

**STUDIES ON VARIABILITY, CHARACTER ASSOCIATION
AND GENETIC DIVERGENCE IN GARDEN PEA
(*Pisum sativum* L. var. *hortense*)**



THESIS

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CERTIFICATE-I

This is to certify that the thesis entitled “**Studies on variability, character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)**” submitted for the degree of **Master of Science (Agriculture)** in the subject of **Horticulture (Vegetable Science)** to the **Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.)** is a bonafied research work carried out by **Mr. Deepak Kumar Gautam, Id. No. HF-4293/08/12** under my supervision and no part of this thesis has been submitted for any other degree.

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

Kumarganj, Faizabad
Dated: July, 2014

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CERTIFICATE-II

This is to certify that the thesis entitled “**Studies on variability, character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)**” submitted by **Mr. Deepak Kumar Gautam, Id. No. HF-4293/08/12** to the **Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.)**, in partial fulfilment of the requirement for the degree of **Master of Science (Agriculture)** in subject of **Horticulture (Vegetable Science)** has been evaluated satisfactory by external examiner and approved by student’s advisory committee after an oral examination.

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INTRODUCTION

Garden Pea (*Pisum sativum* L. var. *hortense*) belongs to family leguminosae sub family Fabaceae and is an important legume vegetable grown throughout world during cool season. It is a self pollinated crop having diploid chromosome number $2n=14$. It is most extensively cultivated in the temperate regions and restricted to cooler altitudes in the tropics and winter season in the sub tropics.

It is highly nutritious and capable of using atmospheric nitrogen. Pea has low nitrogen requirement and does not show any marked response to application of nitrogenous fertilizer. Phosphorus is however essential for growth of nitrogen-fixing organism. On poor soil as well as on soil where the crop is newly grown inoculation of the soil with bacterial culture and adequate manuring with complete fertilizer are essential to increase the yield and to improve the quality of pod.

India ranks third in area after China and USSR under pea (vegetable and pulse pea) cultivation. The total area covered by peas is 4, 22000 hectare with the production of 38, 67000 metric tonnes whereas, productivity is 8.6 metric tonnes per hectare (Anonymous, 2012).

The major growing states of pea are Uttar Pradesh, Bihar, Madhya Pradesh and Maharashtra. Uttar Pradesh is the leading producer of pea having alone about 50% of its area and production. It is also grown as summer season crop in the hills. The major area under pea cultivation is

under mid season because of its suitability in various agro-climatic zones. Fresh pod of garden pea is high nutritive containing high percentage of digestible protein along with carbohydrate, vitamins and minerals (Chaudhary, 1996). Large proportion of garden pea are processed (canned, frozen and dehydrated and pickle) for consumption. It is mostly consumed as green and fresh grains. Being a legume, it fixes atmospheric nitrogen in the roots and increases the soil fertility.

It is a rich source of essential amino acids particularly lysine and tryptophane which is low in cereals. Among the pulses, peas have the highest protein digestibility, being 93.3% as compared to 59.5% to 90.7% in other pulses. It is rich in protein, carbohydrate, vitamin A and C, calcium and phosphorus.

The main objectives in breeding pea crop are yield, regional adaptability, suitable plant type, lodging and shattering resistance disease and insect resistance, environmental stress resistance, quality and effective nitrogen fixation.

At present, the yield potential of pea for green pod as well as for the grain is very low and there exists a scope for its improvement. The environmental factor limiting the yield should be taken into account, while developing genotypes for yield. Pod and grains characteristics, which directly influence the yield and its quality, should be given due consideration. Well-filled medium size pods having better shelling percentage and wrinkled types seed are considered better quality and yielding factors being considered in breeding pea (Nath, 1976).

Garden pea being most important to growers and consumer, therefore, it is imperative pressing need to increase its productivity to fulfil the increasing demands throughout the year. The information usually needed for developing high yielding varieties in a particular species pertains to the extent of genetic variability for desirable traits in the available germplasm.

Evaluation of germplasm is the basic tool for identification of important genotypes. The great extent of natural variation available for various characters among the genotypes suggests good scope for improvement in economic traits. Large variability ensures better chance of producing new forms.

Variability parameters like genotypic and phenotypic coefficient of variations, heritability and genetic advance, and degree of association between the various characters and direct effect of yield contributing characters on total yield, is of paramount significance in formulating an appropriate breeding strategy aimed at exploiting the inherent variability of the original population. Phenotypic variability changes under different environmental conditions, while genetic variability remains unchanged and more useful to a plant breeder for exploitation in selection or hybridization.

Yield is a complex trait controlled by several yield contributing components. Mahalanobis D^2 analysis was utilized for assessment of

genetic diversity among the genotypes and the contribution of each character to the total diversity. Greater the genetic distance better are the chances of obtaining desirable hybrids or segregates after hybridization between diverse groups.

Keeping above in view, the present investigation entitled “**Studies on variability, character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)**” was under taken during Rabi 2012- 2013, with the following objectives:

1. To assess variability, heritability and genetic advance for the quantitative characters,
2. to estimate correlation co-efficient among the important economic traits,
3. to analyze the direct and indirect effects of yield components on yield by path co-efficient analysis and
4. to estimate genetic divergence among the available germplasm for yield and its component traits.

REVIEW OF LITERATURE

A brief review of literature available in garden pea with respect to various aspects of the present investigation has been presented in the chapter under following headings:

2.1 Coefficients of variation, heritability and genetic advance,

2.2 Correlation coefficients

2.3 Path coefficient analysis

2.4 Genetic divergence (D^2)

2.1 Coefficient of variation, heritability and genetic advance:

The nature and extent of variability forms the basis of crop improvement programme. Genetic variability is the raw material on which selection acts to evolve superior genotypes or varieties in plant breeding programme. The variability exploited in breeding programme is derived from the naturally occurring variants and the wild relative of crops as well as artificially developed strains and genetic stocks by human – efforts. The reservoir of variability for different characters of a plant species resulting from available natural or artificially synthesized variants or strains constitution is germplasm.

The concept of heritability is important to determining whether phenotypic differences observed among various individuals are due to genetic changes or due to the effects of environmental factors.

Heritability indicates the possibility and extent on which improvement can be brought about through selection. It is a useful measure for considering the ratio of genetic variance to the total variance and is generally represented in percentage. **Lush (1949)** defined the heritability in broad sense is a ratio of genetic variance to the total variance expressed in per cent.

The genetic gain is the product of heritability and selection differential expressed in terms of phenotypic standard deviation of that character, heritability and genetic advance both are the components of direct selection parameters. It is necessary to utilize heritability estimates in conjunction with selection differential which indicates the expected genetic gain.

Singh (1995) worked out range, mean, coefficient of variation (phenotypic, genotypic and environmental) on seven yield related traits in thirty pea genotypes. The results indicated considerable genetic variability for pod yield and other traits.

Kumaran *et al.* (1995) derived information on genetic variability from data on twenty one yield components in forty pea genotypes grown during 1993-94 at Vijayanagaram. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for number of pods per plant, weight of seeds per pod, number of branches per plant and pod yield per plant. High heritability estimates coupled with

high genetic advance as percentage of mean were observed for number of branches per plant, weight of seed per pod, number of pods per plant and pod yield per plant. These traits could be exploited for improvement through selection.

Vikas *et al.* (1996) evaluated twenty eight genotypes of pea for yield components. They found that estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for harvest index, seed yield per plant, number of pods per plant, number of seeds per pod and biological yield per plant.

Singh *et al.* (1996) studied genetic variability and yield correlations derived from data on six yield related traits in twenty eight genotypes grown during winter 1993. They found greatest variability for plant height, number of pods per plant and green pod yield per plant.

Puzio-Idzkowska (1996) observed high variability for number of pods per plant and number of seeds per plant. The multi-podded genotype (3 pods per node), Kortowska, was bred, which might become the first three-podded field pea cultivar native to Poland.

Kumar and Ojha (1997) studied thirty one strains each of tall and dwarf groups in pea and observed higher genotypic and phenotypic coefficient of variation for number of pods per plant, grain yield per plant, biological yield, partitioning index and straw yield in both the dwarf and tall groups indicating that the greater amount of the variability was among the genotypes of the tall and dwarf groups.

Tyagi *et al.* (1997) observed significant difference for all the traits in forty seven genotypes except the pod length and harvest index. The result indicated that the characters plant height, biological yield and seed yield per plant had high genotypic and phenotypic coefficients of variability.

Kumar *et al.* (1998) recorded considerable genetic variability among the thirty one dwarf and thirty one tall genotypes in relation to characters like plant height, biological yield, seed yield per plant, number of pods per plant

Ramesh *et al.* (2002) observed estimates of broad sense heritability and genetic advance for plant height, inter node length, node of the first fruit and number of pods per plant. High heritability with moderate genetic advance were observed for mean pod weight and reducing sugar content in the edible grain.

Sureja and Sharma (2000) found considerable genetic variability for pod yield and its component characters were observed. High heritability in association with high genetic advance observed for plant height, length of inter node, pod yield per plant, number of pods per plant, seed yield per plant, number of primary branches and 100-seed weight, indicating additive gene effects and emphasized the effectiveness of selection for these traits to improve economic yield.

Roy and Das (2000) evaluated thirteen lines and analysis of variance revealed significant differences among the genotype for all

characters studied. Genetic variability was higher for days to 50% flowering, plant stand, plant height and seed yield per plant.

Mahant *et al.* (2001) studied twenty four advanced lines with one check variety for variability. Data revealed that DPFPD-8 was the highest yielder followed by KPFD-59 having moderate susceptibility to powdery mildew. Similarly in the result the PCV and GCV of all traits which showed low environment influence.

Tyagi and Srivastava (2002) reported wide range of variability for plant height, pod per plant and biological yield per plant among twenty varieties of pea including Indian and exotic origin.

Kumar (2003) studied thirty two strains/varieties to assess genetic variability. The analysis of variance revealed wide range of variability for plant height, days to flowering, number of pods per plant, grain yield per plant, days to maturity and harvest index. Estimates of GCV and PCV were highest for grain yield per plant followed by number of pods per plant, number of seed per pod and 100 grain weight.

Kumar and Jain (2003) evaluated thirty-six pea genotypes and reported that the genotypic coefficient of variation was high for pod yield per plot, plant height, number of primary branches and pod weight. The highest phenotypic coefficient of variation was observed for seed yield per plant. The heritability estimate was highest for plant height.

Sharma *et al.* (2003) evaluated sixty-three pea genotypes and reported that the seed yield per plant, biological yield per plant, harvest

index, plant height, 100-seed weight, number of seeds per pod, number of pods per plant, days to 50 per cent flowering, pod length and days to maturity exhibited significant variability. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for seed yield per plant. High heritability was observed for all characters, except for days to maturity. High genetic advance along with high heritability and GCV was observed for seed yield per plant, biological yield per plant and number of pods per plant.

Kumar *et al.* (2004) evaluated heritability, genetic advance, and correlations of 12 different characters with the yield. Heritability was highest for number of pods per plant. The following characters showed positive and significant correlation: days to flowering with first pod bearing node and days to first picking; plant height with shelling percentage; pod length with green pod yield and 100-green seed weight; number of pods per plant with green pod yield and protein content of green seeds; and 100-green seed weight with green pod yield.

Kumar *et al.* (2004) found that genetic advance was highest for plant height, followed by green pod yield per plant. However, the genetic advance as a percentage of mean was maximum for green pod yield (83.6%), followed by the number of pods per plant, plant height, 100-green seed weight, shelling percentage and the protein content of edible green seeds. Genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic value, indicating the low influence of the environment and the main role of genetic factors in the expression of characters.

Singh and Dhillon (2004) noted that the pod yield per plant ranged from 9.12 to 101.45g whereas the number of pods per plant ranged from 4.36 and to 38.60. The pod weight, number of grains per pod, plant height and number of primary shoots varied from 1.03 to 5.02 g, 3.62 to 6.84, 38.35 to 256.76 cm and 1.04 to 8.92, respectively. The highest GCV (64.07) was associated with highest heritability of 94.25% resulting in a fair amount of expected genetic gain of 128.13 as percent was observed for the number of primary shoots.

Ranjan *et al.* (2006) studied the genotypic coefficient of variation (GCV) for yield and its component (days to flower, plant height, number of branches per plant, days to maturity, number of pods per plant, number of seed per pod and 100-seed weight). The genotype differed significantly for all the traits except the number of branches per plant. Most of the yield components showed high heritability values. Seed yield per plant expressed high GCV indicating the preponderance of additive gene effects.

Gupta *et al.* (2006) assessed genetic variability and heritability for 18 yield characters were assessed in 83 indigenous and exotic genotypes of garden pea and their F₁ hybrids during 2001/02 in Pantnagar, Uttaranchal, India. Analysis of variance revealed highly significant differences for all characters studied. Coefficient of variation ranged from 2.44% (days to seed maturity) to 16.93% (number of green pods per plant). Both phenotypic and genotypic coefficients of variation were

highest for green pod yield. Heritability ranged from 36.05% for total soluble solids to 99.16% for early yield per plant.

Gupta *et al.* (2006) advocated that genetic advance was highest for green pod yield per plant. High heritability coupled with high genetic advance was observed for days to first flowering nodes, plant height, number of first flowering nodes, dry matter weight per plant, green pod yield per plant and number of primary branches per plant, indicating the preponderance of additive gene effects and the potential of selection for these characters to improve garden pea yield.

Singh and Singh (2006) observed that variability was greatest for seed yield per plant followed by number of pods per plant, plant height, number of branches per plant and 100-seed weight.

Saradana *et al.* (2007) assessed genetic variability in 210 accessions of field pea germplasm assembled from diverse eco-geographic regions of the world. High germplasm variability was observed for quantitative as well as qualitative traits. Based on agro-morphological traits, 33 diverse germplasm were found for high pods per plant, high number of seed per plant. Correlation and path analysis revealed that primary branches and 100 seed weight were the most important yield component that could be used as selection indices for further improvement in pea germplasm. Grouping of germplasm and hybridization among genetically diverse Germplasm of cluster 4th (IC-

208375, (IC-212631), 3rd (EC-342007), 1th (EC-381866) would be helpful in developing new varieties and broadening their genetic base.

Chadha *et al.* (2008) found that sufficient genetic variation was observed for marketable pod yield, number of pod per plant, duration of availability of pod and grains per pod.

Kumar (2008) told that wide range of variation exhibited for plant height, days to flower, number of pods per plant, grain yield per plant, days to maturity and harvest index. Significant differences for all the characters except number of primary branches and highest GCV and PCV was recorded for grain yield per plant followed by number of pods per plant, number of seeds per pod and 100 grain weight.

Srivastava *et al.* (2009) recorded high heritability coupled with high genetic advance for number of pods per plant, plant height, length of first fruiting node and days to flowering. Moderate heritability coupled with moderate genetic advance was recorded for pod length and shelling percentage.

