VARIABILITY AND DIVERSITY STUDIES IN PEA

(*Pisum sativum* L.)

A thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI-413 722, DIST. AHMEDNAGAR,
MAHARASHTRA STATE, (INDIA)

by

MISS KATORE TRUSHNA DHANRAJ

in partial fulfilment of the requirements for the degree of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY

(CYTOGENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
MAHATMA PHULE KRISHI VIDYAPEETH
COLLEGE OF AGRICULTURE,
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MAHARASHTRA

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CANDIDATE'S DECLARATION

I hereby declare that the thesis entitled **"Variability And Diversity Studies In Pea (*Pisum sativum* L.)"** or part there of has not been submitted by me or any other person to any other university or institute for a Degree or Diploma.

Place : Pune

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CERTIFICATE

This is to certify that the thesis entitled, **"Variability And Diversity Studies In Pea (*Pisum sativum* L.)"** submitted to the faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra, in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE (Agriculture)** in **Agricultural Botany (Cytogenetics and Plant Breeding)** embodies the results of a piece of *bonafide* research work carried out by **Miss Katore T. D.** under my guidance and supervision, and that no part of the thesis has been submitted for any other degree or Diploma.

The assistance and the help received during the course of this investigation have been duly acknowledged.

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Place : *Pune –5*

Date : */ / 2006* *(Trushna Katore)*

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ABSTRACT

"Variability and Diversity Studies in Pea (*Pisum sativum* L.)"

By

MISS KATORE TRUSHNA DHANRAJ

A candidate for the degree of

Master of Science (Agriculture)

In

AGRICULTURAL BOTANY

(Cytogenetics and Plant Breeding)

Research Guide	**:**	Dr. P.A. Navale
Discipline	**:**	Agricultural Botany
Major Field	**:**	(Cytogenetics and Plant Breeding)

The investigation on "Variability and Diversity Studies in Pea (*Pisum sativum* L.)" was undertaken to know the extent of genetic variability, heritability, genetic advance and genetic divergence among 50 genotypes of Pea collected from NBPGR, New Delhi.

The experiment was laid at Botany Farm, during *Rabi* 2004 at College of Agriculture, Pune. The material was evaluated in randomized block design with three replications.

Observations were recorded on 9 quantitative and 10 qualitative characters. In quantitative characters, days required for flowering ranged from 45.33 to 59.67 days, days required for maturity ranged between 100.67 to 127.67 days, plant height varied between 44.47cm to 128.53cm, number of branches per plant ranged from 6.47 to 14.53, number of pods per plant varied between 27.07 and 57.73, pod length ranged from

3.43cm to 8.13cm, number of seeds per pod ranged from 3.20 to 6.47, 100-seed weight ranged between 6.0g to 19.53g and seed yield per plant ranged between 10.85g and 41.01g

In case of qualitative characters, foliage colour exhibited three types of colour *viz.,* yellowish, green and faint green, stem colour showed three types of colour *viz.,* yellow, green and faint green, flower colour recorded only two types of colour i.e. purple and white, pod shape recorded two types of shape i.e. inflated and constricted.

Likewise, there were two types of pod position i.e. axillary and terminal position recorded by pod, cotyledon colour exhibited yellow, white and green colour, seed colour exhibited white, grey brown and grey colour of seeds, there were only two types of seeds shape recorded i.e. round and wrinkled and two types of growth habit i.e. viny and non viny.

The treatment mean sum of squares were significant for all characters, indicating good amount of variability for various characters studied.

The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were of high magnitude for 100-seed weight, followed by seed yield per plant, pod length, number of branches per plant and plant height at harvest. The maximum magnitudinal difference between PCV and GCV was observed for seed yield per plant, followed by days to flowering and number of seeds per pod, indicating the role of environment in the expression of these characters.

The characters 100-seed weight (98.84 per cent), followed by plant height at harvest (93.57 per cent), number of branches per plant (87.49 per cent), seed yield per plant (84.77 per cent), number of seeds per pod (84.07 per cent), number of pods per plant (83.53 per cent), days to maturity (77.41 per cent) and days to flowering (61.29 per cent) showed

high heritability estimates however the characters were coupled with varied genetic advance.

In correlation studies the seed yield per plant was significantly and positively correlated with 100-seed weight, pod length, number of seeds per pod, days to maturity and days to flowering, indicating dependency of seed yield per plant for these characters. path analysis revealed that 100-seed weight, number of seeds per pod and pod length exhibited high direct effects along with highly significant correlation, indicating the true and perfect relationship between these characters and suggesting that direct selection for these traits will help in yield improvement.

Diversity analysis revealed presence of appreciable amount of diversity among the genotypes studied. D^2 values ranged between 8.838946 to 1510.318. All the 50 genotypes studied were grouped into 20 clusters. Cluster I emerged as the largest cluster with 6 genotypes, followed by cluster II, III and cluster IV and V. Cluster XV, XVI, XVII, XVIII, XIX and XX were monogenotypic. Maximum intracluster distance was observed for cluster XIV (D^2 = 52.24) followed by cluster XIII (D^2 = 51.67) and cluster I (D^2 = 51.21). Whereas, maximum inter-cluster distance was observed between cluster II and XIV (D^2= 1215.38) indicating wide divergence between these clusters. The 100-seed weight followed by number of seeds per plant and plant height at harvest were major contributors towards divergence.

Based studies following ten potent genotypes were identified for tentative breeding programme.

1) EC -398604	5) IC- 356172	8) IC – 267161
2) EC -387113	6) IC- 356332	9) IC-356337
3) IC – 267142	7) IC – 381861	10) IC-296677
4) IC - 267169		

1. INTRODUCTION

India is the largest producer and consumer of pulses in the world, accounting about 25 per cent of global production and 27 per cent of consumption. Pea (*Pisum sativum* L.) is one of the popular vegetables grown in India, belonging to family leguminoseae and subfamily papilionaceae. Ethiopia is main center of origin. Two species *viz.*, garden pea (*P. sativum* sub spp. hortense) and field pea (*P. sativum sub.* Spp. arvense) are commonly being cultivated throughout the world. It is also called as pois proteagineux in French, pisello in Itallian and Matar in Hindi.

Field pea is the third most important crop at global level after dry pea (*Phaseolus vulgaris*) and chick pea (*Cicer arietinum* L.). The field peas are distributed in Asia, Africa, Europe, N. America and Australia. In India, field pea occupies on area of 0.62 million ha with an annual production of 0.56 million tonnes. The average production is 906 kg/ha. The major field pea growing states are Uttar Pradesh, Madhya Pradesh, Bihar and Maharashtra. Besides these states, it is also cultivated in Delhi, West Bengal, Punjab, Haryana and Himachal Pradesh. The area, production and productivity of pea in important states for year 2001-2002 is given in Table 1.1 (Anonymous, 2004).

Table 1.1 Area, production and productivity of pea in important states during 2001-2002

Sr. No.	States	Area	Production (lakh ton)	Productivity (kg ha^{-1})
1	Uttar pradesh	410.4	540.1	1316
2	Madhya pradesh	186.8	76.5	410
3	Orrisa	32.4	20.2	623
4	Maharashtra	12.1	7.9	603
5	Assam	28.4	17.2	606

Pea is very rich in protein, carbohydrate, vitamin A and C, calcium and phosphorous and the nutritive value of fresh green peas has been presented as under. The protein concentration of pea range from 15.5 to 39.7% (Davies *et al*, 1985, Bressani and Elias, 1988).

Composition of pea (100 g of edible portion)

Calories	44
Protein	6.2 g
Fat	0.4 g
Carbohydrate	16.9 g
Calcium	32 mg
Phosphrous	102 mg
Potassium	350 mg
Ascorbic acid	27 mg

Dried peas contain 22.9% protein, 1.4% fat, 60.7% carbohydrate, 1.4% crude fibre, and 2.7% Ash, (Duke, 1981; Hulse, 1994). An average amino acid composition, reported in terms of grams per 100 grams of protein : 6.9 to 8.2 lysine, 1.4 to 2.7 methionine + cystine, 3.9 threonine, 0.9 treptophan, 0.8 to 1.7 cystine (Huisman and Van der poel, 1994). Methionine and Cystine are the main limiting amino acids. Pea hay (at 88.6% DM) contains 10.7 to 21.6% crude protein, 1.5 to 3.7% fat, 41.9 to 50.6% N-Free extract (Duke, 1981).

Pea is an excellent food for human consumption taken either as a vegetable or in soup. Large proportion of peas are processed (Canned, frozen on dehydrated) for consumption in the off season. pea straw is nutritious fodder. Pea is very rich in protein, therefore, very valuable for the vegetarians.

Garden peas are harvested in an immature condition and cooked at fresh or canned for subsequent uses. The field pea is generally grown for

dry seeds, which are used for a variety, for preparation of snacks and Dal. Pea is an important legume vegetables, as it fixes 30-140 kg N/ha (Sekhon *et al.* 1990).

Pea is self pollinated crop with chromosome number 2n=14. It is an annual herbaceaceous plant with well developed tap root and many slender lateral branches. Stem is angular or round, fistular and non-pigmented leaves are compound , having 1-3 Pinnate of oval shape of 25-50 mm length with micronate tips .Inflorescence axillary, long peduncled, receme with 1-2 flowers having 10 Anthers and diadulphous conditions. Pods are of variable length and breadth curved or straight having 4-10 seeds per pod.

Though pea is important crop in India, very little work has been done in Maharashtra to study the varietal characters and to improve the quality of pods and yield. Therefore, necessary to study the variability and diversity in 50 lines (Exotic and Indigenous) received from NBPGR, New Delhi. There is good scope for increasing production by developing high yielding varieties looking to the present status and low productivity of the crop. There is need to develop and identify superior genotypes by exploiting the available variation, simulteneously to understand the association between various yield contributing characters with their degree of divergence.

Correlation studies are helpful in determining the yield components, but don’t provide an exact picture of the relative importance of direct and indirect influence of each of the component characters towards yield, path analysis splits correlation coefficient into measures of direct and indirect effects and measures the direct and indirect combination of various independent variables on the dependent variable (Dewey and Lu, 1959).

Indirect selection for the component fruit with a view to improve yield is possible by path analysis. A greater yield response is obtained when the character for which indirect selection is practiced has a high heritability and a high correlation with yield.

The extent of genetic variability available in crop is a prerequisite for its improvement due to the fact that the efficiency of selection mainly depends on it. Multivariate analysis by means of Mahalanobis D^2 statistics is a powerful tool in quantifying the degree of divergence among genotypes. The distance between two clusters is the measure of the degree of diversification.Genotypes can be grouped into different clusters by following Tocher's method (Rao, 1952). Principle component (canonical) analysis provided relative contribution of different traits to the total variation (Singh and Chaudhary, 1977).

Keeping in view the above aspects, present investigations were undertaken to study the path analysis and genetic diversity in pea, with the following objectives:

1) To study the variability for yield and yield contributing characters.
2) To study the association between different characters with direct and indirect effects.
3) To measure genetic divergence among various germplasm lines.

2. REVIEW OF LITERATURE

Success of breeding programme depends on effective selection. The efficient selection depends upon the knowledge of genetic architexure of quantitative traits. In present chapter attempt is being made to review the result obtained on pea by earlier authors so that we could have a sound knowledge on their findings. These results are reviewed under the following heads.

2.1 Genetic variability

2.2 Heritability and Genetic Advance

2.3 Correlation and path analysis

2.4 Genetic divergence

2.1 Genetic variability

Johannsen (1909) demonstrated the destination between genotype and phenotype and proof by Nilsson – Ehle (1909) and East (1916) that quantitative characters were inherited according to Mendels laws. It becomes clear that variability is resulted from the joint action of the genotype and environment (Fisher, 1930). Charles and Smith (1939) and Power *et al.* (1950) partitioned genetic variance from total variance by use of estimated of environmental variance from the non-segregating population. This work made possible to use genotypic coefficient of variance (GCV) as a relative magnitude on genetic diversity present in the material and helps to compare the genetic variability present for different characters.

Hutchinson (1940) provided means to compare genetic variability present in population of various traits. The statistical method to calculate

the genetic component of variance was given by Frankel (1947), Burton (1952) and Panse and Sukhatme (1985).

Singh and Saklani (1973) studied quantitative variability in eight characters i.e. Days to flowering, Days to first picking, length of pod (cm), Number of seeds per pod, Number of pods per plant, shelling percentage 100- seed weight and green seeds yield per plant in garden pea. A wide range of variability was observed in all characters except the pod length and number of pods per plant. The highest and lowest GCV was found in Green seed yield per plant (57.31g) and Number of pods per plant (7.65).

Kalloo *et al.* (1976) studied variability and correlation in nine characters of 64 varieties of pea. The highest PCV and GCV was found in 50 per cent flowering i.e. 69.56 and 34.74. The lowest PCV and GCV was found in pod length which is 16.73 and 7.79. Correlation studies indicated positive association of yield with number of branches, number of pods and number of clusters. Number of pods was negatively associated with length of pods.

Singh *et al.* (1977) observed variability, heritability and genetic advance in seven characters of pea. Node number with first pod exhibited highest PCV (21.6) and GCV (19.8). Number of seeds per pod exhibited lowest PCV (6.6) and GCV (4.9). Heritability and genetic advance was high for all characters except number of seeds per pod.

Jermyn and Slinkard (1977) studied variability of per cent protein and its relationship to seed yield and seed shape in 1,100 lines of peas from the USDA world pea collection. The ranges for the lines were 85.1 to 118.7 per cent of the population mean for protein percent, 34.7 to 172.4 per cent for seed yield, 33.7 to 165.55 for protein yield and 29.9 to 273.4 per cent for seed weight. There were highly significant negative correlations between percent protein and seed yield, extremely high

correlations between seed yield and protein yield. Wrinkled seeded lines were significantly higher in per cent protein and seed weight, significantly lower in seed yield but not different in protein yield than smooth-seeded lines.

Hobbs and Mahon (1982) studied seven quantitative and physiological characters i.e. photosynthetic CO_2, exchange rate (CER), specific leaf weight, N_2 (C_2H_2) fixation, growth duration and relative growth rate in 25 genotypes of pea. Genetic coefficient of variation for physiological characters varied from 2 to 13 per cent. The CER was correlated with these physiological characters.

Singh and Joshi (1982) studied variation in six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of five yellow round seeded field pea for characters such as pods per plant, pod length, seeds per pod, 100-seed weight and seed yield. They revealed the additive gene action was more important than non additive gene action for pods per plant, number of seeds per pod, 100-seed weight and seed yield.

Kuksal *et al.*, (1983) revealed genetic variability in 14 exotic pea varieties under U.P. hills Agroclimatic conditions. The genetic coefficient of variation varied from 4.70 to 71.80 for various characters. Pod length had the highest value 71.80 which was followed by plant height (33.27) and number of pods per plant (30.80).

Gupta *et al.*, (1983) studied variability, heritability and genetic advance in physiological and yield traits in pea. The highest and lowest GCV value was found in 100-seed weight (38.12g) and days to maturity (5.86). The highest and lowest PCV value was found in branches per plant (38.82) and days to maturity (6.23). Both high heritability and high genetic advance were observed in case of seed weight, first fruiting weight and length of fruiting zone which may be attributed to additive gene effect.

Rastogi *et al.*, (1987) evaluated genetic analysis of yield in pea. The variance for general and specific combining ability in F_1 and F_2 were significant in both the generations, indicating that both additive and non-additive gene action were playing role in the inheritance of pod yield but the values were higher for gca, showing the importance of additive genetic variance. gca value in F_1 and F_2 was 610.95 and 642.62. sca value in F_1 and F_2 was 410.09 and 262.57.

Korla and Singh (1988) revealed genetic variability and Genotype x Environment interaction in thirty diverse cultivars of pea. A wide range of variability was observed for all characters. The highest range was in case of yield per plant (12.61 to 66.87 g) followed by weight of 15 pods (64.44 to 126.00 g). The Genotype x Environment interaction components were less than the genotypic variation for number of pods per axil, number of grains per pod, shelling percentage and yield per plant. Whereas, it was higher than genotypic variance for weight of 15 pods and pod length.

