over percentage of mean was found 32.88 which is medium indicating both additive and non- additive genes controlled the trait.

4.2.10 Seeds per plant

The mean number of seeds per plant was 378.63. Significant differences were found among the genotypes with respect to number of seeds per plant (Table 2). The values were ranged from 227.33 to 631.67, in the genotype "BD- 4205"and "BD-4190" respectively. The genotypic variance was found 9795.64 and phenotypic variance was found 10308.96. From the analysis it is found that phenotypic variance (10308.96) was higher than genotypic variances (9795.64). It indicates that influence of environment on

the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 26.14 and phenotypic co-efficient of variation was found 26.82. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (95.02%) for this trait was high, genetic advance was 198.74 found high and genetic advance over percentage of mean was found 52.49 which is medium indicating both additive and non- additive genes controlled the trait.

4.2.11 Seed diameter (mm)

The mean seed diameter was 5.07mm. Significant differences were found among the genotypes with respect to seed diameter (Table 2). The values were ranged from 3.93 mm to 7.90 mm, in the genotype "BD-41580"and "BD-4205" respectively. The genotypic variance was found 1.55 and phenotypic variance was found 1.56. From the analysis it is found that phenotypic variances (1.56) were higher than genotypic variances (1.55). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 24.59 and phenotypic co-efficient of variation was found 24.62. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (97.74%) for this trait was high, genetic advance was found 2.56 and genetic advance over percentage of mean was found 50.58 which are medium indicating both additive and non- additive genes controlled the trait.

4.2.12 100 Seed weight (g)

The mean of 100 seed weight was 9.07g. Significant differences were found among the genotypes with respect to 100 seed weight (Table 2). The values were ranged from 4.93g to 18.23g, in the genotype "BD- 4157"and "BD-4171" respectively. The genotypic variance was found 16.80 and phenotypic variance was found 16.82. From the analysis it

is found that phenotypic variances (16.82) were higher than genotypic variances (16.80). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 45.21 and phenotypic co-efficient of variation was found 45.22. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (98.98%) for this trait was high, genetic advance was 8.44 found low and genetic advance over percentage of mean was found 93.13 which is high indicating additive genes controlled the trait.

4.2.13 Days to maturity

The mean of days to maturity was 84.10 days. Significant differences were found among the genotypes with respect to days to maturity (Table 2). The values were ranged from 79.33 to 90.67 days, in the genotype "BD- 4161"and "BD-4182" respectively. The genotypic variance was found 10.31 and phenotypic variance was found 16.06. From the analysis it is found that phenotypic variances (16.06) were higher than genotypic variances (10.31). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 3.82 and phenotypic co-efficient of variation was found 4.76. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (64.2%) for this trait was moderately high, genetic advance was 5.3 found low and genetic advance over percentage of mean was found 6.3 which is low indicating non- additive genes controlled the trait.

4.2.14 Seed Yield (ton/ha)

The mean seed yield was 1.27 ton/ha. Significant differences were found among the genotypes with respect to seed yield (Table 2). The values were ranged from 0.59 to 2.71 ton/ha , in the genotype "BD- 4157"and "BD-4223" respectively. The genotypic variance

was found 0.52 and phenotypic variance was found 0.54. From the analysis it is found that phenotypic variances (0.54) were higher than genotypic variances (0.52). It indicates that influence of environment on the expression of trait controlling genes was higher and considerable. The genotypic co-efficient of variation was found 56.90 and phenotypic co-efficient of variation was found 57.00. The difference between phenotypic co-efficient of variation and genotypic co-efficient of variation was found very low which indicates less environmental effect on this character. The estimation of heritability (98.68%) for this trait was high, genetic advance was 1.48 found low and genetic advance over percentage of mean was found 117.03 which is high indicating additive genes controlled the trait.

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 result 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.

Plate 5: The smallest seed from G1

Plate 6: The largest seed from G6

Plate 7: Phenotypic comparison between smallest (G1) and largest seed (G6)

4.3.1 Germination percentage

Germintion percentage had negative and significant correlation with plant height (-0.314 and -0.290) in both genotypic and phenotypic level. With days to maturity (-.283) and seed yield (-.253) germination percentage had negative and significant relationship in only genotypic level (Table 4).

4.3.2 Days of 50% flowering

Days of 50% flowering had positive and significant correlation with plant height (.253) at genotypic level only. It had negative and highly significant correlation with primary branches per plant (-0.430 and -0.336) at both level. It had negative and highly significant correlation with flowers per plant (-0.336), pods per plant (-0.333) at only genotypic level, with flowers per plant (-0.264), pods per plant (-0.258) and seeds per plant it had negative and significance correlation at phenotypic level (Table 4).

4.3.3 Plant Height (cm)

Plant height had a positive and highly significant relationship with leaf length (0.749 and 0.747), leaf diameter (0.746 and 0.739), pod length (0.698 and 0.695), seed diameter (0.664 and 0.662), hundred seed weight (0.567 and 0.566) and seed yield (0.802 and 0.800) at both the level. There was a negative and highly significant relationship between plant height and primary branches per plant (-0.516 and -0.511) at both level. There was a significant and negative relationship between plant height and flowers per plant (-0.284 and -0.283) at both levels (Table 4).

4.3.4 Primary branches per plant

Primary branches per plant had a positive and highly significant correlation with flowers per plant (0.891 and 0.869) , pods per plant (0.794 and 0.778) and seeds per plant (0.762 and 0.739) at both level whereas days to maturity (0.369) at only genotypic level. There were negative and highly significant correlation between days of 50% flowering(-0.516 and -0.511) plant height (-0.430 and -0.336), leaf length (-0.530 and -0.523), leaf

diameter(-0.707 and -0.691), pod length (-0.667 and -0.657), seed diameter (-0.770 and -0.759), hundred seed weight(-0.843 and -0.833), seed yield (-0.699 and -0.693) at both genotypic and phonotypic level (Table 4) .

4.3.5 Leaf Length (cm)

Leaf length had a positive and highly significant correlation with plant height (0.749 and 0.747), leaf diameter (0.787 and 0.777), pod length (0.736 ad 0.731) , seed diameter (0.719 ad 0.716) , hundred seed weight (0.683 and 0.681) and seed yield (0.795 and 0.791) whereas negative and highly significant correlation with primary branches per plant (-0.530 and -0.523) flowers per plant(-0.418 and -0.415) and pods per plant (-0.354 and –o.353) at both genotypic and phenotypic level (Table 4) .

4.3.6 Leaf diameter (cm)

Leaf diameter had positive and highly significant correlation with plant height (0.746 and 0.739), leaf length (0.787 and 0.777), pod length(0.849 and 0.840), seed diameter (0.858 and 0.849), hundred seed weight (0.843 and 0.836) and seed yield (0.858 and 0.851) at both levels whereas negative and highly significant correlation with primary branches per plant (-0.707 and -0.691) , flowers per plant (-0.480 and -0.473) and pods per plant(-o.342 and -0.340) at both genotypic and phenotypic level (Table 4) .

4.3.7 Flowers per plant

Flowers per plant had positive and highly significant correlation with primary branches per plant (0.891 and 0.869), pods per plant (0.960 and 0.942) and seeds per plant (0.936 and 0.896) in both level whereas negative and highly significant with leaf length (-0.418 and -0.415), leaf diameter (-0.480 and -0.473), pod length (-0.496 and -0.490) , seed diameter (-0.678 and -0.672), hundred seed weight (-0.731 and -0.726) and seed yield (-0.566 and -0.560) at both genotypic and phenotypic level(Table 4) .

4.3.8 Pods per plant

Pods per plant had positive and highly significant correlation with primary branches per plant (0.794 and 0.778), flowers per plant (0.960 and 0.942), seeds per plant (0.964 and 0.939) at both levels whereas negative and highly significant correlation with leaf length (-0.354 and -0.353), leaf diameter (-0.342 and -0.340), pods length (-0.475 and -0.472) , seed diameter (-0.562 and -0.554), hundred seed weight (-0.640 and -0.633) and seed yield (-0.498 and -0.493) at both genotypic and phenotypic level (Table 4) .

4.3.9 Pod length (cm)

Pod length had positive and highly significant correlation with pod length (0.698 and 0.695), pod length (0.736 ad 0.731) , leaf diameter (0.849 and 0.840), seed diameter (0.779 and 0.776), hundred seed weight (0.797 and 0.795) and seed yield (0.848 and 0.845) at both genotypic and phenotypic level whereas negative and highly significant correlation with primary branches per plant (-0.667 and -0.657) , flowers per plant (-0.496 and -0.490), pods per plant (-0.475 and -0.472), seeds per plant (-0.350 and -0.343) at both genotypic and phenotypic level (Table 4) .

4.3.10 Seeds per Plant

Seeds per plant had positive and highly significant correlation with primary per plant (0.762 and 0.739), flowers per plant (0.936 and 0.896), pods per plant (0.964 and 0.939) , seed diameter(-0.506 and -0.491), hundred seed weight (-0.596 and -0.580) and seed yield (-0.368 and -0.357) whereas it had negative and highly significant correlation with leaf length (-0.258 and -0.251) and pod length (-0.350 and -0.343) at both genotypic and phenotypic level (Table 4) .

4.3.11 Seed diameter (mm)

Seed diameter had positive and highly significant correlation with plant height (0.664 and 0.662) , leaf length (0.719 and 0.716), leaf diameter (0.858 and 0.849), pod length (0.779 and 0.776), hundred seed weight (0.930 and 0.929) and seed yield (0.899 and 0.897)

whereas it showed negative and highly significant correlation with primary branches per plant (-0.770 and -0.759), flowers per plant (-0.678 and -0.672), pods per plant (-0.562 and -0.554) and seeds per plant (-0.506 and -0.491) at both genotypic and phenotypic level (Table 4) .

4.3.12 Hundred seed weight

Hundred seed weight had positive and highly significant correlation with plant height (0.567 and 0.566), leaf length (0.716 and 0.683), leaf diameter (0.849 and 0.843), pod length (0.797 and 0.795), seed diameter (0.930 and 0.929) and seed yield (0.890 and 0.888) whereas it showed negative and highly significant correlation with primary branches per plant (-0.843 and -0.833), flowers per plant (-0.731 and -0.726), pods per plant (-0.640and -0.633) and seeds per plant (-0.596 and -0.580) at both genotypic and phenotypic level (Table 4) .