Chaudhary *et al.* (2010) study indicated existence of considerable amount of genetic variability for all the characters except pod breadth. Number of pods per plant, green pod yield per plant and plant height exhibited higher values of genotypic and phenotypic coefficient of variation. High estimates of heritability, genotypic coefficient of variation and genetic advance were observed for plant height, number of pods per plant and green pod yield per plant

Lal et al. (2011) evaluated thirty field pea genotypes were during *rabi* of 2009-10 for 12 quantitative traits to examine the nature and magnitude of variability, correlation and path coefficient analysis. Analysis of variance revealed that the differences among 30 genotypes were significant for all the characters. Moderate to high levels of genotypic coefficient of variability (GCV), heritability and genetic advance were observed for plant height, number of primary branches per plant, pods per plant, seeds per pod, cluster per plant, 100 seed weight, harvest index, biological yield per plant and grain yield per plant. Among all traits plant height exhibited high estimates of GCV and PCV (38.8 and 38.82) followed by biological yield (36.88 and 37.1) and harvest index (32.13 and 33.78). Broad sense heritability was high for plant height (99%) and biological yield (99%) followed by number of pods per plant (97) and cluster per plant (97), which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. Correlation and path coefficient analysis revealed that pod per plant, harvest index and biological yield but pod per plant and harvest index were the most important yield components that could be used as selection indices for further improvement in field pea.

Singh et al. (2012) carried out an experiment at Meerut, Uttar Pradesh, India, during *rabi* 2009-10, involving forty eight field pea crosses. They recorded observation on plant height, productive branches per plant, pods per plant, seeds per pod, 100-seed weight, biological yield

per plant, seed yield per plant, harvest index, days to 50% flowering and days to maturity. The phenotypic coefficient of variation and genotypic coefficient of variation were high (>25%) for plant height, productive branches per plant, pods per plant, biological yield per plant and seed yield per plant. High heritability (in narrow sense) estimates were recorded for pods per plant, seed yield per plant and biological yield per plant. High genetic advance was recorded for plant height, pods per plant, productive branches per plant, seeds per pod, biological yield per plant and seed yield per plant.

Sharma and Sharma (2013) carried out a field investigation was to estimate the genetic variability, heritability and genetic advance in the garden pea. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) in all the characters. The highest GCV was observed for the leaf area followed by number of nodules per plant. The lowest GCV was observed for total soluble solids. High heritability in association with high genetic advance observed for 100 pod weight followed by leaf area. High heritability accompanied with low genetic advance observed for days to first picking, pod diameter, pod length, number of pods per plant and number of branches per plant. Number of seeds per pod and shelling percentage were observed with moderate heritability associated with low genetic advance.

Pal and Singh (2013) evaluated and found the genotype VRP-345 with maximum plant height (173.50 cm). Days to first flower emergence

(36.90 days) days to 50% flower emergence (41.70 days), days to 1st pod set (41.80 days) and days to maturity of green pod (63.30 days) was recorded minimum in the genotype VRP-5. The number of seeds/pod was observed in genotype VRPMR-10 (8.70) and it ranged from 5.60 to 8.70. The 100-seed weight varied from 19.98 g to 28.20 g and maximum in VRP-22. Maximum shelling percentage was recorded in genotype VRP-86 (55.84%). The phenotypic variance and PCV were higher as compared to genotypic variance and GCV for all the characters. Maximum GCV and PCV were recorded for plant height followed by number of pods per plant and green pod yield/plant. The highest heritability was recorded for green pod yield/plant and days to 50 per cent flower emergence and its higher value may be attributed to additive gene action. The estimate of genetic advance showed a wide range from 0.07 to 73.38 and it was highest for green pod yield per plant.

Dar *et al.* (2013) results indicated considerable genetic variability for pod yield and other traits. Heritability estimates were generally high for all the characters. High genetic advance coupled with high heritability for pods per plant, pod width, seeds per pod and pod yield per plant indicated that selection for these traits should be effective for improving economic yield

2.2: Correlation coefficient analysis

Correlation measures the degree and direction of relationship between two or more variable. Study of character association helps breeder in fixing a selection criteria for grain yield in parental lines such that selection will be effective in isolation than correlating the correlation of phenotypic values and subjected to change in the environment. It measures the environmental deviation together with non- additive gene action. Hence, knowledge of association between different characters is highly essential for planning a sound breeding programme.

Several workers have studied the correlation coefficient in pea. A brief review of studies on the association of characters in garden pea is presented below:

Kumar *et al.* (1995) performed correlation and path-coefficient analyses for ten yield components in thirty-one tall and thirty-one dwarf genotypes. They observed that straw yield had the highest positive direct effect on yield, followed by harvest index and number of pods per plant in tall types, while number of seeds per pod showed highest positive direct effect on yield followed by number of pods per plant in dwarf types.

Golaszowski and Idzkowska (1996) reported that number of pods per plant, number of seeds per pod, number of seeds per plant and 100-seed weight have predominant positive direct effects on seed yield in edible field pea cultivar Kortowska.

Sharma and Bala (1997) reported that the selection for green pod yield should be based upon pods per plant and pod breadth. However, pod length had indirect effects on green pod yield *via* pod breadth. Significant positive association between pods per plant and plant height, shelling percentage, grains per pod, pod length and breadth were also observed by evaluating 32 genotypes.

Kumar and Ojha (1997) studied correlation for seed yield and its components. Pod length harvest index and seed yield per plant were identified as most promising trait for selection.

Tyagi *et al.* (1997) observed that seed yield per plant has positive correlation with plant height, pods per plant, biological yield and harvest index.

Kumar *et al.* (1998) reported significant positive correlation of seed yield with plant height, pod length, number of pods per plant and straw yield per plant.

Gupta *et al.* (1998) reported that days to 50 per cent flowering exhibited significant phenotypic association with pods per plant, number of seeds per plant, pods weight per plant and 100-seed weight. Number of pods per plant was positively and significantly correlated with pods weight per plant and negatively correlated with pod length, 100-seed weight and protein content. Number of seeds per pod and pod weight per plant showed significant negative association with protein content, while 100-seed weight expressed positive and significant association with protein content.

Shinde *et al.* (1998) observed that yield per plant was positively correlated with number of pods per plant, yield per hectare, weight of pod, length of pod, number of grains per pod and 100-seed weight. Yield per hectare showed positive association with weight of pod, length of pod, number of grains per pod and 100-seed weight.

Singh (1999) reported positive and significant correlation between seed yield per plant and number of pods per plant, biological yield, number of seeds per pod, 100-seed weight and harvest index.

Kumar *et al.* (1999) studied thirty-one dwarf and thirty-one tall pea genotypes and observed that yield potential in the dwarf type can be increased by selection for biological yield, pods per plant, seeds per pod and pod length. Yield potential in tall type can be improved through selection for biological yield, straw yield per plant, pods per plant and 100 seed weight.

Bhardwaj and Kohli (1999) studied fifteen genetically diverse genotypes of garden pea and observed the correlation coefficient among ten characters. Significant differences were observed for all the ten characters. Yield had significant and positive association with node number bearing first flower, days to 50 per cent flowering, shelling percentage and number of pods per plant. Path analysis indicated that number of pods per plant and shelling percentage had high direct effect on yield, showing that these characters were the main yield determinants and could be taken as an index to improve the seed yield through selection.

Roy and Das (2000) investigation revealed that the seed yield per plot had a significant and positive association with all the traits except plant stand. Days to maturity, plant height, primary branches per plant and pods per plant showed significant positive correlation with seed yield.

Mahant *et al.* (2001) observed that yield per plant exhibited positive correlation with branches per plant, pods per plant, seeds per pod and 100- seed weight.

Pratap *et al.* (2001) observed highly significant and positive correlation in both field peas and vegetable peas between days to first flower and number of nodes bearing first flower, height of node bearing the first flower plant height, numbers of pods per plant, seeds per plant, 100-seed weight and yield per plant.

Ramesh *et al.* (2002) observed a considerable amount of phenotypic coefficient of variation and genotypic coefficient of variation was observed for most of the characters such as number of pods per plant, weight of pods per plant, internode length, plant height, mean pod weight and weight of grains per pod, while the variation was low for the other characters tested

Singh *et al.* (2002) reported that seed yield per plant was positively and significantly associated with pods per plant, harvest index and primary branches per plant.

Tyagi and Srivastava (2002) reported that seed yield per plant is strongly associated with biological yield per plant, plant height, days to maturity and number of seeds per pod.

Kumar *et al.* (2003) reported that genotypic correlation was greater than corresponding phenotypic correlation. Path coefficient analysis revealed that the number of pods per plant had greater direct effect on yield per plant.

Chaudhary and Sharma (2003) evaluated twenty-eight crosses obtained from eight genotypes and reported that the genotypic correlation coefficient were higher than phenotypic correlation coefficients. Path coefficient analysis revealed that the number of grains per pod, number of pods per plant and 100-seed weight had the greatest direct effect on pod yield per plant. The greatest negative direct effects on pod yield were exhibited by number of days to 50 per cent flowering.

Arya *et al.* (2004) reported that grain yield was significantly and positively, correlated with number of nodes, height at which the first pod appears, plant height, number of primary branches per plant, pod length and 100-seed weight. These characters were positively correlated with each other also.

Singh *et al.* (2005) recorded observation for nine traits, i.e., days to flower, plant height, number of branches per plant, number of pod per plant, number of seed per pod, pod length, 100-seed weight, harvest index

and grain yield per plant. Genotypic correlation coefficients were higher than the respective phenotypic correlation coefficient, suggesting the existence of inherent association among the traits studied.

Patel *et al.* (2006) studied inter-relationships among yield and yield attributing characters and their direct and indirect effects in forty-seven divergent field pea genotypes. They reported positive correlation between seed yield per plant with number of pods per plant, number of branches per plant, pod length, days to maturity and shelling percentage at genotypic and phenotypic level. Whereas, 100-seed weight was negatively correlated with seed yield per plant. Path coefficient analysis recorded strong positive direct effect of pods per plant followed by 100-seed weight, number of branches per plant, seeds per pod and shelling percentage on seed yield per plant.

MA and Cyhan (2006) made correlation studies and showed that the pod yield was significantly and positively correlated with pods per plant and 100-seed weight.

Singh *et al.* (2008) observed that plant height; length and width of pods and 100-seed weight were associated positively and significantly with grain yield.

Rahman *et al.* (2009) recorded observation for protein, non protein methionine and total sulfur content in addition to biological value of pea cultivars and strains as per standard procedure. Content was highly significant and positive relationship between total sulfur content and methionine content.

Ghobary, (2010) determined the relationship among yield and some yield components using correlation and path analysis. In the experiment traits, i.e., vine length, number of branches per plant, pod length, number of seeds per pod, 100–seed weight and seed yield per plant were recorded. Positive and significant relationship was found among seed yield per plant and number of pods per plant, pod length, 100-seed weight and number of branches per plant. The results of path coefficient analysis indicated that numbers of pods per plant, pod length, 100-seed weight were having a strong and direct positive effect on seed yield per plant.

Singh *et al.* (2011) reported that numbers of pods per plant, plant height, number of primary branches per plant, 100 seed weight and number of clusters per plant were the major characters contributing to grain yield as these traits were significantly and positively associated with grain yield per plant. Number of pods per plant recorded highest positive direct effect on grain yield per plant via positive indirect effects of plant height and number of primary branches per plant.

Sharma and Sharma (2013) carried out a field investigation to estimate the genetic variability, heritability and genetic advance in the garden pea. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) in all the characters. The highest GCV was observed for the leaf area followed by number of nodules per plant. The lowest GCV was observed for total soluble solids.

High heritability in association with high genetic advance observed for 100 pod weight followed by leaf area. High heritability accompanied with low genetic advance observed for days to first picking, pod diameter, pod length, number of pods per plant and number of branch per plant. Number of seeds per pod and shelling percentage were observed with moderate heritability associated low genetic advance

2.3 Path coefficients analysis

Path coefficients analysis is a standardized partial regression coefficient, which splits the correlation coefficients into measures of direct and indirect effects and also measures the direct and indirect contribution of various independent variables on dependent variables. Correlation in combination with path analysis would give better insight into cause and effect relationship between different pair of characters. The works of different workers are reviewed below:

Kumar *et al.* (1995) showed that straw yield followed by harvest index and number of pods per plant in tall while number of seeds per pod followed by number of pods per plant in dwarf types showed the highest positive direct effect on yield.

Roy and Das (2000) revealed that days to 50% flower had a high positive direct effect on grain yield.

Singh *et al.* (2002) observed that pods per plant had the highest direct effect followed by harvest index on seed yield.

Arya *et al.* (2004) path analysis confirmed that the major yield components were number of nodes and height at which the first pod appears, number of primary branches per plant and 100-seed weight, although the direct effect of 100-seed weight was negative. The number of pods per plant had the greatest direct effect on seed yield followed by height at which the first pod appears, plant height, node number which the first pod appears and number of primary branches per plant

Singh *et al.* (2008) indicated that 100-seed weight followed by number of primary branches and pods per plant had high direct effect on grain yield. Most of the yield contributing traits affected yield indirectly via seed weight.

Ram *et al.* (2010) found that correlation coefficients provides the information about inter relationship among yield and its components. The information on character association may be used in the prediction of correlated response to directional selection construction of selection indices and identification of some characters which may have no value by themselves but are useful as indicators of the more important ones under consideration. Correlation and path analysis furnish information regarding the nature and magnitude of various associates and help in measurement of direct effect of one variable on other. It is most important to know the direct and indirect effect on yield component for selecting suitable genotypes for improving the yield.

2.4 Genetic divergence

Genetic diversity is an essential requirement for increasing crop productivity through breeding. Selection of diverse parent in breeding programmes help in isolation of superior recombinant using cluster analysis, such as D^2 analysis, principal component analysis and metrologlyph analysis which have shown to be useful in selecting genetically distant parent. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advance generation.

D^2 analysis is useful in identification of divergent parent for use in the hybridization programme. The D^2 analysis is only possible by replicated data. In D^2 analysis the genetic diversity is depicted by the cluster representing number of groups in which a population can be classified on the basis of D^2 statistics. A brief review of studies on genetic diversity in garden pea is presented below:

Singh (1999) study on genetic divergence (D^2 statistics) among forty-five pea genotypes from different eco-geographic regions in India over two environments indicated the existence of considerable diversity. These genotypes were grouped in to four (F_1) and nine (each E_2 and pooled) clusters. Cluster I was the largest and consisted of five (E_1), twelve (E_3) and eighteen genotypes (pooled). The genotypes included in other cluster of E_2 were four in cluster IV; three in cluster V, sixteen in

cluster VI and three in cluster VII (E_2), whereas cluster IV (E_1) and V, VI, VII (pooled) and VII and IX (E_2 and pooled) had single genotype each. The diversity among the genotypes measured by inter-cluster distance was adequate for improvement of pea by hybridization and selection. The genotypes included in the diverse clusters may be used as promising parents for hybridization for obtaining better segregants in pea.

