GENETIC VARIABILITY FOR YIELD AND HORTICULTURAL TRAITS IN GARDEN PEA (*Pisum sativum* L.)

THESIS

By

AJAY BHARDWAJ (A-2009-30-46)

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in

Partial fulfilment of the requirements for the degree

of

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I can feel you to be along with me, In every walk of irony, Which my life has made me to see. It's your love holding my hand when no one was with me. My reason to live, my destiny you are, Every day I pray for what my God you are.

You here, you there, I can see you everywhere, When you are not around, life is nowhere.

Love you mom love you dad!

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CERTIFICATE – I

This is to certify that the thesis entitled "Genetic variability for yield and horticultural traits in garden pea (*Pisum sativum* L.)" submitted in partial fulfilment of the requirements for the award of the degree of Master of Science (Agriculture) in the discipline of Vegetable Science of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by Mr. Ajay Bhardwaj (Admission No. A-2009-30-46) son of Sh. Ratan Chand under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

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

Place : Palampur Dated : October 19, 2011

(Dr Akhilesh Sharma) Major Advisor

CERTIFICATE - II

This is to certify that the thesis entitled "Genetic variability for yield and horticultural traits in garden pea (Pisum sativum L.)" submitted by Mr. Ajay Bhardwaj (Admission No. A-2009-30-46) son of Sh. Ratan Chand to the CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfilment of the requirements for the degree of Master of Science (Agriculture) in the discipline of Vegetable Science has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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"Pride, Praise and Perfection Belongs to "Lord Hanuman"

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Needless, to say, errors and omissions are mine.

Place: Palampur. Date: October 19, 2011.

Ajay Bhardwaj)

TABLE OF CONTENTS

Chapter	Title	Page
1.	INTRODUCTION .	1-3
2.	REVIEW OF LITERATURE	4-27
3.	MATERIALS AND METHODS	28-49
4.	RESULTS AND DISCUSSION	50-111
5.	SUMMARY AND CONCLUSIONS	112-116
	LITERATURE CITED	117-131
	APPENDICES	132-137
	BRIEF BIODATA OF THE STUDENT	

Sr. No.	Abbreviation	Meaning
1	et al.	et alii (and others)
2	i.e.	Id est (that is)
3	viz.	Vi delicet (namely)
. 4	р	Page
5	pp	Pages
6	°C	Degree Celsius
7	g	gram
8	kg	kilogram
9	1	litre
10	1	Per
11	%	Per cent
12	Fig.	Figure
13	cm	centimeter
14	ml	milliliter
15	mg	milligram
16	mm	millimeter
17	nm	nanometer
18	a.i.	active ingredient
19	&	and
20	@	at the rate
21	v/s	against
22	ppm	parts per million
23	amsl	above mean sea level
24	df	degree of freedom
25	N	north: normal solution
26	E	east
27	conc.	concentrated
28	ha	hectare

LIST OF ABBREVIATIONS USED

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Table no.	Title	Page
4.1	Analysis of variance for different characters in garden pea during the years 2009-10 and 2010-11	51
4.2	Pooled analysis of variance over years for different characters in garden pea	52
4.3	Estimates of parameters of variability for different characters in garden pea during 2009-10 and 2010-11	67
4.4	Estimates of different parameters of variability for different characters in garden pea in pooled over years	68
4.5	Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different pairs of horticultural traits in garden pea during 2009-10	74
4.6	Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different pairs of horticultural traits in garden pea during 2010-11	75
4.7	Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different pairs of horticultural traits in garden pea in pooled over years	76
4.8	Estimates of direct and indirect effects of different traits on pod yield per plant at phenotypic (P) and genotypic (G) levels in garden pea during 2009-10	85
4.9	Estimates of direct and indirect effects of different traits on pod yield per plant at phenotypic (P) and genotypic (G) levels in garden pea during 2010-11	86
4.10	Estimates of direct and indirect effects of different traits on pod yield per plant at phenotypic (P) and genotypic (G) levels in garden pea in pooled over years	87
4.11	Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in garden pea during 2009-10	90

LIST OF TABLES

Table no.	Title	Page
4.12	Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in garden pea during 2010-11	91
4.13	Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in garden pea in pooled over years	92
4.14	Cluster compositions in garden pea following multivariate analysis in 2009-10, 2010-11 and pooled over years	96
4.15	Average intra and inter-cluster distances in garden pea during 2009-10	102
4.16	Average intra and inter-cluster distances in garden pea during 2010-11	103
4.17	Average intra and inter-cluster distances in garden pea in pooled over years	104
4.18	Cluster means for different characters in garden pea during 2009-10	106
4.19	Cluster means for different characters in garden pea during 2010-11	107
4.20	Cluster means for different characters in garden pea in pooled over years	108
4.21	Contribution of various traits towards genetic divergence in garden pea during 2009-10, 2010-11 and pooled over years	110

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Fig. No.	Title	Page
1	Mean weekly weather conditions during the cropping seasons	31
2	Dendrogram showing grouping of 41 garden pea genotypes generated using D^2 cluster analysis (Tocher's method) during 2009-10	97
3	Dendrogram showing grouping of 41 garden pea genotypes generated using D^2 cluster analysis (Tocher's method) during 2010-11	98
4	Dendrogram showing grouping of 41 garden pea genotypes generated using D^2 cluster analysis (Tocher's method) in pooled over years	99

LIST OF PLATES

Plate No.	Title	Page
1	General view of the crop	54
2	Genotypes with different plant characteristics	56
. 3	The best performing genotypes at vegetative and flowering stage	58
4	The best performing genotypes at pod bearing stage	60
5	Pod characteristics of the best performing genotypes	61
6	Variability in different genotypes for pod shape, size and colour	62

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ABSTRACT

The present investigation entitled, "Genetic variability for yield and horticultural traits in garden pea (Pisum sativum L.)" was undertaken to assess the nature of genetic variability, association of various traits with yield and their direct and indirect effects for effective selection, and to study the extent of genetic diversity during winters 2009-10 and 2010-11. The experimental material comprising of 41 genotypes was evaluated in randomized complete block design with three replications and data were recorded on fresh pod and seed yield per plant along with component traits and reaction to powdery mildew disease. Sufficient genetic variability was observed for all morphological, yield and yield contributing, and quality traits during both the years of 2009-10 and 2010-11. Genotypes 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPM-72', 'DPPMFWR-11' and 'DPPM-07-4' observed to be promising on the basis of pod characters and yield. High heritability coupled with high genetic advance was observed for pods per plant, pod yield per plant, total biomass, seed yield per plant and harvest index which revealed the importance of additive gene action and phenotypic selection would be effective for improvement in the early generations. Correlation and path coefficient analysis revealed that pods per plant, pod length, seeds per pod and nodes per plant for fresh pod yield per plant, and total biomass, pod yield per plant, pods per plant and harvest index for seed yield per plant could be considered as the best selection parameters for evolving high yielding genotypes. The multivariate analysis revealed considerable genetic diversity present in the 41 genotypes studied and were arranged into 8, 13 and 5 clusters in 2009-10, 2010-11 and pooled over years, respectively with maximum genotypes in cluster I. The clustering pattern indicated absence of any relationship between genetic divergence and geographical distribution. Harvest index, total biomass and 100-seed weight contributed maximum towards total genetic divergence in the respective years and pooled over years. On the basis of genetic divergence, genotypes 'Punjab-89', 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPMFWR-4', 'DPPMFWR-30-2' and 'DPP-25G' offer promise as a breeding stock for utilization in hybridization as parents for the isolation of transgressive segregants in garden pea.

(Ajay Bhardwaj) Student Date: 19.10.2011

Head of the Departmen

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Major Advisor Date: 19.10.2.11

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1. INTRODUCTION

Garden pea (*Pisum sativum* L.), a member of *Papilionaceae* family, is one of the principal vegetable crops of the temperate and sub-tropical areas of the world. It is the second most important food legume worldwide after *Phaseolus vulgaris* (Tar'an *et al.* 2005). It is of Mediterranean origin, and the Near East and Ethiopia are considered as secondary habitats (Blixt 1970).

Besides, being a rich source of health building substances *viz.*, proteins, vitamins, minerals, and also lysine (a limiting essential amino acid in cereals), it plays an important role in the economy of growers. It is quite palatable and nutritious for human consumption and is eaten as fresh, canned, frozen or in dehydrated forms. It ranks next to tomato as a processed vegetable (Talbert 1953). Being biological nitrogen fixing legume, its value has long been recognized for maintaining and restoring soil fertility, conservation and improvement of physical properties of the soil by virtue of its deep root system.