4.3.13 Days to maturity

Days to maturity had positive and highly significant correlation with primary branches per plant (0.369) at only genotypic level whereas it showed positive and significant correlation with primary branches per plant (0.285) at only phenotypic level. It showed positive and significant correlation with germination percentage (-0.283),leaf diameter (-0.294) at genotypic level only (Table 4) .

4.3.14 Seed Yield

Seed yield had positive and highly significant correlation with plant height (0.802 and 0.800), leaf length (0.795 and 0.791), leaf diameter (0.858 and 0.851), pod length (0.848 and 0.845), seed diameter (0.899 and 0.897) and hundred seed weight (0.890 and 0.888) at both genotypic and phenotypic level whereas it showed negative and highly significant correlation with primary branches per plant (-0.699 and -0.693), flowers per plant (-0.566 and -0.560), pods per plant (-0.498 and -0.493) and seeds per plant (-0.368 and -0.357) at both genotypic and phenotypic level (Table 4) .

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) and Singh *et al*., (1997) who also noticed positive association of number of fruits per plant with fruit yield per plant.

Table 4: Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for 21 genotype of pea

	correlation	GP	D50F	PH (cm)	PBP	LL (cm)	LD (cm)	FPP	PPP	PL (cm)	SPP	SD (mm)	1000 SW (g)	DM
D50F	Genotypic	0.004												
	Phenotypic	0.001												
PH (cm)	Genotypic	-0.314*	0.253*											
	Phenotypic	-0.290*	0.196											
PBP	Genotypic	0.190	-0.430**	-0.516**										
	Phenotypic	0.174	-0.336**	-0.511**										
LL (cm)	Genotypic	0.033	0.035	0.749**	-0.530**									
	Phenotypic	0.027	0.020	0.747**	-0.523**									
LD (cm)	Genotypic	-0.201	0.049	0.746**	-0.707**	0.787**								
	Phenotypic	-0.186	0.020	0.739**	-0.691**	0.777**								
FPP	Genotypic	0.091	-0.336**	-0.284*	0.891**	-0.418**	-0.480**							
	Phenotypic	0.074	-0.264*	-0.283*	0.869**	-0.415**	-0.473**							
PPP	Genotypic	0.082	-0.333**	-0.215	0.794**	-0.354**	-0.342**	0.960**						
	Phenotypic	0.089	-0.258*	-0.214	0.778**	-0.353**	-0.340**	0.942**						
PL (cm)	Genotypic	-0.122	0.247*	0.698**	-0.667**	0.736**	0.849**	-0.496**	-0.475**					
	Phenotypic	-0.114	0.203	0.695**	-0.657**	0.731**	0.840**	-0.490**	-0.472**					
SPP	Genotypic	-0.028	-0.260*	-0.031	0.762**	-0.258*	-0.251*	0.936**	0.964**	-0.350**				
	Phenotypic	-0.010	-0.158	-0.032	0.739**	-0.251*	-0.239	0.896**	0.939**	-0.343**				
SD (mm)	Genotypic	-0.160	0.122	0.664**	-0.770**	0.719**	0.858**	-0.678**	-0.562**	0.779**	-0.506**			
	Phenotypic	-0.155	0.098	0.662**	-0.759**	0.716**	0.849**	-0.672**	-0.554**	0.776**	-0.491**			
1000 SW (g)	Genotypic	-0.154	0.130	0.567**	-0.843**	0.683**	0.843**	-0.731**	-0.640**	0.797**	-0.596**	0.930**		
	Phenotypic	-0.141	0.105	0.566**	-0.833**	0.681**	0.836**	-0.726**	-0.633**	0.795**	-0.580**	0.929**		
DM	Genotypic	-0.283*	0.039	-0.216	0.369**	-0.227	-0.294*	0.170	0.081	-0.231	0.104	-0.213	-0.243	
	Phenotypic	-0.132	0.106	-0.179	0.285*	-0.199	-0.241	0.130	0.070NS	-0.182	0.090	-0.177	-0.193	
SY (ton/ha)	Genotypic	-0.253*	0.227	0.802**	-0.699**	0.795**	0.858**	-0.566**	-0.498**	0.848**	-0.368**	0.899**	0.890**	-0.033
	Phenotypic	-0.232	0.185	0.800**	-0.693**	0.791**	0.851**	-0.560**	-0.493**	0.845**	-0.357**	0.897**	0.888**	-0.020

** = Significant at 1%. * = Significant at 5%.

GP: germination percentage, D50F: days to 50% flowering, PH (cm): plant height (cm), PBP: primary branches per plant, LL (cm): leaf length (cm), LD (cm): leaf diameter (cm), FPP: flowers per plant, PPP: pods per plant, PL (cm): pod length (cm), SPP: seeds per plant, SD (mm): seed diameter (mm), 100 SW: seed weight (g), DM: days to maturity and SY (ton/ha): seed yield (ton/ha)

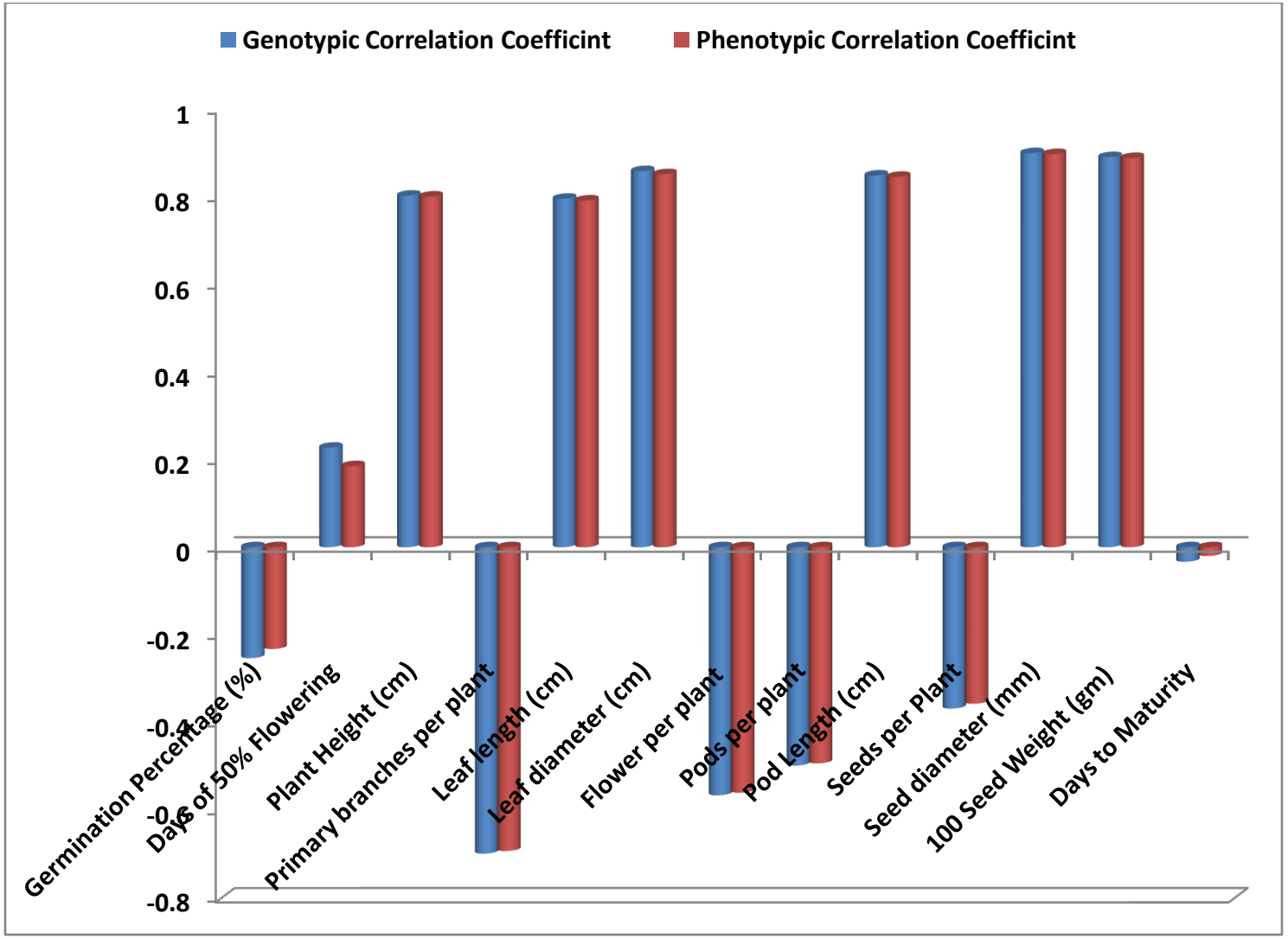

Figure 3: Genotypic and Phenotypic Correlation Coefficient of thirteen characters with seed yield in Pea

4.4 Path Co-efficient Analysis

Though correlation analysis denotes the association pattern of components traits with yield, they basically represent the overall effect 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 effect of one variable upon other. Such information would be of great value in enabling the breeder to exclusively identify the important component traits of yield and use the genetic resources for improvement in a planned way.

In path coefficient analysis the direct effect of a trait on seed yield per plant and its indirect effect through other characters were calculated and the results are presented in Table 8.

4.4.1 Direct effect

Ten out of thirteen characters had positive direct effect on yield per plant. The characters which had positive direct effects are days to 50% flowering (0.116), plant height (0.386), primary branches per plant(0.375), leaf length (0.065), leaf diameter (0.035), pods per plant (0.01), pod length (00.06), seeds per plant(0.07), hundred seed weight (0.087), days to maturity(0.16) . However characters viz., germination percentage (-0.004), flowers per plant (-0.193) and seed diameter (-0.02) had negative direct effect on seed yield per plant (Table 5).