Sureja and Sharma (2001) studied genetic divergence for sixteen quantitative traits among thirty indigenous and exotic genotypes of garden pea. Analysis of variance showed highly significant differences among genotypes for all traits. Mahanalobis D^2 analysis grouped the genotypes into four clusters, with I, II and III each comprising six genotypes and IV comprising twelve genotypes. The grouping pattern of the genotypes was random, indicating that geographical diversity of genetic divergence were unrelated.

Dixit *et al.* (2002) used fifty-three genotypes of field pea to study genetic divergence using Mahalanobis D^2 analysis. Genotypes were grouped into eleven different clusters. Plant height contributed maximum to the genetic diversity.

Singh and Singh (2003) reported genetic divergence for ten traits (number of days to 50 per cent flowering, number of days to maturity, plant height, pod length, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield, seed yield per plant and harvest index. The genotypes grouped into eleven clusters based on multivariate

analysis using Mahalanobis D^2 statistics. The highest intra cluster D^2 values were recorded for cluster IX (2.47), whereas the highest inter cluster D^2 values was observed between cluster III and IX. The genotypes include in cluster IX gave the highest seed yield per plant, biological yield, number of pods per plant, and pod length. The genotypes in cluster VIII had high 100-seed weight and average seed yield per plant. Whereas those in cluster III had the highest harvest index, average 100-seed weight and seed yield per plant.

Tiwari *et al.* (2004) evaluated 34 genotypes of pea for their genetic diversity. The genotypes were grouped into six clusters. The first cluster containing only one genotype was the most divergent. The inter-cluster distance was minimum between cluster third and fourth and was the maximum between cluster first and second. These finding suggested that there was much diversity in the population of 34 genotypes. Cluster I, II, III and IV would be amplified for hybridization programme.

Gupta and Singh (2006) studied Mahalanobis D^2 statistical analysis and grouped 83 genotypes into 27 clusters. Cluster I had the highest number of genotypes (17). Inter-cluster variation was highest between cluster VI and XXIV (2127.75) and lowest between cluster XVII and XXVII (0). Cluster XII had the highest mean for green pod yield per plant (81.6g) whereas cluster XXIV had the highest mean for earliness (89.6), number of first flowering nodes (20.4), number of days to first green pod picking (103.0) and shelling percentage (51.5%). Cluster XXII

had highest mean for pod length (9.2) and 100-green pod weight (776.9). Cluster XIX recorded the highest mean for number of seeds (9), number of green pods (20.1) and days to maturity. Early yield per plant had the highest contribution to the genetic divergence among the genotypes tested.

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

Singh and Mishra (2008) studied the genetic divergence using Mahalanobis D^2 statistic in 21 genetically diverse pea genotypes for days to flower, plant height, and pods per plant, seeds per pod, pod weight per plant and 100-seed weight. The genotypes were grouped into 6 cluster. Cluster I was the biggest with 11 genotypes followed by cluster II and III with 4 and 3 genotypes respectively. Cluster IV, V and VI were unique since they had only one genotype each. The maximum intra cluster distance was observed between cluster II and VI and was followed by cluster II and V and cluster III and VI indicating wide divergence among these cluster, which also suggested that the genetic architecture of the

genotype in one cluster differed entirely from those included in other cluster. The diversity among the genotype measuring intra-cluster distance (D value) was adequate for improvement of pea by hybridization and selection. The genotype included in the diverse cluster can be used as promising parents for hybridization programmes for obtaining high helrotic response and thus better segregates.

Katiyar and Dixit (2009) conducted study during 2006-07 to assess the genetic divergence available in field pea germplasm, based on Euclidian distance for the identification of genetically diverse and agronomically superior accessions which may generate putative transgressive segregates on hybridization. Based on the results obtained in field experiments, designed in augmented one, wide morphological divergence were obtained for all the traits under study. Principal component analysis, which transformed all the metric traits into single index of similarity, yielded 8 vector and roots. Based on first 4 principal components (which accounted for 86.51% of the total variation), non-hierarchical Euclidean cluster analysis grouped the 480 fieldpea accessions into 8 well characterized groups (based on aggregates effect of similarity in traits). There were no parallelism between genetic diversity and geographical origin of accession.

Yadav *et al.* (2009) studied the genetic divergence existing among 62 genotypes of field pea. These genotypes were evaluated for 10 characters. Cluster showing maximum intra- and inter-cluster values

suggested that genotypes included in these clusters may show high heterotic response and will produce better segregants in response to high degree of genetic divergence in the genotype.

Katore *et al.* (2010) grouped fifty germplasm lines into 20 clusters. The D2 statistics showed adequate diversity among the genotypes with D² values ranging from 8.83 to 1510.31. Based on D² values and cluster mean performance following parents have been selected for hybridization programme in order to obtain better recombinants IC-356172, IC-267142, IC-212393, IC-208368, IC-243334, IC-3 10834, IC-356144, IC-356272, IC-356332, EC-412882, EC-412883, IC-267155 and IC-3 10833. Geographic diversity is not correlated with genotypic diversity.

Cupic *et al.* (2011) observed that Characterization of the important traits of pea genotypes (yield and yield components) can facilitate the creation of breeding populations for further selection. Research work was conducted on 23 genotypes of peas with the aim of grouping and determination of holders of quantitative traits (yield and yield components) for future breeding process. Cultivar selection was done based on the cultivars presence in large scale production in South-East Europe. Field trial was conducted during two vegetation years, major quantitative traits were measured and major qualitative traits were evaluated. The resulting data were analyzed by basic statistical methods (mean and standard deviation), analysis of variance, principal component analysis and hierarchical cluster analysis. Statistically significant genetic

diversity was found for most researched traits. Most of the researched traits were under great influence of the environment, while the environment influence had least impact on the absolute grain mass. In PC analysis first two PC axes explained 79.16% of differences. The strongest association between the traits was obtained for: height of the first pod and total plant height; grain yield and the absolute mass of grains. These two groups were in opposition. The product of the hierarchical cluster analysis was five clear clusters grouped on the basis of nine quantitative traits and three morphological traits.

Srivastava *et al.* (2012) examined that selection of genetically divergence parents is an essential step in hybridization. An attempt was made to analyze the relatedness and distances among 30 field pea genotypes using 12 agro-morphological characters. Based on D^2 analysis, by using agro-morphological characters, all genotypes were grouped into six clusters. Among the six clusters, cluster VI comprised nine genotypes forming the largest cluster followed by cluster III (6 genotypes) cluster II (5 genotypes) and V (5 genotypes). The maximum intra cluster distance was observed for cluster II (570.95). Maximum inter cluster distance was observed between clusters I and VI (12652.99). Cluster I showed highest mean for seed yield per plant (15.15 g) followed by cluster IV (12.89 g), cluster V (12.88 g) and cluster II (12.08 g). Cluster I also showed high mean value for plant height (163.35 cm) and biological yield per plant (68.50 g). Among the all characters studied, plant height (69.66%) contributed maximum to the manifestation of genetic divergence.

MATERIALS AND METHODS

The present research work entitled “**Studies on variability, character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)**” was carried out during *Rabi* season 2012-13, at the Main Experiment Station, Department of Vegetable Science, N.D. University of Agriculture and Technology (Narendra Nagar), Kumarganj, Faizabad (U.P.). The materials and methods use are described in detail in the subsequent paragraphs.

3.1 Experimental site:

Geographically, Narendra Nagar, falls under humid sub-tropical climate and is located in between 24.47⁰ and 26.56⁰ N latitude and 82.12⁰ and 83.98⁰ E longitude at an altitude of 113 m above the mean sea level in the Genetic Alluvial Plains of Eastern Uttar Pradesh.

Soil type: The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorous, potash, and slightly alkaline in nature with pH 8.5. The mechanical composition of soil was 60.9 per cent, 27.8 per cent silt and 11.3 per cent clay.

3.2 Environmental conditions:

Narendra Nagar falls under humid subtropical region, receiving an annual mean rainfall about 1200 mm. The winter months are usually cool and dry but occasional light showers are also not uncommon.

The temperature during crop season varied between 34.0 (max) to 2.5 (min). The weather data recorded at meteorological observatory of university during experimentation have been given in table-3.1.

Table-3.1: Weekly average weather data for the cropping period (October 2012 to March 2013)

Month	Standard weeks	Temperature		Average R.H	Wind speed (km/ha)	Sunshine (hrs)	Rainfall
		Min.	Max.				
Oct.	40	21.8	32.3	70.7	2.0	7.9	0.00
	41	19.4	33.0	71.2	1.9	7.7	0.00
	42	18.1	32.8	69.0	1.5	8.0	0.00
	43	14.9	31.0	72.2	1.7	7.1	0.00
	44	12.7	30.4	60.4	1.2	7.4	0.00
Nov.	45	12.1	29.2	68.2	1.3	4.2	0.00
	46	11.0	28.9	71.2	1.1	5.9	0.00
	47	9.5	27.6	68.1	1.5	6.2	0.00
	48	7.8	26.1	61.8	2.4	6.9	0.00
Dec.	49	7.3	26.0	53.0	2.9	5.9	0.00
	50	9.5	26.0	72.7	1.8	3.9	0.00
	51	9.0	20.6	70.2	4.2	4.0	0.00
	52	5.1	14.8	82.5	1.6	1.2	0.00
Jan.	1	4.3	15.2	81.0	2.6	1.5	0.00
	2	2.9	18.1	73.2	2.1	2.0	0.00
	3	9.6	22.6	70.6	3.8	2.7	3.2
	4	5.0	17.3	78.6	2.0	3.2	0.00
	5	6.2	23.5	70.1	1.8	5.5	0.00
Feb.	6	7.7.0	23.4	71.4	2.7	6.5	25.9
	7	10.2	23.5	76.0	4.3	5.0	41.2
	8	11.1	24.5	75.5	2.5	5.7	15.5
	9	11.5	26.3	66.0	4.3	8.3	0.00
Mar.	10	12.9	30.6	59.7	1.8	8.7	0.00
	11	14.0	31.3	57.8	3.2	6.5	0.00
	12	14.7	33.0	54.2	4.4	7.3	0.00
	13	15.0	32.8	62.2	5.5	7.2	0.00

Source: Department of Agro- meteorology, N.D. University of Agriculture & Technology, Kumarganj, Faizabad (U.P.)

3.3 Experimental material:

The experimental material for the present investigation comprised 38 genotypes of garden pea collected from different places in India and being maintained at main experiment station in the Department of Vegetable Science, N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.). The list of genotypes is given below-

Table-3.2: List of vegetable pea genotypes used for the study and their source of origin.

S. No.	Name of genotypes	Source of origin
1	NDVP-421	N.D.U.A.&T, Faizabad
2	NDVP-422	N.D.U.A.&T, Faizabad
3	NDVP-423	N.D.U.A.&T, Faizabad
4	NDVP-424	N.D.U.A.&T, Faizabad
5	NDVP-425	N.D.U.A.&T, Faizabad
6	NDVP-426	N.D.U.A.&T, Faizabad
7	NDVP-429	N.D.U.A.&T, Faizabad
8	NDVP-430	N.D.U.A.&T, Faizabad
9	NDVP-432	N.D.U.A.&T, Faizabad
10	NDVP-433	N.D.U.A.&T, Faizabad
11	NDVP-434	N.D.U.A.&T, Faizabad
12	NDVP-437	N.D.U.A.&T, Faizabad
13	NDVP-439	N.D.U.A.&T, Faizabad
14	NDVP-440	N.D.U.A.&T, Faizabad
15	AP-3(C)	CSAUT, Kanpur
16	VRP-6 (C)	IIVR, Varanasi

17	NDVP-502	N.D.U.A.&T, Faizabad
18	NDVP-503	N.D.U.A.&T, Faizabad
19	NDVP-504	N.D.U.A.&T, Faizabad
20	NDVP-512	N.D.U.A.&T, Faizabad
21	NDVP-514	N.D.U.A.&T, Faizabad
22	NDVP-515	N.D.U.A.&T, Faizabad
23	NDVP-516	N.D.U.A.&T, Faizabad
24	NDVP-517	N.D.U.A.&T, Faizabad
25	NDVP-518	N.D.U.A.&T, Faizabad
26	NDVP-521	N.D.U.A.&T, Faizabad
27	NDVP-522	N.D.U.A.&T, Faizabad
28	NDVP-523	N.D.U.A.&T, Faizabad
29	NDVP-526	N.D.U.A.&T, Faizabad
30	NDVP-528	N.D.U.A.&T, Faizabad
31	NDVP-529	N.D.U.A.&T, Faizabad
32	NDVP-532	N.D.U.A.&T, Faizabad
33	NDVP-534	N.D.U.A.&T, Faizabad
34	Arka Ajit	IIHR, Bengalooru
35	IP-3	GBPUAT, Panthnagar
36	VP-233	VPKAS, Almora
37	PC-531(C)	PAU, Ludhiana
38	VRP-7- (C)	IIVR, Varanasi

3.4 Experimental design:

The experiment was conducted in Randomized Complete Block Design with three replications during *Rabi* season in 2012-13 to assess the performance of 38 genotypes. Each treatment consisted of five rows each with 30 replicated and plants thrice. The seed were shown on 24-10-

2012. Each entries were grown in the plot size of and 3 m x 1.5 m. The line sowing was done with the spacing of 30 cm and 10 cm born seed to seed. All the recommended agronomic package of practices and plant protection measures were followed to raise a good crop.

3.5 Observations recorded:

Observations were recorded on five randomly selected plants from each genotypes in each replications. The observations recorded on the five plants were summed up and divided by five to get mean value. The procedure is described under the respective sub-heads.

3.5.1 Days to 50% flowering:

It was recorded as number of days taken from the date of sowing to the date when first flower anthesis was absorbed in 50% plant of each and recorded in days

3.5.2 Nodes per plant

All the nodes of five tagged plant were counted separately and summed at last harvesting of the crop and mean values were worked out.

3.5.3 Internodal length (cm)

Plant height at last harvest was measured for five tagged plant averaged and divided by node per plant to get intermodal length.

3.5.4 Nodes to first flowers appearance `

Number of node at which first flower appeared was counted from the base of plant, in all the five plant of a plot. The average value was

calculated by adding all the observations on five plants of the particular plot and dividing it by five.

3.5.5 Primary branches per plant:

The branches arising from the base of plant were considered as primary branches. Their number was recorded and averaged.

3.5.6 Plant height (cm):

The height of the plant after last picking was measured in centimeters from the base of the plant to the apex of the main shoot.

3.5.7 Number of pods per plant:

Total number of pods per plant in five tagged plant were counted at the time of maturity and averaged.

3.5.8 Pod length (cm):

Pods were harvested was measured in centimeter with the help of meter scale and thus, the mean pod length was calculated.

3.5.9 Pod width (cm):

Pods were harvested count the number of pods per plant from the randomly tagged plants. Five pods were taken to measure the pod width . The width was measured in centimeter with the help of meter scale and thus, the mean width per pod was calculated.