At the global level, garden pea is cultivated over an area of 1,164.15 thousand hectares with the production of 9168.67 thousand tonnes (Anonymous 2011). It is a leading vegetable crop in the North-Western Himalaya region of India comprising the states of Himachal Pradesh, Jammu and Kashmir, and Uttarakhand (Sharma *et al.* 2010). In India, it occupies an area of 364.90 thousand hectares with the production of 3,029.40 thousand tonnes (Anonymous 2010).

Owing to diverse agro-climatic conditions in Himachal Pradesh, the crop is grown round the year, yielding lucrative returns to the growers. The consumers have their special preference for hill grown peas because of its characteristic flavour, sweetness and freshness. In the high altitude areas, it is grown as an off-season cash crop during summer whereas in winter, it is cultivated in low and mid hills. Accordingly, pea holds a very coveted position in the state by covering more than one-fourth of the total area under vegetable crops and ranks first with an acerage of 21.74 thousand hectares and annual production of 237.28 thousand tonnes (Anonymous 2010).

High yield, long and dark green pods, sweetness and resistance to pests and diseases are the main criteria which are being taken into consideration by the breeders for its genetic improvement. Despite continuous breeding efforts, its average yield is low due to farmer's preference for specific cultivars, biotic and abiotic stresses, genetic drift in the cultivars and development of the new pathogen races. Besides high yield, visual appearance of the produce plays a vital role under Indian conditions as sweet, long and dark green pea pods find favour among the consumers and accordingly the age old varieties like 'Azad P-1', 'Lincoln', 'Arkel' etc. are still preferred by the growers.

The success of any breeding programme depends upon the nature and magnitude of genetic variability present in the germplasm (Adunga and Labuschangne 2003) which provides better chances of selecting desirable types (Vavilov 1951). Therefore, genetic restructuring of pea germplasm is the first step to identify the potential genotypes for use in breeding programme. Most of the desirable traits are quantitative in nature and their expression is influenced by the environment. These traits exhibit continuous variation and are under the control of heritable and non-heritable factors (Fisher 1918). The response of selection depends upon the relative proportion of the heritable component in the continuous variation (Singh *et al.* 2009) which is due to genotype while the non-heritable portion is mainly due to the environmental factors. Hence, it is essential to partition overall variability into heritable and non-heritable components with the help of genetic parameters namely, coefficient of variation, heritability and genetic advance.

Since yield is a complex trait, indirect selection through correlated, less complex and easier measurable traits would be an advisable strategy to increase the yield. Efficiency of indirect selection depends upon the magnitude of association between yield and target yield components (Esposito *et al.* 2009). Correlation coefficient, in general, shows association among characters which is not sufficient to describe their relationship when the causal association among characters is needed (Toker and Cagirgan 2004). Direct selection of one of the characters on the basis of genetic correlation between two traits may cause change in the other. The correlation *per se* does not give the complete picture of their interrelationships when more than two variables are involved (Fakorede and Opeke 1985). The path analysis has been used by the breeders (Ali *et al.* 2009) to identify traits that are useful selection criteria to improve crop yield as it identifies the causes, measures the relative importance of the association, and is used to determine the amount of direct and indirect effect of causal components on the effect component (Dewey and Lu 1959). Therefore, determination of correlation and path-coefficients between yield and yield components is important for the selection of desirable plant types for effective pea breeding programmes.

The genetic study based on multivariate analysis is a powerful tool for determining the degree of divergence among genotypes in the population and nature of forces operating at different levels. The inclusion of diverse parents in hybridization programmes serves the purpose of combining desirable genes to obtain desirable recombinants.

Keeping this in view, the present investigation entitled "Genetic variability for yield and horticultural traits in garden pea (*Pisum sativum* L.)" was undertaken with the following objectives:

Objectives

- i. To assess the nature and quantum of genetic variability,
- ii. to study the association of characters and contribution of direct and indirect effects on pod yield, and
- iii. to identify the promising genotypes.



REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

The knowledge of genetic variances, association of characters with yield and path coefficient analysis is essential for obtaining superior varieties with high yield potential and other desirable characters. The relevant literature available on various aspects included in the present study is briefly reviewed under the following subheadings:

- 2.1 Genetic variability
- 2.2 Quality parameters and powdery mildew incidence
- 2.3 Correlation studies
- 2.4 Direct and indirect effects
- 2.5 Genetic divergence studies

2.1 Genetic variability

Genetic variability is the basis of all plant improvement programmes. Sufficient genetic variability, if present, can be exploited for developing superior cultivars. Vavilov (1951) was the first to realise that a wider range of variability in any crop provides better chances of selecting the desirable types. The continuous variation exhibited by a quantitative character includes the heritable and non-heritable components, the concept of which was first given by Johannsen (1909). He demonstrated in beans that variation within the pure line was environmental (non-heritable) while that between the lines was heritable. Since phenotype is the result of interaction between genotype and environment, and selection pressure is exercised on the phenotype, it is, therefore, important to score the phenotypic variability expressed in population for yield and other contributing traits.

A knowledge of heritability for different component traits gains importance for any crop improvement programme because the heritable component is transmitted from generation to generation. The heritability estimates indicate only the effectiveness of selection with the genotype on the basis of their phenotypic performance but fail to indicate the real progress. Wright (1921) reported that heritability components comprised

of additive and non-additive portion and it was the former which responds to selection. Effective selection depends on the heritability of a trait in question. However, high heritability alone does not mean high genetic gain, therefore, sufficient to make improvement through selection. Thus, the estimation of expected genetic advance is important to have an idea of effectiveness of selection. Burton (1952) suggested that genotypic coefficient of variation (GCV), heritability and genetic advance would give better information about efficiency of selection. Burton and De Vane (1953) suggested that genetic gain, together with heritability estimates, gives a reliable indication of the extent of improvement expected from selection and further remarked that expected genetic gain under particular system supplies true practical information which is needed by a breeder. Johnson et al. (1955 a) suggested that heritability estimate along with genetic advance were more reliable than heritability alone for predicting the response of selection. High heritability coupled with high genetic advance might be due to the action of the additive genes (Panse 1957) whereas, the high heritability associated with low genetic advance might be due to the non-additive gene action which includes dominance and epistasis (Liang and Walter 1969). The relevant literature in this aspect in garden pea is reviewed as follows:

Bhag Mal (1969) found higher values of genetic variability, heritability and genetic advance for pod yield, pod number per plant and plant height while Singh and Singh (1970) observed the higher values of these estimates for pod length, seeds per pod and pods per plant.

Srivastava *et al.* (1972) reported high heritability and low genetic advance for days to flowering and pod length, medium heritability and high genetic advance for seeds per pod and low heritability and low genetic advance for pod yield per plant. On the other hand, Nandpuri *et al.* (1973) revealed wide range of phenotypic variability, genetic coefficient of variation and genetic advance for yield per plant, pods per plant, pod weight, seeds per pod, shelling (%) and plant height. High heritability was evident for all the characters except shelling (%). High heritability coupled with high genetic advance were observed for pod yield per plant and number of pods per plant, indicating additive gene effects, while high heritability and low genetic advance showing non-additive gene effects were found for plant height, number of seeds per pod and pod weight.

Singh and Saklani (1973) found a wide range of variation for days to flower, days to first picking, pod length, seeds per pod, shelling (%) and pod yield per plant. Genetic coefficient of variation (GCV) for pod length, pods per plant and shelling (%) were comparatively less than the other traits. Heritability was high for days to flower, days to first picking, pod yield per plant, seeds per pod and pods per plant and low for shelling (%) and pod length. Expected genetic advance was high for pod yield per plant and pods per plant, whereas it was moderate for days to flower and seeds per pod and low for other traits.

Kuksal *et al.* (1983) reported the role of additive gene effects for the inheritance of pods per plant and yield per plant, while non-additive effects predominated for pod length and seeds per pod. Broad sense heritability estimates of more than 90% were obtained for all the eight characters studied. Ponnuswami and Irulappan (1983) observed high estimates of coefficient of variation, heritability and genetic advance for pods per plant, yield per plant and plant height indicating the role of additive gene effects in the inheritance of these traits and thus offering great scope for selection.

Singh (1985) in a study involving 30 pea varieties reported variation for days to 50% flowering, days to maturity, plant height and pods per plant. Phenotypic and genotypic coefficients of variation were maximum for number of pods per plant followed by plant height. Heritability was highest for days to 50% flowering, plant height and days to maturity, whereas it was moderate for pods per plant. Genetic advance was maximum for plant height followed by pods per plant while it was low for days to maturity and days to 50% flowering. Korla and Singh (1988) reported that pods per axil, pod weight and pod yield per plant exhibited high heritability, medium to high genetic coefficient of variation, medium to high heritability and low genetic advance.