Awasthi (1989) studied 12 varieties of co-ordinated varital trial (CVT) and 14 varieties of state varietal trial (SVT). They analysed seed yield, protein-N, Albumin and PER in different pea varieties, which ranged from 11.15-15.63 q/ha, 3.178-3.954, 3.94-5.44 per cent and 1.38-2.39 during 1975-76 and 14.04-30.19 q/ha, 3.136-3.925, 3.94-5.37 per cent and 1.38-2.34 in 1976-77 in CVT whereas, 19.33-27.97 q/ha, 3.402-3.878, 3.80-5.44 per cent and 1.19-2.4 in 1975-76 and 14.63-21.0 q/ha, 3.227-3.845, 4.1-5.1 per cent and 1.54-2.29 in 1976-77 in SVT respectively.

Singh and Singh (1990) reported genetic analysis of 10 quantitative characters in pea. The variance due to gca and sca were highly significant for all the characters in both F_1 and F_2 generations. The magnitude of additive component was comparatively one for all the

characters except number of pods, primary branches, and yield per plant. Yield showing higher proportion of the non-additive genetic variance, while the yield components such as pods per plants, pod length, seeds per pod and test weight had relatively higher estimates of the additive genetic variance.

Dumoulin *et al.,* (1994) reported that yield in peas highly depend on seed number. The periods of seed set and seed filling were studied in field for two years at two sowing dates. Seed water content at the beginning of the seed filling and at physiological maturity correspondent to 0.85 and 0.55 g g^{-1} fresh weight, respectively. The delimitation of seed set period showed genetic variability for the beginning of period depending upon the first reproductive node number and its duration.

Singh *et al.,* (1997) studied genetic variation of seven quantitative traits in fifteen lines of crossed with two testers of peas, significant estimates of both Additive (D) and Dominance (H) components were observed for all the characters except for pod length. The F_1 value was positive and significant for days to flowering, plant height and pods per plant. Seed weight, seed yield per plant showing iso-directional nature of dominance.

Narayan *et al.* (1999) observed genetics of yield and quality components from six generations of crosses Bonneville x Lincoln, Bonneville x Solan Nirog, Bonneville x Kinnauri, Lincoln x Solan Nirog and Lincoln x Kinnauri. Significant positive values of additive effects were observed for pod yield per plant in all the crosses except Bonneville x Lincoln. All the five crosses showed significant positive dominance effects for shelling percentage, while for protein content, no cross showed significant positive dominance effect.

Bhardwaj *et al.* (2001) in their studies on generation mean reported the values for sugar, days to 50 per cent flowering, seeds per pod, pods

per plant, and pod yield per plant as 49.98, 383.18, 768.31, 361-80 and 7972.56 respectively. Inheritance of all the characters except sugar content was associated with additive, dominance and epistastis components of genetic variation.

Ramesh *et al.* (2002) reported that considerable amount of PCV and GCV in most of characters such as number of pods per plant, weight of pods per plant, internode length, plant height, mean pod weight and weight of seeds per pod.

Sharma and Kalia (2002) studied genetic analysis for pod yield and its contributing traits in garden pea. The Hayman's genetic component analysis indicates that gene action for most of traits had significant additive (D) and non additive (H_1) genetic variance with the preponderance of the latter in both F_1 and F_2 generations. However, D components was found to be non-significant for pod yield per plant and pods per plant in F_1 and TSS in both F_1 and F_2 generations.

Tyagi and Shrivastava (2002) reported a wide range of variability in twenty varieties of pea comprising of lines (15) x tester (5) evaluated at two dates of sowing, normal and late. The phenotypic and genotypic coefficient of variability was higher for normal sown as compared to late sown crop. The higher values of PCV and GCV were recorded for plant height 30.55 and 30.07, pods per plant 29.99 and 28.46 and for biological yield per plant 25.86 and 24.88, respectively for normal and late sown cultivars.

Belimov *et al.*, (2003) reported genetic variability in tolerance to cadmium and accumulation of heavy metal in 99 wild varieties of pea. The coefficients of variation between pea genotypes for heavy metal concentration were high varying from 23 to 39 percent depending on metal. The distribution patterns for varieties based on cd tolerance (sand culture) and HM concentration (soil culture) were characterized by

positive skewness coefficients, suggesting that high genetic variability exists in pea with regards to cd tolerance and heavy metal concentration.

Chaudhari and Sharma (2003) studied genetic variability correlation and path analysis is for green pod yield and its components in 10 characters of garden pea. Significant genetic variation was observed among the F_1 hybrids for all the characters. Plant height, number of pods per plant and first flowering node recorded the greatest phenotypic coefficient of variation.

Kumar *et al.* (2003) studied variability, heritability and genetic advance in 36 pea cultivars. The GCV was high for pod yield per plot, plant height, number of primary branches and pod weight. The highest PCV was observed for seed yield per plot.

Sharma *et al.* (2003) studied genetic variability, heritability and character association in 63 genotypes of pea. All characters exhibited significant variability. The GCV and PCV were highest for seed yield per plant, followed by pods per plant and biological yield per plant.

Singh *et al.* (2003) studied genetic variation, heritability and genetic advance for 8 traits in 10 pea cultivars. The magnitude of variability was higher for pod length and number of pods per plant in F_1 population, and these traits were moderately influenced by non-additive gene action.

2.2 Heritability and Genetic Advance

Heritability is the relative role of heredity in expression of phenotypes (Falconer, 1960 and Allard, 1961). More specifically, it could be also defined as the proportion of total variability that is due to genetic cause. Knowledge of heritability of a character is heritability of a character is important to the breeder since it indicate the possibility and extent to which improvement is possible through selection (Robinson *et*

al. 1949). The genetic advance is a product of heritability, phenotypic standard deviation as a standardized selection differential (Burton and Devane, 1953). This is a measure of expected genetic progress based on selection procedure.

Lush (1949) classified heritability estimates into 3 categories *viz.*, Low (5-10 per cent) medium (10 to 30 per cent) and High (above 30 per cent).

Robinson *et al.* (1951) proposed that expected genetic advance is the variable traction of selection differential in a single generation.

On the basis of above concepts different workers studied heritability and genetic advance in pea eludicated below.

Singh and Singh (1970) reported high heritability estimates for all the traits except shelling percentage and seed yield. Genetic advance was high for number of branches and pods per plant and 100- seed weight.

Srivastrava *et al.* (1972) studied heritability and genetic advance in pea. The heritability ranged from 13.14 per cent (yield per plant), 84.48 per cent (days to flower) and genetic advance from 8.66 per cent (yield per plant) to 25.61 per cent (number of seeds per pod).

Nandpuri *et al.* (1973) revealed that high heritability was associated with high genetic advance and high genotypic coefficient of variation for yield per hectare, yield per plant and number of pods per plant. Heritability was low for weight of pod. Expected genetic advance and coefficient of genotypic variation were also low for this character.

Singh and Saklani (1973) concluded that heritability estimates were high for all the characters except length of pod and shelling percentage. High values of heritability were associated with high values and genetic advance in case of yield per plant, number of pods per plant and 100- seed weight.

Srivastava and Sachan (1974) reported that heritability percentage was maximum for shelling percentage and minimum for 100- seed weight. High heritability value in conjunction with high genetic advance as percentage of mean was observed for branches per plant and seeds per pod.

Narsinghani *et al.* (1977) reported that the heritability estimates were high for 100 -seed weight followed by height of plant and pods per plant. The value of genetic advance was high for number of branches and pods per plant.

Kuksal *et al.* (1983) reported that high heritability was accomplished by genetic advance in number of pods per plant and pod yield per plant showing additive gene effects, while pod length and seeds per pod had high heritability but low genetic advance showing non additive gene effects.

Singh *et al.* (1986) reported heritability in a 10 x 10 diallel of 10 varieties of field pea. Heritability estimates were high for seeds per pod (68.93 per cent) followed by pods per plant (58.45 per cent). Lowest heritability was found in protein content (12.92 per cent).

Dubey and Lal (1988) concluded that narrow sense heritability for yield per plant and other characters ranged from 2.6 to 72.5 per cent. The highest heritability was for days to flowering and 100- seed weight. Genetic advance was highest for 100- seed weight and pod length. High heritability with moderate to high genetic advance was observed for yield per plant, seeds per pod and shelling percentage.

Rastogi (1988) studied broad and narrow sense heritability in green seeds of pea. Narrow sense heritability in F_1 and F_2 generation was 0.28 and 0.22 per cent and broad sense heritability in F_1 and F_2 generation was 0.92 and 0.95 per cent respectively.

Rastogi *et al.* (1989) reported genetic analysis of protein content in pea seed. Narrow sense heritability in F_1 and F_2 generation was 0.07 and 0.08 per cent and broad sense heritability in F_1 and F_2 generation was 0.91 and 0.98 per cent respectively.

Baswana and Tewatia (1994) studied variability, heritability and genetic advance in pea under dry land condition. Heritability was high for number of pods per plant (89.82 per cent) and low for pod yield per plant(61.60 per cent). Genetic advance was high for number of pods per plant (96.20 per cent)and low for plant height(52.38 per cent).

Sharma *et al.* (1997) studied genetic variability, heritability and genetic advance for yield and its contributing traits in pea. Highest and lowest heritability was found in plant height (98.90 per cent) and number of seeds per pod (5.10 per cent) and highest and lowest genetic advance was found in plant height (39.07 per cent) and number of seeds per pod (0.11 per cent) respectively.

Dixit (1998) studied heritability for certain yield contributing traits in grass pea, heritability was highest for pods per plant 45.1 per cent followed by seeds per pod 14.57 per cent and lowest for number of primary branches 3.97 per cent.

Sharma *et al.* (2003) studied gene action and combining ability studies for earliness in pea. The narrow sense heritability was quite high for earliness in pea. i.e. ranging from 54.90 to 74.81 per cent.

Venkateswarlu and Singh (1982) studied narrow sense heritability in F_1 and F_2 generations of ten parents diallel in pea and reported that both additive and non additive components were significant for all the character except yield. The number of alleles or allele group showing dominance (h^2 /H_2) was more than one for plant height, secondary branches, pods per plant and seed yield. Heritability values for all the characters except seed weight were lower in F_1 than F_2 generation.

2.3 Correlation and path analysis

The yield is a complex character in inheritance and depends on many other attributes of plant. The correlation studies helps in under studying the association between such traits and making efficient selections. The chief cause of correlation is pleiotropy and linkage (Falconer, 1960). So it became difficult to get the actual idea about positive or negative effects of segregating genes. The path coefficient analysis is the most probable solution to such problems as it measures direct as well as indirect effects of various traits on yield.

Robinson *et al.* (1951) observed that the correlation values are of potential importance, since selection is usually concerned with changing two or more traits. Dewey and Lu (1959) used these correlation coefficient first time in plant for path analysis by following Wright (1921).

Chaudhary and Singh Arya (1971) studied genotypic and phenotypic correlation coefficient in 13 varieties of pea for yield and yield contributing characters. The yield per plant was found to be highly and positively correlated with the number of pods per plant, number of seeds per pod and 100- seed weight but was not significantly correlated with height of the plant. The length of the pod was found to be positively correlated with the breadth of pod.

Wlakankar *et al.* (1974) studied correlation in 32 varieties of pea and concluded that pod number and 100- seed weight were significantly and positively correlated with green pod yield. Positive but non – ssignificant correlations were observed between pod number and pod length.

Pande and Gritten (1975) revealed that the plant height often positively correlated with pods per plant, seeds per plant and yield per plant, indicating superior yielding ability of taller plants.

Korla and Rastogi (1977) studied the correlation in 30 varieties of pea. Number of pods per cluster showed positive significant correlation with pod yield and negative significant correlation with days taken to first picking.

Narsinghani *et al.* (1978) studied correlation and path analysis in 65 diverse varieties of pea and revealed that there was maximum direct effect on yield by number of seeds per plant, followed by 100- seed weight, number of days to maturity, height and protein percentage and other components had negative direct effects. Most of characters had an indirect effect *via* number of seeds per plant.

Teotia *et al.* (1983) studied correlation and path analysis in 42 genotypes of garden pea for 12 characters. Yield was positively associated with number of seeds per pod, pod length and number of pods per plant at both genotypic and phenotype levels. Number of seeds per pod had positive and significant correlation with pod length at phenotypic level only. The yield components except 100- seed weight were positively correlated with each other.

Singh (1985) studied correlation in 30 varieties of pea for 8 characters and reported that the days to 50 per cent flowering, plant height, pods per plant and branches per plant were positively associated with seed yield.

Singh *et al.* (1985) studied correlation and path analysis in F_1 and F_2 progenices for 10 quantitative characters i.e. Days to flowering, plant height, branches per plant, pods per plant, seeds per pod, pod length, days to maturity, 100- seed weight, Harvest index and protein content with seed yield in pea. Considering direct effect of each character on seed yield, pods per plant had highest positive effect followed by 100- seed weight, seeds per pod and harvest index in both F_1 and F_2 generations. Days to flowering, plant height, branches per plant and harvest index had

high positive correlation with seed yield and low positive effect in both the generations, while number of seeds per pod had weak association with seed yield and exhibited considerable positive direct effect in both the generations.

Singh *et al.* (1987) studied genotypic and phenotypic correlation coefficient between 11 characters in F_1 and F_2 generations of 10 parent diallel cross in pea. Seed yield per plant was correlated positively with pods per plant, plant height, branches per plant, days to flowering and days to maturity in both the generations. Seed yield was not associated with seeds per pod, pod length and protein content.

Solanki *et al.* (1987) studied correlation and path analysis in 27 genotypes of pea. The number of seeds per pod had maximum contribution to pod yield followed by days to maturity and number of primary braches per plant and indirect negative influence through number of seeds per pod.

Ramesh and Tewatia (2002) studied correlation and path analysis in 36 genotypes of garden pea, pod weight per plant was significantly and positively associated with number of pods per plant (0.709), number of seeds per pod (0.484), mean pod weight (0.383), weight of seeds per pod (0.363), plant height (0.329) and length of pod (0.328). The number of pods per plant had highest positive contribution towards pod weight per plant (0.908).

Chaudhary and Sharma (2003) studied correlation and path analysis for green pod yield and its components in garden pea. The genotypic correlation coefficient were higher than phenotypic correlation coefficient. Pod yield per plant showed positive correlation coefficient with pod length, number of seeds per pod, number of pods per plant and shelling percentage. They revealed that number of seeds per pod, pod

length, number of pods per plant and 1000 seed weight had greatest direct effect on pod yield per plant.

Kumar *et al.* (2003) studied correlation and path analysis in pea. Pod yield per plant exhibited significant and positive correlation with number of pods per plant (0.752), mean pod weight (0.423), weight of edible seeds per pod (0.397 g), days to first picking (0.375), number of edible seeds per pod (0.359), internodel length (0.324 cm), shelling percentage (0.286) and number of branches per plant (0.279). Path coefficient analysis indicated that the number of pods per plant exerted highest positive direct effect on pod yield per plant (0.879g) followed by mean pod weight (0.446 g).

Pathak *et al.* (2002) studied variability and correlation analysis in 9 traits of garden pea. The genotypic correlation coefficients were generally higher than the corresponding phenotypic correlation coefficients. At the phenotypic level, pods per plant was positively correlated with number of pods per plant, plant height and average pod weight. Positive associations were also observed between days to 50 per cent flowering and days to maturity, pods per plant and plant height, pod length and seeds per pod and average pod weight and number of seeds per pod and average pod weight.

2.4 Genetic diversity

Genetic diversity is the genetic differences as observed between the individual or genetic stocks with respect to individual traits or an array of traits. It is a result of inherent genetic variations present in the germplasm. The knowledge of nature and degree of genetic divergence is useful in selecting the desirable parents for breeding programme. The selections based on the genetic divergence has been successfully utilized by different workers in various corps.

Mahalanobis (1936) described D^2 statistics as a tool for quantitative estimate of genetic divergence between the population. Rao (1952) suggested more flexible method which would replace the measurements on large number of characters all the which contribute in some degree towards discrimination by relatively few measurements.

Mahalanobis *et al.* (1949) applied D^2 statistics in detailed statistical study of anthropometric data of Uttarpradesh, India.

Moll *et al.* (1962) found that the genetic diversity is not affected due to geographic distribution and genetic diversity and its reflection in expression of heterosis.

Narsinghani *et al.* (1978) studied the genetic divergence in peas. Nine variables were evaluated in respect of 65 varieties of diverse genotype and geographical origin. Multivariate analysis by the D^2 statistics and vector analysis showed that the seed size, plant height and days to maturity were the most important factors contributing to the genetic divergence. The grouping pattern of varieties was random, indicating that the geographical and genetic diversities were not related.