Path coefficient analyses revealed that seed yield per plant was directly influenced by days of 50% flowering, plant height, primary branches per plant, leaf length, leaf diameter, pod per plant, pod length, seed per plant, hundred seed weight and days to

maturity. Hence selection of any of these traits can be done for the improvement of genotypes.

4.4.2 Indirect effect

4.4.2.1 Germination Percentage

Germination percentage showed a positive indirect effect on seed yield through days of 50% flowering (0.00), primary branches per plant (0.071), leaf length (0.002), pods per plant (0.00), seed per plant (0.00) and seed diameter. However it had indirect negative effect on seed yield through plant height (-0.121), leaf diameter (-0.007) , flowers per plant (-0.0.18), pod length (-0.01) , hundred seed weight(-0.12) and days to maturity(-0.046) (Table 5).

4.4.2.2 Days of 50% flowering

Days of 50% flowering showed a positive indirect effect on seed yield through plant height (0.098), leaf length (0.002), leaf diameter (0.002), flowers per plant (0.065), pod length (0.02), hundred seed weight (0.10) and days to maturity (0.006). Though it showed a negative indirect effect on seed yield through primary branch per plant (-0.161), seeds per plant (-0.02) (Table 5).

4.4.2.3 Plant Height

Plant height showed a positive indirect effect on seed yield through germination percentage (0.001), days of 50% flowering (0.029), leaf length(0.049), leaf diameter (0.026), flowers per plant (0.055), pod length(0.04) and hundred seed weight(0.46). Though it showed a negative indirect effect on seed yield through primary branches per plant (-0.194), seed diameter (-0.01) and days to maturity (-0.035) (Table 5).

4.4.2.4 Primary branches per plant

Primary braches per plant showed a positive indirect effect on seed yield through seeds per plant (0.05), seed diameter (0.01) and days to maturity (0.06). However it showed a

negative indirect effect germination percentage (-0.001), days of 50% flowering (-0.050), plant height (-0.199), leaf length (-0.034), leaf diameter (-0.025), flowers per plant (-0.172), pod length (-0.04) and hundred seed weight (-0.68) (Table 5).

4.4.2.5 Leaf Length (cm)

Leaf length showed a positive indirect effect on seed yield through days of 50% flowering (0.04), plant height (0.289), leaf diameter (0.28), flowers per plant (0.081), pod length (0.04) and hundred seed weight (0.55). Though it showed a negative indirect effect o seed yield through primary braches per plant (-0.199), seeds per plant (-0.02), seed diameter (-0.01) and days to maturity (-0.037) (Table 5).

4.4.2.6 Leaf diameter

Leaf diameter showed a positive indirect effect on seed yield through germination percentage (0.001), days of 50% flowering (0.006), plant height (0.288), leaf length (0.051), flowers per plant (0.093), pod length (0.05) and hundred seed weight (0.68). whereas it showed a negative indirect effect on seed yield through primary branches per plant (-0.265), seeds per plant (-0.02), seed diameter (-0.01) and days to maturity (-0.048) (Table 5).

4.4.2.7 Flowers per plant

Flowers per plant showed a positive indirect effect on seed yield through primary branches per plant (0.334), pods per plant (0.01), and seeds per plant (0.06), seed diameter (0.01) and days to maturity (0.028). Though it showed a negative indirect effect on seed yield through days of 50% flowering (-0.039), plant height (-0.110), leaf length (-0.027), leaf diameter (-0.017), pod length (-0.03) and hundred seed weight (-0.59) (Table 5).

4.4.2.8 Pods per plant

Pods per plant showed a positive indirect effect on seed yield through primary branches

per plant (0.3), seeds per plant (0.06), seed diameter (0.01) and days to maturity (0.028).

Pods per plant showed a positive indirect effect on seed yield through primary branches per plant (0.3), seeds per plant (0.06), seed diameter (0.01) and days to maturity (0.028). Though it showed a negative indirect effect on seed yield through days of 50% flowering (-0.04), plant height (-0.08), leaf length (-0.02), leaf diameter (-0.01), flowers per plant (-0.19), pod length (-0.03) and hundred seed weight (-0.52) (Table 5).

4.4.2.9 Pod length (cm)

Pod length showed a positive indirect effect on seed yield through days of 50% flowering (0.03), plant height (0.27), leaf length (0.05), leaf diameter (0.03), flowers per plant (0.10) and hundred seed weight (0.64) . Though it showed a negative indirect effect on seed yield through primary branches per plant (-0.25), seeds per plant (-0.02), seed diameter (-0.01) and days to maturity (-0.038) (Table 5).

4.4.2.10 Seeds per plant

Seeds per plant showed a positive indirect effect on seed yield through primary branches per plant (0.29), pods per plant (0.01), seed diameter (0.01), and days to maturity (0.017). Though it showed a negative indirect effect on seed yield through days of 50% flowering (-0.03), plant height (-0.01), leaf length (-0.02), leaf diameter (-0.01), flowers per plant (-0.18), pod length (-0.02) and hundred seed weight (-0.48) (Table 5).

4.4.2.11 Seed diameter (mm)

Seed diameter showed a positive indirect effect on seed yield through days of 50% flowering (0.01), plant height (0.26), leaf length (0.05), leaf diameter (0.03), flowers per plant (0.13), pod length (0.05) and hundred seed weight (0.75) . Though it showed a negative indirect effect on seed yield through primary branches per plant (-0.29), seeds per plant (-0.03) and days to maturity (-0.035) (Table 5).

4.4.2.12 Hundred seed weight (g)

Hundred seed weight showed a positive indirect effect on seed yield through days of 50% flowering (0.02), plant height (0.22), leaf length (0.04), leaf diameter (0.03), flowers per plant (0.14), pod length (0.05). Though it showed a negative indirect effect on seed yield through primary branches per plant (-0.32), seeds per plant (-0.04) and days to maturity (-0.040) (Table 5).

4.4.2.13 Days to maturity

Days to maturity showed a positive indirect effect on seed yield through primary branches per plant (0.14) and seeds per plant (0.01). Though it showed a negative indirect effect on seed yield through plant height (-0.08), leaf length (-0.01), leaf diameter (-0.01), flowers per plant (-0.03), pod length (-0.01) and hundred seed weight (-0.20) (Table 5).

From the Path analyses it can be concluded that for improvement of seed yiled selection would be effective for the traits plant height , leaf length, leaf diameter, pod length , seed diameter and hundred seed weight and selection should not be done for the traits for primary branches per plant ,flowers per plant , pods per plant and seeds per plant.

Plate 8: A pea plant with purple flower

Plate 9: A pea plant with white flower

Table 5: Partitioning of genotypic correlations into direct (bold) and indirect effects of thirteen important characters by path analysis of pea

	GP	D50F	PH (cm)	PBP	LL (cm)	LD (cm)	FPP	PPP	PL (cm)	SPP	SD (mm)	1000 SW (g)	DM	Genotypic correlation with seed yield
GP	**-0.004**	0.000	-0.121	0.071	0.002	-0.007	-0.018	0.00	-0.01	0.00	0.00	-0.12	-0.046	-0.253*
D50F	0.000	**0.116**	0.098	-0.161	0.002	0.002	0.065	0.00	0.02	-0.02	0.00	0.10	0.006	0.227
PH (cm)	0.001	0.029	**0.386**	-0.194	0.049	0.026	0.055	0.00	0.04	0.00	-0.01	0.46	-0.035	0.802**
PBP	-0.001	-0.050	-0.199	**0.375**	-0.034	-0.025	-0.172	0.00	-0.04	0.05	0.01	-0.68	0.060	-0.699**
LL (cm)	0.000	0.004	0.289	-0.199	**0.065**	0.028	0.081	0.00	0.04	-0.02	-0.01	0.55	-0.037	0.795**
LD (cm)	0.001	0.006	0.288	-0.265	0.051	**0.035**	0.093	0.00	0.05	-0.02	-0.01	0.68	-0.048	0.858**
FPP	0.000	-0.039	-0.110	0.334	-0.027	-0.017	**-0.193**	0.01	-0.03	0.06	0.01	-0.59	0.028	-0.566**
PPP	0.00	-0.04	-0.08	0.30	-0.02	-0.01	-0.19	**0.01**	-0.03	0.06	0.01	-0.52	0.013	-0.498**
PL (cm)	0.00	0.03	0.27	-0.25	0.05	0.03	0.10	0.00	**0.06**	-0.02	-0.01	0.64	-0.038	0.848**
SPP	0.00	-0.03	-0.01	0.29	-0.02	-0.01	-0.18	0.01	-0.02	**0.07**	0.01	-0.48	0.017	-0.368**
SD (mm)	0.00	0.01	0.26	-0.29	0.05	0.03	0.13	0.00	0.05	-0.03	**-0.02**	0.75	-0.035	0.899**
1000 SW (g)	0.00	0.02	0.22	-0.32	0.04	0.03	0.14	0.00	0.05	-0.04	-0.02	**0.81**	-0.040	0.890**
DM	0.00	0.00	-0.08	0.14	-0.01	-0.01	-0.03	0.00	-0.01	0.01	0.00	-0.20	**0.16**	-0.033

Residual effect: 0.113 ** = Significant at 1%. * = Significant at 5%.

GP: germination percentage, D50F: days to 50% flowering, PH (cm): plant height (cm), PBP: primary branches per plant, LL (cm): leaf length (cm), LD (cm): leaf diameter (cm), FPP: flowers per plant, PPP: pods per plant, PL (cm): pod length (cm), SPP: seeds per plant, SD (mm): seed diameter (mm), 100 SW: seed weight (g), DM: days to maturity and SY (ton/ha): seed yield (ton/h

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 58.97% of the total variation among the genotypes, while 10 of these with Eigen values above unity accounted for 99.77% presented in Table 5. Based on principal component scores I and II obtained from the principal component analysis, a two dimensional scatter diagram (Z1-Z2) 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 present considerable diversity existed among the genotypes which are given in Fig 5.