Dev *et al.* (1993) observed high phenotypic and genotypic coefficients of variation for pod yield and pods per plant alongwith high heritability for pod yield, seeds per pod and plant height and genetic advance for pod yield. Kumaran *et al.* (1995) reported high GCV, PCV, heritability and genetic advance for pods per plant, pod weight and pod yield per plant indicating that these traits could be exploited for improvement through selection in pea.

Kumar *et al.* (1998) studied genetic variability in 62 genotypes of pea and reported wide variation for days to maturity, plant height, pod length, number of pods per plant and pod yield per plant. High GCV, PCV, heritability and genetic advance were noticed only for plant height, pod yield per plant and pods per plant. Sureja and Sharma (2000) observed considerable genetic variability for pod yield and its component characters. High heritability in association with high genetic advance were observed for plant height, length of internode, 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 the effectiveness of selection for these traits to improve economic yield.

Tiwari *et al.* (2001) found highest variability for seed yield per plant, number of pods per plant, plant height and number of primary branches per plant. Low to very high heritability coupled with low to moderate genetic advance was observed for most of the characters, indicating little scope for the selection of these characters due to the non-additive gene action. Pathak and Jamwal (2002) recorded high genotypic coefficient of variation (GCV) coupled with high heritability and genetic advance (GA) for pod yield per plant. Moderate GA along with moderate to high GCV were recorded for number of days to 50% flowering and plant height and that of high heritability with low GA and high GCV for number of days to first picking, pod length and average pod weight, and high heritability with low GA and high GCV for ascorbic acid content and number of pods per plant.

Ramesh *et al.* (2002 b) observed high estimates of heritability and genetic advance for plant height, internode length, node of the first fruit and number of pods per plant in 36 genotypes of garden pea including five field pea genotypes and that of high heritability with moderate genetic advance for mean pod weight and reducing sugar content. A considerable amount of phenotypic and genotypic coefficient of variation was observed for pods per plant, weight of pods per plant, internode length, plant height, mean pod weight and weight of grains per pod. Chaudhary and Sharma (2003) observed significant high phenotypic coefficient of variation for plant height, pods per plant and first flowering node. High heritability coupled with high genetic advance was observed for pod yield per plant, plant height, number of pods per plant and 1000-seed weight.

Sharma *et al.* (2003) studied 63 genotypes and found that all the characters namely, seed yield per plant, biological yield per plant, harvest index, plant height, 100-seed weight, seeds per pod, pods per plant, days to 50% flowering, pod length and days to maturity exhibited significant variability. The genotypic and phenotypic coefficients of variation were the highest for seed yield per plant, followed by pods per plant and biological yield per plant. High heritability was observed for all characters, except for days to maturity. High genetic advance along with high heritability and GCV was observed for seed yield per plant, biological yield per plant and pods per plant indicating thereby that selection for these characters would be effective for further improvement. Kumar *et al.* (2004) found highest heritability for pods per plant and that of genetic advance was maximum for green pod yield, followed by the pods per plant, plant height, 100-green seed weight, shelling (%) and the protein content of edible green seeds.

Singh and Dhillon (2004) observed significant mean square estimates for all the characters through analysis of variance and found wide variation for pod yield per plant (9.12 to 101.45 g), pods per plant (4.36 to 38.60), pod weight (1.03 to 5.02 g), grains per pod (3.62 to 6.84), plant height (38.35 to 256.76 cm), primary shoots (1.04 to 8.92), internodal length (2.47 to 11.53 cm) and days to flower initiation (32.93 to 63.07 days). High heritability and genetic gain were observed for primary shoots and pod yield per plant whereas the lowest GCV associated with moderate heritability and low genetic advance were observed for grains per pod. Kalloo *et al.* (2005) observed significant variability for all plant, pod and seed morphological and biochemical traits with maximum variation for plant height and yield per plant. Mehta *et al.* (2005) reported significant differences for node at which first flower appears, plant height, pods per plant, pod yield per plant, pod length, pod width, grains per pod, shelling (%), TSS and reducing sugars.

Gupta *et al.* (2006) noticed highly significant differences for all 18 yield characters with coefficient of variation ranging from 2.44% (days to seed maturity) to 16.93% (number of green pods per plant). The highest phenotypic and genotypic coefficients of variation were observed for green pod yield. 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. Sirohi *et al.* (2006) revealed significant variation for all the characters under study with the highest estimates of phenotypic and genotypic coefficients of variation for plant height.

Jan *et al.* (2007) found significant differences with respect to yield and quality attributes among the genotypes which indicated the extent of diversity and degree of genetic variability present in the genotypes. They further inferred that pods per plant, seeds per pod, pod size, pod weight and shelling (%) might have contributed to higher pod yield. Rana and Jamwal (2007) revealed sufficient variation for all the traits and suggested that the maximum improvement through direct selection can be brought for only plant height whereas pod yield per plant, days to 50% flowering, days to first harvest, pods per plant, average pod weight and pod length can be improved through recombination breeding.

Rathi and Dhaka (2007) found wide range of variability for most of the characters under study. Significant differences in the magnitude of PCV and corresponding GCV were observed for branches per plant, pods per plant, seed yield and harvest index suggesting greater role of environment in the expression of these traits. Plant height, grain yield per plant, dry matter yield, 100-seed weight and number of pods per plant had high phenotypic and genotypic coefficient of variations coupled with moderate to high estimates of heritability and expected genetic advance. Sharma *et al.* (2007) observed high phenotypic and genotypic coefficients of variation for plant height and moderate for pods per plant and pod yield per plant. The heritability and genetic advance were high for plant height and moderate for pods per plant and pod yield per plant indicating the additive and non-additive gene action for their expression, respectively.

Chadha *et al.* (2008) observed sufficient genetic variation for marketable pod yield, pods per plant, duration of availability of pods and grains per pod. Marketable pod yield exhibited high heritability associated with high genetic advance, whereas pods per plant, grains per pod and duration of marketable pods had high heritability with moderate genetic advance. Kumar (2008) found wide range of variation for plant height, days to flowering, pods per plant, grain yield per plant, days to maturity and harvest index. The

highest GCV and PCV were recorded for grain yield per plant followed by pods per plant, seeds per pod and 100-grain weight. Heritability coupled with genetic advance was the highest for grain yield per plant followed by seeds per pod, pods per plant, 100-grain weight and harvest index while genetic advance was maximum for grain yield per plant.

Nawab *et al.* (2008) revealed highly significant differences among genotypes for days to emergence, days to 50% flowering, pods per plant, weight of pods per plant, pod length, seeds per pod, 100-seed weight and green pod yield. Green pod yield per plot, 100-seed weight, pods per plant and weight of pods per plant showed high genetic coefficient of variation (GCV) along with high heritability and genetic advance. Guleria *et al.* (2009) noticed high genotypic and phenotypic coefficient of variations for seeds per pod, plant height, internodal length, grain yield and number of pods. High heritability estimates were observed for almost all the characters except for seeds per pod which had moderate value. Heritability alone in predicting the value of selection. High genetic advance was predicted in seeds per pod, shoot height and internodal length, which indicated that fix ability of heritable characters was high.

Sharma *et al.* (2009) observed wide range of variation for all the characters under study. Phenotypic and genotypic coefficients of variation were high for pod yield per plant and number of pods per plant indicating that there is good scope for improvement these characters through selection. Kumar *et al.* (2010) found high genetic variability for number of pods per plant followed by yield per plot. Higher genetic advance was exhibited by number of pods per plant with their high magnitude of genotypic coefficient of variability and heritability indicating the presence of additive effects for these characters.

Singh *et al.* (2011) observed significant differences for all the characters studied. Moderate to high heritability coupled with moderate genetic advance was recorded for plant height, pod length and 100-seed weight indicating role of additive gene action.

2.2 Quality parameters and powdery mildew incidence

Avakimova (1974) observed variation for ascorbic acid content and reported higher ascorbic acid content in the late varieties than in the early strains. The highest ascorbic acid content of 22.40 mg/100 g was recorded in P₈ cultivar of pea (Ullah and Haq 1975). Pandey and Gritton (1975) reported that the heritability for protein content in pea genotypes ranged from 45-65%. On the other hand, low to moderate estimates of broad and narrow sense heritability were recorded by Jermyn (1977) for this trait.

Kaur *et al.* (1976) studied seven varieties of pea for different quantitative and nutritional traits and found that Bonneville had the highest protein and sugar contents, while the highest vitamin C content of 15 mg/100 g was recorded in GC-3 cultivar. Putinsev *et al.* (1976) reported that protein content in different varieties of pea ranged from 21.00 to 33.40% and varied by as much as 4-10% from year to year. Benken and Makasheva (1977) reported variations of 22.80 to 34.10% for protein contents in 50 genotypes of pea.

Krarup (1977) observed variation ranging from 14.90-27.60% for protein content in all the high yielding pea lines derived from the cross 1236493 x L2-1-7.