3.5.10 Number of seeds per pod:

Five pods were randomly taken from total pods of five randomly selected plants from each germplasm. Total numbers of seeds of these pods were counted and their mean value was expressed as the number of seeds per pod.

3.5.11 Shelling (%):

Shelling percentage of ten green pods was calculated applying given formula:

$$\text{Shelling(\%)} = \frac{\text{Weight of green pod seed}}{\text{Total weight of pods}} \times 100$$

3.5.12 100-seed weight (g)

The seeds of randomly selected plants from each plot were mixed to draw a representative sample of 100-seeds which was weighed in grams.

3.5.13. Total soluble solids (⁰ Brix):

Total soluble solids (⁰ Brix) of garden pea were determined with the help of Hand refracto meter. The values were corrected at 20⁰c with the help of distilled water and mean value expressed as per cent total soluble solids.

3.5.14. Pods per cluster:

Total number of pods in a cluster was counted for each plant. It was repeated for five plants in a plot. Average has been calculated by adding all five data and dividing by five.

3.5.15. Pods weight (g)

Pods were selected randomly and weighted on a physical balance. The weight was recorded in gram and mean pod weight was calculated by dividing the total weight by the number of pods.

3.5.16. Pod yield per plant (g):

Total weight of pod up to third picking was considered as an early yield and obtained by summing up the pod weight from first to third picking and averaged.

3.6 Statistical analyses:

The experimental data was compiled by taking the mean value of the 38 genotypes of garden pea for 16 yield and its components traits from all the three replications. Then it was subjected to the following statistical analyses.

3.6.1. Analysis of variance for the design of experiment (Panse and Sukhatme, 1967).

3.6.2. Heritability and genetic advance (Burton and de Vane, 1953).

3.6.3. Genetic advance in per cent of mean (Johnson *et al.*, 1955).

3.6.4. Correlation coefficient (Al- Jibouri *et al.*, 1958).

3.6.5. Path coefficient analysis and (Dewey and Lu, 1959).

3.6.6. Genetics divergence (D^2) analysis (Mahalanobis, 1928).

3.6.1 Analysis of variance for the design of experiment

The analysis of variance for the design of experiment was carried out according to the procedure outlined by **Panse and Sukhatme** (1967).

The significance of differences among treatment means was tested by 'F' test. To test the hypothesis $H_0: t_1 = t_2 \dots t_n$, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of i^{th} entry in the j^{th} replication

μ = General mean

t_i = Effect of the i^{th} entry ($i=1, 2, \dots$)

b_j = Effect of the j^{th} replication ($j=1, 2, \dots$)

e_{ij} = Environment effect

ANOVA for the experiment:

Source of variation	Degree of freedom	Mean sum of square	F ratio
Replication	$r-1$	MSR	MSR/MSE
Treatments	$t-1$	MST	MST/MSE
Error	$(r-1)(t-1)$	MSE	
Total	$(rt-1)$		

Where,

r = Number of replications

t = Number of treatments

MSR = Mean square due to replications

MST = Mean square due to treatments

MSE = Mean square due to error

The mean square due to replications and treatments were tested against corresponding error mean square and the calculated 'F' value was compared with table value of 'F' at P=0.005 and P=0.01.

The standard error, critical difference and coefficient of variation were calculated as follows:

$$SEm(\pm) \text{ of mean} = \sqrt{\frac{MSE}{r}}$$

3.6.1.1. Critical difference:

Critical difference was calculated to find out the superiority of one variety over the other by following formula.

$$CD = \sqrt{\frac{2MSE}{r}} \times t \text{ value at 5\% and 1\% error d.f.}$$

Where,

$$SEd = \sqrt{\frac{2 \times \text{variance due to error}}{\text{no. of replication}}}$$

t = Table value of 't' distribution at error d.f. on P<0.05 and 0.01.

3.6.1.2. Coefficient of variation (C.V.):

$$CV\% = \frac{\sqrt{MSE}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = General mean

3.6.1.3. Range :

Lower and upper limits of mean values for each character were arranged to measure the range of variation for the character.

3.6.1.4. Estimation of variance:

The mean squares for error was subtracted from the mean squares due to genotypes and the difference was divided by number of replications for obtaining the genotypic variance, which was calculated according to the method suggested by Burton (1952). Environmental variance is the mean squares due to error. Phenotypic variance was calculated by adding genotypic variance and environmental variance, which was suggested by Burton and de Vane (1953).

$$\text{Environmental variance } (\sigma^2_e) = \text{M.S.E.}$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{M.S.T.} - \text{M.S.E.}}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

M.S.T. is genotypes/ varieties mean square

M.S.E. is error mean square and

r is number of replications

3.6.2. Estimation of coefficient of variation:

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following Burton and de Vane (1953).

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean } (\bar{X})} \times 100$$

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean } (\bar{X})} \times 100$$

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

3.6.3. Heritability and genetic advance:

(a) Heritability:

Heritability in broad sense (h^2_{bs}) was calculated using the formula suggested by **Burton and de Vane (1953)**.

$$H^2_{bs} = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e} \text{ or } \frac{\sigma^2 g}{\sigma^2 p}$$

$$h^2_{bs} (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

(b) Genetic advance:

Genetic advance (Ga) was estimated by the method suggested by **Johnson et al. (1955)**.

$$Ga. = \frac{\sigma^2 g}{\sigma^2 p} K. \sigma_p$$

$$= h^2 . K. \sigma_p$$

Where,

K=Selection differential at 5% selection intensity (2.06).

h^2 =Heritability

σ_p = Phenotypic standard deviation

Genetic advance in percent of mean ($\overline{Ga}$ %)

$$\overline{Ga} (\%) = \frac{\text{genetic advance}}{\overline{X}}$$

3.6.4. Correlation coefficient:

The correlations between different characters at genotypic (g) and phenotypic (p) levels were worked out between characters as suggested by **Searle** (1961).

i) Phenotypic correlation coefficient between characters X and Y

$$r_{xy(p)} = \frac{\text{Cov.}_{xy(p)}}{\sqrt{\text{Var. X (p). Var. Y (p)}}}$$

ii) Genotypic correlation between characters X and Y

$$r_{xy(g)} = \frac{\text{Cov.}_{xy(g)}}{\sqrt{\text{Var. X (g). Var. Y (g)}}}$$

Where,

r_{xy} =Correlation coefficients between X and Y.

Covariance XY=Co-variance between characters X and Y

Var.X=Variance for X character

Var.Y=Variance for Y character

The significance of phenotypic correlation coefficients was tested against (n-2) degrees of freedom at 5% and 1% probability level. Where, n is the number of germplasm on which the observations were recorded.

3.6.5. Path-coefficient analysis:

Path-coefficient analysis was carried out according to **Dewey and Lu (1959)**. Yield per plant was assumed to be dependent variable (effect) which is influenced by all the characters, the independent variable (causes), directly as well as indirectly through other characters. The variation in total yield per plant unexplained by the fifteen causes was presumed to be contributed by residual factor (x) which is uncorrelated with other factors. Path-coefficients were estimated by solving the following simultaneous equations indicating the basic relationship between correlation and path-coefficient. The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{j=1}^{15} r_{ij} P_{jy}, \text{ for } i = 1, 2, \dots, 15$$

$$r_{iy} = P_{iy} + \sum_{j=1}^{15} r_{ij} P_{jy}, \text{ for } r_y = 1.$$

The above equation can be written in the form of matrix.

$$[A]_{15 \times 1} = [B]_{15 \times 1} [C]_{15 \times 1}$$

Where,

A is column vector of correlations r_{iy}

B is the correlation matrix of r_{ij} , and

C is the column vector of direct effects, P_{iy}

Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_j P_{iy} r_{iy}$$

The r_{ij} 's i.e., $r_{1.2}$ to r_{13-14} denote correlations between all possible combination of independent characters P_{1y} to P_{15y} denote direct effect of various characters on character y.

r_{iy} = Correlation coefficient between i^{th} and y character.

p_{iy} = Direct effect of i^{th} character on Y.

3.6.6. Estimation of genetic divergence (D^2):

The genetic divergence of thirty eight genotypes of garden pea was worked out using **Mahalanobis** (1928) D^2 statistics. The sixteen quantitative characters in pea were included for these analyses.

The calculation of D^2 the values involved following steps:

- I. A set of uncorrelated linear combinations (y, s) was obtained by pivotal condensation of the common dispersion matrix of set of correlated variables (x, s). The common dispersion matrix was arranged with the help of error mean squares and mean sum of products.
- II. Using the relationship between y, s and x, s the mean values of different characters and (X_1 to X_{16} in peas) were transferred in to the mean values of a set of uncorrelated linear combinations (Y_1 to Y_{16}) in garden pea.

III. The ' D^2 ' values between i^{th} and j^{th} genotypes for k^{th} characters was calculated as under.

$$D^2 = K (Y_{it} - Y_{jt})$$

Where, $t = 1$

The K components were calculated separately and added to get D^2_{ij} .

IV. The 'K' component and ' D^2_{ij} ' for each combination were ranked in descending order of magnitude.

V. These ranks were added up for each component D^2_{ij} over combinations of i and j the rank totals were obtained.

VI. **Group constellation:** The D^2 values were arranged in an increasing order of magnitude. The grouping of the strains in to different cluster was done using Tocher's methods (Rao, 1952). The two most closely associated groups were chosen and third group was found which had the smaller average D^2 value from the first two. Similarly the fourth was chosen to have the smallest average D^2 from the first three and so on. The D^2 value did not fit with the former group and was, therefore, taken as another cluster.

VII. **Intra and inter-cluster distance:** The intra-cluster D^2 was calculated as the sum of $n(n-1)/2$ genotypes within a cluster divided by total number of combinations. All possible D^2 values between the groups of two clusters were added and then divided by $n_1 \times n_2$ for computing inter-cluster distance.

Where,

n_1 and n_2 = the number of genotypes in two clusters.

VIII.Cluster mean: The cluster mean for the particular character is the summation of mean values of the strains included in a cluster divided by number of strains in the cluster.

IX.Testing of the significance of D^2 values: The D^2 values obtained for a pair of population were taken as the calculated value of χ^2 and is tested against tabulated value of χ for 'P' degree of freedom.

Where,

P = number of characters considered

X.Per cent contribution of each character towards genetic divergence was calculated as below:

$$\text{Percentage contribution of character X} = \frac{N}{C} \times 100$$

Where,

N= Number of genotype combinations which was ranked first for character X.

C= All possible combinations of genotypes involved in D^2 analysis.

EXPERIMENTAL FINDINGS

The results obtained in respect of the experiment conducted under present investigation have been described in this chapter under following heads:

- 4.1 Analysis of variance,
- 4.2 mean performance of genotypes,
- 4.3 coefficients of variations,
- 4.4 heritability and genetic advance in per cent of mean
- 4.5 correlation coefficients,
- 4.6 path coefficients analysis and
- 4.7 genetic divergence (D^2).

4.1 Analysis of variance:

The data recorded on sixteen traits from the experiment were subjected to analysis of variance. Mean squares due to genotypes were highly significant for all the sixteen traits (Table 4.1), indicating therefore significant differences among the genotypes with respect to the traits under study.

4.2 Mean performance of genotypes-:

The mean performance, general means and range of 38 entries for sixteen characters had been given in table 4.2.

4.2.1 Days to 50% flowering-:

Days to 50 per cent flowering ranged from 40.00 days (NDVP-429, NDVP-430, NDVP-432, and NDVP-434) to 69.33days (NDVP-532).

Table-4.1 Analysis of variance (mean squares) for sixteen quantitative characters in garden pea.

S. No	Characters	Source of variation		
		Replications	Treatments	Error
	d.f.	2	37	74
1.	Days to 50% flowering	2.64	255.09 **	2.90
2.	Nodes per plant	0.71	27.51 **	0.37
3.	Internodal length (cm)	0.47	1.84 **	0.17
4.	Nodes to first flower appearance	0.082	13.75**	0.19
5.	Primary branches per plant	0.026	0.96**	0.084
6.	Plant height (cm)	0.68	1154.40**	16.06
7.	Pods per plant	0.71	29.50**	0.30
8.	Pod length (cm)	0.09	1.84**	0.10
9.	Pod width (cm)	0.00	0.05**	0.010
10.	Seeds per pod	0.051	2.22**	0.038
11.	Shelling (%)	14.43	39.05**	5.61
12.	100 seed weight (g)	0.42	27.4**	0.92
13.	T.S.S. (⁰ Brix)	0.18	2.46**	0.15
14.	Pods per cluster	0.00	0.32**	0.08
15.	Pod weight(g)	0.04	3.25**	0.11
16.	Pod yield per plant (g)	5.5	151.40**	2.75

*, ** - significant at 5 % and 1 % probability level, respectively.

Experimental Findings

Table- 4.2 Mean performance of thirty eight genotypes for sixteen characters in garden pea.