Kalloo *et al.* (1980) studied the genetic divergence in garden pea. Significant differences revealed between 56 varieties for 9 characters. There was no consistant relationship between genetic divergence and geographical distribution but the result suggested that the crosses between selected varieties from widely separated clusters were most likely to give desirable recombinents.

Chandel and Joshi (1981) studied genetic diversity in 30 genotypes of yellow seeded Indian field pea for 8 yield contributing characters. They grouped these 30 genotypes into 10 clusters. The genotypes in cluster III produced maximum number of branches, cluster IV, V, VI, VII and VIII had maximum number of pods per plant and pod bearing penduncles, cluster VI was earliest to flower and fewest seeds per pod

(3.75) and cluster X had maximum seeds per pod (5.94). Maximum genetic diversity was between cluster III and VI and minimum diversity between cluster III and IV and also between II and V.

Dobhal and Ram (1985) reported the genetic divergence for yield and yield attributes through multivariate analysis in 32 indigeneous and exotic lines of pea which were grouped into 11 character. Cluster II showed high green pod yield (77.14g), primary branches (2.31) and shelling percentage (49.09). The highest number of green pods per plant (30.56) was in cluster V while, cluster VI had the highest value for seeds per pod (6.92) with high green pod yield. Genetic divergence was maximum between cluster I and VII (39.81) followed by VII and VIII (35.52) and I and IV (33.22).

Singh and Tripathi (1985) studied the genetic diversity in 100 pea germplasm lines and grouped them into 14 clusters. They reveled that the maximum intercluster distance was observed between cluster I and XIV followed by VII and XIV. Cluster XI was more diverse than others.

Singh and Ram (1988) studied genetic diversity in 80 germplasm lines for two years and grouped them into fifteen clusters. The maximum intercluster distance was observed between clusters IV and VII and V and VII. Days to flowering (12.6 per cent), 100 green pod weight (17 per cent), pod length (8 per cent) and plant height (8 per cent) were important contributors towards divergence.

Shinde *et al.* (1995) reported the genetic diversity among 73 varieties of pea obtained form different eco-geographical regions of India. D^2 value ranging form 1.46 to 940.64. Yield, days to flowering and crude protein content ranging from 28.4 to 95 q/ha, 44.0 to 58.0 and 3.7 to 19.2 per cent respectively.

Dixit *et al.* (2002) studied genetic diversity in 53 genotypes of field pea and grouped them into 11 different clusters. Plant height contributed

maximum to genetic diversity. Intracluster distance was highest in cluster III followed by clusters I and II. Inter cluster distance was maximum between cluster IV and X followed by cluster IV and XI and minimum between clusters X and XI, IV and VIII and III and IV.

Singh and Singh (2003) studied genetic divergence among 50 genotypes of pea. Genotypes were grouped into XI clusters and observed maximum intra-cluster value in cluster IX (2.47) followed by cluster VI (2.17) and cluster VIII (1.73). Maximum inter–cluster D^2 values were observed between cluster III and IX.

Tiwari *et al.* (2004) evaluated the genetic diversity in 34 genotypes of pea and grouped them into six clusters. The inter–cluster distance was minimum (11.84) between cluster III and VI and was maximum (41.77) between cluster I and II. Thus there was much diversity in population of 34 genotypes of cluster I, II, III and IV. They could be exploited for hybridization.

Sureja and Sharma (2001) studied genetic divergence in garden pea (*Pisum sativum* L. sub. Spp. hortense asch and graebn) of 30 genotypes. They revealed that cluster I showed maximum intra-cluster value (11.11) and cluster III showed minimum intra-cluster value (6.28). At inter-cluster level, minimum D^2 values was obtained between cluster II and IV (13.71) indicating, close relationship among genotypes included in these clusters. Minimum inter-cluster D^2 values were observed between cluster I and II (30.38) and cluster I and II (29.93) which indicated that genotypes included in these clusters had maximum divergence.

MATERIAL AND METHODS

The present investigation on variability and diversity studies in pea (*Pisum sativum* L.)" was carried out at Botany farm, College of Agriculture, Pune during *Rabi,* 2005. The details of the material and methods used to carry out the experiment and statistical procedures followed are described in this chapter.

3.1 Material

The experimental material consist 50 germplasm lines obtained from NBPGR (IARI campus), New Delhi 110012 (India). The list of germplasm lines used for the study is given in Table 3.1.

3.2 Methods

3.2.1 Experimental Design

The experiment was conducted in Randomized Block Design with three replications. Each plot consist of a single row of 4.5 m length with spacing of 45 cm between rows and 15 cm between plants within rows. One border row was sown at both the sides of block to avoid the border effects.

3.2.2 Sowing and cultural practices

The land was prepared by ploughing followed by two cross harrowings. The dose of 25kg N and 50 kg P_2O_5 per ha. was applied before sowing. The remaining half dose of Nitrogen was applied at the interval of 30 days after sowing.

The sowing of pea experiment was carried on 11th October 2005. The thinning and Gap filling operations were carried out after 20 days of

sowing. The usual cultural practices like weeding, irrigation etc**.** were carried out at regular intervals.

Table 3.1 : The list of Exotic and Indigenous lines used for present study

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1	EC-341782	18	IC-212393	35	IC-310834
2	EC-381866	19	IC-242725	36	IC-332113
3	EC-381897	20	IC-242733	37	IC-332118
4	EC-384139	21	IC-243334	38	IC-347185
5	EC-384890	22	IC-267127	39	IC-356144
6	EC-385247	23	IC-267142	40	IC-356147
7	EC-387113	24	IC-267151	41	IC-356172
8	EC-389374	25	IC-267155	42	IC-356268
9	EC-398604	26	IC-267161	43	IC-356272
10	EC-398611	27	IC-267169	44	IC-356274
11	EC-398612	28	IC-267182	45	IC-356310
12	EC-412882	29	IC-268254	46	IC-356332
13	EC-412883	30	IC-268275	47	IC-356337
14	IC-207167	31	IC-268276	48	IC-356373
15	IC-208368	32	IC-279120	49	IC-356378
16	IC-208384	33	IC-296677	50	IC-381861
17	IC-208391	34	IC-310833		

3.2.3 Harvesting

The crop was harvested after the physiological maturity of the pods. The following symptoms were considered for the physiological maturity of pea.

a. Yellowing of foliage
b. The mature pods developed yellowish brown colour and seed becomes hard.

3.2.4 Observations recorded

Following observations were recorded on five randomly selected plants from each treatment in each replication and averages were worked out.

3.2.4.1 Days to flowering (Nos.)

Number of days required for flowering of each observational plant was recorded from the date of sowing.

3.2.4.2 Days to maturity (Nos.)

Number of days required from sowing till the physiological maturity of the last fruit on the observational plant was considered as days to maturity.

3.2.4.3 Plant height at harvest (cm)

Plant height was recorded from ground level to tip of plant in centimeters at maturity on selected observational plants.

3.2.4.4 Number of branches per plant

Number of branches produced on the stem of each observational plant were counted and recorded.

3.2.4.5 Number of pods per plant

Total number of pods on each observational plant were counted and recorded at maturity after harvesting.

3.2.4.6 Pod length (cm)

Length of pods was measured from base (without pedicel) to the tip of pod for five randomly selected pods of each observational plant.

3.2.4.7 Number of seeds per pod

Number of seeds per pod were counted from each of the five randomly selected pods of observational plants and their average value was estimated.

3.2.4.8 Seed yield per plant (g)

Seed yield per plant was recorded by taking the total seed weight of randomly selected observational plants.

3.2.4.9 Weight of 100 seeds (g)

Weight of randomly selected hundred seeds was recorded in grams.

3.3 Statistical analysis

The mean value of randomly selected observational plants for nine different traits were used for statistical analysis.

The following statistical measures/ parameters were calculated for presentation of data on different quantitative attributes.

3.3.1 Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in the following form

Source of variation	DF	MSS	Expected mean square
Replication	(r-1)	MSr	$\sigma^2e + t\sigma^2r$
Treatment	(t-1)	MSt	$\sigma^2e + r\sigma^2r$
Error	(r-1) (t-1)	MSe	σ^2e
Total	(rt-1)		

Where,

r = Number of replications

t = Number of treatments

3.3.2 Estimation of mean and range

The mean value for each character was worked out by using following formula

$$\bar{\xi} = (1/n) \sum_{i=1}^{n} X_i$$

Where,

Σ Xi = Sum total of the each character

n= Number of observations

The lowest and the highest values from mean of each character were recorded as range.

3.3.3 Estimation of standard error of mean, standard error of difference and critical difference

The SE of mean difference was calculated as

i) SE of mean [SE(m)] = $\sqrt{\sigma^2 e/r}$

ii) The standard error of difference between two means was calculated as

SE difference = SE (m) x $\sqrt{2}$

iii) The critical difference between only two means was calculated as

CD = SE (d) x 't' error d.f.

3.3.4 Estimation of components of variation

The phenotypic and genotypic variances were calculated by utilizing the respective mean square values (Johnson *et al.* 1955).

i) Environmental Variance ($\sigma^2 e$) = MSe

ii) Genotypic Variance (σ^2g) = (MSg-MSe)/r

iii) Phenotypic Variance (σ^2p) = $\sigma^2g + \sigma^2e$

Where,

M Sg = Genotypic mean sum of squares

M Se = Error mean sum of squares

r = Number of replications

3.3.5 Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated by following Burton and Devane (1953)

i) Phenotypic coefficient of variation (PCV)

$$PCV = \sqrt{\sigma^2p / \xi} \times 100$$

Where,

σ^2p = Phenotypic variance

ξ = General mean of the character

ii) Genotypic coefficient of variation (GCV)

$$GCV = \sqrt{\sigma^2g / \xi} \times 100$$

Where,

σ^2g = Genotypic variance

ξ = General mean of the character

3.3.6 Estimation of heritability percentage

Heritability percentage in broad sense was estimated for various characters as per the formulae suggested by Hanson *et al.* (1956).

$$h^2 (b.s.) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where,

σ^2g = Genotypic Variance

σ^2p = Phenotypic Variance

3.3.7 Estimation of Genetic Advance

The genetic advance was calculated in per cent by the formulae suggested by Johnson *et al.* (1955).

$$G\ A = \sigma^2 g / \sigma^2 p \times \sigma p \times K$$

or

$$G\ A = K \times h^2\ (b\ s) \times \sigma^2 p$$

$$G\ A \text{ as percentage of mean} = \frac{G\ A}{\xi} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

K = Selection differential at 5 per cent selection intensity (i.e. 2.06)

h^2 (b.s.) = Heritability (broad sense)

ξ = Mean of the character.

3.3.8 Correlations

To understand the association between the characters, genotypic and phenotypic correlation coefficients were worked out by following Singh and Chaudhary (1977).

i) Phenotypic correlation coefficient (rp)

It is derived by

$$r_{p\ 1.2} = \frac{(cov_{p\ 1.2})}{\sqrt{(\sigma^2 p_1) \,.\, (\sigma^2 p_2)}}$$

Where,

$r_{p\ 1.2}$ = Phenotypic correlation between character 1 and 2

$cov_{p1.2}$ = Phenotypic co-variance between character 1 and 2

$\sigma^2 p_1$ and $\sigma^2 p_2$ = Phenotypic variance of character l and 2, respectively.

ii) Genotypic correlation coefficient (rg)

It is derived by

$$r_{g\ 1.2} = \frac{(cov_{g\ 1.2})}{\sqrt{(\sigma^2 g_1) \,.\, (\sigma^2 g_2)}}$$

Where,

$r_{g.1.2}$ = Genotypic correlation between character 1 and 2

$Cov_{g.1.2}$ = Genotypic co-variance between character 1 and 2

$\sigma^2 g_1$ and $\sigma^2 g_2$ = Genotypic variance of character 1 and 2, respectively

The significance of the phenotypic and genotypic correlation coefficients were tested by 't' test (Panse and Sukhatme, 1985)

$$t = r\sqrt{(n-2) / 1 - r^2}$$

Where,

r = Correlation coefficient

n = Total number of observations

The calculated 't' value was tested with table 't' value for respective (n-2) degree of freedom for significance.

3.3.9 Path analysis

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959). If 'y' is the effect and 'x_1' is the cause, the path coefficient for the path from cause x_1 to the effect y is $\delta x_1/\delta y$. Direct and indirect effects were worked out by using genotypic correlations as below:

Direct effect of x_1 on y = $Px_1.y$

Where,

Px_1 = Path coefficient of x_1 on y. Similarly, direct effects of other attributes on yield were calculated.

Indirect effects of x_1 via x_2 on y = px_2. y x rx_1. x_2

Where,

$Px_2.y$ = Path coefficient of the component character x_2 on y.

$rx_1.x_2$ = Genotypic correlation between x_1 and x_2

Similarly, indirect effect on all possible combinations were calculated for all component characters. The residual effect (R) was calculated as below

$$R = [1- (Px_1y. rx_1y)-(Px_2y.rx_2y) \ldots\ldots (Px_ny. r x\ _ny)]^{½}$$

Where,

Px_1y, Px_2y, ------, Px_ny = Direct effects of respective character on seed yield

Rx_1y, rx_2y, ------, rx_ny = Correlation coefficient between respective characters and yield.

3.3.10 Mahalanobis generalized distance (D^2)

The generalized distance between two population is defined by Mahalanobis (1936) as $D^2 = \lambda i.j.\ di.\ dj.$

Where,

$\lambda i.j$ = Reciprocal matrix to the common dispersion matrix

d_i = difference between the mean values of two populations for i^{th} character

d_j = difference between the mean values of two populations for j^{th} character

Estimation of D^2 values from the above formula is very complicated in the present study, since it requires the inversion of a nineth order determinant and then the evaluation of 9(9+2)/2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with such transformed variables reduced to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Chaudhary, 1977). The coefficient for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.3.11 Determination of gene constellation

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is not well defined term. The only criteria appeared to be that any two groups belonging to the same cluster should at least on an average show a smaller D^2 than those belonging to the two different clusters. A simple device suggested by K.D. Tocher is to start with the two closely associated groups and find a third group which has the smaller D^2 from the two. Similarly, the fourth is chosen to have the smaller D^2 from the first three and so on. If at any stage the average D^2 of a group form those already listed appears to be high. Then this group does not fit in the former groups and is therefore, taken outside the former cluster. The group of first cluster are then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to inclusion of an additional group. If the changes are appreciable, then newly added group has to be considered as outside the cluster.

3.3.12 Average intra and inter cluster D^2 and D Values

3.3.12.1 Average intra cluster D^2

$$D^2 = \Sigma Di^2 / n$$

Where,

'Di' is sum of distances between all possible combinations (n) of the population included in a cluster.

3.3.12.2 Average inter cluster D^2

D^2 = Σ Distances between the population of cluster 1 and j./ni nj

Where,

ni = Number of populations in the cluster i

nj = Number of populations in the cluster j

3.3.12.3 Average intra and inter - cluster distance

$D = \sqrt{D^2}$

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

4. EXPERIMENTAL RESULTS

The results obtained in the present investigation on variability and diversity studies in pea (*Pisum sativum* L.) on various quantitative and qualitative characters are described in the chapter.

4.1 Analysis of variance

The analysis of variance (Table 4.1) revealed highly significant differences among genotypes for all characters studied. The mean sum of squares for plant height at harvest, days to maturity, seed yield per plant and number of pods per plant were of high magnitude compared to the other characters.

4.2 Mean performance

The mean performance of nine characters in 50 genotypes of pea is presented in Table 4.2.

4.2.1 Days to flowering (Nos.)

The days required for flowering ranged from 45.33 to 59.67 days respectively. The genotypes IC-296677, IC-212393, IC-242733, IC-268275, IC-279120, IC-310834, IC-243334 and IC-381861 flowered earlier i.e. in less than 46 days. While, the genotype EC-341982 was very late to flower (59.67). Out of 50 genotypes, twenty flowered earlier than the population mean (52.21) days.