Tyagi *et al.* (1978) conducted a study on varietal resistance of powdery mildew disease in Rajasthan and reported that pea lines P 185 and P 6587 were immune to *Erysiphe polygoni* amongst the large number of varieties screened under natural conditions of infection and also following artificial inoculation.

Kalia (1985) screened 145 cultivars of garden pea in the mid hills of Himachal Pradesh against *Erysiphe polygoni* under natural and artificial epiphytotic conditions and reported wide variation. Only seven cultivars *viz.*, P 185, P 388, P 6583, P 6587, P 6888, T 10 and Sugar Giant were found to be highly resistant.

Thakur and Verma (1988) screened 70 cultivars of pea in the mid hills of Himachal Pradesh against powdery mildew (E. *Polygoni*) and reported HFP-6 to be highly resistant. On the other hand, Kuo (1988) from China reported Taichung 12 (bred from Taichung 11 X Manoa Sugar) as highly resistant to powdery mildew.

Haeder (1989) reported sugar content in the range of 4.40-8.30% in garden peas and 0.70-2.60% in field peas, however, it was slightly higher in the leafless cultivars. Thakur *et al.* (1996) tested 86 lines of garden pea against powdery mildew disease in the dry temperate zone of Himachal Pradesh and reported seven lines *viz.*, Sugar Giant, Pant P-8, DPP-54, PMR-3, JP-71, DPP-26 and HPPC-95 as resistant (<10% infection), 14 were rated as moderately resistant (<25% infection) and remaining lines were found to be moderately (<50% infection) to highly (>51% infection) susceptible.

Hybl et al. (1998) found that the starch content varied from 31.00 to 56.50% in field peas and 17.60 to 49.30% in garden peas.

Ramesh *et al.* (2002 a) evaluated nutrient quality of 36 genotypes of pea and recorded significant variation in the total sugar (5.13-9.52%), reducing sugar (1.34-5.31%) and non-reducing sugars (2.62-5.44%) in matured seeds of peas. The genotypes JP-501-A/2, PH-1-5 and PH-1 recorded the highest sugar content and soluble protein in both edible grains and matured seeds.

Nair and Khare (2009) revealed high heritability and genetic advance for total sugar and reducing sugar indicating use of direct selection for its improvement. Genotypes 'Arkel', 'Pusa Pragati' and 'VRP 6' had high total sugar (>10%) with 80% as reducing sugar.

2.3 Correlation studies

Correlation coefficient is the measure of the degree of association between the two traits (Hayes *et al.* 1955). Yield is a very complex entity, polygenically controlled and subject to the fluctuating environment, and hence, the selection of superior genotypes based on the performance of yield as such is usually not effective. To raise the genetic potential of a crop, the knowledge of nature and magnitude of association among different characters is of immense value to any breeding programme and forms a basis for selection (Robinson *et al.* 1951). The correlation among the different pairs of characters and their influence on yield assume special significance because selection for any character invariably affects number of other associated characters while bringing out improvement. Johnson *et al.* (1955 b) stressed the importance of both phenotypic and genotypic correlation among the characters in planning and evaluating breeding programmes. Correlation coefficients for a given trait vary with the genotypes and the environment where the study is carried out.

Kohli *et al.* (1971) reported that pod yield per plant was positively and significantly correlated with plant height, pod length, seeds per pod and pod weight. On the other hand, Jandial (1972) observed strong association between pod yield and number of pods per plant.

Srivastava *et al.* (1972) found significant and positive genotypic correlations of pod yield with days to flowering, pods per plant and seeds per pod and that of pod length with seeds per pod and days to flowering with pod length while significant negative association was noticed between pod length and pods per plant. Nandpuri *et al.* (1973) reported significant positive correlations between pod yield per plant and pods per plant whereas negative correlation was observed between shelling (%) and pods per plant and that of plant height with pod weight and seeds per pods.

Audiberti *et al.* (1973) reported positive correlation between protein content and plant height whereas Peshin (1975) observed negative correlation of seeds per pod and plant height with protein content. He also noticed positive correlation between yield and pods per plant. Pandey and Gritton (1975) also observed strong positive phenotypic and genotypic correlation between pod yield per plant and pods per plant and that of plant height with pods per plant and yield per plant.

Korla and Rastogi (1977) reported pods per cluster positively correlated with pod yield and negatively with days taken to first picking. Strong association was also observed between pod weight, seeds per pod, shelling (%), pod length and days taken to first picking but their correlations with pod yield were non-significant. Narsinghani *et al.* (1978) revealed that pods per plant were positively correlated with plant height whereas both these traits showed negative association with protein content. Correlation coefficients of days to maturity and plant height with days to flowering were positive.

Teotia *et al.* (1983) reported that yield per plant was positively associated with seeds per pod, pod length and pods per plant at both phenotypic and genotypic levels and negatively with plant height and days to first picking. Positive correlation was also noticed for days to first picking with plant height, seeds per pod and pod length at genotypic level and that of seeds per pod with pod length at phenotypic level.

Katiyar and Ram (1987) revealed that pods per plant, pod length, harvest index and seeds per pod in powdery mildew resistant lines of pea were positively and significantly correlated with marketable yield. Singh *et al.* (1987) noticed that seed yield per plant was positively correlated with pods per plant, plant height, branches per plant, days to flowering and days to maturity. Negative correlations were also observed between harvest index and seed protein content on the one hand and days to flowering, days to maturity and 100-seed weight on the other. Harvest index was considered a suitable criterion for selection to improve both seed yield and protein content. El-Murabaa *et al.* (1988) also observed significant positive association of total green pod yield with pod length and pod weight.

Srivastava and Singh (1989), in a study with 178 germplasm lines of pea, reported positive correlation coefficients of pod length with seeds per pod and days to maturity, days to flowering with days to maturity and pods per plant, and days to maturity with plant height. Partap *et al.* (1995) showed that days to flowering were positively associated with growth characters and negatively with pod and seed characters. On the other hand, pod yield, pod and seed characters were positively inter-related.

Dev *et al.* (1996) derived information on correlations of different quality traits with pod yield and revealed that none of the quality traits showed significant association with yield per plant. Kumar *et al.* (1998) reported significant and positive correlations of pod yield with plant height, pod length and pods per plant and that of plant height with pod length and pods per plant.

Sharma and Kalia (1998) observed that pod yield per plant was found to have significantly positive association with pods per plant, plant height, pod length, seeds per pod in BIP's as well as F_3 . Bhardwaj and Kohli (1999) noticed that yield had significant and positive association with node number bearing first flower, days to 50% flowering, shelling (%) and pods per plant. Seed yield per plant exhibited a significant and positive correlation with plant height, number of pods per plant, 1000-seed weight, number of grains per pod and harvest index (Tiwari *et al.* 2001).

Pathak and Jamwal (2002) found generally higher genotypic correlation coefficients than the corresponding phenotypic correlation coefficients and reported positive correlation of pod yield per plant with pods per plant, plant height and average pod weight at the phenotypic level. Ramesh and Tewatia (2002) observed that pod weight per plant had strong positive association with pods per plant, grains per pod, mean pod weight, pod length, plant height and grain weight per pod.

Singh and Mishra (2002) observed that seed yield per plant was positively and significantly associated with pods per plant, harvest index and primary branches per plant. Chaudhary and Sharma (2003) construed higher genotypic correlation coefficients than the phenotypic correlation coefficients and revealed positive phenotypic correlation of pod yield per plant with pod length, grains per pod, pods per plant and shelling (%).

Kumar *et al.* (2003) noticed that yield per plant was positively associated with pods per plant, primary branches, plant height, pod length and seeds per pod at the genotypic level. Similarly, positive association was observed for days to flowering with days to maturity and seeds per pod; plant height with secondary branches, pods per plant and harvest index; primary branches with secondary branches, days to maturity, pods per plant, seeds per plant, pod length, and 100-grain weight; secondary branches with pod length and pods per plant; days to maturity with 100-grain weight and seeds per pod; and pod length with pods per plant and seeds per pod.

Arya *et al.* (2004 a) noticed 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 and these characters were also positively correlated with each other. Kumar *et al.* (2004) found higher genotypic correlation coefficients 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 and observed positive and significant correlation for days to flowering with first pod bearing node and days to first picking; plant height with shelling (%); pod length with green pod yield and 100-green seed weight; pods per plant with green pod yield and protein content of green seeds; and 100-green seed weight with green pod yield.

Kalloo *et al.* (2005) revealed significant positive correlation of first flowering node with days to flower and plant height and that of pod length with average pod weight. Green pod yield had significant and positive association with green pods per plant, number of grains per pod, shelling (%) and pod length (Mehta *et al.* 2005).