S. No	Characters Genotypes	Days to 50% flowering	Nodes per plant	Internodal length (cm)	Nodes to first flower appearance	Primary branches per plant	Plant height (cm)	Pods per plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Shelling (%)	100 seed weight (g)	T.S.S. (° Brix)	Pods per cluster	Pod weight (g)	Pod Yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Early season types																	
1.	NDVP-421	41.66	12.00	7.66	8.66	2.49	67.93	12.10	7.90	1.92	5.73	32.66	31.33	11.40	1.00	6.63	31.26
2.	NDVP-422	41.33	12.33	7.90	8.60	2.56	60.20	10.93	8.20	1.92	6.70	45.13	34.00	12.53	1.00	5.36	29.54
3.	NDVP-423	43.00	12.6	7.50	7.60	2.60	58.0	11.73	8.33	2.28	7.90	45.33	34.00	10.46	1.00	6.44	24.78
4.	NDVP-424	52.33	11.86	6.66	9.46	2.10	71.63	11.56	9.30	1.91	7.16	45.66	32.00	12.53	1.00	5.53	33.71
5.	NDVP-425	45.00	11.60	7.33	9.53	1.73	61.73	11.13	9.23	1.91	6.30	45.00	36.33	12.34	1.00	3.40	28.07
6.	NDVP-426	42.33	12.46	7.34	7.70	2.60	67.33	10.83	8.20	1.96	6.93	45.33	32.00	10.64	1.20	6.70	24.00
7.	NDVP-429	40.00	11.86	7.66	8.36	2.56	54.86	6.90	9.32	2.02	6.66	46.00	30.00	11.72	1.06	5.09	29.21
8.	NDVP-430	40.00	9.80	8.14	9.00	3.00	55.26	13.43	7.72	1.92	5.93	44.33	29.00	12.46	1.06	4.90	31.59
9.	NDVP-432	40.00	12.60	6.83	8.46	2.26	42.20	8.03	7.86	2.01	5.93	45.33	33.00	12.02	1.26	5.04	23.54
10.	NDVP-433	61.66	11.53	6.94	9.53	2.43	74.69	11.03	8.14	2.26	6.36	35.33	30.33	9.66	1.20	4.90	22.76
11.	NDVP-434	40.00	11.73	6.36	7.50	2.50	35.26	10.73	8.11	1.98	5.90	42.33	32.33	12.80	1.13	4.13	30.02
12.	NDVP-437	41.33	11.60	6.36	8.70	2.93	58.66	13.13	9.79	1.86	6.33	46.00	37.00	12.76	1.13	5.55	29.24
13.	NDVP-439	44.33	12.40	6.03	7.60	2.63	56.53	13.90	8.40	2.02	7.36	42.33	25.66	11.53	1.13	6.16	24.42
14.	NDVP-440	44.33	12.73	6.16	9.26	3.06	59.73	10.70	9.58	1.84	7.20	43.33	41.00	10.53	1.40	6.09	25.69
15.	AP-3(C)	45.00	12.06	7.86	8.50	1.90	61.26	7.86	8.26	2.07	6.56	45.00	36.00	12.66	1.00	6.14	29.31
16.	VRP-6 (C)	43.66	11.70	7.83	9.53	2.50	53.46	9.50	8.33	2.30	6.00	47.66	35.00	13.42	1.00	3.50	30.00
Mid season types																	
17.	NDVP-502	53.66	18.30	8.66	13.53	4.13	62.93	11.53	9.36	1.86	6.56	48.00	27.00	11.80	1.93	3.56	40.61
18.	NDVP-503	53.66	18.06	6.40	13.53	2.83	111.06	19.30	8.33	1.90	6.23	46.00	29.00	11.94	1.33	3.59	41.81
19.	NDVP-504	44.00	16.93	6.76	13.26	2.76	97.59	12.46	7.66	1.90	6.63	47.33	32.00	12.73	1.73	4.46	35.38
20.	NDVP-512	52.33	16.13	7.06	11.53	3.40	67.00	13.13	8.63	1.96	7.30	45.33	28.66	13.00	1.33	3.57	41.09
21.	NDVP-514	48.16	16.53	6.91	12.53	3.08	82.29	12.80	8.15	1.93	6.96	46.33	29.00	12.86	1.53	4.02	38.24

Contd.....

Experimental Findings

S. No	Characters Genotypes	Days to 50% flowering	Nodes per plant	Internodal length (cm)	Nodes to first flower appearance	Primary branches per plant	Plant height (cm)	Pods per plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Shelling (%)	100 seed weight (g)	T.S.S. (° Brix)	Pods per cluster	Pod weight (g)	Pod Yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
22.	NDVP-515	50.66	18.20	7.40	12.26	2.98	72.60	10.60	9.30	1.83	6.26	40.00	32.00	13.93	1.66	3.95	35.90
23.	NDVP-516	59.00	16.73	7.13	13.60	3.36	94.13	13.80	8.92	1.86	6.43	44.66	31.00	13.00	1.66	4.69	41.71
24.	NDVP-517	56.33	18.73	7.20	12.26	2.40	84.46	12.36	8.03	1.87	5.63	45.00	33.00	13.49	1.80	4.86	47.71
25.	NDVP-518	64.33	17.80	8.73	12.53	1.76	80.53	20.30	7.90	1.80	5.10	41.66	33.00	12.73	1.73	4.09	39.12
26.	NDVP-521	55.00	18.50	7.90	13.30	2.40	84.98	14.10	7.76	1.78	4.70	38.00	27.33	11.54	1.33	4.28	46.76
27.	NDVP-522	67.33	20.40	6.36	12.63	2.63	93.53	12.00	7.33	1.71	5.46	40.66	37.00	13.06	1.46	5.29	45.33
28.	NDVP-523	62.33	19.73	6.10	12.33	4.00	100.26	10.06	10.53	1.94	8.46	44.00	32.66	12.80	1.20	7.07	22.62
29.	NDVP-526	52.66	17.50	6.20	12.50	2.70	82.26	15.20	9.90	1.96	8.03	47.66	31.66	13.40	2.00	5.66	25.71
30.	NDVP-528	57.5	18.30	6.15	13.76	3.35	91.26	12.63	10.21	1.95	8.45	45.83	34.00	13.10	1.60	6.37	24.17
31.	NDVP-529	62.00	15.46	7.86	12.56	3.33	83.78	15.40	8.25	1.75	6.46	48.66	30.66	13.00	1.00	5.95	37.45
32.	NDVP-532	69.33	17.26	6.90	12.60	2.40	76.20	12.40	9.30	1.94	5.83	43.00	30.00	12.26	1.73	5.65	35.40
33.	NDVP-534	67.66	15.60	6.93	13.46	2.66	94.53	13.20	8.56	2.00	6.46	48.66	33.66	12.50	1.66	4.61	38.88
34.	Arka Ajit	66.33	16.40	6.23	12.00	1.60	96.00	15.86	8.54	1.82	6.00	47.83	31.00	12.23	1.80	4.78	27.62
35.	IP-3	61.00	18.33	5.73	12.26	2.40	120.26	7.83	7.23	1.80	5.60	49.16	32.00	13.00	1.93	3.37	37.30
36.	VP233	59.00	17.13	5.61	11.73	2.26	110.33	17.56	8.33	1.90	6.23	39.00	32.33	12.33	1.53	4.88	36.83
37.	PC-531(C)	49.33	18.00	7.23	12.46	3.26	86.26	13.40	8.66	2.03	6.43	46.00	30.00	12.63	1.53	4.43	34.26
38.	VRP-7- (C)	54.66	17.33	6.30	12.60	3.50	91.53	20.50	8.69	1.88	6.00	46.00	30.00	12.30	1.86	3.88	37.42
	Mean	51.90	15.22	7.01	10.98	2.71	76.38	12.63	8.58	1.93	6.49	44.35	32.07	12.34	1.39	4.96	33.12
	C.V.	3.28	4.02	5.93	4.06	10.69	5.20	4.36	3.77	5.20	3.01	5.34	2.99	3.18	20.79	6.76	5.01
	S.E.	0.98	0.35	0.20	0.25	0.16	6.52	0.31	0.18	0.05	0.11	1.36	0.55	0.22	0.16	0.19	0.95
	CD 5 %	2.77	0.99	0.67	0.72	0.47	8.65	0.89	0.52	0.16	0.31	3.85	1.56	0.64	0.47	0.54	2.69
	Range	40.00	9.80	5.61	7.50	1.60	35.26	6.90	7.23	1.71	4.70	32.66	25.66	9.66	1.00	3.37	22.62
		69.33	20.40	8.73	13.76	4.13	120.26	20.50	10.53	2.30	8.86	49.16	41.00	13.93	2.00	7.07	47.71

The grand mean for days to 50 per cent flowering was 51.90 cm. Out of 16 genotypes of early group only four genotypes NDVP-429, NDVP-430, NDVP-432 and NDVP-434 were found significant (40 days) for earliness over the best check VRP-6 (43.66 days). While among mid season only one genotype NDVP-504 was found earlier (44.00 days) than the best check PC-531 (49.33 days) for days to 50% flowering.

4.2.2 Nodes per plant-:

The nodes per plant varied from 9.80 (NDVP-430) to 20.40 (NDVP-522). The grand mean for nodes per plant was 15.22 cm. Only one genotype NDVP-423 (12.60) was found significant for nodes per plant than the best check AP-3 (12.06) in early type. While, among mid season group seven genotypes namely NDVP-504 (16.93), NDVP-516(16.73), NDVP-514(16.53), Arka Ajit (16.40), NDVP-512 (16.13), NDVP-534(15.60) and NDVP-529 (15.46) were found significant for higher nodes per plant than the best check PC-531 (18.00).

4.2.3 Internodal length (cm)-:

The internodal length varied from 5.61cm (VP-233) to 8.73cm (NDVP-518). The grand mean for internodal length was 7.01 cm. Among early genotypes seven genotypes viz NDVP-433 (6.94 cm), NDVP-432 (6.83 cm), NDVP-424 (6.66 cm), NDVP-4434 (6.36 cm), NDVP-437 (6.36 cm), NDVP-440 (6.16 cm) and NDVP-439 (6.03 cm) were found significant for shorter internodal length than the best check AP-3 (7.86 cm) while, among mid season group six genotypes namely NDVP-503

(6.40 cm), NDVP-522 (6.36 cm), Arka Ajit (6.23 cm), NDVP-526 (6.20 cm), NDVP-428 (6.15 cm), and NDVP-523 (6.10 cm) were found significant for smaller internodal length than the best check PC-531 (7.23 cm).

4.2.4 Nodes to first flower appearance:-

Nodes to first flower appearance varied from 7.50 (NDVP-434) to 13.76 (NDVP-528). The grand mean for nodes to first flower appearance was 10.98. Out of 16 genotypes all the genotypes were found significant for lower nodes to first flower appearance than the best check VRP-6 (9.53) except NDVP-424 (9.46), 9.53 (NDVP-425 and NDVP-433) NDVP-440 (9.26) and NDVP-430 (9.00) in early type. While among mid season type only one genotype VP-233 (11.73) was found significant for lesser nodes to first flower appearance than the best check PC-531 (12.46).

4.2.5 Primary branches per plant:-

The primary branches per plant ranged from 1.60 (Arka Ajit) to 4.13 (NDVP-502). Out of 16 genotypes of early groups two genotypes NDVP-440 (3.06) and NDVP-430 (3.00) were found significant for higher primary branches per plant than the best check VRP-6 (2.50). Whereas in mid season groups only two genotypes namely NDVP- 502 (4.13) NDVP-523 (4.00) were found significant for primary branches per plant than the best check VRP-7 (3.50).

4.2.6 Plant height (cm):-

Plant height ranged from 35.26 cm (NDVP-434) to 120.26 cm (IP-3). Out of 16 genotypes of early groups genotypes NDVP-433 (74.69 cm) and NDVP-424 (71.63cm) were found significant for the taller plant height over the best check AP-3 (61.26cm) while among mid season group four genotypes viz. IP-3 (120.26cm), NDVP-503 (111.06cm) and VP-233 (110.33cm) were found significant for larger plant height than the best check VRP-7 (91.53).

4.2.7 Pods per plant:-

Pods per plant ranged from 6.90 (NDVP-426) to 20.50 (VRP-7). Out of 16 genotypes all the genotypes were found significant for higher pods per plant than the best check VRP-7 (20.50) except NDVP-432(8.03) and NDVP- (6.90) while among mid season group none of the genotypes were found significant for higher pods per plant than the over best check VRP-7 (20.50).

4.2.8 Pod length (cm):-

Pod length of the genotypes ranged from 7.23 cm (IP-3) to 10.53 cm (NDVP-523). Five genotypes NDVP-437 (9.79cm), NDVP-440 (9.58) , NDVP-429 (9.32cm) , NDVP-424 (9.30cm) and NDVP-425 (9.23 cm) were found significant for longer pod length than the best check VRP-6 (8.33 cm) in case of early group. Whereas in mid season groups six genotypes viz. NDVP-523 (10.53cm), NDVP-528 (10.21cm), NDVP-

526 (9.90cm), NDVP- (9.36) NDVP-515 (9.30cm) and NDVP-532 (9.30cm) were found significant for longer pod length than the best check VRP-7 (8.69cm).

4.2.9 Pod width (cm):-

Pod width (cm) of genotypes ranged from 1.71 cm (NDVP-522) to 2.23 (VRP-7). None of the genotypes were found significant for wider pod width in either of the groups than their respective best checks.

4.2.10 Seeds per pod:-

Seeds per pod ranged from 4.70 seeds (NDVP-521) to 8.86 seeds (NDVP-523). Out of 16 genotypes four genotypes NDVP-423 (7.90 seeds), NDVP-439 (7.36 seeds), NDVP-440 (7.20) and NDVP-424 (7.16 seeds) were found significant for more number of seeds per pods than the best check AP-3 (6.56) in early group, while genotypes NDVP-523 (8.46 seeds) NDVP-528 (8.45 seeds) and NDVP-526 (8.03 seeds) were found significant against best check PC-531(6.43 seeds) in mid season group for this traits.

4.2.11 Shelling (%):-

The shelling per cent varied from 32.66 % (NDVP-421) to 49.16% (IP-3). None of the genotypes in either of the groups were found significant for higher shelling % than the best checks.

4.2.12 100 seed weight (g):-

100 seed weight at optimum edible maturity stage ranged from 25.26g (NDVP-439) to 41.00g (NDVP-440). Only one genotypes

NDVP-440 (41.00g) was found significant for higher 100 seed weight than the best check AP-3 (36.00g) in early group. Whereas none of the genotype was found significant for higher 100 seed weight than the best check 30.00 (PC-531 and VRP-7) in mid season group.

4.2.13 Total soluble solids (⁰ Brix)-:

Total soluble solids (⁰ Brix) varied from 9.66 (NDVP-433) to 13.96 (NDVP-515). Out of 16 genotypes none of the genotypes found significant for TSS over best check 13.42 (VRP-6) in early group. While two genotypes NDVP-515 (13.93) and NDVP-517 (13.49) were found significant against best check PC-531(12.63) in mid season group for high TSS.

4.2.14 Pods per cluster-:

The pods per cluster varied from 1.0 (AP-3 and VRP-6) to 2.0 (NDVP-526). Out of 16 genotypes none of the genotypes were found significant for more pods per cluster than the best check 1.00 (AP-3 and VRP-6) in early group. Whereas, none of the genotypes were found significant for higher pods per cluster than the best check VRP-7(1.86) in mid season group.

4.2.15 Pod weight (g)-:

Pod weight at picking stage ranged from 3.37g (IP-3) to 7.07g (NDVP-523). In case of early group none of the genotype was found significant for heavier pod weight than the best check 6.14 (AP-3). While

among mid season groups four genotypes NDVP-523 (7.07g), NDVP-528 (6.37g), NDVP-526 (5.66g) and NDVP-522 (5.29g) were found significant for heavier pod weight than the best check PC-531 (4.43g).

4.2.16 Pod yield per plant (g):-

The pod yield per plant ranged from 22.62g (NDVP-423) to 47.71g (NDVP-517). Among early groups only one genotype NDVP-424 (33.71g) was found significant for higher pod yield per plant over the best check 30.00g (VRP-6). While among mid season type seven genotypes namely NDVP-517 (47.71g), NDVP-521 (46.76g), NDVP-522 (45.33g), NDVP-504 (41.81g), NDVP-516 (41.71g), NDVP-502 (40.71g) and NDVP-512 (41.09g) were found significant for higher pod yield per plant than the best check VRP-7 (37.42g).

4.3 Coefficient of variation:-

The estimates of genotypic and phenotypic coefficients of variation for sixteen characters of garden pea germplasm had been presented in table 4.3.

The estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters. The highest phenotypic as well as genotypic coefficients of variation were observed in case of pods per cluster followed by plant height, pods per plant, primary branches per plant, pod yield per plant and pod weight, nodes per plant and nodes to first flower appearance.