In order to, assess the diversity and grouping genotypes based on the characteristics and parameter was performed Principal Component Analysis. PCA shows that the first three traits correspond to the whole percentage of the variance in the dataset. The first three main PCAs are extracted from the complicated components, the total cumulative variance of these three factors amounted to 84.40% and these components had eigen values >1. The PCA grouped the estimated pea variables into three main components which PCA_1 accounted for about 58.97% of the variation; PCA_2 for 16.91%; PCA_3 8.52%. The first PCA was related to plant height, leaf length, leaf diameter, pod length, seed diameter, 100 seed weight and seed yield whereas the second PCA was related to seeds per plant and pods per plant. The third PCA contrasts variables that are related solely to days to maturity (Table 6).

Table 6: Factor analysis for 13 studied traits in pea genotypes

	Component		
	PCA1	PCA2	PCA3
Germination Percentage %	-0.173	-0.170	-0.624
Days of 50% Flowering	0.225	-0.252	0.478
Plant Height (cm)	0.705	0.537	0.157
Primary branches per plant	-0.894	0.281	0.006
Leaf length (cm)	0.770	0.380	-0.171
Leaf diameter (cm)	0.857	0.397	-0.075
Flower per plant	-0.798	0.559	0.012
Pods per plant	-0.726	0.634	-0.034
Pod Length (cm)	0.855	0.258	0.005
Seeds per Plant	-0.627	0.734	0.086
Seed diameter (mm)	0.924	0.129	-0.032
100 Seed Weight (gm)	0.941	0.018	-0.061
Days to Maturity	-0.209	-0.093	0.722
Seed Yield (ton/ha)	0.911	0.282	0.164
Eigen value	7.666	2.198	1.108
Cumulative%	58.97	75.88	84.40

Table 7: Eigen values and yield percent contribution of thirteen characters of 21 pea genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	7.666	58.97	58.97
II	2.198	16.91	75.88
III	1.108	8.52	84.40
IV	0.924	7.11	91.51
V	0.375	2.88	94.39
VI	0.260	2.00	96.39
VII	0.181	1.39	97.78
VIII	0.143	1.10	98.88
IX	0.075	0.58	99.46
X	0.041	0.31	99.77
XI	0.016	0.12	99.89
XII	0.011	0.08	99.97
XIII	0.003	0.03	100.00

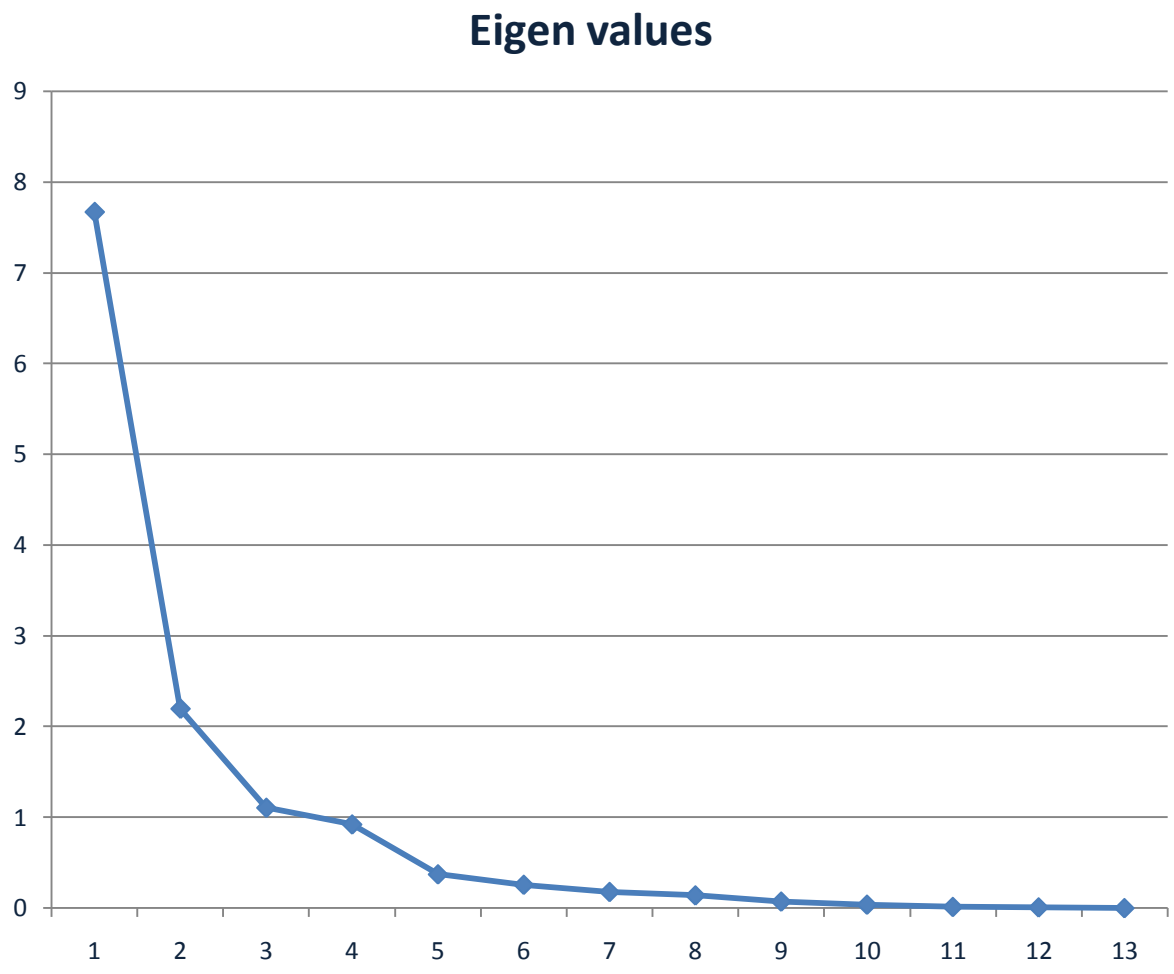

Fig 4: Graphical representation of Eigen values for component number of Pea

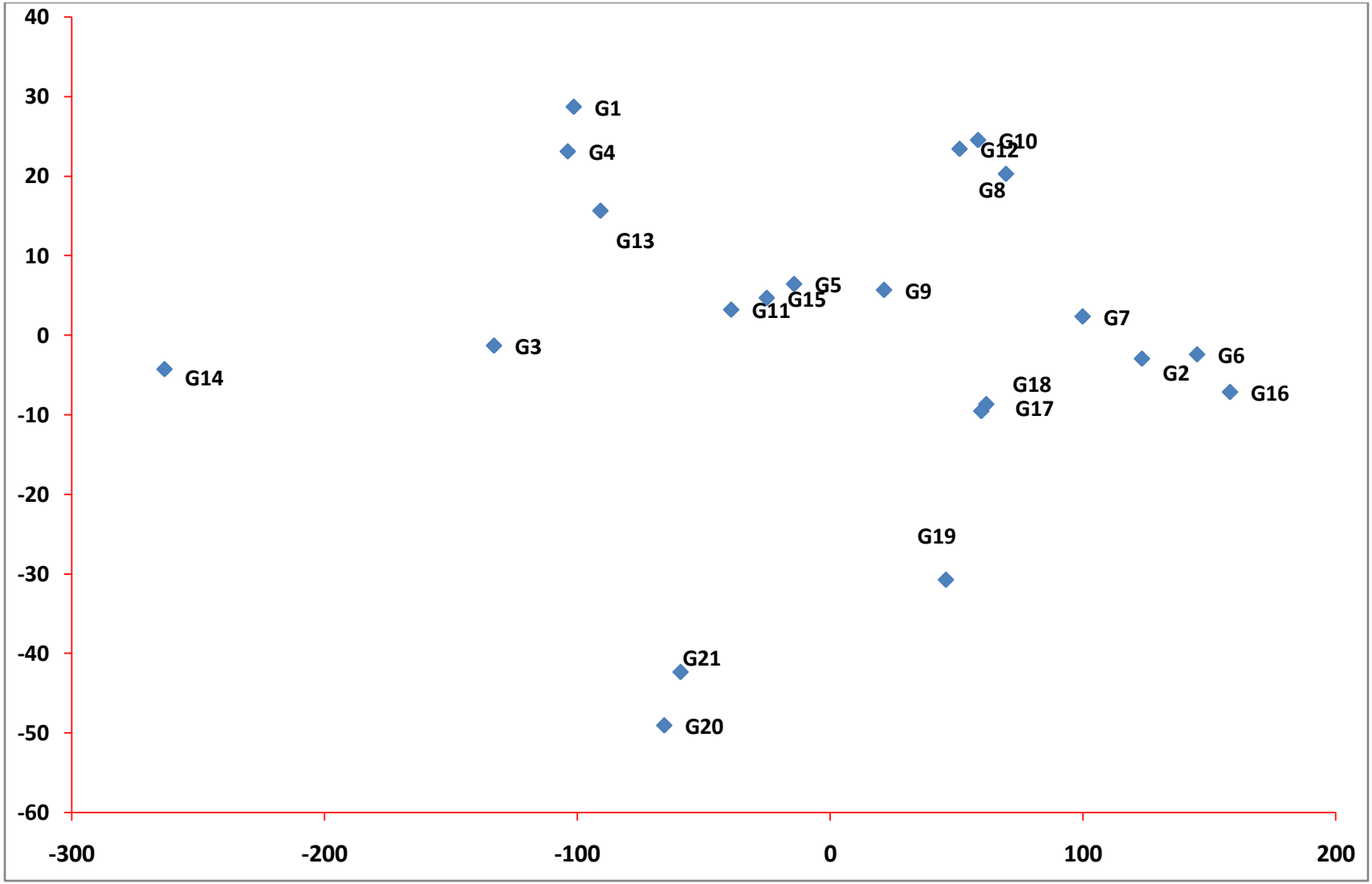

Figure 5: Scatter diagram of pea genotypes of based on their principal component scores.