4.2.2 Days to maturity (Nos.)

Days required for maturity ranged between 100.33 to 127.67. The genotype IC-242733 was earlier to mature (100.33) followed by genotypes IC-208384, IC-332118, IC-310834, IC-243334, IC-356274, IC-381861, EC-398611 and IC268275. While, the genotype IC-208391

Table 4.1 : Analysis of variance (MSS) for 9 characters in pea

Sr. No.	Characters	Mean sum of square		
		Replications (3)	Treatment (50)	Error (150)
1.	Days to flowering	23.6562	57.9018*	10.0682
2.	Days to maturity	24.6250	203.3214*	18.0281
3.	Plant height at harvest (cm)	169.6250*	1420.7550*	31.8176
4.	No. of branches per plant	0.51074	20.2284*	0.92014
5.	No. of pods per plant	137.6875*	180.5612*	11.1320
6.	Pod length (cm)	10.1208	17.3381*	10.8024
7.	No. of seeds per pod	0.0514	2.8216*	0.16765
8.	100-seed weight (g)	1.3750*	37.0732*	0.1446
9.	Seed yield per plant (g)	99.4922*	124.5169*	7.0341

* Significant at 5 per cent level

was most late to mature (127.67 days). Out of 50 genotypes, twenty two matured earlier than the population mean (110.17).

4.2.3 Plant height at harvest (cm)

Plant height varied between 44.47 cm and 128.53 cm. The genotype EC-398604 was tallest (128.53) followed by IC-268275, IC-356332, IC-310834, IC-267142, IC-356337 and IC-267169. The genotype EC-412883 was dwarfest (44.47) followed by EC-412882. Twenty four genotypes recorded more plant height than population mean (88.89).

4.2.4 Number of branches per plant (Nos.)

The variation for number of branches per plant ranged from 6.47 to 14.53. The genotype IC-356172 produced maximum (14.53) number of branches per plant followed by IC-267182, IC-310834, IC-347185, IC-267169, IC-356332, IC-356272, IC-268276, IC-356144 and IC-268275. The genotype EC-341782 recorded lowest (6.47) number of branches per plant followed by EC-384139 and IC-356378. Twenty three genotypes recorded more number of branches per plant than population mean (10.39).

4.2.5 Number of pods per plant

Number of pods per plant varied between 27.07 and 57.73. The genotype IC-356332 recorded highest (57.73) number of pods per plant followed by IC-356172, IC-243334, IC-212393, IC-267127 and IC-356337. However, the genotype EC-381866 recorded lowest number of pods per plant followed by IC-208391 and EC-341782. Among the genotypes studied, twenty five recorded maximum number of pods per plant than the population mean (44.12).

4.2.6 Pod length (cm)

Pod length ranged from 3.43 cm to 8.13 cm. The genotype IC-267169 had highest pod length (8.13 cm) followed by IC-267142, IC-

356172, IC-356378, EC-384139, EC-384890 and IC-356337. While, the genotype IC-356147 had lowest (3.43 cm) pod length. Twenty one genotypes recorded highest pod length than population mean (5.03).

4.2.7 Number of seeds per pod

The range of 3.20 to 6.47 was observed for number of seeds per pod. The genotypes IC-267142, IC-267169 and IC-356172 had maximum number of seeds per pod (6.47) followed by IC-208368, EC-384139, IC-381861 and IC-356378. The genotype IC-356274 recorded lowest number of seeds per pod. Twenty two genotypes recorded greater number of seeds per pod than population mean (4.65).

4.2.8 100-seed weight (g)

The variation for 100-seed weight ranged between 6.0 g to 19.53 g. The genotype EC-387113 had highest 100-seed weight (19.53 g) followed by EC-381866, EC-385247, EC-341782, EC-398612, IC-332113 and EC-412883. The genotype IC-212393 recorded lowest 100-seed weight (6.0 g). Twenty genotypes gave greater 100-seed weight than population mean (11.44 g).

4.2.9 Seed yield per plant (g)

Seed yield per plant ranged between 10.85 g and 41.01 g. The genotype IC-267142 recorded highest (41.01 g) seed weight per plant followed by IC-267161, EC-385247, IC-356172, IC-267155, EC-387113 and IC-267169. The genotype IC-267151 recorded lowest (10.85 g) seed yield per plant. Twenty eight genotypes showed high seed yield per plant than population mean (22.39 g).

4.3 Parameters of Genetic variability

The parameters of genetic variability *viz.*, Range of variability, PCV, GCV, Heritability (bs), and Genetic advance are summarized in Table 4.3. The important findings are described below.

4.3.1 Coefficient of variation

The magnitude of PCV was higher than GCV for all nine characters under study. The magnitude of PCV was highest for 100-seed weight (30.8591) followed by seed yield per plant (30.3539), pod length (28.008) and number of branches per plant (26.0993). While, the magnitude of PCV was medium for plant height at harvest (25.0237) followed by number of seeds per pod (22.0385) and number of pods per plant (18.6377) and magnitude of PCV was low for days to flowering (9.7681) and days to maturity (7.9637).

The magnitude of GCV was highest for 100-seed weight (30.6794) followed by seed yield per plant (27.9476) and pod length (27.8578). The magnitude of GCV was medium for number of branches per plant (24.4125) followed by plant height at harvest (24.2057), number of seeds per pod (20.2067) and number of pods per plant (17.0343). While, days to flowering (7.6476) and days to maturity (7.006) recorded lowest GCV estimates.

The maximum difference between PCV and GCV magnitude was observed for seed yield per plant followed by days to flowering, number of branches per plant and number of seeds per pod. The PCV and GCV was of same magnitude for days to maturity, plant height at harvest, pod length and 100-seed weight.

4.3.2 Heritability (bs)

The medium (10 to 30 per cent) and high (above 30 per cent) heritability was recorded for all characters studied. The character 100-seed weight exhibited highest heritability (98.84) followed by plant height at harvest (93.57), number of branches per plant (87.49),

seed yield per plant (84.77), number of seeds per pod (84.07), number of pods per plant (83.53), days to maturity (77.41) and days to flowering (61.29). The medium and lowest magnitude of heritability (bs) was recorded for pod length (16.78).

4.3.3 Genetic advance

The plant height recorded highest genetic advance (42.8761) followed by days to maturity (14.2438), number of pods per plant (14.1493) and seed yield per plant (11.8692). However, pod length gave lowest magnitude of genetic advance (1.2456) followed by number of seeds per pod (1.7765), number of branches per plant (4.8883), days to flowering (6.44) and 100-seed weight (7.1854).

The highest heritability and genetic advance was recorded in plant height at harvest, seed yield per plant, number of pods per plant and days to maturity. While, pod length and days to flowering recorded lowest heritability and genetic advance.

4.4 Correlation

The simple correlation between yield and yield contributing characters in pea is presented in Table 4.4.

4.4.1 Association between seed yield and its components

The characters 100- seed weight (0.675) recorded the highest significant positive correlation with seed yield per plant followed by pod length (0.636), number of seeds per pod (0.607), days to maturity (0.483) and days to flowering (0.404). However, the association between seed yield and number of pods per plant was negative and non significant. Number of branches and plant height were associated non significantly.

4.4.2 Association between other component characters

Days to flowering recorded the highest significant positive correlation with days to maturity (0.755) followed by 100- seed weight (0.551). While, plant height at harvest (-0.356) was significantly and negatively correlated with days to flowering followed by number of pods per plant (-0.521) and number of branches per plant (-0.525).

Days to maturity recorded the highest significant positive correlation with 100-seed weight (0.566) followed by pod length (0.364) and number of seeds per pod (0.307). However, its association was significantly negative with number of pods per plant (-0.504) followed by number of branches per plant (-0.372).

Plant height at harvest recorded the highest significant positive correlation with number of branches per plant (0.631) followed by number of pods per plant (0.500), however, its association was significantly negative with 100-seed weight (-0.288).

Number of branches per plant was significantly and positively correlated with number of pods per plant (0.598), however, its association was significantly negative with 100-seed weight (-0.401).

Number of pods per plant was significantly and negatively correlated with 100-seed weight (-0.627) followed by number of seeds per pod (-0.304) and pod length (-0.302).

Pod length had highest significant positive correlation with number of seeds per pod (0.874).

4.5 Path analysis

The path analysis suggested by Dewey and Lu (1959) is used to reveal the direct and indirect contribution of each character to yield. The path analysis on yield contributing components were carried out

to have a clear view of individual characters contribution to seed yield per plant.

The direct and indirect effects of nine characters on seed yield per plant is presented in Table 4.5.

4.5.1 Direct effect

Looking to data on direct effects in path analysis (Table 4.5) it was observed that the character 100- seed weight produced the highest direct effect (0.94958) followed by number of pods per plant (0.54602), number of seeds per pod (0.46048) and pod length (0.25386). The correlation coefficient of these characters with seed yield were positively significant except number of pods per plant which was positively and non significantly correlated with seed yield.

Pod length recorded medium direct effect and its correlation with seed yield was positively significant.

Number of branches per plant recorded magnitudinally low direct effect with yield and was positively non significant.

Days to flowering recorded low direct effect and its correlation with yield was positively significant, however, days to maturity showed low and negative direct effect and its correlation with yield was positively significant.

Plant height at harvest recorded negative and lowest direct effect and its association with seed yield was non significant.

4.5.2 Indirect effects

Looking to the indirect effects of various characters it was observed that days to flowering contributed *via* 100- seed weight and number of seeds per pod positively and number of pods per plant negatively. Days to maturity contributed indirectly *via* 100-seed weight and number of seeds per pod positively.

The attribute plant height at harvest contributed indirectly *via* number of pods per plant, number of seeds per pod, pod length and number of branches per plant positively and 100-seed weight negatively. The trait number of branches per plant had maximum positive indirect effect *via* number of pods per plant and number of seeds per pod and maximum negative indirect effect through 100-seed weight.

The number of pods per plant showed indirect effect *via* number of branches per plant and days to maturity positively and 100-seed weight and number of seeds per pod negatively. Pod length exhibited maximum positive indirect effect *via* number of seeds per pod and 100-seed weight and maximum negative indirect effect *via* number of pods per plant.

Likewise, number of seeds per pod showed maximum positive indirect effect through pod length and 100-seed weight and maximum negative indirect effect through number of pods per plant. The 100-seed weight showed indirect effect *via* number of seeds per pod and pod length positively and number of pods per plant negatively.

4.6 Genetic divergence

Genetic divergence in 50 lines was measured by following Mahalanobis D^2 statistics. The D^2 values between all possible pair of 50 lines ranged between 8.8389 (genotypes 19 and 24) to 1510.31 (genotypes 2 and 20).

4.6.1 Cluster formation

The cluster formation was done as per Tocher's method as suggested by Rao (1952). The 50 genotypes were grouped into twenty clusters. Cluster I was the largest and comprises maximum of 6

genotypes, followed by cluster II and III with 5 genotypes each. Likewise, cluster IV and V accommodated 4 genotypes each, cluster VI and VII with 3 genotypes each, Cluster VIII, IX, X, XI, XII, XIII and XIV were with 2 genotypes each and cluster XV, XVI, XVII, XVIII, XIX, and XX were monogenotypic.

Table 4.6 Distribution of 50 Genotypes into different clusters

Cluster number	Number of genotypes included	Genotypes
I	6	EC-398611, IC-208384, IC-268254, IC- 332118, IC-356274, IC-356373
II	5	EC-389374, IC-20167, IC-242725, IC-242733, IC-267151
III	5	IC-243334, IC-310834, IC-356144 IC-356272, IC-356332
IV	4	EC-412882, EC-412883, IC-267155, IC-310833
V	4	IC-267182, IC-268275, IC-268276, IC-2996677
VI	3	EC-381897, EC-384890, IC-356378
VII	3	IC-267127, IC-356310, IC-356337
VIII	2	EC-385247, EC-387113
IX	2	EC-398604, IC-267169
X	2	IC-27912, IC-356147
XI	2	EC-341782, IC-208391
XII	2	IC-332113, IC-347185

XIII	2	IC-356268, IC-381861
XIV	2	EC-381866, IC-267161
XV	1	EC-384139
XVI	1	EC-398612
XVII	1	IC-208368
XVIII	1	IC-2123933
XIX	1	IC-267142
XX	1	IC-356172

4.6.2 Intra and Inter cluster formation

The intra and inter cluster distances were worked out by D^2 solutions. The mean D^2 values of cluster elements were used as measure of intra and inter cluster distance (Table 4.7b).

The maximum intra cluster distance was found in cluster XIV (D^2 = 52.24) followed by cluster XIII (D^2 = 51.67), cluster I (D^2 = 51.21), cluster XII (D^2 = 48.92), cluster XI (D^2 = 48.24), cluster V (D^2 = 45.58), cluster X (D^2=45.48), cluster IV (D^2 = 43.33), cluster II (D^2 = 38.15), cluster III (D^2 = 34.39), cluster VI (D^2 = 33.00), cluster IX (D^2 = 26.58) and cluster VII had D^2 = 26.65. The clusters XV, XVI, XVII, XVIII, XIX and XX being monogenotypic, recorded no intracluster distance. The minimum intracluster distance was observed for cluster VIII (D^2 = 10.40).

The maximum inter-cluster distance was found between cluster II and XIV (D^2 = 1215.38) followed by cluster XIV and XVIII (D^2 = 1046.43) and cluster II and XIX (D^2 = 1016.93). The inter-cluster distance between cluster VIII and XVI (D^2 = 42.34) was minimum.

The cluster I showed the maximum inter-cluster distance with cluster XIV (D^2 = 632.23) followed by cluster VIII (D^2 = 431.67). The cluster I was closer to cluster X (D^2 = 72.59).

The maximum inter-cluster distance of cluster II was observed with cluster XIV (D^2 = 1215.38) followed by cluster XIX (D^2 = 1016.93). While, cluster II was closer to cluster X (D^2 = 81.40).

The cluster III was most distant from cluster XV (D^2 = 664.97) followed by cluster XVII (D^2 = 463.25) and closer to cluster XX (D^2 = 67.78).

The cluster IV was most distant from cluster XVIII (D^2 = 369.14) followed by cluster XIX (D^2 = 314.14) and closer to cluster XVI (D^2 = 67.73).

The cluster V was most distant from cluster XIV (D^2 = 619.45) followed by cluster VIII (D^2 = 472.21) and closer to cluster VII (D^2 = 91.77).

The cluster VI was most distant from cluster XIX (D^2 = 496.22) and closer to cluster XVII (D^2 = 63.89).

The cluster VII showed the maximum inter-cluster distance with cluster XIV (D^2 = 475.56) followed by cluster XV (D^2 = 401.41). The cluster VII was closer to cluster XX (D^2 = 80.30).

The cluster VIII was most distant from cluster XVIII (D^2 = 793.88) followed by cluster XV (D^2 = 750.88) and closer to cluster XVI (D^2 = 42.34).

The cluster IX was most distant from cluster XV (D^2 = 684.17) followed by cluster XVII (D^2 = 445.18) and closer to cluster XIX (D^2 = 62.17).

The cluster X was most distant from cluster XIV (D^2 = 870.13) followed by cluster XIX (D^2 = 644.34) and closer to cluster XVIII (D^2 = 69.24).

The cluster XI was most distant from cluster XVIII (D^2 = 400.67) followed by cluster XV (D^2 = 392.40) and closer to cluster XIII (D^2 = 77.68).

The cluster XII was most distant from cluster XV (D^2 = 686.24) followed by cluster XVII (D^2 = 583.95) and closer to cluster XIII (D^2 = 106.43).

The cluster XIII was most distant from cluster XV (D^2 = 494.73) followed by cluster XVIII (D^2 = 327.20) and closer to cluster XVI (D^2 = 116.69).

The cluster XIV was most distant from cluster XVIII (D^2 = 1046. 43) followed by cluster XV (D^2 = 978.36) and closer to cluster XVI (D^2 = 115.16).

The cluster XV was most distant from cluster XIX (D^2 = 891.26) followed by cluster XX (D^2 = 573.87) and closer to cluster XVII (D^2 = 96.76).

The cluster XVI was most distant from cluster XVIII (D^2 = 572.62) followed by cluster XVII (D^2= 444.56) and closer to cluster XIX (D^2 =184.83).

The cluster XVII was most distant from cluster XVIII (D^2 = 648.48) followed by cluster XX (D^2 = 419.85) and closer to cluster XVIII (D^2 =207.89).

The cluster XVIII was most distant from cluster XIX (D^2 = 676.97) and closer to cluster XX (D^2 = 299.27).

The cluster XIX was most distant from cluster II (D^2 = 1016.93) and closer to cluster IX (D^2 = 62.17).

The cluster XX was most distant from cluster II (D^2 = 615.01) followed by cluster XV (D^2 = 573.87) and cluster XVII (D^2 = 419.85).

The cluster XX was closer to cluster III (D^2 = 67.78).

4.7 Cluster means

The cluster mean for nine characters studied are given in Table 4.8. There mean values for individual characters are described below.