Table-4.3 Estimates of range, grand mean, phenotypic (PCV), genotypic (GCV), and environmental (ECV) coefficient of variation, heritability in broad sense, genetic advance(Ga) and Ga (in per cent of mean) for sixteen characters in garden pea.

S. No.	Characters	Range		Grand mean	PCV (%)	GCV (%)	ECV (%)	Heritability broad sense (%) (h^2_{bs})	Genetic advance (Ga)	Genetic advance in per cent of mean (Ga)
		Lowest	Highest							
1.	Days to 50% flowering	40.0	69.33	51.90	17.96	17.66	3.28	96.70	23.79	45.85
2.	Nodes per plant	9.80	20.40	15.22	20.15	19.75	4.02	96.00	7.78	51.09
3.	Internodal length (cm.)	5.61	8.73	7.01	12.18	10.64	5.93	76.20	1.72	24.53
4.	Nodes to first flower appearance	7.50	13.76	10.98	19.77	19.35	4.06	95.80	5.49	50.01
5.	Primary branches per plant	1.60	4.13	2.71	22.70	20.03	10.69	77.80	1.26	46.65
6.	Plant height (cm)	35.26	120.26	7638	26.03	25.50	5.24	95.90	50.37	65.94
7.	Pods per plant	6.90	20.50	12.63	25.08	24.70	4.33	97.00	8.11	64.23
8.	Pod length (cm)	7.23	10.53	8.58	9.63	8.86	3.77	84.60	1.84	21.52
9.	Pod width (cm)	1.71	2.30	1.93	7.91	5.96	5.20	56.70	0.23	11.85
10.	Seeds per pod	4.70	8.86	6.49	13.49	13.15	3.02	95.00	2.19	33.84
11.	Shelling per cent	32.66	49.16	44.35	9.23	7.52	5.34	66.50	7.18	16.20
12.	100 seed weight (g)	25.66	41.00	32.07	9.73	9.26	2.99	90.50	7.46	23.26
13.	T.S.S. ($^{\circ}$ Brix)	9.66	13.93	12.34	7.79	7.11	3.18	83.30	2.11	17.12
14.	Pods per cluster	1.00	2.00	1.39	28.99	20.20	20.79	48.60	0.51	37.17
15.	Pod weight (g)	3.37	7.07	4.96	21.67	20.59	6.76	90.03	2.56	51.66
16.	Pod yield per plant (g)	22.62	47.71	33.12	21.83	21.25	5.01	94.70	18.08	54.61

4.4 Heritability and Genetic Advance:-

Estimates of heritability (broad sense) and genetic advance for different characters has been presented in table 4.3

The heritability in broad sense ranged from 48.60 per cent in case of yield per plant to 97.00 per cent for TSS. High estimates of heritability ($>75\%$) were recorded for 13 characters viz. pods per plant (97%), days to 50% flowering (96.70%), nodes per plant (96%), plant height (95.90%), nodes to first flower appearance (95.8%), seeds per pod (95%), pod yield per plant (94.7%), 100 seed weight (90.50%), pod weight (90.03%), pod length (84.60%), TSS (83.30%), primary branches per plant (77.80%), and internodal length (76.20%). However, moderate heritability ($>50\%$ and $<75\%$) was observed for shelling per cent (66.50%) followed by pod width (56.70%) and lower heritability ($<50\%$) was estimated for pods per cluster (48.60%). Highest value of genetic advance in per cent of mean was shown by plant height (65.94). While pods per plant exhibited lowest value (11.85) for this parameter. The characters which observed very high estimates of genetic advance were plant height (65.94), pods per plant (64.23), pod yield per plant (54.61) pod weight (51.66), nodes per plant (51.09), nodes to first flower appearance (50.01), primary branches per plant (46.65), days to 50% flowering (45.85), pods per cluster (37.17), seeds per pod (33.84), internodal length (24.53), 100 seed weight (23.26), and length of pod (21.52). The moderate estimates for genetic advance were found for TSS (17.12) and shelling per cent (16.20). Lowest genetic advance in per cent of mean was estimated for width of pod (11.85).

4.5 Correlation coefficient:-

The phenotypic and genotypic correlation coefficient computed among the sixteen characters under study had been presented in table 4.4 and 4.5.

In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, suggesting therefore, a strong inherent relationship in different pairs of characters in garden pea genotypes. The most important trait pod yield per plant had exhibited highly significant and positive phenotypic correlation with nodes to first flower appearance (0.604), nodes per plant (0.599), pod width (0.444), plant height (0.432), days to 50% flowering (0.398), pods per plant (0.367), TSS (0.362) and pod per cluster (0.344) while, seeds per pod (-0.537), pod weight (-0.513), and pod length (-0.339) exhibited significant and negative correlation with pod yield per plant. Most important positive and significant association was estimated between nodes to first flower appearance and pod yield per plant. Nodes to first flower appearance was also found to had significant and positive correlation with days to 50 per cent flowering (0.709), nodes per plant (0.855), primary branches per plant (0.326), plant height (0.751), pods per plant (0.451), TSS (0.412), pods per cluster (0.596) while, it showed negative significant correlation with pod width (-0.398) and pod weight (-0.352). This showed that traits having significant positive correlation with pod yield per plant also showed significant and positive correlations with some other traits as well.

Experimental Findings

Table- 4.4: Estimates of phenotypic correlation coefficients between sixteen characters in garden pea

Characters	Nodes per plant	Internodal length(cm)	Nodes to first flower appearance	Primary branches per plant	Plant height (cm)	Pods per plant	Pod length (cm)	Pod width (cm)	Seed per pod	Shelling (%)	100 seed weight (g)	T.S.S. (⁰ Brix)	Pods per cluster	Pod weight (g)	Pod Yield per plant (g)
Days to 50% flowering	0.667**	-0.192	0.709**	0.013	0.691**	0.375*	0.041	-0.305*	-0.126	-0.010	-0.099	0.179	0.452**	-0.095	0.398*
Node per/plant		-0.199	0.855**	0.300	0.739**	0.379*	0.077	-0.426**	-0.044	0.085	-0.162	0.384*	0.605**	-0.211	0.559**
Internodal length(cm)			-0.085	-0.035	-0.375*	-0.077	-0.200	0.090	-0.270	-0.035	-0.121	-0.071	-0.180	-0.137	0.182
Nodes to first flower appearance				0.326*	0.751**	0.451**	0.102	-0.398*	-0.085	0.181	-0.208	0.412*	0.596**	-0.352*	0.604**
Primary branches per plant					0.118	0.044	0.347*	-0.066	0.418**	0.163	-0.209	0.124	0.182	0.046	0.098
Plant height (cm)						0.431**	-0.048	-0.321*	-0.028	0.090	-0.107	0.227	0.487**	-0.136	0.432**
Pods per plant							-0.045	-0.275	-0.170	-0.037	-0.262	0.065	0.286	-0.184	0.367*
Pod length (cm)								0.067	0.616**	0.151	0.147	0.093	0.080	0.264	-0.339*
Pod width (cm)									0.278	-0.008	0.009	-0.281	-0.256	0.134	0.444**
Seeds per pod										0.250	0.073	-0.035	-0.071	0.483	-0.537**
Shelling (%)											0.053	0.294	0.099	-0.188	-0.0009
100 seed weight (g)												0.060	-0.147	0.217	-0.247
T.S.S. (⁰ Brix)													0.248	-0.290	0.362*
Pods per cluster														-0.301	0.344*
Pod weight (g)															-0.513**

*, ** - significant at 5 % and 1 % probability level, respectively.

Experimental Findings

Table- 4.5: Estimates of genotypic correlation coefficients between sixteen characters in garden pea germplasm

Characters	Nodes per plant	Internodal length(cm)	Nodes to first flower appearance	Primary branches per plant	Plant height (cm)	Pods per plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Shelling (%)	100 seed weight (g)	T.S.S. (⁰ Brix)	Pods per cluster	Pod weight (g)	Pod Yield per plant (g)
Days to 50% flowering	0.7020	-0.2159	0.7340	0.0310	0.7164	0.3924	0.0519	-0.3760	-0.1321	0.0054	-0.1141	0.1971	0.6420	-0.0868	0.4251
Nodes per plant		-0.2286	0.9029	0.3514	0.7647	0.3858	0.0728	-0.5569	-0.0427	0.1071	-0.1753	0.4436	0.8761	-0.2314	0.5885
Internodal length(cm)			-0.1037	-0.0196	-0.4297	-0.0938	-0.2150	0.1034	-0.3287	-0.0744	-0.1619	-0.0442	-0.3028	-0.1395	0.2131
Nodes to first flower appearance				0.3667	0.7910	0.4712	0.1071	-0.5347	-0.0910	0.2138	-0.2211	0.4625	0.8692	-0.3664	0.6467
Primary branches per plant					0.1158	0.0658	0.4318	-0.1114	0.4624	0.2331	-0.2315	0.0914	0.1658	0.0533	0.1129
Plant height (cm)						0.4490	-0.0664	-0.4697	-0.0355	0.1116	-0.1114	0.2414	0.6596	-0.1494	0.4430
Pods per plant							-0.0561	-0.3758	-0.1712	-0.0556	-0.2859	0.0768	0.4174	-0.1949	0.3724
Pod length (cm)								0.0190	0.6870	0.2188	0.1706	0.1060	0.0544	0.3030	-3867
Pod width (cm)									0.3610	-0.0267	0.0426	-0.4122	-0.5170	0.1029	-0.4944
Seeds per pod										0.3115	0.0837	-0.0692	-0.1664	0.5244	-0.5760
Shelling (%)											0.0741	0.4200	0.3529	-0.2105	.0077
100 seed weight (g)												0.0832	-0.1766	0.2406	-0.2544
T.S.S. (⁰ Brix)													0.3677	-0.3294	0.4141
Pods per cluster														-0.4018	0.4704
Pod weight (g)															-0.5514

*, ** - significant at 5 % and 1 % probability level, respectively.

Nodes per plant showed significant positive correlation with nodes to first flower appearance (0.855), plant height (0.739), days to 50 per cent flowering (0.667), pod per cluster (0.605) and TSS while highly significant and negative correlation with pod width (-0.426). Internodal length showed significant negative correlation with plant height (-0.375). Primary branches per plant had highly significant and positive correlation with seeds per pod (0.418) followed by pod length (0.347) and nodes to first flower appearance (0.326). Plant height had highly significant positive correlation with nodes to first floweres appeararance (0.751) followed by nodes per plant (0.739) days to 50 per cent flowering (0.691) pod per cluster (0.487) pods per plant (0.431) while, significant and negative correlation with pod width (-0.321). Pod length had highly significant positive correlation with seeds per pod (0.616) and primary branches per plant. Seeds per pod had highly significant and positive correlation with pod weight (0.483).

4.6 Path coefficient analysis-:

The path coefficient analysis was carried out from phenotypic and genotypic correlation coefficient to resolve direct and indirect effect of sixteen characters on pod yield per plant

The direct and indirect effects of different characters on pod yield at phenotypic and genotypic level had been presented in table 4.6 and 4.7 The higher magnitude of positive direct effect on pod yield was exerted by number of nodes per plant (0.2312) followed by internodal length

Experimental Findings

Table-4.6 Direct and indirect effect of fifteen characters on pod yield per plant (g) at phenotypic level in garden pea

Characters	Days to 50% flowering	Nodes per plant	Internodal length(cm)	Nodes to first flower appearance	Primary branches per plant	Plant height (cm)	Pod per plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Shelling (%)	100 seed weight (g)	T.S.S. (⁰ Brix)	Pods per cluster	Pod weight (g)	Correlation with Pod Yield per plant (g)
Days to 50% flowering	-0.0048	0.1543	-0.0293	0.1036	0.0020	0.0691	0.0215	-0.0054	0.0312	0.0425	0.0003	0.0046	0.0250	-0.0294	0.0132	0.3985
Nodes per plant	-0.0032	0.2312	-0.0304	0.1250	0.0442	0.0739	0.0218	-0.0101	0.0436	0.0148	-0.0024	0.0076	0.0535	-0.0393	0.0293	0.5594
Internodal length(cm)	0.0009	0.0462	0.1523	-0.0125	-0.0052	-0.0375	-0.0045	0.0264	-0.0093	0.0907	0.0010	0.0057	-0.0099	0.0117	0.0191	0.1827
Nodes to first flower appearance	-0.0034	0.1979	-0.130	0.1461	0.0480	0.0751	0.0259	-0.0135	0.0407	0.0288	-0.0050	0.0098	0.0574	-0.0387	0.0489	0.6048
Primary branches per plant	-0.0001	0.0696	-0.0054	0.0478	0.1470	0.0118	0.0025	-0.0457	0.0068	-0.1405	-0.0045	0.0098	0.0173	-0.0119	-0.0064	0.0980
Plant height (cm)	-0.0033	0.1709	-0.0571	0.1078	0.0174	0.0999	0.0248	0.0064	0.0328	0.0094	-0.0025	0.0050	0.0316	-0.0317	0.0190	0.4323
Pods per plant	-0.0018	0.0878	-0.0119	0.0660	0.0065	0.0431	0.0574	0.0059	0.0281	0.0573	0.0010	0.0123	0.0091	-0.0186	0.0255	0.3679
Pod length (cm)	-0.0002	0.0178	-0.0305	0.0150	0.0511	-0.0049	-0.0026	-0.1316	-0.0069	-0.2069	-0.0042	-0.0069	0.0130	-0.0053	-0.0366	-0.3395
pod width (cm)	0.0015	-0.0986	0.0138	-0.0583	0.0097	-0.0321	-0.0158	0.0089	-0.1021	-0.0934	0.0002	-0.0005	-0.0392	0.0167	-0.0186	-0.4448
Seeds per pod	0.0006	-0.0102	-0.0412	-0.0125	0.0615	-0.0028	-0.0098	-0.0811	-0.0284	-0.3356	-0.0069	-0.0034	-0.0050	0.0047	-0.0670	-0.5371
Shelling (%)	0.0001	0.0196	-0.0055	0.0266	0.0240	0.0091	-0.0021	-0.0199	0.0008	-0.0840	-0.0277	-0.0025	0.0410	-0.0065	0.0261	-0.0009
100 seed weight (g)	-0.0005	-0.0375	-0.0185	-0.0305	-0.0307	-0.0107	-0.0151	-0.0194	-0.0010	-0.0245	-0.0015	-0.0468	0.0084	0.0096	-0.0301	-0.2477
T.S.S. (⁰ Brix)	-0.0009	0.0889	-0.0108	0.0603	0.0182	0.0227	0.0037	-0.0123	0.0287	0.0120	-0.0082	-0.0028	0.1392	-0.0161	0.0402	0.3629
Pods per cluster	-0.0022	0.1399	-0.0275	0.0871	0.0268	0.0487	0.0164	-0.0106	0.0262	0.0240	-0.0028	0.0069	0.0345	-0.0650	0.0418	0.3443
Pod weight (g)	0.0005	-0.0489	-0.0210	-0.0516	0.0068	-0.0137	-0.0106	-0.0348	-0.0137	-0.1623	0.0052	-0.0102	-0.0404	0.0196	-0.1385	-0.5135