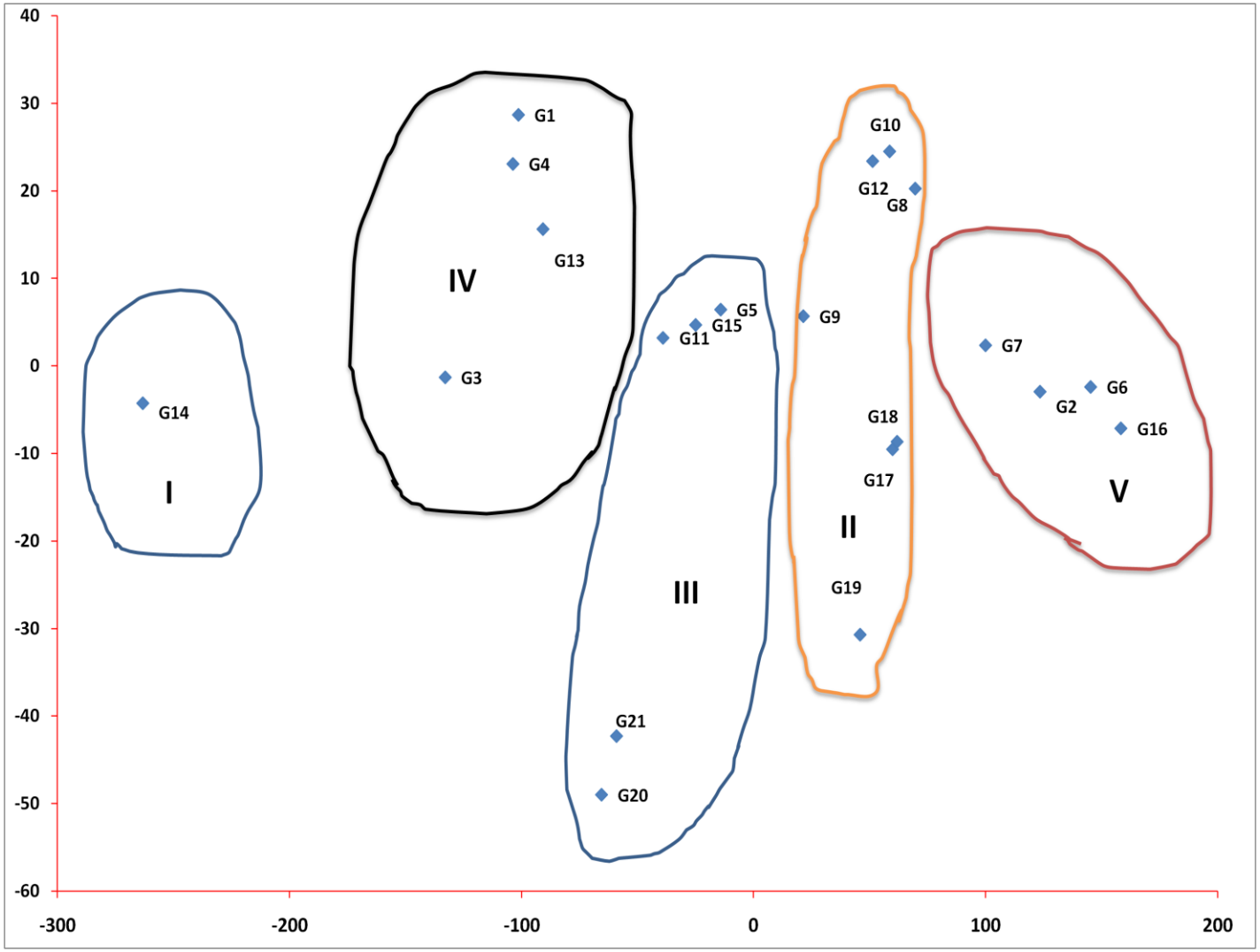

Figure 6: Cluster diagram showing average intra and inter cluster distances of 21 genotypes in Pea

4.5.2 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 21 pea genotypes were grouped into five different clusters. It is stated that highest 33.33% genotypes were included in cluster II and it was followed by 23.81% in cluster III, 19.05% in cluster IV and V. The remaining 4.76% genotypes were in cluster I. The composition of clusters with different genotypes is presented in Table 8.

From Table 9 cluster II had the maximum 7 genotypes (G8, G9, G10, G12, G17, G18, G19) followed by cluster III(G5, G11, G15, G20, G21), cluster IV (G1, G3, G4, G13) and cluster V(G2, G6, G7, G16) had 4 genotypes. Cluster I comprised with only one genotypes (G14) (Table 8).

The result confirmed the clustering pattern off the genotype according to the principal component analysis. Composition of various clusters regarding their genotypes in each cluster is presented in Table 9. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. For that reason it can be said that the results obtained through PCA were established by nonhierarchical clustering.

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Table 8: Distribution of 21 genotypes in different clusters

Cluster no.	Genotypes	No. of populations	Percentage	Genotypes
I	G14	1	4.76%	BD 4190,
II	G8, G9, G10, G12, G17, G18, G19	7	33.33%	BD 4176, BD 4178, BD 4182, BD 4186, BD 4206, BD 4207, BD 4220
III	G5, G11, G15, G20, G21	5	23.81%	BD 4161, BD 4183, BD 4193, BD 4222, BD 4223
IV	G1, G3, G4, G13	4	19.05%	BD 4150, BD 4154, BD 4157, BD 4188
V	G2, G6, G7, G16	4	19.05%	BD 4151, BD 4171, BD 4172, BD 4205
	Total	21		

4.5.3 Canonical variate analysis

The inter cluster D^2 values are given in Table 11 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 9. The inter cluster D^2 values were maximum (49.46) between the cluster I and cluster V, followed by I and II (37.74) ,IV and V (33.88) and I and III (29.93). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and V as well as V and I indicated the genotypes in these clusters were diverse than those clusters. The minimum distance was observed between clusters II and III (8.62) and III and II (8.62) indicated close relationship among the genotypes included. So the crossing between the genotypes derived from cluster V and I will bring desired result.

The intra cluster D^2 values were given in Table 10. The intra cluster distance was observed in the clusters II, III, IV and V. The intra cluster distance was higher in cluster II (4.62) followed by cluster III (3.13), IV (2.52) and lowest in cluster V (1.43). No intra cluster distance was observed for cluster I because of one genotype included in this cluster. The intra cluster distances in all the clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

Table 9: Intra (Bold) and inter cluster distances (D^2) for 21 pea genotypes

Cluster	I	II	III	IV	V
I	**0.00**	37.74	29.93	16.58	49.46
II		**4.62**	8.62	22.07	12.06
III			**3.13**	15.34	20.00
IV				**2.52**	33.88
V					**1.43**

Table 10: The nearest and farthest clusters from each cluster between D^2 values in pea

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	IV (16.58)	V (49.46)
2	II	III (8.62)	I (37.74)
3	III	II (8.62)	I (29.93)
4	IV	III (15.34)	V (33.88)
5	V	II (12.06)	I (49.46)

4.5.4 Cluster mean analysis

The cluster means of 13 different characters (Table 11) were indicated and compared considerable differences among clusters for all the characters studied. Maximum days of 50% flowering were found in cluster V (44.60) whereas minimum was found in cluster I (40.00). Maximum plant height was observed in cluster III (90.40) and minimum was observed in cluster IV (62.25). Number of primary branches per plant was observed maximum in cluster I (17.00) and minimum was in cluster V(4.00).Leaf length was found maximum in cluster V (3.37 cm) and minimum was found in cluster I (2.50 cm). Maximun leaf diameter was found in cluster V (1.82 cm) and minimum was found in cluster IV (1.34cm). Flowers per plant were maximum in cluster I (155.67) and minimum in cluster V (79.08) (Table 11).

Pods per plant were found maximum in cluster I (145.67) and minimum in cluster V (60.67). Pod length was found maximum in cluster V (5.27cm) and minimum in cluster I (3.93 cm). Seed per plant was found maximum in cluster I (631.67) and minimum in cluster V (254.00). Seed diameter was found highest in cluster V (6.17 mm) and lowest in cluster I (3.93 mm) (Table 11).

Hundred seed weight was found maximum in cluster IV (13.24 g) whereas minimum in cluster I (5.03g). Days to maturity was recorded highest in cluster IV (85.25 days) and lowest in cluster I (81.33 days). Seed yield was found highest in cluster V (1.69 ton/ha) whereas lowest in cluster I (0.59 ton/ha) (Table 11).

Table 11: Cluster mean for thirteen yield and yield related characters in 21 pea genotypes

Characters	I	II	III	IV	V
Days of 50% Flowering	40.00 (L)	41.67 (I)	42.60 (I)	42.00 (I)	44.00 (H)
Plant Height (cm)	76.00 (I)	75.62 (I)	90.40 (H)	62.25 (L)	79.42 (I)
Primary branches per plant	17.00 (H)	8.86 (I)	11.40 (I)	15.00 (I)	4.00 (L)
Leaf length (cm)	2.50 (L)	3.10(I)	3.26 (I)	2.75 (I)	3.37 (H)
Leaf diameter (cm)	1.47 (I)	1.62 (I)	1.59 (I)	1.34 (L)	1.82 (H)
Flower per plant	155.67 (H)	103.33 (I)	115.07 (I)	138.33 (I)	79.08 (L)
Pods per plant	145.67 (H)	78.62 (I)	89.33(I)	118.50 (I)	60.67 (L)
Pod Length (cm)	3.93 (L)	5.06 (I)	5.07 (I)	4.51 (I)	5.27 (H)
Seeds per Plant	631.67 (H)	327.33 (I)	420.13 (I)	477.91 (I)	254.00 (L)
Seed diameter (mm)	3.93 (L)	5.18 (I)	5.03 (I)	4.10 (I)	6.17 (H)
100 Seed Weight (gm)	5.03 (L)	9.69 (I)	8.42 (I)	5.60 (I)	13.24(H)
Days to Maturity	81.33 (L)	84.14 (I)	84.60 (I)	85.25 (H)	82.92 (I)
Seed Yield (ton/ha)	0.59 (L)	1.30 (I)	1.48 (I)	0.69 (I)	1.69 (H)

H: high value
L: low value
I: intermediate value

4.5.5 Cluster diagram

With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Fig 6) was constructed, which showed the relationship between different genotypes. However, the diagram was not following exact scale. It was apparent from the (Fig 6) that the genotypes from the cluster V were far diverse (49.46) from the genotypes of the cluster I and where the genotypes belonging to III- II were the least diverse (8.62). Genotypes of cluster I and II (37.74) and I-III (29.93) were moderately diverse from each other. The genotypes included between the clusters IV-V (33.88) were also diverse.