4.7.1 Days to flowering (Nos.)

The genotypes in cluster XVIII were earliest to flowering (45.67) followed by cluster V (48.08), cluster I (48.22), cluster III (48.47) and cluster XIII (49.33). However, genotypes in cluster XI (57.83) flowered late.

4.7.2 Days to maturity (Nos.)

Based on the cluster means, it was observed that the genotypes in cluster XIII were earliest to mature (104.17) followed by cluster I (104.67), cluster XII (105.00), cluster XIII (105.33) and cluster III (105.99). Genotypes in the cluster XI were very late to mature (124.33) followed by cluster VIII (122.33) and cluster XVI (120.67).

4.7.3 Plant height at harvest (cm)

Cluster IX included the tallest genotypes (119.73) followed by cluster XIX (117.00) and cluster III (111.99). Cluster XV included dwarf genotypes (51.87).

4.7.4 Number of branches per plant

Cluster XX exhibited the highest number of branches per plant (14.53) followed by cluster V (14.02), cluster III (13.63) and cluster IX (13.13). While, cluster XV had lowest number of branches per plant (6.73) followed by cluster XI (7.10) and cluster XVI (7.27).

4.7.5 Number of pods per plant

Cluster XX exhibited maximum number of pods per plant (56.80) followed by cluster XVIII (54.80), cluster III (53.16), cluster VII (52.59) and cluster V (50.97). The cluster XI exhibited lowest number of pods per plant (31.40) followed by cluster XIV (33.63).

4.7.6 Pod length (cm)

Cluster XIX exhibited maximum length of pods (7.96) followed by cluster XVII (7.15), cluster IX (6.93) and cluster XX (6.87). The cluster XVIII (3.54) exhibited lowest length of pods.

4.7.7 Number of seeds per pod

Cluster XVII (6.53) exhibited highest number of seeds per pod followed by cluster XIX and XX exhibited the same number of seeds per pod (6.47) followed by cluster XV (6.20). The cluster XVIII (3.40) exhibited lowest number of seeds per pod followed by cluster XII (3.70).

4.7.8 100-seed weight (g)

The genotypes in the cluster VIII (19.32) had maximum 100-seed weight followed by cluster XIV (17.53) and cluster XVI (17.50). The cluster XVIII exhibited minimum weight of 100-seeds (6.00) followed by cluster V (7.3) and cluster II (7.68).

4.7.9 Seed yield per plant (g)

A wide range of variation was observed for this character. The cluster XIX (41.01) exhibited highest seed yield per plant followed by cluster XIV (31.22), cluster XX (30.78), cluster VIII (30.99) and cluster IX (28.24). The cluster XVIII exhibited lowest seed yield per plant (11.79) followed by cluster II (13.12) and cluster X (16.33).

4.8 Per cent contribution of various characters towards divergence

The 50 lines of pea were studied for nine characters and the data collected were used to determine the contribution of individual character towards genetic divergence (Table 4.9). Out of nine characters studied 100- seed weight (36.98 per cent) contributed the highest for divergence followed by number of seeds per pod (18.12 per cent) and seed yield per plant (14.61 per cent). However,

contribution of plant height at harvest (9.14 per cent), number of pods per plant (6.86 per cent) and days to maturity (5.14 per cent) were of a moderate magnitude. The number of branches per plant (2.94 per cent) contributed the lowest for divergence followed by days to flowering and pod length i.e. 3.10 per cent.

Table 4.9 : Percent contribution of various characters to divergence in pea

Sr. No.	Characters	Percent contribution
1	Days to flowering	3.10
2	Days to maturity	5.14
3	Plant height at harvest (cm)	9.14
4	No. of branches per plant	2.94
5	No. of pods per plant	6.86
6	Pod length (cm)	3.10
7	No. of seeds per pod	18.12
8	100-seed weight (g)	36.98
9	Seed yield per plant (g)	14.61
	Total	100

4.9 Morphological character variation in pea

The morphological character variation was recorded on all the 50 genotype lines on 10 qualitative characters and presented in Table 4.10.

4.9.1 Foliage colour

Looking to the foliage colour variation among 50 genotypes, 27 genotypes exhibited yellowish foliage colour and was followed by green (22) and faint green (1).

4.9.2 Stem colour

The 50 genotypes were grouped in three stem colours *viz.*, green (30), yellow (18) and faint green (2).

4.9.3 Flower colour

There were only two types of flower colour variations recorded. Of the 50 genotypes, 26 exhibited purple flower colour and 24 were white in flower colour.

4.9.4 Pod shape

There were only two types of pod shape variations recorded. Of the 50 genotypes, 38 exhibited inflated pod shape and 12 were constricted in pod shape.

4.9.5 Pod position

There were only two types of pod position variations. Of the 50 genotypes, 26 exhibited axillary and 24 were terminal in pod position.

4.9.6 Cotyledon colour

Looking to the cotyledon colour variation among 50 genotypes, 33 genotypes exhibited yellow cotyledon colour and was followed by white (12) and green (5).

4.9.7 Seed colour

Looking to the seed colour variation among 50 genotypes, 29 genotypes exhibited white seed colour was followed by grey brown (17), green (2) and grey (2).

4.9.8 Seed shape

There were only two types of seed shape variations recorded. Of the 50 genotypes, 42 exhibited round shape and 8 were wrinkle shaped.

4.9.9 Growth habit

There were only two types of growth habit variations recorded. Of the 50 genotypes, 31 exhibited viny habit and 19 were non-viny in habit.

4.9.10 Natural incidence of pest and disease

Powdery mildew diseases was recorded only in 9 genotypes of pea.

5. DISCUSSION

Success of any breeding programme mainly depends on available variability and intensity of selection imposed. Biometrical genetics offered various analytical techniques to assess the available variability. Genotypic and phenotypic coefficient of variation, estimates the extent of variability present in material under investigation, while heritability suggests the relative role of genetic factors in expression of phenotypes (Falconer, 1960) and also an index of transmissibility of particular trait to its offspring. However, the knowledge of heritability alone does not help in formulating breeding programme. Genetic advance along with heritability helps to ascertain the possible genetic control for any particular trait. All these genetic parameters suggested breeding technique to be adopted. Whereas, the association, analysis and path coefficient explain the nature of dependency of yield and yield contributing characters on each other. The D^2 statistics as suggested by Mahalanobis (1936) and clustering Rao (1952) helps to search genetically diverse types for hybridization programme.

In the present investigation entitled “Variability and Diversity studies in pea” (*Pisum sativum* L.) attempts were made to study the variability and diversity for 9 quantitative and 10 qualitative morphological characters among the 50 genotypes, the association between the dependent and independent variables along with their direct and indirect effects and also the genetic diversity among them. The results obtained are discussed in the chapter under the following sub headings.

5.1 Mean performance

5.2 Components of genetic variation

5.3 Heritability and genetic advance

5.4 Correlations

5.5 Path analysis

5.6 Genetic divergence

5.7 Morphological character variation

5.1 Mean performance

Based on analysis of variance for various characters the mean sum of squares due to treatments were significant for all the nine characters indicating the presence of good amount of variability for all the characters studied. The earlier findings of Singh and Saklani (1973), Singh *et al.* (1977), Kuksal *et al.* (1983), Korla and Singh (1988), Bhardwaj *et al.* (2001) and Singh *et al.* (2003) were similar to present results.

Looking to the range of variation for various characters, good amount of differences were observed in *per se* performance for various characters studied.

The variation for seed yield ranged between 10.85 g to 41.01 g per plant with a population mean of 22.39 g. The genotype IC-267142 recorded highest seed yield per plant (41.01g) followed by IC-267161, EC-385247, IC-356172, IC-267155, EC-387113 and IC-267169 (Table 4.3). These lines exhibited more than 29.00g of seed yield per plant indicating their high yielding potential. The present result confirm the findings of Gupta *et al.* (1983), Korla and Singh (1988), Awasthi (1989) and Tyagi and Srivastava (2002).

In respect of components characters, genotypes IC-296677, IC-212393, IC-242733, IC-268272, IC-279120, IC-310834, IC-243334 and IC-381861 exhibited early flowering i.e. less than 46 days. The lines IC-242733, IC-208384, IC-332118, IC-310834, IC-243334, IC-356274, IC-381861, EC-398611 and IC-268275 matured earlier i.e. before 104 days.

The earlier findings of Gupta *et al.* (1983) and Tyagi and Srivastava (2002) were similar to present results.

Similarly, genotypes EC-398604, IC-268275, IC-356332, IC-310834, IC-267142 and IC-356337 were taller i.e. more than 118cm. Genotypes IC-356172, IC-267182, IC-310834, IC-347185, IC-267169 and IC-356332 had high number of branches per plant. While, genotypes IC-356332, IC-356172, IC-243334, IC-212393 and IC-267127 had maximum number of pods per plant. The genotypes IC-267169, IC-267142, IC-356172, IC-356378 and EC-384139 had greater pod length. Number of seeds per pod were greater in genotypes IC-267142, IC-267169, IC-356172, IC-208368 and EC-384139. The 100-seed weight were highest in genotypes EC-38113, EC-381866, EC-385247, EC-341782 and EC-398612. The seed yield per plant were highest in genotypes IC-267142, IC-267161, EC-385247, IC-356172 and IC-267155. The present results confirm the findings of Korla and Singh (1988) for yield per plant and weight of 15 pods and Bhardwaj *et al.* (2001) for days to 50 per cent flowering.

The variability studied between 50 genotypes indicated the presence of good amount of variation for all nine characters studied. Variability observed for seed yield per plant ranged between 10.85 g to 41.01 g. Likewise, other characters also showed wide range of variability as, days to flowering (45.37 to 59.67 days), days to maturity (100. 33 to 127.67 days), plant height at harvest (44.47 to 128.53 cm), number of branches per plant (6.47 to 14.53 cm), number of pods per plant (27.07 to 57.73), pod length (3.43 to 8.13 cm), number of seeds per pod (3.20 to 6.47) and 100-seed weight (6.0 to 19.53 g).

Among the 50 genotypes studied, genotype IC-296677 for early flowering, IC-242733 for early maturity, EC-398604 for plant height at harvest, IC-356172 for number of branches per plant, IC-356332 for

number of pods per plant, IC-267169 for pod length, IC-267142, IC-267169 and IC-356172 for number of seeds per pod, EC-387113 for 100-seed weight and IC-267142 for seed yield per plant recorded the highest *per se* performance for respective characters.

5.2 Components of genetic variation

Looking to GCV and PCV the indices of variability it was observed that PCV estimates were magnitudinally greater than GCV for all nine characters revealing the role of environment in phenotypic expression of these traits. This also suggested the fact that in variability studies one should not rely upon phenotypes alone. It is always better to consider PCV and GCV together with heritability.

The character 100-Seed weight recorded highest magnitude of PCV and GCV followed by seed yield per plant, pod length, number of branches per plant and plant height at harvest suggesting the presence of good amount of variability for these traits. These results confirm the earlier findings of Kalloo *et al.* (1976), Kuksal *et al.* (1983), Gupta *et al.* (1983), Tyagi and Shrivastava (2002), Chaudhary and Sharma (2003), Kumar *et al.* (2003), Sharma *et al.* (2003) and Singh *et al.* (2003).

The GCV and PCV estimates were of moderate magnitude for number of seeds per pod and number of pods per plant. Whereas, the characters days to flowering and days to maturity had low PCV and GCV estimates, suggesting narrow range of variation for these characters in the 50 genotypes evaluated. These results were in agreement with those obtained by Kalloo *et al.* (1976), Gupta *et al.* (1983) and Ramesh *et al.* (2002).

In the studies on magnitudinal differences between PCV and GCV it was observed that the magnitudinal difference between PCV and GCV were very high for the traits *viz.*, seed yield per plant, days to flowering,

number of seeds per pod, number of branches per plant and number of pods per plant, indicating the role of environment in the expression of these characters. The result of the present research confirmed the earlier finding of Singh *et al.* (1977) for node number with first pod and number of seeds per pod and Tyagi and Shrivastava (2002) for pods per plant and biological yield per plant.

The magnitudinal difference between PCV and GCV for days to maturity, plant height at harvest, pod length and 100-seed weight were low, suggesting a little role of environment in expression of these traits. These results confirm the earlier finding of Kuksal *et al.* (1983) and Ramesh *et al.* (2002).

5.3 Heritability and Genetic Advance

Heritability is the resemblance between parents and their progeny (Falconer, 1960) while, genetic advance provides knowledge about expected genetic gain for particular trait after selection. In general in self pollinated crops characters with high heritability posses genetic advance of higher magnitude but phenotypic variation in the population is low, genetic advance also tends to be low and vice versa. This indicated the importance of variation and heritability in breeding programme.

When heritability is moderate to high with higher magnitude of expected genetic advance for a particular trait indicates the additive gene action and if the results are reversed and either of the conditions like high heritability coupled with low genetic advance is observed for any given trait, then presence of non-additive gene action may be suspected.

The medium to high heritability was recorded for all characters under study. The maximum per cent of heritability was observed for 100-seed weight (98.84) followed by plant height at harvest (93.57), number of branches per plant (87.49), seed yield per plant (84.77), number of

seeds per pod (84.07), number of pods per plant (83.53), days to maturity (77.41) and days to flowering (61.29). Among these characters, plant height at harvest, seed yield per plant, number of pods per plant and days to maturity with high magnitude of expected genetic advance suggested existence of additive gene action. These results coincide with those obtained by Singh and Singh (1970), Singh and Saklani (1973), Singh *et al.* (1986), Dubey and Lal (1988) for days to flowering and 100-seed weight, Baswana and Tewatia (1994) and Dixit (1998) for pods per plant.

High heritability coupled with moderate genetic advance was observed for characters 100-seed weight, days to flowering and number of branches per plant. These results were in agreement with those recorded by Dubey and Lal (1988) for yield per plant, seeds per pod and shelling percentage.

The characters *viz.*, 100-seed weight, number of seeds per pod and days to flowering had high heritability with low genetic advance and pod length showed moderate heritability coupled with low genetic advance. This situation suggested the presence of non-additive genetic variation for expression of these traits.

5.4 Correlation

Correlation coefficient is a statistical measure which is used to find out the degree (strength and direction of relationship between two or more variables). The information on the inter-relationship among the traits facilitated the choice of breeding method to be applied and selecting the parents for crop improvement.

In the present investigation, the character seed yield per plant showed significant positive association with 100-seed weight, pod length, number of seeds per pod, days to maturity and days to flowering, suggesting dependency of yield on these characters. However, seed yield

was significantly and negatively correlated with number of pods per plant. Similar findings were reported by Chaudhary *et al.* (1971) for 100-seed weight and number of seeds per pod, Singh (1985) for days to 50 per cent flowering, Singh *et al.* (1985) for 100-seed weight, seeds per pod and days to flowering and Singh *et al.* (1987) for days to maturity and days to flowering.

In association between component characters, days to flowering recorded the highest significant positive correlation with days to maturity and 100-seed weight. The days to maturity recorded significant positive correlation with 100-seed weight, pod length and number of seeds per pod. While, pod length had significant positive correlation with number of seeds per pod. These results suggested the interdependency of these characters on each other. These results coincide with Teotia *et al.* (1983) for pod length with number of seeds per pod.

5.5 Path analysis

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into direct and indirect effects. In present investigation, path analysis was worked out by following Dewey and Lu (1959) to estimate the magnitude and direction of direct and indirect effects of various yield and yield contributing characters. Correlation coefficient along with path effects together provides reliable information which can be between causal factor and direct effect is more or less of equal magnitude, it explains the true and perfect relationship between the traits and direct selection through these traits will be rewarding. However, if the correlation coefficient is positive and the direct effect is negative or negligible the indirect causal factors are to be considered in simultaneous selection (Singh and Kakar, 1977).

5.5.1 Direct effects

In the present investigation path coefficient analysis was calculated. This was done to ascertain a clear view by which individual traits contributed to yield. It was observed that the character 100-seed weight (0.94958) produced the highest direct effect followed by number of pods per plant (0.54602), number of seeds per pod (0.46048) and pod length (0.25386).

Along with the direct effect of these characters on yield, the correlation coefficient between seed yield with 100-seed weight, number of seeds per pod and pod length were significantly positive indicating the true and perfect association between these characters.

The days to flowering recorded low direct effects and its correlation with yield was significantly positive. The days to maturity also produced magnitudinally low and negative direct effect but its association with seed yield was significantly negative.