Singh and Singh (2005) revealed that the magnitude of genotypic correlation coefficients was higher than the phenotypic correlation coefficients, suggesting the existence of inherent association among the traits studied. Grain yield per plant showed positive and significant correlation with pods per plant, branches per plant, plant height, pod length and seeds per pod. Singh *et al.* (2005) found that fruit yield per plant was positively correlated with pods per plant, seeds per pod, shelling (%) and days to marketable maturity.

Singh and Yadav (2005) noticed that seed yield had strong positive genotypic and phenotypic correlation with pods per plant, branches per plant, seeds per pod and pod length. The number of days to 50% flowering exhibited significant negative genotypic and phenotypic correlation with seed yield, number of pods per plant, and number of branches per plant. Gupta and Singh (2006) observed significant and positive correlation of green pod yield per plant with pod length, pods per plant and 100-green pod weight at genotypic and phenotypic level except pod length whereas it had significant negative correlation with days to first flowering, first flowering node, nodes per main stem and plant height, indicating selection for longer pods, more number and weight of green pods per plant, early flowering, flowering at lower nodes, less number of nodes per main stem and dwarf plants would be highly desirable and effective.

Kumar and Sharma (2006) revealed that pod yield per plant had significant positive correlation with pods per plant, node number of first flower and plant height. Days to first flowering had highly significant positive correlation with node number of first flower and days to first green pod harvest and negative significant correlation with 1000-seed weight. Pods per plant exhibited significant positive correlation with pod yield per plant and biomass weight of plant while its association with shelling (%) was significantly negative. Patel *et al.* (2006) noticed that genotypic correlations were higher than the phenotypic correlations among all the combinations, except for yield per plant with branches per plant, pod length, seeds per pod, 100-seed weight and harvest index, which would be due to the masking or modifying effects of the environments. Yield per plant was found positively correlated with pods per plant, branches per plant, pod length, days to maturity and shelling (%) at genotypic and phenotypic levels.

Sirohi *et al.* (2006) showed positive and significant association of seed yield with protein content, and that of biological yield per plant with harvest index. Among the inter se associations, positive and significant associations at phenotypic level were noticed for days to flowering with days to maturity, pods per plant and pod length; primary branches with plant height, pods per plant and pod length; plant height with pod length and harvest index; and plant height with pods per plant.

Kaur *et al.* (2007) noticed highly significant and positive correlation of green pod yield per plant with pods per plant, seeds per pod, pod length, crude protein content, days taken to flower initiation, number of branches and shelling (%), suggesting that these are the major yield contributing characters. Mahajan *et al.* (2007) revealed positive association of seed yield with pod length and negative association with days to flower and maturity. Pods per plant, seeds per pod and pod length are important characters which are least influenced by the climatic condition in mid-altitudes over years.

Rathi and Dhaka (2007) observed negative association of seed yield with days to 50% flowering, days to green pod picking and days to maturity. Sharma *et al.* (2007) revealed positive association of pod yield per plant with pods per plant, pod length, seeds per pod and total soluble solids. Singh (2007) found that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients, indicating the strong inherent association among different characters. Seed yield showed strong and positive correlation with number of pods per plant, number of branches per plant, number of seeds per pod and pod length.

Usmani and Dubey (2007) observed that seed yield was positively and significantly correlated with harvest index, biological yield, pod bearing length, plant height, number of effective nodes, number of nodes and number of pods. Green pod yield per plot had positive and significant correlation with seeds per pod and weight of pods

per plant at genotypic and phenotypic levels (Nawab *et al.* 2008). Plant height, pod length and 100-seed weight were positively associated with grain yield (Singh *et al.* 2008).

Togay *et al.* (2008) noticed positive and significant relationship among seed yield and pods per plant and biological yield in both years. Pod number and seeds per pod had strong correlation coefficient with yield and should be selected to increase the grain yield (Guleria *et al.* 2009). Sharma *et al.* (2009) found highly significant and positive correlation between green pod yield per plant and plant height, pods per plant, and node at which first flower appears. Significant and positive association between green pod yield per plant and node at which first flower appears indicated that selection for higher yield can be practiced as soon as the first pod develops.

Devi *et al.* (2010) revealed that days to first flower and seed yield had the highest positive and significant correlation with length of internodes, days to first green pod harvest, number of primary branches, length of pods, number of seeds per pod, number of pods per plant, pod yield per plant. Dhama *et al.* (2010) observed that the value of genotypic correlations was higher than phenotypic correlations for all the characters in all the eight environments. Number of pods per plant exhibited significant and positive association with seed yield per plant in all environments while it was significantly and positively associated with protein content at genotypic level in E5. Seed yield per plant exhibited significant and positive correlation with number of pods per plant, number of branches per plant and 100-green seed weight (Kumar *et al.* 2010).

Awasthi *et al.* (2011) found positive and significant correlation for plant height, pods per plant and primary branches per plant with seed yield at genotypic and phenotypic levels suggesting their potential use as selection indices for improvement of garden pea genotypes for higher yield. Pods per plant, plant height, primary branches per plant and 100-seed weight were the major characters contributing to grain yield as these traits were significantly and positively associated with grain yield per plant (Singh *et al.* 2011).

2.4 Direct and indirect effects

Path analysis splits the correlation coefficients into the measures of direct and indirect effects of a set of independent variables on the dependent variable. The estimates of correlation coefficients provide only the inter-relationship of the characters, but do not furnish information on the cause and effect. Due to mutual association, the development of dependent variable is determined by the degree of the direct effect of independent variables and direct effects exerted via other characters, arising inevitably as an integral part of the growth pattern. Under such complex situations, the total correlation is insufficient to explain the real association for an effective and fruitful manipulation of the character. Wright (1921) provides a better knowledge by revealing direct and indirect a given correlation and measures the relative importance of each causal factor. Dewey and Lu (1959) were the first to demonstrate the utility of path coefficient analysis in breeding programme, using crested wheat grass progenies.

Wakankar *et al.* (1974) and Peshin (1975) reported the highest direct positive effect of pods per plant on green pod yield. However, Peshin (1975) also revealed that days to flowering and days to maturity had positive indirect effects on pod yield per plant through pods per plant and plant height.

Chandel and Joshi (1976) observed positive direct effects of seeds per pod, pods per plant and plant height towards pod yield and that of negative direct effect at phenotypic level through days to flower and pod length. However, the indirect positive effects of days to flower via pods per plant, pod length via days to flower, and plant height via pods per plant were also recorded. Positive direct contribution of number of pods per plant towards pod yield has also been observed by Kallo and Dhankar (1977).

Narsinghani *et al.* (1978) revealed that number of days to maturity, plant height and protein content exhibited direct positive effects on pod yield. Teotia *et al.* (1983) found that pods per plant, seeds per pod, protein content and TSS had direct positive effects on yield at genotypic level, while plant height, pod length, shelling (%), days to first picking and ascorbic acid had negative direct effects on yield. Singh and Singh (1985) showed that pods per plant, days to flowering and seeds per pod had the maximum direct positive contributions to pod yield. Similar observations were also recorded by Katiyar and Ram (1987). Pods per plant, seeds per pod and pod length are the major yield component affecting pod yield per plant (Singh and Ram 1988).

Joshi and Narsinghani (1992) construed that pods per plant and days to maturity had direct effects on seed yield per plant. It was suggested that pods per plant in pea was the most reliable component in breeding programmes for increased yield potential. Seeds per pod showed the highest positive direct effect on yield followed by pods per plant in dwarf types (Kumar *et al.* 1995)

Ramesh and Tewatia (2002) revealed that pods per plant had maximum direct genotypic effect on pod weight per plant, followed by mean pod weight, total sugars in edible grain, number of nodes on main stem per plant, days to first picking and grain weight per pod. Pods per plant had the highest direct effect followed by harvest index on seed yield and the selection based on pods per plant, harvest index and primary branches per plant will give fruitful results for yield improvement in pea (Singh and Mishra 2002).

Chaudhary and Sharma (2003) found that the grains per pod, pod length, pods per plant, and 1000-seed weight had the greatest direct effect on pod yield per plant. Arya *et al.* (2004 a) revealed that pods per plant had the greatest direct effect on seed yield, followed by height at which the first pod appears, plant height, node number at which the first pod appears, and number of primary branches per plant.

Singh *et al.* (2005) reported that pods per plant and shelling (%) had the maximum direct effect on green pod yield. Singh and Singh (2005) found that number of pods per plant had the maximum positive direct effect on grain yield, followed by number of seeds per pod, 100-seed weight and pod length. Plant height, branches per plant, seeds per pod, pod length and harvest index had the highest indirect effects on grain yield per plant via pods per plant.
Singh and Yadav (2005) revealed that the number of pods per plant had the greatest direct genotypic and phenotypic effects on seed yield, followed by pod length and should be considered important in any selection programme for the improvement of pea yield. Patel *et al.* (2006) revealed that pods per plant, branches per plant, shelling (%) and harvest index should be given more emphasis in selection programme of peas.