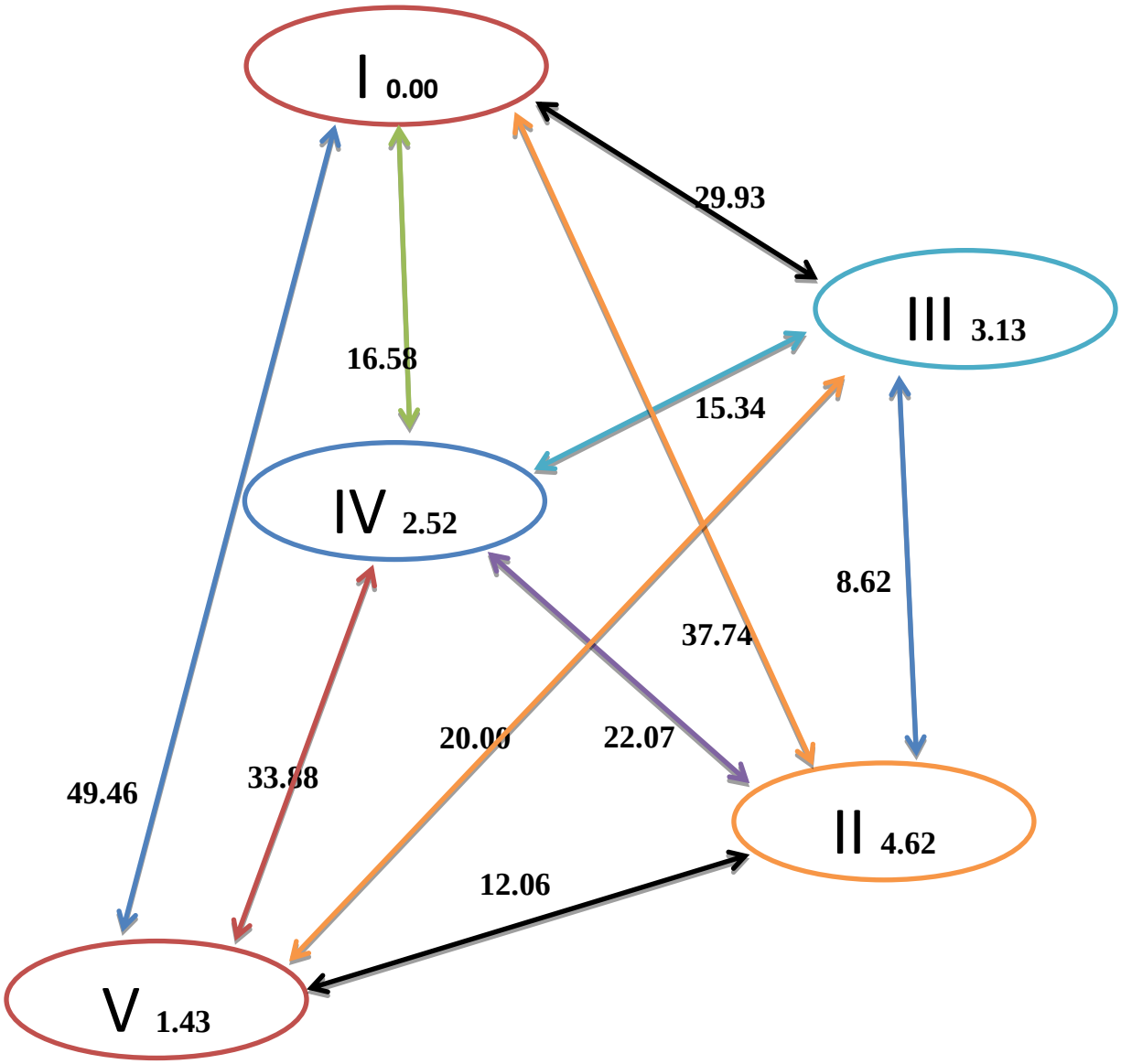

Fig 7: Intra and inter cluster distances of 21 genotypes in pea

4.5.6 Contribution of characters towards divergence of the genotypes

Contribution of characters towards the divergence obtained from canonical variates analysis is presented in Table 12. In this method vectors were calculated to represent in the graphical form. This is helpful in cluster analysis as it facilitated the study of group constellation and also serves as a pictorial representation of the configuration of various groups. The absolute magnitude of the coefficients in the first two canonical vectors also reflected to a great extent, the importance of the characters for primary and secondary differentiation. The character which gave absolute magnitude for vector 1 was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If the same character gave equal magnitude for both vectors then the character was considered responsible for primary as well as secondary differentiation.

Table 12: Relative contributions of the thirteen characters of 21 varieties to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days of 50% Flowering	0.095	0.196
Plant Height (cm)	0.252	-0.355
Primary branches per plant	-0.326	-0.187
Leaf length (cm)	0.278	-0.274
Leaf diameter (cm)	0.309	-0.276
Flower per plant	-0.291	-0.374
Pods per plant	-0.264	-0.427
Pod Length (cm)	0.309	-0.184
Seeds per Plant	-0.232	-0.490
Seed diameter (mm)	0.333	-0.094
100 Seed Weight (gm)	0.339	-0.021
Days to Maturity	-0.090	0.072
Seed Yield (ton/ha)	0.327	-0.189

In vector (Z_1) obtained from principal component analysis (PCA), the important characters responsible for genetic divergence in the axis of differentiation were days of 50% flowering (0.095), plant height (0.258), leaf length (0.278), leaf diameter (0.309), pod length (0.309), seed diameter (0.333), hundred seed weight (0.339) and seed yield (0.327). In vector 2 (Z_2) the second axis of differentiation days of 50% flowering (0.196) and days to maturity (0.072) were important because all these characters had positive signs. On the other hand primary branches per plant (-0.326), flowers per plant (-0.291), pods per plant (-0.264), seeds per plant (-0.232) and days to maturity (-0.090) possessed the negative sign in the first axis of differentiation and plant height (-0.355), primary branches per plant (-0.187), leaf length (-0.274), leaf diameter (-0.276), flowers per plant (-0.374), pods per plant (-0.427), pod length (-0.184), seeds per plant (-0.490), seed diameter (-0.094), hundred seed weight (-0.021) and yield (-0.189) possessed negative signs in the second axis of differentiation that means it had minor role in the genetic diverse. Days of 50% flowering had positive sign in both the vectors, which indicated it was the important component character having higher contribution to the genetic divergence among the characters studied.

4.5.7 Selection of genotypes as parent for hybridization program:

Selection of genetically distant parents is a vital step for hybridization program. So the genotypes should be selected on the basis of specific objectives. A high heterosis could be created from the crosses between genetically distance parents, (Falconer, 1961; Moll *et al*., 1962; 1962 Ramanujan *et al*., 1974; Ghaderi *et al*., 1984). Therefore considering group distance and other agronomic performance the inter-genotypic crosses between BD 4190 and BD 4151, BD 4190 and BD 4171, BD 4190 and BD 4172, BD 4190 and BD 4205) may be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify the characters contributing to genetic diversity, identify divergent parents for hybridization program, identify the characters which contribute to genetic diversity, measure the magnitude of genetic divergence in genotypes and find out the variability regarding yield and some yield contributing characters, the degrees of association among the characters under study and their indirect and direct effects of 21 genotypes of *Pisum sativum* L. at the experimental plot of Sher-E-Bangla Agricultural University farm, Dhaka, during December 2016 to March 2017. The most important findings of the present study have been summarized on the basis of the characters under study.

The ANOVA (analysis of variance) showed significant differences among the genotypes for all the characters under study. The accession BD- 4188 showed highest germination percentage (96.67%) while the lowest (82.33%) was recorded in BD-4207. The minimum days of 50% flowering was 39.67 days in the genotype BD- 4188 and maximum days of 50% flowering was to 48.67 days in the genotype BD-417. The lowest plant height was 52 cm in BD- 4157 and highest was 123 cm in the genotype BD-4222. The minimum number of primary branches per plant was 3 in BD- 4207 and maximum was 17 in BD-4190. The minimum length of leaves was 2.07cm in BD- 4152 and maximum was 4.47cm in BD-4220. The genotype BD- 4150 showed minimum diameter of leaves 0.97 cm whereas BD-4223 showed maximum diameter of leaves 2.33 cm. The minimum number of flowers per plant was recorded 71 in BD- 4171 and maximum number of flowers per plant was recorded 155.67 in BD-4190.

The highest number of pods per plant was found 145.67 in BD-4190 and lowest number of pods per plant was found 57.67 in BD- 4171 genotype. The maximum pod length was found 6.38 cm in BD-4223 whereas minimum length of pod was found 3.93 cm in BD-4190. The lowest number of seeds per plant was recorded 227.33 in BD- 4205 whereas the highest number of seeds per plant was recorded 631.67 in BD-4190. The maximum seed diameter was found 7.90 mm in BD-4205 whereas BD-41580 showed minimum seed diameter 3.93 mm. The minimum hundred seed weight was found 4.93g in BD-4157 whereas maximum hundred seed weight was found18.23g in BD-4171. The maximum days to maturity was recorded 90.67 days in BD-4182 whereas the minimum days to maturity was 79.33 days in BD- 4161genotype. The maximum seed yield was

recorded 2.71 ton/ha in BD-4223 whereas minimum seed yield was 0.59 ton/ha in BD-4157.

The phenotypic coefficients of variation were higher than genotypic coefficients of variation in all the characters under study. Phenotypic coefficients of variation were also near to genotypic coefficients of variation for all of the characters under study. High heritability (> 60%) was observed for all the characters under study. The highest heritability was found for seed yield (98.68%). The high heritability coupled with high genetic advance in percent of mean observed in plant height, primary branches per plant, leaf length, Leaf diameter, flower per plant, pods per plant, pod length, seeds per plant, seed diameter, 100 seed weight and seed yield which would be selected for future breeding program. . High heritability coupled with low genetic advance in percent of mean was observed in germination percentage, days of 50% flowering and days to maturity.