Similar results were obtained by Narsinghani *et al.* (1978), Teotia (1983), Singh (1985), Singh *et al.* (1985), Chaudhary and Sharma (2003) and Pathak *et al*. (2002).

However, the direct effect of number of pods per plant showed negative correlation with seed yield per plant suggesting these characters do not contribute directly but may influence the yield *via* other component characters.

5.5.2 Indirect effects

Among the various characters days to flowering contributed indirectly through 100-seed weight and number of seeds per plant positively and number of pods per plant negatively. Days to maturity contributed indirectly through 100-seed weight and number of seeds per pod positively. Pod length contributed indirectly through 100-seed weight positively and through number of pods per plant negatively.

Likewise, number of seeds per pod showed positive indirect effect through pod length and 100-seed weight and negative indirect effect through number of pods per plant. The 100-seed weight showed positive indirect effect through number of seeds per pod and pod length and negatively through number of pods per plant.

From the above results, it is implicated that increase in the performance of these traits which contributed indirectly and positively, ultimately leads to increase in seed yield per plant.

The residual effects determines how best the causal factors accounted for the variability of dependent factors i.e. seed yield per plant. In the present study, the residual effect was 0.22902, indicating that besides the characters studied, there are some other attributes which contributed to the yield.

5.6 Genetic Divergence

The most important and difficult task is initiation of hybridization programme by selecting genotypes with high *per se* performance for yield and yield contributing components with suitable genetic divergence among them. From the genetic variability estimates it would be possible to identify desirable genotypes but unless we have sound knowledge about average between them its difficult to expect any extra ordinary results from their progeny.

D^2 statistics a concept developed by Mahalanobis (1936) is important tool to plant breeder. It is useful tool to study the degree of divergence between biological population at genotypic level and to asses the relative contribution of different components to the total divergence at both intra and inter-cluster level. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding.

5.6.1 Intra and Inter-cluster distances

The basic idea behind formation of clusters is to get the intra and inter-cluster distances. This serves as index for selection of parents with diverse origin. The intra and inter-cluster values are means derived from D^2 values of cluster elements. The crossing between the genotypes placed in clusters with large inter cluster distance will be more correct approach to get desirable results.

In the present investigation the 50 lines were grouped into 20 clusters. The genotypes EC-381866 and IC-242733 were genetically distanced as they show maximum D^2 values (1510.31) between them and were placed in different clusters. While, genotypes IC-242725 and IC-267151 were most closely related (D^2 =8.8389) and placed in same cluster. This indicated the relationship between genotypes and individual distances from each other with clustering pattern.

The 20 different clusters formed in the present study indicated that the available genotypes possess variability for nine different characters under study. The cluster I had larger number of 6 genotypes followed by cluster II and III with 5 genotypes each, cluster IV and V had 4 genotypes each, cluster VI and VII with 3 genotypes each, cluster VIII, XI, X, XI, XII, XIII, XIV with 2 genotypes each and cluster XV, XVI, XVII, XVIII, XIX, XX were monogenotypic. Wide range of diversity was also reported by Chandel and Joshi (1981) who grouped 30 genotypes into 10 clusters, Dhobal and Ram (1985) grouped 32 genotypes into 11 clusters, Singh and Tripathi (1985) grouped 100 germplasms into 14 clusters, Dixit *et al.* (2002) grouped 53 genotypes into 11 clusters and Singh and Singh (2003) grouped 50 genotypes into 11 clusters.

The maximum intra cluster distance was observed for the genotypes falling in cluster XIV (D^2 = 52.24) followed by cluster XIII (D^2 = 51.67) and I (D^2 = 51.21). This implies that cluster XIV, XIII and I

have the genotypes with varied genetic architecture, while the genotypes falling in the cluster VIII (D^2 = 10.40) exhibited minimum intra cluster distance, impling that genotypes falling in the cluster VIII were genetically resembling to each other and might have come from common gene pool, while the cluster XV, XVI, XVII, XVIII, XIX and XX showed zero intracluster distance due to monogenotypic nature.

Genotypes falling between cluster II and XIV exhibited maximum inter-cluster distance (D^2 = 1215.38), cluster XIV and XVIII (D^2 = 1046.43) and cluster II and XIX (D^2 = 1016.93) indicating that genetic makeup of genotypes falling in this clusters may be entirely different from one another. While, the cluster VIII and XVI recorded lowest distance (D^2 = 42.34) followed by cluster IX and XIX (D^2 = 62.17) suggesting that genotypes in these clusters were genetically close to each other.

5.6.2 Mean performance

Based on the cluster means for a characters (Table 4.8) it was observed that cluster XIX recorded highest seed yield per plant (41.01) and was characterized as comparatively larger number of seeds per pod, pod length and plant height at harvest. The cluster XX, VIII and IX showed medium seed yield per plant as most of the yield components were intermediary in nature. The cluster XVIII was least yielder among the clusters, which was mainly due to early flowering, shorter pods, less number of seeds per pod and less weight of 100-seeds.

Cluster mean for plant height at harvest was maximum for cluster IX similarly, number of branches per plant, number of pods per plant for cluster XX, pod length for cluster XIX, number of seeds per pod for cluster XVII and 100-seed weight for cluster VIII exhibited maximum cluster mean.

5.6.3 Relative contribution of characters towards divergence

In present investigation 100-seed weight (g) showed maximum (36.98 per cent) relative contribution towards divergence followed by number of seeds per pod (18.12 per cent) and seed yield per plant (14.61 per cent) indicating that these characters were considerably responsible for the total divergence in the material under study.

Plant height at harvest, number of pods per plant and days to maturity contributed moderately for genetic divergence, while number of branches per plant, days to flowering and pod length contributed least for genetic divergence.

The results obtained in the present investigation indicated that yield indictors responsible for divergence varied substantially and may be attributed to differences in the genetic constitution of material and the environment in which they were are grown.

5.6.4 Genetic divergence as a measure of choosing potent parent for crossing

The success of any crossing programme lies primarily in the selection of parents with high expression for economically important characters. Since genetic make up of self pollinated crops remains constant, it is important to have divergent parents with good performance for yield as well as other quantitative traits for hybridization to obtain a desirable segregant through selection in the subsequent generations. Among the different approaches of selecting parents, selection based on diversity had its own merit. Therefore, in the present investigation diversity among different genotypes was studied, which yielded valuable information that could be useful in suggesting potent parents for hybridization.

Bhatt (1970) advocated that the statistical distance of all possible cluster combinations may be considered arbitrarily as a guideline and

suggested that crosses belonging to different clusters showing an inter cluster distance equal to mean statistical distance or more might be attempted.

Timothy (1963) had also suggested, genetic divergence as one of the criteria for selecting the parents in plant breeding as a mean to generate crosses which will segregate in later generations into transgressive segregants possessing performance better than the parents involved.

In the present investigation, attempts were made to the cluster combinations into four divergence classes as per the method suggested by Arunachalam and Bandopadhyay (1984). The statistical distances (D) given in table 4.7 represent the index of genetic diversity among cluster. The mean (M) calculated for intra and inter cluster distances was 15.39 with a standard deviation (S) of 8.52. The minimum (X) and maximum (Y) divergence class values were 3.225 and 34.862 respectively. The divergence classes are presented in Table 5.1.

Arunachalam and Bandopadhyay (1984) reported that crosses between divergent classes DC_2 and DC_3 will be more heterotic and promising than other combinations. In the present investigations, the maximum clusters were included in DC_2 and DC_3. To reduce the risk form the view point of heterosis, high yielding genotypes from the clusters selection should be used. However, while selecting genotypes from clusters other practical considerations, like yield quality, resistance to disease should be taken into account. The list of 10 genotypes, which deserve to be considered as a potent parents for crossing are as indicated below.

Sr. No.	Name of Genotype	Cluster	Characteristics
1	EC-398604	IX	Maximum plant height at harvest, seed yield, 100-seed weight, pod length and number of seeds per pod
2	EC-387113	VIII	Maximum 100-seed weight and seed yield
3	IC-267142	XIX	Maximum seed yield, number of seeds per pod, 100-seed weight, pod length and plant height at harvest.
4	IC-267169	IX	Maximum pod length, number of seeds per pod, seed yield and plant height at harvest.
5	IC-356172	XX	Maximum number of seeds per pod, seed yield, pod length and plant height at harvest
6	IC-356332	III	Maximum number of pods per plant, pod length, seed yield and plant height at harvest.
7	IC-381861	XIII	Early flowering and maturity, maximum seed yield, pod length and number of seeds per pod.
8	IC-267161	XIV	High seed yield, 100-seed weight, pod length and number of seeds per pod.
9	IC-356337	VII	High seed yield, number of pods per plant, plant height and number of branches per plant.
10	IC-296677	V	Early flowering maximum pod length and number of seeds per pod.

Table 5.1 : Distribution of different cluster combinations into four divergence classes based on D values between them

X	M-S	M	M+S	Y
3.225	8.52	15.39	22.26	34.862

DIVERGENCE CLASSES

3.225

DC_4 (XI, XIII), (VIII, XIV), (XVI, XV), (IV, XVI), (VIII, XVI), (VI, XVII), (X, XVIII), (IX, XIX), (III, XX).

8.52

DC_3 (I, II), (I, III), (I, IV), (I, V), (III, V), (IV, V), (I, VI), (II, VI), (IV, VI), (I, VII), (III, VII), (IV, VII), (V, VII), (IV, VIII), (III, IX), (IV, IX), (V, IX), (VII, IX), (VIII, IX), (I, X), (II, X), (IV, X), (V, X), (VI, X), (VII, (X), (I, XI), (III, XI), (IV, XI), (VI, XI), DC_3(VII, XI), (VIII, XI), (IX, XI), (III, XII), (IV, XII), (V, XII), (VII, XII), (VIII, XII), (IX, XII), (XI, XII), (I, XIII), (III, XIII), (IV, XIII), (V, XIII), (VII, XIII), (VIII, XIII), (XI, XIII), (XII, XIII), (IX, XIV), (XII, XIV), (XIII, XIV), (II, XV), (X, XV), (VII, XVI), (IX, XVI), (XI, XVI), (XII, XVI), (XIII, XVI), (XIV, XVI), (I, XVII), (II, XVII), (X, XVII), (XV, XVII), (I, XVIII), (II, XVIII), (V, XVIII), (VII, XVIII), (XVII, XVIII), (III, XIX), (VII, XIX), (VIII, XIX), (XI, XIX), (XII, XIX), (XIII, XIX), (XIV, XIX), (XVI, XIX), (I, XX), (V, XX), (VII, XX), (IX, XX), (XI, XX), (XII, XX), (XIII, XX), (XVI, XX), (XIX, XX).

15.39

DC_2 (II, IV), (III, IV), (III, VI), (V, VI), (II, VII), (VI, VII), (I, VIII), (V, VIII, (VI, VIII,), (VII, VIII), (I, IX), (VI, IX), (III, X), (II, XI), (V, XI), (X, XI), (I, XI), (I, XII), (VI, XII), (X, XII), (VI, XIII), (X, XIII), (III, XIV), (IV, XIV), (VII, XIV), (I, XV), (IV, XV), (V, XV), (VII, XV), (XI, XV), (I, XVI), (III, XVI), (V, XVI), (VI, XVI), (X, XVI), (XV, XVI), (III, XVII), (IV, XVII), (V, XVII) (VII, XVII), (IX, XVII), (XI, XVII), (XIII, XVII), (XVI, XVII), (III, XVIII), (IV, XVIII), (VI, XVIII), (IX, XVIII), (XI, XVIII), (XII, XVIII), (XIII, XVIII), (XV, XVIII), (XVI, XVIII), (I, XIX), (IV, XIX), (V, XIX), (IV, XX), (VI, XX), (VIII, XX), (X, XX), (XIV, XX), (XVII, XX), (XVIII, XX).

22.26

DC_1 (II, III), (II, VIII), (VIII, X), (II, XII), (II, XIII), (I, XIV), (II, XIV), (V, XIV), (VI, XIV), (X, XIV), (III, XV), (VIII, XV), (IX, XV), (XII, XV), (XIII, XV), (XIV, XV), (II, XVI), (VIII, XVII), (XII, XVII), (XIV, XVII), (VIII, XVIII), (XIV, XVIII), (II, XIX), (VI, XIX), (X, XIX), (XV, XIX), (XVIII, XIX), (XVIII, XIX), (II, XX), (XV, XX).

34.862

5.7 Morphological character variation

The observations on the ten qualitative characters of 50 germplasm lines were reveled that they had limited morphological variation.

Foliage colour exhibited three types of colour *viz.*, yellowish, green and faint green, stem colour showed three types of colour *viz.*, yellow, green and faint green, flower colour recorded only two types of colour i.e. purple and white, pod shape recorded two types of shape i.e. inflated and constricted.

Likewise, there were two types of pod position i.e. axillary and terminal position recorded by pod, cotyledon colour exhibited yellow, white and green colour, seed colour exhibited white, grey brown and grey colour of seeds, there were only two types of seed shape recorded i.e. round and wrinkled and two types of growth habit i.e. viny and non-viny.

6. SUMMARY AND CONCLUSIONS

The present investigation entitled “Variability and diversity studies in pea (*Pisum sativum* L.)” was undertaken with following objectives.

1. To study the variability for yield and yield contributing characters.
2. To study the association between different characters with direct and indirect effects.
3. To measure genetic divergence among various germplasm lines.

In the present investigation 50 indigenous and exotic genotypes were planted on 11th Oct. 2005 with 45 cm x 15 cm spacing in randomized block design with three replications. The genotypes were evaluated for nine diverse quantitative characters to have clear view of yield contributing components of seed yield per plant, other characters *viz.*, days to flowering, days to maturity, plant height at harvest, number of branches per plant, number of pods per plant, pod length, number of seeds per pod and 100- seed weight and ten qualitative characters *viz.*, foliage colour, stem colour, flower colour, pod shape, pod position, cotyledon colour, seed colour, seed shape, growth habit and Natural incidence of pest and disease.

The treatment mean sum of squares were significant for all characters studied, suggesting the presence of good variability for various characters studied in genotypes evaluated. Following are some important genotypes which showed the best performance for each of the various characters under study *viz.,* Among the 50 genotypes studied, IC-296677 for early flowering, IC-242733 for early maturity, EC-398604 for plant height at harvest, IC-356172 for number of branches per plant, IC-356332 for number of pods per plant, IC-267169 for pod length, IC-267142 , IC-

267169 and IC-356172 for number of seeds per pod, EC-387113 for 100-seed weight and IC-267142 for seed yield per plant recorded the highest *per se* performance for respective characters.

The variability studied between 50 genotypes indicated the presence of good amount of variation for all nine characters studied. Variability observed for seed yield per plant ranged between 10.85 g to 41.01 g. Likewise, other characters also showed wide range of variability as, days to flowering (45.37 to 59.67 days), days to maturity (100. 33 to 127.67 days), plant height at harvest (44.47 to 128.53 cm), number of branches per plant (6.47 to 14.53), number of pods per plant (27.07 to 57.73), pod length (3.43 to 8.13 cm), number of seeds per pod (3.20 to 6.47) and 100-seed weight (6.0 to 19.53 g).

The estimates of PCV and GCV were of high magnitude for 100-seed weight followed by seed yield per plant, pod length and number of branches per plant indicating, the presence of good amount of variability for these characters. Whereas, plant height at harvest and number of seeds per pod exhibited moderate PCV and GCV values.

The magnitudinal difference between PCV and GCV were high for seed yield per plant and days to flowering indicating, the role of environment in phenotypic expression of these traits. However, it was low for the characters, days to maturity, plant height at harvest, pod length and 100- seed weight suggesting a little role of environment in expression of these traits. The characters 100-seed weight (98.84 per cent), plant height at harvest (93.57 per cent), number of branches per plant (87.49 per cent), seed yield per plant (84.77 per cent), number of pods per plant (83.53 per cent), days to maturity (77.41 per cent) and days to flowering (61.29 per cent) showed high heritability estimates. However, theses characters showed varied expected genetic advance. Plant height at harvest, seed yield per plant, number of pods per plant and

days to maturity showed the high estimates of genetic advance, suggesting the role of additive gene effects for these characters. While, 100-seed weight, number of seeds per pod, days to flowering and pod length showed low estimates of expected genetic advance, suggesting the role of non – additive gene effects for these characters.

Seed yield per plant had positive and significant correlation with 100-seed weight, pod length, number of seeds per pod, days to maturity and days to flowering, this indicating the dependency of seed yield on these characters.