Residual effect- 0.5445 R²- 0.0019

Experimental Findings

Table-4.7 Direct and indirect effect of sixteen characters on pod yield per plant (g) at genotypic level in garden pea

Characters	Days to 50% flowering	Nodes per plant	Inter-nodal length (cm)	Nodes to first flower appearance	Primary branches Per plant	Plant height (cm)	Pods Per plant	Length of pods (cm)	Width of pod (cm)	Seed per pod	Shellin g (%)	100 seed weight (g)	T.S.S. (^o Brix)	Pods Per cluster	Pod weight (g)	Correlati on with yield per plant (g)
Days to 50% flowering	0.3230	-0.2737	-0.0921	-0.2587	0.0115	0.2100	0.0002	-0.0230	0.1586	-0.0392	-0.0020	-0.0098	0.0633	0.3198	0.0374	0.4251
Nodes per plant	0.2268	-0.3899	-0.0975	-0.3182	0.1301	0.2241	0.0002	-0.0323	0.2349	-0.0127	-0.0405	-0.0150	0.1424	0.4364	0.0998	0.5885
Internodal length(cm)	-0.0698	0.0891	0.4267	0.0365	-0.0072	-0.1259	0.0000	0.0955	-0.0436	-0.0976	0.0281	-0.0139	-0.0142	-0.1508	0.0602	0.2131
Nodes to first flower appearance	0.2371	-0.3520	-0.0442	-0.3525	0.1357	0.2318	0.0002	-0.0476	0.2256	-0.0270	-0.0809	-0.0189	0.1484	0.4330	0.1580	0.6467
Primary branches per plant	0.0100	-0.1370	-0.0083	-0.1293	0.3701	0.0339	0.0000	-0.1918	0.0470	0.1373	-0.0882	-0.0198	0.0293	0.0826	-0.0230	0.1129
Plant height (cm)	0.2314	-0.2982	-0.1833	-0.2788	0.0429	0.2931	0.0002	0.0295	0.1981	-0.0105	-0.0422	-0.0095	0.0775	0.3286	0.0644	0.4430
Pods per plant	0.1267	-0.1504	-0.0400	-0.1661	0.0243	0.1316	0.0004	0.0249	0.1585	-0.0508	0.0211	-0.0245	0.0246	0.2079	0.0841	0.3724
Pod length (cm)	0.0168	-0.0284	-0.0917	-0.0377	0.1598	-0.0195	0.0000	-0.4441	-0.0080	0.2040	-0.0828	0.0146	0.0340	0.0271	-0.1307	-3867
Pod width (cm)	-0.1215	0.2171	0.0441	0.1885	-0.0412	-0.1377	0.0002	-0.0084	-0.4218	0.1072	0.0101	0.0036	-0.1323	-0.2575	-0.0444	-0.4944
Seeds per pod	-0.0427	0.0166	-0.1402	0.0321	0.1711	-0.0104	-0.0001	-0.03051	-0.1523	0.2969	-0.1179	0.0072	-0.0222	-0.0829	-0.2262	-0.5760
Shelling (%)	0.0017	-0.0417	-0.0317	-0.0754	0.0863	0.0327	0.0000	-0.0972	0.0112	0.0925	-0.3784	0.0064	0.1348	0.1758	0.0908	.0077
100 seed weight (g)	-0.0368	0.0684	-0.0691	0.0789	-0.0857	-0.0327	-0.0001	-0.0758	-0.0180	0.0248	-0.0280	0.0857	0.0267	-0.0880	-0.1038	-0.2544
T.S.S. (^o Brix)	0.0637	-0.1730	-0.0188	-0.1630	0.0338	0.0707	0.0000	-0.0471	0.1739	-0.0206	-0.1589	0.0071	0.3209	0.1832	0.1421	0.4141
Pods per cluster	0.2074	-0.3416	-0.1292	-0.3064	0.0614	0.1933	0.0002	-0.0242	0.2181	-0.0494	-0.1336	-0.0151	0.1180	0.4982	0.1733	0.4704
Pod weight (g)	-0.0280	0.0902	-0.0595	0.1292	0.0197	-0.0438	-0.0001	-0.1345	-0.0434	0.1557	0.0797	0.0206	-0.1057	-0.2001	-0.4313	-0.5514

Residual effect-0.4749, R² -0.7744

(0.1523), primary branches per plant (0.1470), nodes to first flower appearance (0.1461), TSS (0.1392) and plant height (0.0999). The higher magnitude of negative direct effect on pod yield was exerted by seeds per pod (-0.3356) followed by pod weight (-0.1385), pod length (-0.1316) and width of pod (-0.1021)). Considerable positive indirect effects by days to 50 per cent flowering (0.1543), nodes to first flower appearance (0.1979), plant height (0.1709) and pod per cluster (0.1399) were exerted *via* nodes per plant toward pod yield per plant. Whereas, substantial negative indirect effects on pod yield per plant were exhibited by pod length (-0.2069), pod weight (-0.1623) and primary branches per plant (-0.1405) *via* seeds per pod.

Rest of the estimates of indirect effects were very low. The estimates of the residual factor was high (0.5445) indicating the importance of some other component not included under the present investigation.

4.7 Genetic divergence-:

The study of genetic divergence among the 38 genotypes of garden pea was carried out by using Mahalanobis D^2 statistics. The thirty eight genotypes were grouped into seven different non- overlapping clusters (Table-4.8). Cluster II (14) had highest number of genotypes followed by cluster I (10), cluster III (6), cluster V (4) cluster IV (2) and cluster VI and VII had only one genotypes. The estimates of intra-and inter-cluster distances represented by D^2 values are given in table-4.9. The intra cluster

Table-4.8 Clustering pattern of 38 genotypes of garden pea on the basis of Mahalanobis D² statistics

Cluster number	No. of genotypes	Genotypes
I	10	NDVP-514, PC-531(C), NDVP-504, NDVP-512, NDVP-515, NDVP-516, NDVP-534, NDVP-502, NDVP-529, NDVP-532
II	14	NDVP-432, NDVP-434, NDVP-429, NDVP-422, AP-3(C), NDVP-425, VRP-6(C), NDVP-437, NDVP-430, NDVP-421, NDVP-424, NDVP-426, NDVP-440, NDVP-423,
III	6	NDVP-503 VP-233, VRP-7(C), Arka Ajit, NDVP-518, NDVP-526
IV	2	NDVP-523, NDVP-528,
V	4	NDVP-517, NDVP-522, NDVP-521, IP-3
VI	1	NDVP-439
VII	1	NDVP-433

Table-4.9 Intra and inter clusters D^2 values for seven clusters in garden pea

Cluster number	I	II	III	IV	V	VI	VII
I	71.94	249.57	127.99	177.66	135.24	360.20	223.90
II		72.09	304.16	318.86	446.15	134.51	134.83
III			85.49	189.52	246.16	312.59	213.28
IV				28.03	361.14	312.76	231.21
V					87.50	670.32	428.47
VI						0.00	104.18
VII							0.00

D^2 values ranged from 0.00 (cluster VI and VII) to 87.50 (cluster V). The maximum inter-cluster distance was observed between clusters V and VI (670.32). Which suggested that members of these two clusters are genetically very diverse to each other. The inter-cluster values between cluster II and cluster V (446.15), cluster V to VII (428.47), cluster IV to V (361.14), cluster I to VI (360.20) and cluster II to IV (318.86) were very high. The minimum inter-cluster D^2 value was recorded in case of cluster VI and cluster VII (104.18). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters while, lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. The intra- clusters means for sixteen characters in garden pea had given in table-4.10.

A perusal of table 4.10 showed that cluster means for different traits indicated considerable differences between the clusters. Cluster I showed maximum mean value for shelling per cent (45.80%), nodes to first flower appearance (12.78) and internodal length (7.29cm). Cluster II showed maximum mean value for 100 seed weight (33.76g). Cluster III showed maximum mean value for pods per plant (18.12) and pods per cluster (1.71). Cluster IV showed maximum mean value for nodes per plant (19.02), primary branches per plant (3.68), pod length (10.38cm), seeds per pod (8.66), TSS (12.95) and pod weight (6.72). Cluster V showed maximum mean value for plant height (95.81cm) and pod yield

Experimental Findings

Table-4.10 Cluster mean for sixteen characters in garden pea.

Characters Cluster No.	Days to 50% flowering	Nodes per plant	Internodal length (cm)	Nodes to first flower appearance	Primary branches per plant	Plant height (cm)	Pods per plant	Pod length (cm)
Cluster-I	55.62	16.92	7.29	12.78	3.13	81.73	12.87	8.68
Cluster-II	42.46	11.93	7.26	8.64	2.49	57.68	10.61	8.58
Cluster-III	58.44	17.44	6.58	12.48	2.44	95.29	18.12	8.62
Cluster-IV	59.92	19.02	6.13	13.05	3.68	95.67	11.35	10.38
Cluster-V	59.92	18.99	6.80	12.62	2.46	95.81	11.58	7.59
Cluster-VI	44.33	12.40	6.03	7.60	2.63	56.53	13.90	8.40
Cluster-VII	61.67	11.53	6.94	9.53	2.43	74.69	11.03	8.14

Characters Cluster No.	Pod width (cm)	Seed per pod	Shelling per cent	100 seed weight (g)	T.S.S. (⁰ Brix)	Pods per cluster	Pod weight (g)	Pod Yield per plant (g)
Cluster-I	1.91	6.54	45.80	30.70	12.77	1.58	4.49	37.90
Cluster-II	1.99	6.52	44.22	33.76	12.02	1.09	5.32	28.57
Cluster-III	1.88	6.27	44.69	31.17	12.49	1.71	4.48	34.75
Cluster-IV	1.95	8.66	44.92	33.33	12.95	1.40	6.72	23.40
Cluster-V	1.79	5.35	43.21	32.33	12.78	1.63	4.45	44.28
Cluster-VI	2.02	7.37	42.33	25.67	11.53	1.13	6.16	24.43
Cluster-VII	2.27	6.37	35.33	30.33	9.67	1.20	4.91	22.76

per plant (44.28g). Cluster VII showed maximum mean value for days to 50% flowering (61.67) and pod width (2.27cm) and Cluster II showed minimum mean values for days to 50 % flowering (42.46), plant height (57.68cm), pods per plant (10.61), and pods per cluster (1.09). Cluster V showed minimum mean value for pod length (7.59cm), pod width (1.79cm), seeds per pod (5.35) and pod weight (4.45g). Cluster VI showed minimum mean values for internodal length (6.03cm) nodes to first flower appearance (7.60) and 100 seed weight (25.67cm). Cluster VII showed minimum mean values for nodes per plant (11.53), primary branches per plant (2.43), shelling per cent (35.33%), TSS (9.67 °Brix) and pod yield per plant (22.76g).

The analysis of contribution of characters towards total genetic divergence between thirty eight genotypes of garden pea had been given in table 4.11 The maximum contribution in manifestation of total genetic divergence was made by pod yield per plant (34.57%) followed by pods per plant (20.20%). The minimum contribution was noticed in case of internodal length (0.14%) and length of pod (0.14%) toward genetic divergence. The role of days to 50% flowering (9.39%), nodes per plant (6.12%), nodes to first flower appearance (8.11%), plant height (5.83%) and seeds per pod (5.26%) were very low in manifestation of total genetic divergence in the available germplasm.

Table-4.11 Per cent contribution of sixteen characters towards total genetic divergence in garden pea

S. No.	Sources	Times Ranked 1st	Per cent contribution
1.	Days to 50% flowering	66	9.39
2.	Nodes per plant	43	6.12
3.	Internodal length (cm)	1	0.14
4.	Nodes to first flower appearance	57	8.11
5.	Primary branches per plant	0.01	0.00
6.	Plant height (cm)	41	5.83
7.	Pods per plant	142	20.20
8.	Pod length (cm)	1	0.14
9.	Pod width (cm)	0.01	0.00
10.	Seeds per pod	37	5.26
11.	Shelling per cent	4	0.57
12.	100 seed weight (g)	27	3.84
13.	T.S.S. (° Brix)	11	1.56
14.	Pods per cluster	0.01	0.00
15.	Pod weight (g)	30	4.27
16.	Pod Yield per plant (g)	243	34.57

DISCUSSION

Genetic variability is the back bone of any crop improvement programme and effectiveness of selection depends upon its nature and magnitude in the genetic material at the disposal of plant breeder. In other words genetic variability is the fundamental to selection and to a great extent to the breeding methodology as such. The speed of improvement in any crop depends upon the magnitude and kinds of genetic variability present in the population. The genetic variation is heritable one and hence important in the selection.

A great deal of genetic variability is available in the germplasm of garden pea in centers of its diversity. A number of reports on exploitation of variability in major crops of world are available even in Pre-Mendelian period and this caused improvement in yield. Among the vegetable crops, the garden pea which is grown on a large acreage, it has become necessary to gather basic information on genetic and other biometrical parameters which help in selection and genetic manipulations for improvement in the yield of this crop. With this objective, thirty eight genotypes collected from different places were maintained and evaluated for sixteen characters. The genetic and statistical parameters were estimated for genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance, correlation coefficient, path analysis and genetic divergence. The results of present investigation have

been discussed in the following heads in reference to reported work relevant to this investigation on garden pea.

5.1 Analysis of variance:-

The analysis of variance for different characters had been presented in table 4.1. The mean sum of square due to genotypes/treatments was highly significant for all the characters. In other words, the performances of the genotypes with respect to these characters were statistically different; suggesting that, there exists ample scope for selection in the available germplasm of garden pea.

5.2 Mean performance:-

In order to evaluate the listed genotypes the mean of thirty eight genotypes including respective check for sixteen characters had been presented in table 4.2. A very wide range of variation in mean performance of genotypes were observed for all the characters under study. The comparison of mean performance of thirty eight genotypes of early and mid season groups for sixteen traits using critical differences with checks revealed existence of very high level of variability in the used genotypes. The genotype NDVP-517 (47.71g) significantly out yielded the best check in case of early group. While, in case of mid season genotypes NDVP-521 (46.71g), NDVP-522 (45.33g), NDVP-503 (41.81g), NDVP-516 (41.71g), NDVP-502 (40.61g) and NDVP-534 (38.88g) were found significantly superior for pod yield per plant than the best checks. These genotypes also showed significantly high mean performance for some other characters.

5.3 Coefficient of variation:

The estimate of genotypic coefficient of variation is of prime importance to breeder because genetic variance alone, does not allow a decision as to which characters were showing the highest degree of variability. Therefore, accurate relative comparison can be made with the help of phenotypic and genotypic coefficient of variation. In general, the phenotypic coefficients of variability were higher than the genotypic coefficient of variability for all the characters under study which indicated that environment played very important role in the expression of the traits.