Plant height, leaf length, leaf diameter, pod length, seed diameter and hundred seed weight showed highly significant and positive correlation with seed yield at both genotypic and phenotypic levels. On the other hand primary branches per plant, flowers per plant, and pods per plant and seeds per plant showed negative and highly significant correlation with seed yield per plant at both genotypic and phenotypic levels.

Days to maturity showed positive and highly significant correlation with primary branches per plant, negative and significant correlation with germination percentage, leaf diameter at genotypic level. Hundred seed weight showed positive and highly significant correlation with plant height, leaf length, leaf diameter, pod length, seed diameter and seed yield both genotypic and phenotypic levels whereas it showed negative and highly significant correlation with primary branches per plant, flowers per plant, pods per plant and seeds per plant at both genotypic and phenotypic levels.

Seed diameter showed positive and highly significant correlation with plant height, leaf length, leaf diameter, pod length, hundred seed weight and seed yield at both genotypic and phenotypic levels whereas it showed negative and highly significant correlation with primary branches per plant, flowers per plant, pods per plant and seeds per plant at both genotypic and phenotypic levels. Seeds per plant showed positive and highly significant correlation with primary branches per plant, flowers per plant and pods per plant whereas negative and highly significant correlation with pod length, seed diameter, hundred seed weight and seed yield at both genotypic and phenotypic levels.

Pod length showed positive and highly significant correlation with plant height, leaf length, leaf diameter; seed diameter, hundred seed weight and seed yield whereas negative and highly significant correlation with primary branches per plant, flowers per plant, pods per plant and seeds per plant at both genotypic and phenotypic levels. Pods per plant showed positive and highly significant correlation with primary branches per plant and flowers per plant whereas it showed negative and highly significant correlation with leaf length, leaf diameter, pod length, seed diameter, hundred seed weight and seed yield plant at both genotypic and phenotypic levels.

Flowers per plant showed positive and highly significant correlation with pods per plant and seeds per plant whereas it showed negative and highly significant correlation with days of 50% flowering, leaf length, leaf diameter, pod length, seed diameter, hundred seed weight and seed yield at both genotypic and phenotypic levels. Leaf diameter showed positive and highly significant correlation with plant height, leaf length, pod length, seed diameter, hundred seed weight and seed yield whereas it showed negative and highly significant correlation with primary branches per plant, flowers per plant and pods per plant at both genotypic and phenotypic levels.

Leaf length plant showed positive and highly significant correlation with plant height, leaf diameter, pod length, seed diameter, hundred seed weight and seed yield whereas it showed negative and highly significant correlation with primary branches per plant, flowers per plant, pods per plant and seeds per plant at both genotypic and phenotypic levels. Primary branches per plant showed positive and highly significant correlation with flowers per plant and pods per plant whereas it showed negative and highly significant correlation with days of 50% flowering, plant height, leaf length, leaf diameter, pod length, seed diameter, hundred seed weight and seed yield at both genotypic and phenotypic levels.

Hundred seed weight showed the highest positive direct effect (0.81) with seed yield. On the other hand negative direct effect on seed yield was shown by germination percentage flowers per plant, seed diameter. Days of 50% flowering, plant height, primary branches per plant, leaf length, leaf diameter, pods per plant, pod length, seeds per plant and days to maturity also showed positive direct effect with seed yield per unit area. The highest indirect effect of seed diameter observed with hundred seed weight. Hundred seed weight showed high direct effect on seed yield indicated that direct selection for this trait might be successful and there is a great extent of possibility of improving seed yield through selection based on those characters.

Genetic diversity of twenty one pea genotypes based on fourteen characters was measured through multivariate analysis. The 21 genotypes clustered into five distant clusters. The cluster II comprised the maximum number 7 of genotypes followed by cluster III, 5. The cluster IV, V and I comprised 4, 4 and 1 genotypes, respectively. The highest inter-cluster distance (49046) was observed between the cluster I and V and the highest distant genotypes were G14 (BD-4190) and G 16 (BD-4205). The lowest inter-cluster distance (8.62) was observed between the cluster II and III and the lowest distance genotypes were G10 (BD-4190) and G12 (BD-4186). (Fig 5)

The inter-cluster distances were larger than the intra-cluster distances. The intra cluster distances in the entire five clusters were more or less low indicating that the genotypes within the same cluster were closely related. Plant height, leaf length, leaf diameter, pod length, seed diameter, and seeds per plant hundred seed weight were the important component characters having higher contribution to the genetic divergence.

The result of the present study exposed that a wide variability exists among the syudied and 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 findings could be drawn:

1. The genotype of clusters I was more diverse from the genotypes of cluster V.

2. Wide range of genetic diversity present among the pea genotypes. Wide genetic diversity was found in 21 genotypes of pea, which were grouped into five clusters and most diverse genotypes were G14 and G16. That variability could be used for future breeding program of pea in Bangladesh.

3. Plant height, leaf length, leaf diameter, pod length, seed diameter and hundred seed weight showed highly significant and positive correlation with seed yield at both genotypic and phenotypic levels. This results suggested that seed yield per plant can be increased by improving these characters.

4. High heritability coupled with high genetic advance in percent of mean was observed in plant height, primary branches per plant, leaf length, leaf diameter, flowers per plant, pods per plant, pod Length, seeds per plant, seed diameter, 100 seed weight and seed yield. Hence, yield improvement in pea would be achieved though selection of these characters.

5. Days of 50% flowering, Plant height, primary branches per plant, leaf length, leaf diameter, pods per plant, pod length, seeds per plant, hundred seed weight, days to maturity showed positive direct effect on yield. So yield improvement was associated with these characters.

6. Plant height, leaf length, leaf diameter, pod length, seed diameter, hundred seed weight were found responsible for the maximum diversity. On the other hand, primary branches per plant, flowers per plant and pods per plant have the least responsibility of both the primary and secondary differentiation of genotypes.

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

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

1. Genotypes G2 (BD-4151), G6 (BD-4171), G7 (BD-4172), G14 (BD-4190), G16 (BD-4205) could be included in the furthest study in view of seed yield for releasing as pea verities**.**

2. The genotypes of cluster I and V could be used as parents for future breeding program to developed pea variety.

3. Plant height, leaf length, leaf diameter, pod length, seed diameter, hundred seed weight were found responsible for the maximum diversity So selection based on these characters could be effective for the improvement of pea yield.

CHAPTER VI

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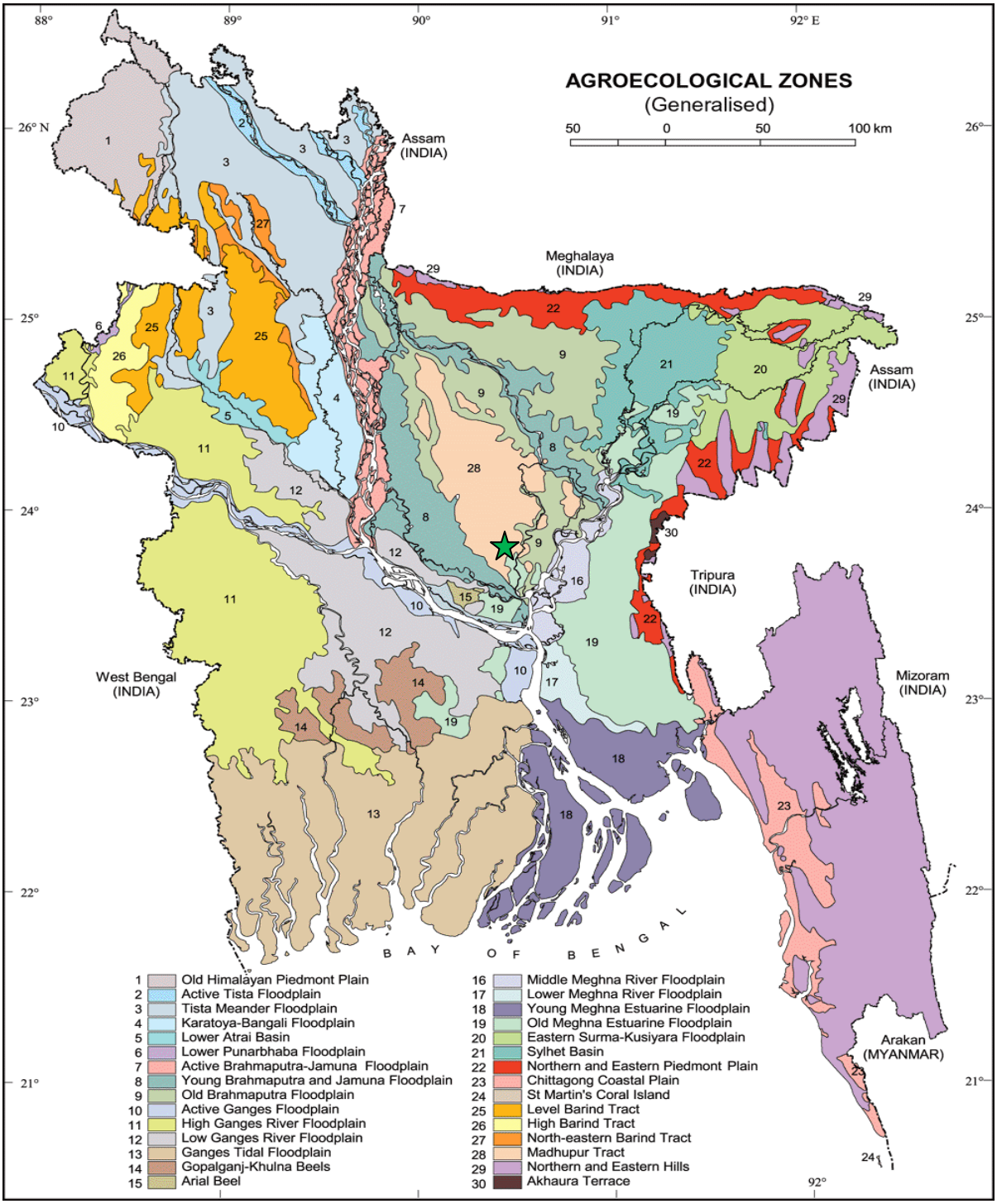
APPENDICES

Appendix I: Map showing the experimental site under the study



Green Star = Experimental Area

Appendix II: Monthly average record of air temperature, rainfall, relative humidity, sunshine hours of the experimental site during study period from December 2016 to March 2017

Month	Air temperature(◦c)		Relative humidity (%)	Rainfall(mm) total	Sunshine (hr)
	Maximum	Minimum			
December,2016	29	13	79	0	8.3
January,2017	28.1	11.1	72	1	7.5
February,2017	33.9	12.2	55	1	8.7
March,2017	34.6	16.5	67	45	7.3

Source: Bangladesh Meteorological Department (Climate & Weather Division) Agargaon

Dhaka- 1212

Appendix III: Physical characteristics and chemical composition of the experimental plot

Soil characteristics	Analytical results
Aprological zone	Madhupur tract
pH	6.00-6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq/100 g soil

Source: Soil Resource and development institute (SRDI), Dhaka 1212

Appendix IV: Principal component score 1 & 2.