The path coefficient analysis revealed that the 100-seed weight, number of pods per plant, number of seeds per pod and pod length recorded high magnitude of direct effects on seed yield per plant. Among them 100 seed weight, number of seeds per pod and pod length showed significantly positive correlation with seed yield, indicating true and perfect relationship between yield and these characters with seed yield suggesting, the fact that the one can rely upon these characters while, making selections for high yielding genotypes in pea.

The 50 genotypes studied in the present investigation were grouped into twenty clusters by D^2 analysis as suggested by Rao (1952). The Tochers clustering method was used to have gene constellations. The maximum D^2 value (1510.31) was observed between the genotypes EC-381866 and IC-242733, while lowest was observed between IC-242725 and IC-267151 (8.8389). This suggested that, genotypes EC-381866 and IC-242733 were most apart genetically. While, genotypes IC-242725 and IC-267151 were most close to each other genetically. Among twenty clusters formed, cluster I comprised maximum number of genotypes i.e. 6, Cluster II and III had 5 genotypes each, cluster IV and V had 4 genotypes each, likewise, cluster VI and VII had 3 genotypes each and

VIII, IX, X, XI, XII, XIII and XIV had 2 genotypes each. while, cluster XV, XVI, XVII, XVIII, XIX and XX were monogenotype.

The intra cluster distance was maximum for cluster XIV, while it was minimum for cluster VIII. The inter cluster distance was maximum between cluster II and XIV, while it was minimum between VIII and XVI.

The variance of cluster means information that the genotypes in cluster XVIII were earliest to flowering. Likewise, genotypes in cluster XIII were earliest to mature, genotypes in cluster IX were tallest for plant height at harvest, genotypes in cluster XX number of pods per plant, genotypes in cluster XIX exhibited maximum length of pods, genotypes in cluster XVII exhibited highest number of seeds per pod, genotypes in cluster VIII had maximum 100-seed weight and genotypes in cluster XIX exhibited highest seed yield per plant.

The 100-seed weight showed highest percentage of contribution towards divergence followed by number of seeds per pod and seed yield per plant. Plant height at harvest, number of pods per plant and days to maturity contributed moderately for genetic divergence.

Looking to the morphological character variation, Foliage colour exhibited three types of colour *viz.,* yellowish, green and faint green, stem colour showed three types of colour *viz.,* yellow, green and faint green, flower colour recorded only two types of colour i.e. purple and white, pod shape recorded two types of shape i.e. inflated and constricted.

Likewise, there were two types of pod position i.e. axillary and terminal position recorded by pod, cotyledon colour exhibited yellow, white and green colour, seed colour exhibited white, grey brown and grey colour of seeds, there were only two types of seed shape recorded i.e. round and wrinkled and two types of growth habit i.e. viny and non viny.

Conclusions

1. **The significant treatment difference for 50 genotypes indicated good amount of variability for all the characters studied.**
2. Following are some important genotypes which showed best *per se* performance for each of the various characters under study *viz.*, IC-296677 for early flowering, IC-242733 for early maturity, EC-398604 for plant height at harvest, IC-356172 for number of branches per plant, IC-356332 for number of pods per plant, IC-267169 for pod length, IC-267142, IC-267169 and IC-356172 for number of seeds per pod, EC-387113 for 100- seed weight and IC-267142 for seed yield per plant recorded the highest *per se* performance for respective characters.
3. In the present investigation 100 -seed weight, seed yield per plant, pod length, number of branches per plant and plant height at harvest recorded high magnitude of PCV and GCV, indicating the presence of good amount of variation for these character among genotypes studied. The highest heritability and genetic advance was recorded for plant height at harvest, seed yield per plant and days to maturity. While, pod length and days to flowering recorded lowest heritability and genetic advance.
4. The characters 100-seed weight, number of seeds per pod and pod length produced the highest direct effect on seed yield per plant. The correlation coefficient of these characters with seed yield per plant was positively significant, indicating the true and perfect association between these characters. This suggested the dependency of seed yield on these characters.
5. The 100-seed weight contributed maximum to the total divergence. The total number of 50 genotypes were grouped in twenty clusters.

The maximum intra cluster distance was observed for cluster XIV and inter cluster distance was maximum between cluster II and XIV.

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*** Originals not seen**

8. VITA

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MASTER OF SCIENCE

In

CYTOGENETICS AND PLANT BREEDING
(AGRICULTURAL BOTANY)

2006

TITLE OF THESIS : "Variability and Diversity studies in pea (*Pisum sativum*(L).

MAJOR FIELD : Cytogenetics and Plant Breeding

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Table 4.1 : Analysis of variance (MSS) for 9 characters in pea

Sr. No.	Characters	Mean sum of square		
		Replications (3)	Treatment (50)	Error (150)
1.	Days to flowering	23.6562	57.9018*	10.0682
2.	Days to maturity	24.6250	203.3214*	18.0281
3.	Plant height at harvest (cm)	169.6250*	1420.7550*	31.8176
4.	No. of branches per plant	0.51074	20.2284*	0.92014
5.	No. of pods per plant	137.6875*	180.5612*	11.1320
6.	Pod length (cm)	10.1208	17.3381*	10.8024
7.	No. of seeds per pod	0.0514	2.8216*	0.16765
8.	100-seed weight (g)	1.3750*	37.0732*	0.1446
9.	Seed yield per plant (g)	99.4922*	124.5169*	7.0341

*, ** Significant at 5 per cent and 1 per cent level

Table 4.9 : Percent contribution of various characters to divergence in pea

Sr. No.	Characters	Percent contribution
1	Days to flowering	3.10
2	Days to maturity	5.14
3	Plant height at harvest (cm)	9.14
4	No. of branches per plant	2.94
5	No. of pods per plant	6.86
6	Pod length (cm)	3.10
7	No. of seeds per pod	18.12
8	100-seed weight (g)	36.98
9	Seed yield per plant (g)	14.61
	Total	100

Table 4.6 Distribution of 50 Genotypes into different clusters

Cluster number	Number of genotypes included	Genotypes
I	6	EC-398611, IC-208384, IC-268254, IC- 332118, IC-356274, IC-356373
II	5	EC-389374, IC-20167, IC-242725, IC-242733, IC-267151
III	5	IC-243334, IC-310834, IC-356144 IC-356272, IC-356332
IV	4	EC-412882, EC-412883, IC-267155, IC-310833
V	4	IC-267182, IC-268275, IC-268276, IC-2996677
VI	3	EC-381897, EC-384890, IC-356378
VII	3	IC-267127, IC-356310, IC-356337
VIII	2	EC-385247, EC-387113
IX	2	EC-398604, IC-267169
X	2	IC-27912, IC-356147
XI	2	EC-341782, IC-208391
XII	2	IC-332113, IC-347185
XIII	2	IC-356268, IC-381861
XIV	2	EC-381866, IC-267161
XV	1	EC-384139
XVI	1	EC-398612
XVII	1	IC-208368
XVIII	1	IC-2123933
XIX	1	IC-267142
XX	1	IC-356172

Table 3.1 : The list of Exotic and Indigenous lines used for present study

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1	EC-341782	18	IC-212393	35	IC-310834
2	EC-381866	19	IC-242725	36	IC-332113
3	EC-381897	20	IC-242733	37	IC-332118
4	EC-384139	21	IC-243334	38	IC-347185
5	EC-384890	22	IC-267127	39	IC-356144
6	EC-385247	23	IC-267142	40	IC-356147
7	EC-387113	24	IC-267151	41	IC-356172
8	EC-389374	25	IC-267155	42	IC-356268
9	EC-398604	26	IC-267161	43	IC-356272
10	EC-398611	27	IC-267169	44	IC-356274
11	EC-398612	28	IC-267182	45	IC-356310
12	EC-412882	29	IC-268254	46	IC-356332
13	EC-412883	30	IC-268275	47	IC-356337
14	IC-207167	31	IC-268276	48	IC-356373
15	IC-208368	32	IC-279120	49	IC-356378
16	IC-208384	33	IC-296677	50	IC-381861
17	IC-208391	34	IC-310833		

Table 4.10 : Morphological character variation in 50 Germplasm lines of pea

Germ-plasm No.	Foliage colour	Stem colour	Flower colour	Pod shape	Pod position	Cotyledon colour	Seed colour	Seed shape	Growth habit	Natural incidence of pest and disease
1	Green	Green	White	Inflated	Terminal	Yellow	White	Round	viny	
2	Green	Green	White	Inflated	Terminal	White	White	Round	nonviny	
3	Yellowish	Yellow	White	Inflated	Terminal	Yellow	White	Wrinkled	nonviny	P.M.
4	Green	Faint green	White	Inflated	Terminal	Yellow	Gray	Wrinkled	nonviny	
5	Yellowish	Yellow	White	Inflated	Terminal	White	White	Round	nonviny	
6	Green	Green	White	Inflated	Terminal	White	White	Round	viny	
7	Green	Green	White	Inflated	Terminal	White	White	Round	nonviny	P.M.
8	Green	Green	White	Inflated	Terminal	White	White	Round	nonviny	
9	Yellowish	Yellow	White	Inflated	Terminal	White	White	Round	viny	
10	Yellowish	Yellow	Purple	Constricted	Axillary	Yellow	Green	Round	viny	P.M.
11	Green	Green	White	Inflated	Terminal	Yellow	Gray brown	Round	nonviny	
12	Faint green	Faint green	White	Inflated	Terminal	Yellow	White	Wrinkled	nonviny	
13	Green	Green	White	Inflated	Terminal	Yellow	Green	Round	nonviny	
14	Yellowish	Yellow	Purple	Inflated	Axillary	Yellow	White	Round	viny	
15	Green	Green	White	Inflated	Terminal	Yellow	White	Round	viny	
16	Green	Green	Purple	Constricted	Axillary	Yellow	White	Wrinkled	viny	P.M.
17	Green	Green	White	Constricted	Terminal	Yellow	White	Round	nonviny	
18	Yellowish	Yellow	Purple	Constricted	Axillary	Yellow	Gray brown	Round	viny	
19	Green	Green	Purple	Inflated	Axillary	Yellow	Gray brown	Round	nonviny	
20	Green	Green	Purple	Constricted	Axillary	Yellow	Gray brown	Round	nonviny	
21	Yellowish	Yellow	Purple	Inflated	Axillary	Yellow	Gray brown	Round	viny	

Table 4.10 contd…….

22	Yellowish	Yellow	Purple	Inflated	Axillary	Yellow	White	Round	viny	P.M.
23	Green	Green	White	Inflated	Terminal	White	White	Round	viny	P.M.
24	Yellowish	Yellow	Purple	Constricted	Axillary	Yellow	White	Round	nonviny	
25	Green	Green	White	Inflated	Terminal	Yellow	White	Round	nonviny	
26	Green	Green	White	Inflated	Terminal	Yellow	White	Round	nonviny	
27	Green	Green	White	Inflated	Terminal	Yellow	White	Round	viny	
28	Yellowish	Yellow	Purple	Inflated	Axillary	Yellow	White	Round	viny	
29	Yellowish	Yellow	White	Constricted	Terminal	Yellow	Gray brown	Round	nonviny	
30	Yellowish	Yellow	Purple	Constricted	Axillary	Yellow	White	Round	viny	
31	Yellowish	Yellow	Purple	Inflated	Axillary	Yellow	Gray brown	Wrinkled	viny	
32	Yellowish	Yellow	Purple	Constricted	Axillary	Yellow	Gray brown	Wrinkled	viny	P.M.
33	Yellowish	Green	Purple	Inflated	Axillary	Yellow	White	Round	viny	
34	Green	Green	White	Constricted	Terminal	White	White	Round	nonviny	
35	Yellowish	Green	Purple	Inflated	Axillary	Yellow	Gray	Round	viny	
36	Green	Green	Purple	Inflated	Axillary	Green	Gray brown	Round	viny	
37	Yellowish	Green	Purple	Inflated	Axillary	Green	Gray brown	Round	viny	
38	Green	Green	Purple	Inflated	Axillary	Green	Gray brown	Round	nonviny	
39	Yellowish	Yellow	Purple	Inflated	Axillary	White	White	Round	viny	
40	Yellowish	Green	Purple	Constricted	Axillary	White	White	Round	viny	P.M.
41	Yellowish	Green	White	Inflated	Terminal	Green	Gray brown	Round	viny	
42	Yellowish	Yellow	Purple	Inflated	Axillary	Yellow	White	Round	viny	
43	Green	Green	Purple	Inflated	Axillary	Yellow	White	Round	viny	
44	Yellowish	Yellow	Purple	Constricted	Axillary	Yellow	Gray brown	Round	viny	
45	Yellowish	Green	Purple	Inflated	Axillary	Yellow	Gray brown	Round	viny	
46	Yellowish	Yellow	Purple	Inflated	Axillary	Green	Gray brown	Wrinkled	viny	
47	Green	Green	White	Inflated	Terminal	White	White	Round	viny	
48	Yellowish	Green	Purple	Inflated	Axillary	White	White	Round	viny	P.M.
49	Yellowish	Green	White	Inflated	Terminal	Yellow	Gray brown	Round	nonviny	
50	Yellowish	Green	White	Inflated	Terminal	Yellow	Gray brown	Wrinkled	viny	

Table 4.3 : Components of genetic variation in 50 germplasm lines of pea for various characters

Sr. No.	Characters	Range	General mean	PCV	GCV	Heritability h^2 (bs)	Genetic advance
1.	Days to flowering	45.37- 59.67	52.21	9.7681	7.6476	61.29	6.44
2.	Days to maturity	100.33-127.67	112.17	7.9637	7.006	77.41	14.2438
3.	Plant height at harvest (cm)	44.47-128.53	88.89	25.0237	24.2057	93.57	42.8761
4.	No. of branches per plant	6.47-14.53	10.39	26.0993	24.4125	87.49	4.8883
5.	No. of pods per plant	27.07-57.73	44.12	18.6377	17.0343	83.53	14.1493
6	Pod length (cm)	3.43-8.13	5.03	28.008	27.8578	16.78	1.2456
7.	No. of seeds per pod	3.20-6.47	4.65	22.0385	20.2067	84.07	1.7765
8.	100-seed weight (g)	6.0-19.53	11.44	30.8591	30.6794	98.84	7.1854
9.	Seed yield per plant (g)	10.85-41.01	22.39	30.3539	27.9476	84.77	11.8692

PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, h^2 (b.s) = Broad sense

Table 4.5 : Direct (diagonal) and indirect (above and below diagonal) path effects of different characters towards yield in pea

Character	Days to flowering	Days to maturity	Plant height at harvest (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Seed yield per plant(g)
Days to flowering	**0.00724**	-0.00506	0.00106	-0.01858	-0.28458	0.06682	0.11375	0.52343	0.404**
Days to maturity	0.00547	**-0.00670**	0.00080	-0.01318	-0.27516	0.09244	0.14147	0.53748	0.483**
Plant height at harvest (cm)	-0.00258	0.00180	**-0.00298**	0.02234	0.27290	0.02634	0.03305	-0.27333	0.078
No. of branches per plant	-0.00380	0.00249	-0.00188	**0.03541**	0.32628	0.01699	0.03075	-038078	0.025
No. of pods per plant	-0.00377	0.00338	-0.00149	0.02116	**0.54602**	-0.07665	-0.13983	-0.59560	-0.247
Pod length (cm)	0.00191	-0.00244	-0.00031	0.00237	-0.16486	**0.25386**	0.40239	0.14310	0.636**
No. of seeds per pod	0.00179	-0.00206	-0.00021	0.00236	-0.16581	0.22184	**0.46048**	0.08840	0.607**
100-seed weight (g)	0.00399	-0.00379	0.00086	-0.01420	-0.34247	0.03826	0.04287	**0.94958**	0.675**

Residual effect = 0.2290258

Table 4.4 Simple correction coefficient between 9 characters in pea

Sr. No.	Characters	Days to flowering	Days to maturity	Plant height at harvest (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Seed yield per plant(g)
1	**Days to flowering**	**1.000**	0.755**	-0.356*	-0.525**	-0.521**	0.263	0.247	0.551**	0.404**
2	**Days to maturity**		**1.000**	-0.268	-0.372**	-0.504**	0.364*	0.307*	0.566**	0.483**
3	**Plant height at harvest (cm)**			**1.000**	0.631**	0.500**	0.104	0.072	-0.288*	0.078
4	**No. of branches per plant**				**1.000**	0.598**	0.067	0.67	-0.401**	0.025
5	**No. of pods per plant**					**1.000**	-0.302*	-0.304*	-0.627**	-0.247
6	**Pod length (cm)**						**1.000**	0.874**	0.151	0.636**
7	**No. of seeds per pod**							**1.000**	0.093	0.607**
8	**100-seed weight (g)**								**1.000**	0.675**
9	**Seed yield per plant (g)**									**1.000**

*, ** Significant at 5 per cent and 1 per cent probability respectively.