Kaur *et al.* (2007) revealed that direct effects were highest for pods per plant, node at which first fertile pod develops, number of branches, seeds per pod and pod length which can serve as reliable variable for selection. Rathi and Dhaka (2007) found that yield per plant is directly affected by pods per plant, dry matter yield, pod length, harvest index and seeds per pod and thus it may be treated as selection criteria for isolating higher yielding genotypes in pea. Highly positive direct effects through pods per plant, plant height and pod length on pod yield were noticed by Sharma *et al.* (2007).

Singh (2007) observed that pods per plant had the highest positive direct effect on seed yield, followed by branches per plant, seeds per pod and pod length. The genotypic path revealed that harvest index showed the highest positive direct effect followed by biological yield on seed yield. The indirect effects of biological yield and harvest index via other yield contributing characters were high and positive (Usmani and Dubey 2007).

Nawab *et al.* (2008) observed that 100-seed weight, pods per plant, number of seeds per pod and days to 50% flowering exhibited maximum positive direct effect on green pod yield per plot. Singh *et al.* (2008) observed that 100-seed weight followed by number of primary branches and pods per plant had high direct effect on grain yield. Biological yield and number of pods per plant recorded the highest positive and direct effects on seed yield, followed by first pod height and number of seeds per pod (Togay *et al.* 2008).

Espósito *et al.* (2009) revealed that number of pod and seeds per plot were the main components of seed yield, having the maximum direct effects and might be used as selection criteria in order to increase the selection efficiency in pea breeding programs. Guleria *et al.* (2009) revealed that flower number, pod number and seeds per pod contributed positively to the grain yield. Sharma *et al.* (2009) reported that pods per plant

recorded highest positive direct effect on pod yield per plant followed by node at which first flower appears and plant height. Direct contribution of these traits indicated that by making selection for these traits, the yield can be substantially improved.

Katore and Navale (2010) noticed that 100-seed weight, pod length, seeds per pod, days to maturity and days to flowering were the major yield contributing characters and emphasis should be given on these characters in selection programmes to develop desirable pea genotypes. Singh *et al.* (2011) recorded highest positive direct effect of number of pods per plant on grain yield per plant via positive indirect effects of plant height and number of primary branches per plant. Awasthi *et al.* (2011) noticed that plant height and pods per plant exhibited high positive direct effect on seed yield.

2.5 Genetic divergence studies

The assessment of genetic diversity using quantitative traits has been of prime importance in differentiating well defined populations. The germplasm in a autogamous crop can be considered as a heterogeneous sets of groups, since each group being homozygous within itself. The selection of parents for hybridization programme is critical because the success depends upon the selection of segregants from the cross combinations to meet out the aim of high yield with desirable horticultural traits.

To help the breeders in the process to identify the parents that nick better, several methods of divergence analysis based on quantitative traits have been proposed to achieve various objectives. The method of Mahalanobis's generalised distance finds a unique place and is efficient to determine the extent of diversity among different genotypes, which quantify the differences among several quantitative traits.

With the development of advanced biometrical techniques, multivariate analysis based on Mahalanobis's D^2 statistic (Mahalanobis 1936) has been used for discriminating divergent populations (Murthi and Quadri 1966) rather than gathering information from earlier indices like morphological similarities, ecographic diversity and phylogenetic relationship. Estimation of degree of divergence between biological population and computation of different components to the total divergence is done completely by Mahalanobis generalised distance estimation of D^2 statistics (Nair and Mukherjee 1960; Maurya and Singh 1977).

Selection of parents in hybridization programme based on Mahalanobis D^2 statistic is more reliable as the requisite knowledge of parents in respect of various characters is available prior to initiation of crossing. Nair and Mukherjee (1960) were the pioneers to use the D^2 statistics as a measure of genetic divergence in the field of plant breeding for classification of teak.

Gupta *et al.* (1992) grouped 35 lines into six clusters in environment I and II and into nine clusters across environments. About 60% of the lines showed consistency in clustering pattern in environment I and II. However, the distribution of lines included in different clusters and the intercluster distance pattern differed significantly between environments. Partap *et al.* (1992) analysed 20 characters in 49 genotypes and indicated that the number of clusters ranged from 9 to 13 depending on the environment, with many clusters containing only one genotype. Clustering behaviour of the genotypes showed that neither the number of clusters formed nor the entries included in each cluster were influenced by the place of origin. Intracluster and intercluster genetic distance values varied widely in the population. The clusterwise mean pod yield per plant for the different environments was not constant which suggested that agronomic practices and human selection pressure had the most effect on cluster patterns. It is proposed that for hybridization and improvement programmes in pea, genotypes can be selected randomly from divergent clusters possessing high mean pod yield.

Kumar *et al.* (1994) subjected 11 yield components in 62 genotypes (31 dwarf and 31 tall) from various geographical regions to clustering analysis and grouped into 9 and 12 clusters, respectively. No clear association was observed between geographical distribution and genetic divergence. Promising genotypes for hybridization based on genetic divergence and per se performance were Pusa 2, DDR8, DDR9 and KFPD5 among dwarf and HFPK20, KPMR60, KPMR65 and HPPC77 among tall. Vikas and Singh (1999) indicated the existence of considerable diversity among 45 pea (*Pisum sativum*) genotypes over two environments and grouped these into four (E1) and nine (each in E2 and pooled) clusters. Clusters I was the largest consisted of 38 (E1), 13 (E2) and 18 genotypes (pooled) followed by cluster II which consisted of five (E1), 12(E2) and 16 genotypes (pooled) whereas cluster IV (E1 & pooled) V, VI, VII (pooled) and

VIII and IX (E2 & pooled) had single genotype each. Maximum intra-cluster values were observed in cluster I followed by clusters III and II in E1; cluster I followed by clusters II and III in E2; and cluster I followed by cluster III in pooled analysis, relaying, some intracluster diversity. Maximum inter-cluster values were observed between cluster III & IV (E1), cluster V & IX (E2) and cluster IV & V (pooled), indicating that the genotypes included in these clusters had maximum divergence.

Sureja and Sharma (2001) grouped the genotypes into four clusters, with I, II and III each comprising six genotypes and IV comprising 12 genotypes. The grouping pattern of the genotypes was random, indicating that geographical diversity and genetic divergence were unrelated. Therefore, selection of genotypes for hybridization should be based on genetic divergence rather than geographical diversity. Singh and Singh (2003) studied genetic divergence for ten traits in 50 accessions of pea and grouped the genotypes into 11 clusters. Cluster XI was the largest (9 genotypes), followed by clusters II, VI, I, V, X, VIII, IV, IX, III, and VII. The highest intra-cluster values were recorded for cluster IX, whereas the highest inter-cluster value was observed between clusters III and IX. Cluster means for the ten traits indicated that the genotypes included in cluster IX gave the highest seed yield per plant, biological yield, number of pods per plant, and pod length, whereas those included in cluster X had the highest number of seeds per pod and pod length, and average 100-seed weight and number of pods per plant. The genotypes in cluster VIII had high 100-seed weight and average seed yield per plant, whereas those in cluster III had the highest harvest index, and average 100-seed weight and seed yield per plant. The results revealed that the genotypes under these diverse clusters had good potential as parents for hybridization studies in pea.

Arya *et al.* (2004 b) found nine clusters for 36 elite genotypes of field pea. Cluster I had the highest number of genotypes, whereas clusters VII, VIII and IX had only one genotype each. The inter-cluster distance was greatest between clusters I and IX, followed by III and IX, I and VI, and I and V, and further suggested that the higher the inter-cluster distance, the greater the diversity between genotypes and vice versa and crosses between genotypes from distant clusters will give better transgressive segregants. Tiwari *et al.* (2004) grouped 34 genotypes into six clusters. The cluster V and VI were

the largest with eight genotypes each while cluster I contained only one genotype and was the most divergent. They further suggested that genotypes of clusters I, II, III and IV could be exploited for hybridization programme based on maximum inter-cluster distance.

Yadav *et al.* (2004) clustered 45 pea lines into 15 groups. Intra-cluster divergence was low for clusters V, VII, VIII and IX. They construed that genetic constitution rather than the geographical placement played a major role in the clustering pattern of the genotypes. Gupta and Singh (2006) determined genetic divergence in 83 garden pea genotypes and grouped the genotypes into 27 clusters. Cluster I had the highest number of genotypes. Inter-cluster variation was highest between clusters VI and XXIV and lowest between clusters XVII and XXVII. Cluster XII had the highest mean for green pod yield per plant, whereas cluster XXIV had the highest mean for earliness, number of first flowering nodes, number of days to first green pod picking and shelling (%). Cluster XXII had the highest mean for pod length and 100-green pod weight. Cluster XIX recorded the highest mean for number of seeds, number of green pods and number of days to maturity. Early yield per plant had the highest contribution to the genetic divergence among the genotypes tested.