Sl No.	PCA 1	PCA 2
G 1	-101.37	28.71
G 2	123.39	-2.93
G 3	-132.92	-1.29
G 4	-103.75	23.10
G 5	-14.21	6.45
G 6	145.20	-2.39
G 7	99.92	2.37
G 8	69.60	20.28
G 9	21.38	5.70
G 10	58.57	24.53
G 11	-39.09	3.22
G 12	51.26	23.42
G 13	-90.80	15.65
G 14	-263.25	-4.25
G 15	-25.01	4.70
G 16	158.24	-7.12
G 17	61.81	-8.65
G 18	59.85	-9.51
G 19	45.86	-30.70
G 20	-65.57	-48.99
G 21	-59.11	-42.29

Appendix V: Analysis of variance for different characters in pea genotypes

Characters/Variety	**Mean sum of square**		
	Replication (r-1) = 2	**Genotype (g-1) = 20**	**Error (r-1)(g-1) = 40**
Germination Percentage %	4.06	45.62**	2.65
Days of 50% Flowering	0.44	13.98**	2.13
Plant Height (cm)	7.76	1103.13**	0.85
Primary branches per plant	5.29	69.87**	0.59
Leaf length (cm)	0.003	1.49**	0.003
Leaf diameter (cm)	0.005	0.67**	0.004
Flower per plant	79.86	1530.93**	8.54
Pods per plant	54.54	1639.15**	11.24
Pod Length (cm)	0.03	1.88**	0.004
Seeds per Plant	3703.63	29900.23**	513.32
Seed diameter (mm)	0.03	4.66**	0.004
100 Seed Weight (gm)	0.01	50.40**	0.003
Days to Maturity	7.05	36.67**	5.75
Seed Yield (tn/ha)	0.001	1.56**	0.002

**** Denote Significant at 1% level of probability**

Appendix VI: Range, mean, CV (%) and standard deviation of 21 pea genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Germination Percentage %	82.33	96.67	89.21	1.82	1.82	1.63
Days of 50% Flowering	39.67	48.67	42.32	3.45	3.45	1.46
Plant Height (cm)	52.00	123.00	77.33	1.19	1.19	0.92
Primary branches per plant	3.00	17.00	10.10	7.58	7.58	0.77
Leaf length (cm)	2.07	4.47	3.10	1.80	1.80	0.06
Leaf diameter (cm)	0.97	2.33	1.59	3.84	3.84	0.06
Flower per plant	71.00	155.67	110.67	2.64	2.64	2.92
Pods per plant	57.67	145.67	88.54	3.79	3.79	3.35
Pod Length (cm)	3.93	6.38	4.95	1.22	1.22	0.06
Seeds per Plant	227.33	631.67	378.63	5.98	5.98	22.66
Seed diameter (mm)	3.93	7.90	5.07	1.26	1.26	0.06
100 Seed Weight (gm)	4.93	18.23	9.07	0.60	0.60	0.05
Days to Maturity	79.33	90.67	84.10	2.85	2.85	2.40
Seed Yield (ton/ha)	0.59	2.71	1.27	3.24	189.32	2.40

Appendix VII: Estimation of genetic parameters in fourteen characters of 21 pea genotypes

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Germination Percentage (%)	16.97	14.32	2.65	4.62	4.24	1.82	84.40	7.16	8.03
Days of 50% Flowering	6.08	3.95	2.13	5.83	4.70	3.45	65.00	3.30	7.80
Plant Height (cm)	368.27	367.43	0.85	24.82	24.79	1.19	92.77	39.44	51.00
Primary branches per plant	23.68	23.10	0.59	48.20	47.60	7.58	95.53	9.78	96.84
Leaf length (cm)	0.50	0.50	0.00	22.84	22.76	1.80	94.38	1.45	46.75
Leaf diameter (cm)	0.23	0.22	0.00	29.98	29.74	3.84	91.36	0.96	60.75
Flower per plant	516.00	507.46	8.54	20.53	20.36	2.64	92.34	46.02	41.58
Pods per plant	553.88	542.64	11.24	26.58	26.31	3.79	94.97	47.50	53.65
Pod Length (cm)	0.63	0.63	0.00	16.06	16.01	1.22	92.42	1.63	32.88
Seeds per Plant	10308.96	9795.64	513.32	26.82	26.14	5.98	95.02	198.74	52.49
Seed diameter (mm)	1.56	1.55	0.00	24.62	24.59	1.26	97.74	2.56	50.58
100 Seed Weight (gm)	16.80	16.80	0.00	45.22	45.21	0.60	98.98	8.44	93.13
Days to Maturity	16.06	10.31	5.75	4.76	3.82	2.85	64.20	5.30	6.30
Seed Yield (ton/ha)	0.52	0.52	0.00	57.00	56.90	3.24	98.68	1.48	117.03

Appendix VIII: Mean performance of different characters of 21 pea genotypes

Genotypes	Name	GP	D50F	PH (cm)	PBP	LL (cm)	LD (cm)	FPP	PPP	PL (cm)	SPP	SD (mm)	1000 SW (g)	DM	SY (ton/ha)
G1	**BD 4150**	90.67	41.00	55.00	**17.00**	**2.07**	**0.97**	150.00	122.33	4.08	468.33	**3.93**	7.13	89.67	0.91
G2	**BD 4151**	94.67	42.00	80.00	4.00	4.07	1.97	82.33	62.33	5.90	261.67	5.90	14.37	79.67	1.72
G3	**BD 4154**	93.67	42.67	80.00	14.00	3.43	1.47	139.67	125.00	4.67	503.33	4.43	5.07	82.67	0.63
G4	**BD 4157**	89.33	**44.67**	**52.00**	13.00	2.43	1.47	131.67	114.00	4.57	476.67	3.97	**4.93**	87.33	**0.59**
G5	**BD 4461**	92.67	42.67	72.00	13.00	2.45	1.02	121.67	85.33	4.67	391.67	3.97	5.27	**79.33**	0.65
G6	**BD 4171**	92.33	44.00	77.00	4.00	3.77	2.07	71.00	57.67	5.67	**242.33**	**7.90**	**18.23**	84.67	2.51
G7	**BD 4172**	88.33	48.67	74.00	5.00	2.23	1.07	86.33	64.33	4.45	284.67	3.95	6.73	83.67	0.81
G8	**BD 4176**	89.33	43.67	62.00	11.00	3.07	1.17	110.67	76.00	4.73	308.33	4.43	8.23	82.67	0.93
G9	**BD 4178**	92.67	41.33	70.00	11.00	2.33	1.47	102.67	81.67	4.53	359.33	4.93	8.23	85.33	0.96
G10	**BD 4182**	90.67	40.67	57.00	15.00	3.07	1.23	111.67	74.67	4.93	319.67	4.03	5.93	**90.67**	0.78
G11	**BD 4183**	85.67	42.67	73.00	13.00	2.48	1.05	117.00	94.33	4.02	416.67	3.93	5.23	87.67	0.63
G12	**BD 4186**	83.33	39.67	56.00	12.00	2.37	1.02	104.00	82.33	4.05	327.33	4.47	6.13	87.67	0.79
G13	**BD 4188**	**96.67**	39.67	62.00	16.00	3.07	1.43	132.00	112.67	4.73	463.33	4.07	5.27	81.33	0.64
G14	**BD 4190**	86.67	40.00	76.00	17.00	2.50	1.47	**155.67**	**145.67**	**3.93**	**631.67**	3.93	5.03	81.33	**0.59**
G15	**BD 4193**	88.33	40.00	71.00	13.00	3.27	1.47	113.00	92.00	4.07	403.33	4.43	7.13	82.33	0.93
G16	**BD 4205**	86.33	41.33	86.67	**3.00**	3.43	2.17	**76.67**	58.33	5.07	227.33	6.93	13.63	83.67	1.72
G17	**BD 4206**	89.33	43.33	88.00	5.00	3.03	2.07	98.33	80.67	5.93	318.67	6.47	12.07	79.67	1.63
G18	**BD 4207**	**82.33**	**40.33**	86.33	**3.00**	3.37	**2.33**	97.33	75.00	6.12	322.33	5.93	15.43	79.67	1.82
G19	**BD 4220**	91.33	42.67	110.00	5.00	4.47	2.03	98.67	80.00	5.13	335.67	5.97	11.83	83.33	2.17
G20	**BD 4222**	83.67	43.00	**123.00**	10.00	4.13	2.07	115.00	90.00	6.23	446.67	6.93	11.93	84.33	2.49
G21	**BD 4223**	85.33	**44.67**	113.00	8.00	**3.97**	**2.33**	108.67	85.00	**6.38**	442.33	5.90	12.53	89.33	**2.71**

GP: germination percentage, D50F: days to 50% flowering, PH (cm): plant height (cm), PBP: primary branches per plant, LL (cm): leaf length (cm), LD (cm): leaf diameter (cm), FPP: flowers per plant, PPP: pods per plant, PL (cm): pod length (cm), SPP: seeds per plant, SD (mm): seed diameter (mm), 100 SW: seed weight (g), DM: days to maturity and SY (ton/ha): seed yield (ton/ha).