The highest phenotypic and genotypic coefficient of variation was observed for pod per cluster followed by plant height, pods per plant, and primary branches per plant, pod yield per plant, pod weight, nodes per plant and nodes to first flower appearance. Similar, results have been reported by Chaudhary *et al.* (2010), Singh *et al.* (2012), Dar *et al.* (2013) and Sharma and Sharma (2013). Moderate PCV along with GCV were recorded for days to 50% flowering, internodal length and seed per pod. Similar result was also reported by Srivastava *et al.* (2009) and Lal *et al.* (2011).

The phenotypic and genotypic coefficients of variations were lower for TSS, 100 seed weight, shelling per cent, and pod width and pod length. Low GCV and PCV for these traits indicated that the genotypes taken for the present study were similar for these traits.

4.4 Heritability and genetic advance:

Heritability in broad sense of a character is important to the breeder since it indicate the possibility and extent to which improvement is possible through selection. It also indicates direction of selection pressure to be applied for a trait during selection because it measures relationship between parents and their progeny, hence widely used in determining the degree to which a character may be transmitted from parents to offspring. However, high heritability alone is not enough to make efficient selection in advanced generation unless accompanied by substantial amount of genetic advance (Burton, 1952). High estimates of heritability along with high genetic advance provides good scope for further improvement in advance generations.

The result on heritability and genetic advance in per cent of mean of present investigation had been presented in table 4.3. The heritability estimates for different characters ranged from 48.60 to 97.00 per cent. High heritability was recorded for almost all the character except pods per cluster, pod width and shelling per cent. High heritability coupled with high genetic advance in per cent of mean were recorded for plant height, pods per plant, pod yield per plant, pod weight, nodes per plant, nodes to first flower appearance primary branches per plant and seeds per pod indicating that these traits were little influenced by environment. Thus, require low selection intensity for improvement. Similar result were also reported by Srivastava *et al.* (2009) and Dar *et al.* (2013),

4.5 Correlation coefficient:

The nature and magnitude of association between yield and its components traits is necessary for effective selection in advance generations. Nature of population under consideration and the magnitude of correlation coefficient could often be influenced by the choice of the individuals upon which the observations are made.

Correlations between character pairs are due to linkage of genes or pleiotropy of genes. Therefore, selection of one traits influence the other linked or pleiotropically affected traits. Considerable importance has been attached to correlation studies in the plant improvement because they are helpful in making effective selection.

In the present study, correlations between sixteen characters were worked out in all possible combinations at phenotypic and genotypic levels and had been presented in table 4.4 and 4.5. In general, the magnitude of genotypic correlation coefficients were higher than the corresponding values of the phenotypic correlation coefficients. This indicated a strong genetic association between the traits and the phenotypic expression which was suppressed due to environmental influence. Singh *et al.* (2011) and Sharma and Sharma (2013) also reported higher estimates of genotypic correlations than the corresponding phenotypic correlations between yield and yield components.

. The most important trait *viz.* pod yield per plant had exhibited highly significant and positive phenotypic correlation with nodes to first

flower appearance, nodes per plant, pod width, plant height, days to 50% flowering, pods per plant, TSS, and pod per cluster. Most important positive and significant association was estimated between nodes to first flower appearance and pod yield per plant. Nodes to first flower appearance was also found to have significant and positive correlation with days to 50 per cent flowering (0.709) , nodes per plant (0.855), primary branches per plant (0.326), plant height (0.751), pods per plant (0.451), TSS (0.412), pods per cluster (0.596), while, it showed negative significant correlation with pod width (-0.398) and pod weight (-0.352). This showed that traits having significant positive correlation with pod yield per plant also had significant and positive correlations with some other traits as well. The available literature has also indicated positive correlation between pod yield per plant and among themselves in garden pea. Similar association of traits in garden pea had also been reported by Ghobary (2010) and Singh *et al.* (2011).

4.6 Path coefficient analysis:

Path coefficient is simply standardized partial regression coefficient which splits the correlation coefficient into the measure of the direct and indirect effects of a set of independent variables on the dependent variable. This analysis provided a measure for separating out direct and indirect effect of different characters on pod yield at phenotypic and genotypic level and had been presented in table 4.6 and 4.7. The higher magnitude of positive direct effect on pod yield was exerted by number of nodes per plant followed by internodal length,

primary branches per plant, nodes to first flower appearance, TSS and plant height. The higher magnitude of negative direct effect on pod yield was exerted by number of seed per pod followed by pod weight, length of pod and width of pod.

This indicated that direct selection based on pod per plant and pod weight would result in an appreciable improvement of pod yield per plant in garden pea.

Considerable positive indirect effects by days to 50 per cent flowering (0.1543), nodes to first flower appearance (0.1979), plant height (0.1709) and pod per cluster (0.1399) were exerted *via* nodes per plant toward pod yield per plant. Whereas substantial negative in direct effects on pod yield per plant were exhibited by pod length (-0.2069), pod weight (-0.1623) and primary branches per plant *via* seeds per pod.

Therefore during selection these characters should also be taken into consideration. Similar results were also reported by Arya *et al.*, Singh *et al.* and Ram *et al.* (2010).

4.7 Genetic divergence:

The result of D^2 analysis are presented in table 4.8, 4.9 4.10 and 4.11. The study of genetic divergence among thirty eight genotype of garden pea were carried out by using Manalanobis D^2 statistics'. In present investigation thirty eight genotypes of garden pea were grouped in seven distinct non- over lapping clusters. This indicated presence of considerable diversity in the genotypes. The major clusters in the above

mentioned genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although the genotypes of same origin or geographic region were also found to be grouped together in the same cluster. The instances of grouping of genotypes of different origin or geographically of same region in same clusters were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity. Grouping of genotypes into VII cluster indicated presence of considerable diversity among the different traits in the available germplasm. Cluster II (14) had highest number of genotypes followed by cluster I (10), cluster III (6), cluster V (4) cluster IV (2) and cluster VI and VII which had only one genotypes. The estimates of intra- and inter-cluster distances represented by D^2 values had given in table No-4.9. The intra cluster D^2 values ranged from 0.00 (cluster VI and VII) to 87.50 (cluster V). The maximum inter-cluster distance was observed between clusters V to VI (670.32), which suggested that members of these two clusters were genetically very diverse to each other. The inter-cluster values between cluster II and cluster V (446.15), cluster V to VII (428.47), cluster IV to V (361.14), cluster I to VII (360.20), cluster II to IV (318.86), and were very high. The minimum inter-cluster D^2 values were recorded in case of cluster VI and cluster VII (104.18). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters. While lower inter-cluster values between the clusters suggested that the genotypes of these clusters were not much genetically diverse from each other. Further the crossing between lines of

distant clusters may give rise to desirable segregates. Similar findings were also recorded by Singh and Mishra (2008), Cupic *et al.* (2011) and Srivastava *et al.* (2012).

The analysis of contribution of characters towards genetic divergence between thirty-eight genotypes of garden pea had been given in table 4.11. The maximum contribution in manifestation of total genetic divergence was made by pod yield per plant followed by pods per plant. While, minimum contribution was noticed in case of internodal length and length of pod. The role of days to 50% flowering, nodes per plant, nodes to first flower appearance, plant height and seed per pod were low in manifestation of total genetic divergence in the available germplasm. The contribution of these traits for total genetic divergence were also reported by Dixit *et al.* 2002 and Srivastava *et al.* (2012).

SUMMARY AND CONCLUSION

The present investigation “**Studies on variability character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)**” using 38 genotypes of garden pea was carried out to study the extent of variability, heritability, genetic advance, correlation and path coefficient analysis at phenotypic and genotypic levels and genetic divergence for sixteen yield and yield attributing traits. The experiment was conducted in Randomized Complete Block Design with three replications at the Main Experiment Station, Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad (U.P.), during *Rabi*, 2012-13. Each treatment consisted of five rows spaced 30cm with plant to plant spacing of 10 cm and replicated thrice. Each entry was grown in the plot size of 3 m x 1.5 m. The observations were recorded on sixteen quantitative traits. The mean data were subjected to the various statistical and biometrical analysis. The salient findings of the study are summarized below:

1. The analysis of variance (mean of squares) for sixteen quantitative characters were highly significant for all the traits indicating ample variation among the genotypes.
2. Based on mean performance only one genotype NDVP-424 in early group and seven genotypes *viz.* NDVP-517 followed by NDVP-521, NDVP-522, NDVP-503, NDVP-516, NDVP-512 and

NDVP-502 in mid-season group were found as significant and most promising genotypes for pod yield per plant along with some other traits.

3. The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits. High magnitude of variability were observed in case of pods per cluster (28.99%), plant height (26.03%), pods per plant (25.08), primary branches per plant (22.70%), pod yield per plant (21.83), pod weight (21.67%), nodes per plant (20.15%) and nodes to first flower appearance (19.77%).
4. High heritability coupled with high genetic advance in per cent of mean were observed for plant height, pods per plant, pod yield per plant, pod weight, nodes per plant, nodes to first flower appearance, primary branches per plant and seeds per pod indicating scope of high selection response.
5. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, suggesting a strong inherent relationship in different pairs of the traits. Nodes at first flower appearance, nodes per plant, width of pod, plant height, days to 50 per cent flowering, pods per plant, TSS, and pod per cluster showed significant and positive correlation with pod yield per plant, while seeds per pod, pod weight, and length of pod showed negative and significant correlation with pod yield per plant and selection for traits with positive correlation would be effective for yield improvement in garden pea.

6. Path coefficient analysis revealed that nodes per plant followed by internodal length, primary branches per plant and nodes at first flower appearance exhibited considerable positive direct effect on yield, while negative direct contribution towards yield were pronounced by seed per pod, pod weight and length of pod both at phenotypic and genotypic levels.
7. Mahalanobis D^2 statistic distributed all the thirty eight genotypes into seven diverse clusters.
8. The inter-cluster values between cluster II and cluster V (446.15), cluster V to VII (428.47), cluster IV to V (361.14), cluster I to VII (360.20) and cluster II to IV (318.86) were high. The minimum inter-cluster D^2 value was recorded in case of cluster VI and cluster VII (104.18).
9. High mean value for yield per plant was estimated in case of cluster V, while it was lowest was within cluster VII.
10. The quantitative traits which contributed maximum towards the genetic distance among the genotypes was pod yield per plant followed by pods per plant.

On the basis of findings of present experiment it may be concluded that considerable variability exists within the genotypes of garden pea. The genotype NDVP-424 from early group and genotypes NDVP-517, NDVP-521, NDVP-522 NDVP-503, NDVP-516, NDVP- 512 and NDVP-502 from mid group were found promising for pod yield per plant and other traits and may be use in future breeding programmes.

Summary and Conclusion

High heritability along with high genetic advance for important traits indicated greater chance of selection response.

Character association indicated that selection for traits like nodes per plant, internodal length, nodes to first flower appearance, primary branches per plant, and TSS may be effective for pod yield improvement. Divergence analysis showed the existence of sufficient diversity in germplasm.

Characters like pod yield per plant and pods per plant contributed maximum towards total genetic divergence. Further clustering patterns indicated that clusters V and VI may give rise to desirable transgressive segregates after hybridization in segregating progenies of garden pea.

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Title: “Studies on variability, character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)”

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ABSTRACT

The present investigation “**Studies on variability, character association and genetic divergence in garden pea (*Pisum sativum* L. var. *hortense*)**” using thirty eight genotypes of garden pea was carried out with a view to study the extent of variability, heritability in broad sense, genetic advance, correlation coefficient, path coefficient analysis at phenotypic and genotypic levels and genetic divergence. The experiment was conducted at Main Experimental Station of Department of Vegetable Science, NDUAT, Kumarganj, Faizabad (U.P.) during *Rabi*, 2012-13. Experimental material for study was consisted of 38 early and mid-season genotypes including four checks (AP-3, VRP-6, PC-531 and VRP-7). The experiment was conducted in Randomized Complete Block Design with three replications. Each treatment consisted of five rows spaced 30cm with plant to plant spacing of 10 cm and replicated thrice. Each entries were grown in the plot size of 3 m x 1.5 m. Observations were recorded on sixteen character *viz.* days to 50 percent flowering (days), nodes per plant, internodal length (cm), nodes to first flower appearance, primary branches per plant, plant height (cm), pods per plant, pod length (cm), pod width (cm), seeds per pod, shelling per cent (%), 100 seed weight (g), T. S.S (°Brix), pod per cluster, pod weight (g), and pod yield per plant (g).

The analysis of variance for design of experiment indicated highly significant differences among the genotypes for all the traits. Based on mean performance only one genotype NDVP-424 among early group and seven genotypes *viz.* NDVP-517 followed by NDVP-521, NDVP-522, NDVP-503, NDVP-516, NDVP-512 and NDVP-502 among mid-season group were found as significant and most promising genotypes for pod yield per plant along with some other traits. The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits. High magnitudes of variability were observed in case of pods per cluster (28.99%), plant height (26.03%), pods per plant (25.08), primary branches per plant (22.70%), pod

yield per plant (21.83%), pod weight (21.67%). While, TSS, width of pod, 100 seed weight, shelling per cent and seed per pod exhibited low variability. High heritability coupled with high genetic advance in per cent of mean were estimated for plant height, pods per plant, pod yield per plant, pod weight, nodes per plant, nodes to first flower appearance, primary branches per plant, days to 50 per cent flowering, internodal length, length of pod, 100 seed weight and TSS which indicated opportunity for selection response. The most important trait, pod yield per plant had exhibited highly significant and positive phenotypic correlation with nodes to first flower appearance, nodes per plant, pod width, plant height, days to 50% flowering, seed per plant and early pods per plant, TSS, and pods per cluster while it showed highly significant and negative correlation with seed per pod, pod weight and length of pod. The higher magnitude of positive direct effect on pod yield was exerted by number of nodes per plant (0.2312) followed by internodal length (0.1523), primary branches per plant (0.1470), nodes to first flower appearance (0.1461), TSS (0.1392) and plant height (0.0999). The higher magnitude of negative direct effect on pod yield was exerted by number of seeds per pod (-0.3356) followed by pod weight (-0.1385), length of pod (-0.1316) and width of pod (-0.1021)). All the thirty eight genotypes into seven diverse clusters. Cluster II (14) had highest number of genotypes followed by cluster I (10), cluster III (6), cluster V (4) cluster IV (2) and cluster VI and VII (1), which had only one genotypes. The Inter-cluster values between cluster II and cluster V (446.15), cluster V to VII (428.47), cluster IV to V (361.14), cluster I to VII (360.20), cluster II to IV (318.86), were very high. The minimum inter-cluster D^2 values were recorded in case of cluster VI and cluster VII (104.18). Pod yield per plant and pods per plant contributed maximum toward total genetic divergence in available germplasm of garden pea. Thus, there exists ample variation and scope of improvement after selection in the available germplasm of garden pea.

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