Kumar *et al.* (2006) grouped 100 pea genotypes into eight clusters, of which, the cluster I was the largest consisting of 32 genotypes, followed by cluster II with 20 genotypes whereas the cluster VIII was the smallest with 3 genotypes. Intra-cluster values revealed that cluster VIII was the most diverse (13.49), followed by cluster VII (8.37) and cluster VI (8.16). The highest inter-cluster value was observed between clusters V and VII (23.15) indicating that genotypes included in these clusters had maximum divergence. There was no parallelism between genetic and geographic diversity. The genotypes 02/1119 and PH-1 (cluster V), HFP-2005 and HFP-9907A (cluster VI), HFP-9937 and MP-Arkel (cluster VII) and 02/1090 (cluster VIII) might be used as promising parents for yield and quality attributes in hybridization for pea improvement programmes. Singh and Singh (2006) evaluated thirty-one advanced genotypes of pea and observed six clusters based on D² values. Cluster I, which had the advanced genotype KPMR632, was more divergent and monogenotypic. Cluster VI was

the largest, with eight genotypes. The inter-cluster distance was lowest between clusters III and VI, and greatest between clusters I and II, closely followed by clusters I and IV. The intermating among the genotypes from clusters I, II and III may be used to improve the grain yield of pea.

Kumar *et al.* (2007) grouped the 100 genotypes into nine clusters. The cluster I had the maximum 22 genotypes followed by 20 in cluster II. The maximum inter-cluster values were observed between clusters VII and IX followed by clusters II and IX, clusters VI and VII, clusters VI and VIII and clusters VII and VIII. Plant height contributed maximum towards total genetic divergence. The grouping pattern did not show any relationship with geographical diversity. Genotypes from divergent clusters are expected to yield potential transgressive segregants for further exploitation in pea breeding programmes. Singh *et al.* (2007) indicated presence of considerable genetic divergence among the 120 genotypes which were grouped into six clusters and suggested that to get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI could be followed as the inter cluster distance was greater between these clusters.

Singh and Mishra (2008) grouped 21 genetically diverse pea genotypes into six dusters. Cluster I was the biggest with 11 genotypes followed by clusters II and III with 4 and 3 genotypes, respectively while cluster IV, V and VI had only one genotype. The maximum inter-cluster distance was observed between clusters II and VI and was followed by clusters II and V, and clusters III and VI indicating wide divergence among these clusters, which also suggested that the genetic architecture of the genotypes in one cluster differed entirely from those included in other clusters. The diversity among the genotypes measured by inter-duster distance (D value) was adequate for improvement of pea by hybridization and selection. Sharma *et al.* (2009) evaluated 14 diverse genotypes of early maturing garden pea for genetic divergence and grouped these into six clusters. Cluster V showed maximum intra-cluster distance while cluster I and V followed by clusters. The maximum divergence in these clusters. The maximum contribution towards divergence was made by number of pods per plant, followed by shelling (%), grains per pod and pod length.

Yadav *et al.* (2009) examined the genetic divergence among 62 genotypes for ten characters and suggested that genotypes included in clusters having maximum intra and inter-cluster values may show high heterotic response and will produce better segregants in response to high degree of genetic diversity in the genotypes. Devi *et al.* (2010) grouped 12 strains into four clusters of which cluster I retained the maximum number of genotypes followed by cluster II and cluster III with three genotypes each while cluster IV accommodated only one genotype. The maximum value of inter-cluster distance was observed for cluster I. Cluster IV showed the maximum value of cluster mean for pod length, pod breadth, seeds per pod, pods per plant, pod yield per plant, seed yield per plant and shelling (%).

It can be concluded from the review of literature that tremendous efforts have been made by the breeders for the genetic improvement of garden pea. Despite continuous breeding efforts, the yield potential of garden pea has reached a plateau and still the age old varieties find favour among the farmers. The major factors posing restrictions to overcome these barriers are consumer's preference for long and dark green pods, shelf life in transit and susceptibility to various biotic stresses. Therefore, to enhance the productivity, genetic restructuring of germplasm of garden pea is required to develop high yielding varieties with desirable horticultural traits. Accordingly, efforts have been made to create variability by following non-conventional and conventional breeding approaches to develop new and valuable alterations in plant characteristics. The present investigation will help in identifying the genotypes from this genetic material for different characters and meet out the requirement of farmers.



MATERIALS AND METHODS

The present investigation was carried out at the Experimental Farm of the Department of Vegetable Science and Floriculture, College of Agriculture, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur during winters 2009-10 and 2010-11. The details of materials used and methods employed in the present investigation are presented below:

3.1 Experimental site

The Experimental Farm is situated at an elevation of 1, 290.8 m above mean sea level with 32^{0} 6 N latitude and 76^{0} 3' E longitude. The location is characterized by humid and temperate climate with an annual rainfall of 2,500 mm of which 80% is received during June to September and represents the mid-hill zone of Himachal Pradesh. The soil is classified as Alfisols typic Hapludalf clay having a pH of 5.7. The mean weekly meteorological data with regard to temperature, relative humidity and rainfall during the cropping period of location is presented in Fig. 1 and Appendix-II.

3.2 Materials and layout of the experiment

3.2.1 Experimental materials

The experimental materials comprised of 41 genotypes of garden pea of which 28 isolated from induced mutations, seven through hybridization followed by selection and six other released varieties. Their details are given below:

Sr. No.	Genotypes	Source
1.	DPPMFWR-1	Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur
2.	DPPMFWR-2	-do-
3.	DPPMFWR-3	-do-
4.	DPPMFWR-4	-do-

5.	DPPMFWR-5	Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur
6.	DPPMFWR-8	-do-
7.	DPPMFWR-11	-do-
8.	DPPMFWR-12	-do-
9.	DPPMFWR-20	-do-
10.	DPPMFWR-27	-do-
11.	DPPMFWR-29	-do-
12.	DPPMFWR-30-1	-do-
13.	DPPMFWR-30-2	-do-
14.	DPPM-1	-do-
15.	DPPM-22	-do-
16.	DPPM-64	-do-
17.	DPPM-65	-do-
18.	DPPM-72	-do-
19.	DPPM-73	-do-
20.	DPPM-74	-do-
21.	DPPM-07-4	-do-
22.	DPPM-07-9	-do-
23.	DPPM-07-30	-do-
24.	DPPMR-09-1	-do-
25.	DPPMR-09-2	-do-
26.	DPPMR-09-3	-do-
27.	DPPMR-09-5	-do-
28.	DPPMR-09-9	-do-
29.	DPP-25G	-do-

30.	DPP-89	Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur
31.	DPP-100	-do-
32.	DPP-168	-do-
33.	DPP-3-1	-do-
34.	DPP-11-2	-do-
35.	DPP-17-2	-do-
36.	VP-215	-do-
37.	Green Pearl	ProAgro seed company
38.	Lincoln (Check)	ICAR-RRS, Katrain
39.	Azad P-1 (Check)	CSAUA&T, Kanpur
40.	Palam Priya (Check)	Department of Vegetable Science & Floriculture, COA, CSKHPKV, Palampur
41.	Punjab-89 (Check)	-do-

3.2.2 Layout plan

The experiment was laid out in Randomized Complete Block Design with three replications. Each genotype was grown in three rows of 3 m length in winter 2009-10 and during winter 2010-11 in one row of 4 m length over the replications. These genotypes were sown on November 12 in 2009 and November 13 in 2010 with inter and intra-row spacing of 45 cm and 10 cm, respectively.

3.2.3 Cultural practices

The experiment field was disked and the recommended FYM @ 20 t/ha was mixed in the soil. The recommended rate of NPK fertilizers @ 50:60:60 kg of N, P_2O_5 and K_2O were applied in the rows at the time of sowing. Seed treatment with 'Bavistin' at the rate of 3g/kg of seed was done. Irrigation was provided prior to sowing and as needed thereafter. The weedicide 'Pendimethalin' @ 1.5 kg a.i./ha was applied immediately after sowing followed by two hand weeding to keep the field weed free.



Fig. 1 Mean weekly weather conditions during the cropping seasons

3.3 Recording of the data

The observations were recorded on randomly taken ten plants of each genotype in each replication followed by computing their means for the following horticultural and quality traits:

3.3.1 Horticultural traits

(I) Morphological traits

1. Days to first flower

Days to first flower were calculated from the date of sowing to the date when flowering appeared on any of the plant of a genotype.