Table 4.7 (b) : Average intra (diagonal) and inter (about diagonal) clusters D^2 values in 20 clusters of 50 genotypes of pea

	C 1	C 2	C 3	C 4	C 5	C 6	C 7	C 8	C 9	C 10	C 11	C 12	C 13	C 14	C 15	C 16	C 17	C 18	C 19	C 20
C 1	**51.21**	208.26	164.15	152.24	84.33	135.62	91.07	431.67	237.31	72.59	172.83	247.71	137.77	632.23	258.74	271.22	145.15	96.77	401.22	194.22
C 2		**38.15**	613.80	364.97	353.49	120.48	401.93	935.86	729.99	81.40	478.77	729.47	517.11	1215.38	100.05	643.52	114.22	179.19	1016.93	615.01
C 3			**34.39**	250.89	90.25	431.05	81.32	306.26	97.81	312.44	216.09	94.66	105.43	428.08	664.97	145.19	463.25	254.37	175..24	67.78
C 4				**43.33**	232.39	129.52	155.26	173.27	215.96	215.99	85.99	172.03	121.83	297.75	260.76	67.73	254.43	369.14	314.14	239.80
C 5					**45.58**	274.70	91.77	472.21	180.23	143.54	239.05	208.55	143.75	619.45	434.56	320.40	272.59	101.00	349.93	102.25
C 6						**33.00**	239.03	496.22	417.79	94.71	190.60	449.20	266.85	708.03	65.21	189.60	63.89	255.63	608.24	401.67
C 7							**26.65**	289.31	130.99	178.04	128.11	151.48	112.31	475.56	401.41	196.38	261.20	182.87	211.40	80.30
C 8								**10.40**	190.86	639.83	150.24	129.78	181.83	67.01	750.88	42.34	683.51	793.88	147.85	319.23
C 9									**26.58**	419.83	117.25	123.80	62.27	276.46	684.17	161.11	445.18	432.46	62.17	93.38
C 10										**45.48**	287.52	422.57	280.60	870.13	141.86	410.37	94.8	69.24	644.34	312.99
C 11											**48.24**	191.91	77.68	306.05	392.40	83.65	255.43	400.67	190.42	222.08
C 12												**48.92**	106.43	192.82	686.24	109.85	583.95	455.33	152.67	132.10
C 13													**51.67**	296.38	494.73	116.69	314.18	327.20	144.31	142.97
C 14														**52.24**	978.36	115.16	936.90	1046.43	221.11	402.58
C 15															**0.00**	478.90	96.76	351.29	891.26	573.87
C 16																**0.00**	446.56	572.62	184.83	227.81
C 17																	**0.00**	207.89	648.48	419.85
C 18																		**0.00**	676.97	299.27
C 19																			**0.00**	157.55
C 20																				**0.00**

Table 4.2 : Mean performance of 50 germplasm lines of Pea for various characters

Sr. No.	Germ-plasms	Days to flowering	Days to maturity	Plant height at harvest (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Seed yield per plant (g)
1	EC-341782	59.67	121.00	96.87	6.47	31.53	5.90	4.60	18.03	25.87
2	EC-381866	57.67	120.33	59.53	9.47	27.07	5.44	5.13	19.43	26.95
3	EC-381897	57.00	119.33	69.60	7.40	35.80	4.67	4.07	12.17	17.66
4	EC-384139	56.00	117.67	51.87	6.73	43.00	6.67	6.20	10.00	26.47
5	EC-384890	54.33	120.00	69.60	7.13	35.40	6.36	5.40	12.23	23.36
6	EC-385247	54.33	117.67	66.07	7.47	35.93	5.07	4.60	19.11	31.48
7	EC-387113	58.00	127.00	68.73	7.67	34.53	4.83	4.00	19.53	30.50
8	EC-389374	55.67	125.33	71.13	8.00	37.53	4.19	3.53	8.87	11.81
9	EC-398604	55.33	120.33	128.53	12.40	36.73	5.73	5.47	12.83	26.90
10	EC-398611	48.00	102.67	97.87	10.47	44.53	3.90	3.73	9.77	15.18
11	EC-398612	55.67	120.00	66.53	7.27	36.93	3.97	5.07	17.50	26.36
12	EC-412882	55.33	119.67	47.40	8.00	37.00	4.45	4.47	13.87	22.93
13	EC-412883	57.67	120.33	44.47	7.27	35.80	4.33	3.67	15.43	20.25
Mean		**55.74**	**119.33**	**72.16**	**8.13**	**36.29**	**5.03**	**4.61**	**14.52**	**23.51**
14	IC-207167	54.67	102.67	84.13	7.53	43.40	4.55	5.33	8.83	17.95
15	IC-208368	54.00	112.00	100.07	7.53	37.60	7.15	5.53	10.23	25.40
16	IC-208384	48.33	101.00	106.33	10.87	49.00	4.37	5.27	8.63	21.31
17	IC-208391	56.00	127.67	97.00	7.73	31.27	5.72	5.40	14.43	24.54

Table 4.2 Contd……

18	IC-212393	45.67	105.33	108.93	12.40	54.80	3.54	3.40	6.00	11.79
19	IC-242725	55.33	104.00	65.27	7.93	46.60	3.69	3.67	7.50	12.07
20	IC-242733	45.67	100.33	69.33	8.27	49.93	4.45	3.73	6.90	12.92
21	IC-243334	46.00	102.00	109.93	12.93	56.20	3.59	3.33	12.03	22.50
22	IC-267127	56.67	116.00	99.13	10.93	54.80	5.05	4.33	11.20	26.96
23	IC-267142	52.67	116.67	117.00	12.13	42.87	7.96	6.47	14.83	41.01
24	IC-267151	48.67	104.33	65.13	9.40	45.20	4.46	3.80	6.30	10.85
25	IC-267155	53.67	115.00	80.10	8.67	41.47	5.62	5.20	14.03	30.41
26	IC-267161	56.00	121.00	54.27	11.87	40.20	5.87	5.80	15.63	35.48
27	IC-267169	54.00	116.00	110.93	13.87	39.80	8.13	6.47	11.16	29.57
28	IC-267182	47.00	105.00	103.93	14.33	51.13	5.47	4.93	7.43	18.28
29	IC-268254	46.67	116.67	79.07	9.33	47.87	3.85	3.73	11.37	19.24
30	IC-268275	45.67	103.33	124.60	13.00	53.00	4.17	3.80	8.73	27.69
31	IC-268276	54.33	108.33	94.20	13.53	53.53	4.18	4.47	6.67	15.96
32	IC-279120	45.67	107.33	79.13	11.60	48.67	5.76	5.07	6.60	16.33
33	IC-296677	45.33	114.33	109.60	14.20	46.20	5.35	5.60	6.47	16.06
34	IC-310833	55.67	117.00	73.27	10.53	36.33	5.01	4.93	11.73	21.10
35	IC-310834	45.67	101.67	117.60	14.27	50.73	5.28	4.47	11.00	24.90
36	IC-332113	54.00	106.33	84.53	10.87	46.27	4.08	3.47	15.57	24.80
37	IC-332118	46.67	101.00	81.73	11.87	43.20	5.17	4.00	9.27	15.95
38	IC-347185	47.33	103.67	72.67	14.07	51.73	4.51	3.93	10.60	22.90
39	IC-356144	49.67	104.67	110.80	13.47	52.93	4.21	3.80	10.07	19.31
40	IC-356147	54.33	111.00	88.87	8.47	48.13	3.43	3.53	9.73	16.33
41	IC-356172	56.00	118.67	109.73	14.53	56.80	6.87	6.47	9.00	30.78

Table 4.2 contd……..

42	IC-356268	52.67	105.67	104.73	11.60	36.67	3.53	3.73	12.63	18.48
43	IC-356272	47.00	103.33	103.20	13.67	48.20	4.41	4.67	9.43	21.21
44	IC-356274	50.33	102.00	110.40	8.47	52.07	3.56	3.20	10.80	18.07
45	IC-356310	51.00	118.00	98.53	8.40	49.20	4.19	3.67	14.00	25.48
46	IC-356332	54.00	118.00	118.40	13.80	57.73	4.31	4.20	9.63	23.25
47	IC-356337	57.33	124.67	116.47	11.40	54.07	6.29	5.20	11.17	29.55
48	IC-356373	49.33	104.67	90.27	11.47	43.00	5.44	5.07	10.39	24.27
49	IC-356378	57.00	115.00	69.70	7.07	36.00	6.85	6.00	10.40	22.69
50	IC-381861	46.00	102.67	97.40	10.93	37.47	5.99	6.13	12.63	28.46
Mean		**48.68**	**105.01**	**105.62**	**12.65**	**51.95**	**5.03**	**4.69**	**8.36**	**21.27**
Population mean		**52.21**	**110.17**	**88.89**	**10.39**	**44.12**	**5.03**	**4.65**	**11.44**	**22.39**
S.E.		**2.59**	**3.46**	**4.60**	**0.78**	**2.72**	**2.68**	**0.33**	**0.31**	**2.16**
C.D. at 5%		**5.07**	**6.79**	**9.02**	**1.53**	**5.33**	**5.25**	**0.65**	**0.60**	**4.24**
C.V.%		**6.07**	**3.78**	**6.34**	**9.23**	**7.56**	**6.20**	**8.79**	**3.32**	**11.84**

Table 4.8 : Cluster means performance for 9 characters in pea

Cluster No.	Characters								
	Days to flowering	Days to maturity	Plant height at harvest (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Seed yield per plant (g)
I	48.22	104.67	94.28	10.40	46.61	4.38	4.17	10.04	19.00
II	52.00	107.33	71.00	8.23	44.53	4.27	4.01	7.68	13.12
III	48.47	105.93	111.99	13.63	53.16	4.36	4.09	10.43	22.23
IV	55.58	118.00	61.31	8.62	37.65	4.85	4.57	13.77	23.67
V	48.08	107.75	108.08	14.02	50.97	4.79	4.70	7.33	17.00
VI	56.11	118.11	69.63	7.20	35.73	5.96	5.16	11.60	21.23
VII	55.00	119.56	104.71	10.24	52.69	5.18	4.40	12.12	27.33
VIII	56.17	122.33	67.40	7.57	35.23	4.95	4.30	19.32	30.99
IX	54.67	118.17	119.73	13.13	38.27	6.93	5.97	12.00	28.24
X	50.00	109.17	84.00	10.03	48.40	4.60	4.30	8.16	16.33
XI	57.83	124.33	96.93	7.10	31.40	5.81	5.00	16.23	25.21
XII	50.67	105.00	78.60	12.47	49.00	4.30	3.70	13.08	23.85
XIII	49.33	104.17	101.07	11.27	37.07	4.76	4.93	12.63	23.47
XIV	56.83	120.67	56.90	10.67	33.63	5.66	5.47	17.53	31.22
XV	56.00	117.67	51.87	6.73	43.00	5.95	6.20	10.00	26.47
XVI	55.67	120.00	66.53	7.27	36.93	3.97	5.07	17.50	26.36
XVII	54.00	112.00	100.07	7.53	37.60	7.15	6.53	10.23	25.40
XVIII	45.67	105.33	108.93	12.40	54.80	3.54	3.40	6.00	11.79
XIX	52.67	116.67	117.00	12.13	42.87	7.96	6.47	14.83	41.01
XX	56.00	118.67	109.73	14.53	56.80	6.87	6.47	9.00	30.78

Table 4.7(a) Average intra (diagonal) and inter (Above) diagonal clusters D values in 20 clusters of 50 genotypes of pea

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20
C1	**7.156**	14.431	12812	12.339	9.183	11.646	9.543	20.777	15.405	8.520	13.147	15.739	11.738	25.144	16.086	16.469	12.048	9.837	20.031	13.936
C2		**6.177**	24.775	19.104	18.801	10.976	20.048	30.592	27.018	9.022	21.881	27.009	22.740	34.862	10.003	25.368	10.687	13.386	31.889	24.7899
C3			**5.864**	15.839	9.500	20.762	9.018	17.500	9.890	17.676	14.700	9.729	10.268	20.690	25.787	15.659	21.523	15.949	13.238	8.233
C4				**6.582**	15.244	11.381	12.460	13.163	14.696	14.697	9.273	13.116	11.038	17.256	16.148	8.230	15.951	19.213	17.724	15.486
C5					**6.752**	16.574	9.580	21.730	13.425	11.981	15.461	14.441	11.989	24.889	20.846	17.900	16.510	10.050	18.706	10.112
C6						**5.745**	15.460	22.276	20.440	9.732	13.806	21.194	16.336	26.609	8.075	17.018	7.993	15.988	24.663	20.042
C7							**5.162**	17.009	11.445	13.343	11.318	12.308	10.598	21.807	20.035	14.014	16.162	13.523	14.540	8.961
C8								**3.225**	13.887	25.295	12.257	11.392	13.485	8.186	27.402	6.507	26.144	28.176	12.159	17.867
C9									**5.156**	20.490	10.828	11.127	7.891	16.627	26.157	12.693	21.099	20.796	7.885	9.663
C10										**6.744**	16.956	20.556	16.751	29.498	11.911	20.258	9.725	8.231	25.384	17.692
C11											**6.946**	13.853	8.814	17.494	19.809	9.146	15.982	20.017	13.799	14.902
C12										.		**6.994**	10.317	13.886	26.196	10.481	24.165	21.338	12.356	11.494
C13													**7.188**	17.216	22.243	10.802	17.725	18.089	12.013	11.957
C14														**7.228**	31.279	10.731	30.609	21.349	14.870	20.064
C15															**0.000**	21.884	9.837	18.743	29.854	23.956
C16																**0.000**	21.132	23.930	13.595	15.93
C17																	**0.000**	14.418	25.465	20.490
C18																		**0.000**	26.019	17.299
C19																			**0.000**	12.552
C20																				**0.000**

Table 4.8 : Cluster means performance for 9 characters in pea

Cluster No.	Characters								
	Days to flowering	Days to maturity	Plant height at harvest (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100-seed weight (g)	Seed yield per plant (g)
I	48.22	104.67	94.28	10.40	46.61	4.38	4.17	10.04	19.00
II	52.00	107.33	71.00	8.23	44.53	4.27	4.01	7.68	13.12
III	48.47	105.93	111.99	13.63	53.16	4.36	4.09	10.43	22.23
IV	55.58	118.00	61.31	8.62	37.65	4.85	4.57	13.77	23.67
V	48.08	107.75	108.08	14.02	50.97	4.79	4.70	7.33	17.00
VI	56.11	118.11	69.63	7.20	35.73	5.96	5.16	11.60	21.23
VII	55.00	119.56	104.71	10.24	52.69	5.18	4.40	12.12	27.33
VIII	56.17	122.33	67.40	7.57	35.23	4.95	4.30	19.32	30.99
IX	54.67	118.17	119.73	13.13	38.27	6.93	5.97	12.00	28.24
X	50.00	109.17	84.00	10.03	48.40	4.60	4.30	8.16	16.33
XI	57.83	124.33	96.93	7.10	31.40	5.81	5.00	16.23	25.21
XII	50.67	105.00	78.60	12.47	49.00	4.30	3.70	13.08	23.85
XIII	49.33	104.17	101.07	11.27	37.07	4.76	4.93	12.63	23.47
XIV	56.83	120.67	56.90	10.67	33.63	5.66	5.47	17.53	31.22
XV	56.00	117.67	51.87	6.73	43.00	5.95	6.20	10.00	26.47
XVI	55.67	120.00	66.53	7.27	36.93	3.97	5.07	17.50	26.36
XVII	54.00	112.00	100.07	7.53	37.60	7.15	6.53	10.23	25.40
XVIII	45.67	105.33	108.93	12.40	54.80	3.54	3.40	6.00	11.79
XIX	52.67	116.67	117.00	12.13	42.87	7.96	6.47	14.83	41.01

XX	56.00	118.67	109.73	14.53	56.80	6.87	6.47	9.00	30.78