2. First flower node

Recorded from the ground level to the node number which bears first flower.

3. Days to 50% flowering

Calculated from the date of sowing to the appearance of first flowering in 50% plants of a genotype.

4. Days to first picking

The number of days taken from sowing date to the date of first marketable picking of green pods were calculated.

5. Number of branches

The numbers of primary structural branches arising from the main stem were counted in the randomly taken plants.

6. Internodal length (cm)

The distance between two central nodes was measured on the main branch of the randomly taken plants in centimeters.

7. Nodes per plant

The total numbers of nodes on the main branch were counted in the randomly taken plants at the time of final picking in each genotype.

8. Plant height (cm)

Plant height was measured in centimeters from the base to the highest tip of the plant at the time of final harvest in each genotype in centimeters.

(II) Yield and yield contributing traits

1. Pod length (cm)

Pod length of 10 randomly taken fresh pods from the base to the tip was measured in centimeters in each genotype.

2. Seeds per pod

Seeds of each of the pods whose length was measured were counted.

3. Shelling (%)

Shelling (%) was worked out on 25 randomly harvested pods by using the following formula:

Shelling (%) = $\frac{\text{Seed weight of 25 pods (g)}}{\text{Pod weight of 25 pods (g)}} \times 100$

4. Pods per plant

The total number of pods picked from randomly taken plants at each harvest were counted and finally summed-up to work out the total number of pods per plant.

5. Pod yield per plant (g)

The number of pods at each picking were weighed and added to get the average pod yield per plant in grams.

6. Total biomass (g)

The randomly taken plants harvested at seed maturity were weighed along with pods to obtain total biomass in grams.

7. Seed yield per plant (g)

The harvested plants were threshed to obtain seed. After cleaning and grading, seeds were weighed to work out seed yield per plant in grams.

8. Harvest index (%)

Harvest index was calculated as a ratio of seed yield per plant to the total biomass per plant and expressed in percentage.

9. 100-seed weight (g)

One hundred dry seeds of each genotype were counted and weighed in grams.

10. Incidence of powdery mildew disease (%)

Observations on incidence of infection under natural conditions were recorded at maturity stage, when the disease was at its peak. The tagged plants in each treatment of each replication were categorized as under in relation to their resistance to the parasite as per the methodology given by Munjal *et al.* (1963).

Grade	Per cent infection	Description
0	0	Plant completely healthy with no trace of infection on any part (completely resistant).
1	25	Plant shows slight infection with roughly one in every four leaves infected, a fine coating of the powdery growth on the upper surface, the plant as a whole has green appearance, stems free from infection, plant size normal (moderately resistant).
2	50	Infection moderate, nearly 50 per cent leaves infected, the upper ones more severely, slight stem infection, normal plant size (moderately susceptible).
3	75	Nearly 75 per cent of the foliage infected, the whole plant appears to be covered with white powdery coating, stem also severely infected, plant slightly stunted (susceptible).
4	100	All the leaves of the plant as well as stem heavily coated with the fungal growth, leaves turn pale green to yellow and start drying up, the plant becomes conspicuous because of stunted growth (highly susceptible).

Per cent Disease Intensity (PDI) was calculated by using the formula of McKinney (1923).

	Total sum of all numerical rating
PDI =	× 100
	Number of observations taken × maximum disease score

3.3.2 Quality Characters

1. Total soluble solids (^oBrix)

Seeds of fresh pods from second picking were crushed in pestle-mortar and the liquid extract obtained was used to record the total soluble solids with the help of ERMA hand refractrometer.

2. Ascorbic acid (mg/100 g fresh weight basis)

The ascorbic acid contents were estimated by titration method as described by AOAC (1970).

Requirements

2% and 1% oxalic acid, distilled water, activated charcoal, Whatman filter paper, dye solution, burette, pipette, flasks, beakers, grinder etc.

Reagents

Dye solution

52 mg of 2, 6-dichloroindophenol dye was diluted in 100 ml distilled water and boiled for 5 minutes. Then, solution was allowed to cool. The volume was made up to 200 ml with distilled water. Then, 42 mg Na_2HCO_3 was added and mixed properly to obtain dye solution.

Procedure

- Determination of dye factor 20 mg standard ascorbic acid and 100 ml of 1% oxalic acid were mixed well and 5 ml volume of this solution was titrated against the dye to get pink colour which persisted for at least 15 seconds.
- Dye factor was calculated by using following formula-

Dye factor

=

1 _____ Titre

- 100 g of fresh pea seeds were grounded with 100 ml of 2% oxalic acid in grinder and slurry was made and then weighed.
- 20 g of above slurry was taken in beaker and was diluted with 100 ml of 1% oxalic acid.

- After shaking well, charcoal treatment was given, by adding 500 mg activated charcoal.
- Above solution was filtered with Whatman filter paper and clear solution was taken in flask.
- Then known volume of this filterate was titrated against dye.
- The end point was the appearance of rose pink colour which persisted for atleast 15 seconds.

Ascorbic acid (mg/100 g) = $\frac{D \times T \times V_1 \times W_2}{20 \text{ g} \times W_1 \times V_2} \times 100$

Where,

D	=	Dye factor
Т	=	Sample reading of titration
V_1	=	Volume made up
V_2	=	Volume used for titration
W_1	=	Weight of sample
W_2	=	Total weight of slurry.

3. Protein content (AOAC, 1990)

Reagents

Concentrated sulphuric acid

Digestion mixture : K_2 SO₄ and CuSO₄ were mixed in the ratio 10 : 1

30% sodium hydroxide

0.01 N Hydrochloric acid

Methyl Red indicator

2% Boric acid

Procedure

Dry pea seeds were grounded to a fine powder. Nitrogen contents in these sample were estimated by Microkjeldahl Method (AOAC 1990) to calculate protein content as:

Protein content (%) = Estimated Nitrogen \times 6.25

Digestion of sample

- 0.5 g of sample was taken in digestion flask along with 5 g digestion mixture and then 20 ml conc. H₂ SO₄ was added to it.
- The above material was left overnight for pre-digestion.
- The material was digested on heater till the material turned transparent and then allowed to cool.
- Flask was shaken well after adding 15 ml water to it and then final volume was made to 100 ml.

Distillation

- From prepared volume, 10 ml of aliquot was taken in distillation apparatus and 10 ml of 30% NaOH was slowly added to it and was distilled for 5 minutes.
- The ammonia liberated was collected in 100 ml conical flask containing 10 ml of 2% boric acid to which methyl red indicator was previously added.

Titration

- This content of the flask was titrated against 0.01 N HCl till the colour changed from light blue to pink and the reading was noted for the volume of HCl used.
- Reading was also taken for a blank sample.

Calculations

Weight of the sample (W)	=	0.5 g
Volume made	=	100 ml
Volume taken for distillation	=	10 ml
Amount of acid used for titration of sample	=	S ml
Amount of acid used for titration of blank	=	B ml
Actual acid consumed	=	(S-B) ml

Now,

N (04)	_	(S-B) \times 0.014 \times volume of digest \times normality of acid used	v 100
19 (70)	-	Aliquot taken × W	× 100

Protein content (%) = N (%) \times 6.25

4. Total sugars (%)

Total sugar was estimated by following the method of Dubois et al. (1956).

Reagents Used

- Phenol 5%: 50 g phenol (reagent grade) was dissolved in water and diluted to 1 litre.
- Sulphuric acid: 95.5% reagent grade.
- Standard Glucose Solution: Stock solution-100 mg glucose was dissolved in 100 ml distilled water. Working standard-10 ml of stock solution diluted to 100 ml with distilled water.

Procedure

100 mg sample of dry seeds was taken and grounded in pestle and mortar with 50 ml 80% ethanol. It was transferred into a beaker and was put on a hot plate till volume was reduced to half. Then, it was centrifuged and supernatant was used for testing total sugars. The supernatant was collected and 0.1 ml and 0.2 ml aliquots were taken for analysis. The standard was prepared by taking 0, 0.2, 0.4, 0.6, 0.8 and 1.0 ml of the working standard taking 0 as blank. The volume was made up to 1 ml in all the tubes including the sample tubes by adding distilled water. Then, 1 ml of phenol solution was added to each tube. After that 5 ml of 95.5% sulphuric acid was added to each tube and was shaken well. After 10 minutes, each tube was shaken again and placed in water bath at 25-30°C for 20 minutes. The contents were cooled and intensity of colour was read at 490 nm on Genesys 10 Vis Spectrophotometer. A standard curve was prepared by plotting concentration of the standards on X-axis versus absorbance on the Y-axis. From the graph, the amount of sugars (%) present in the sample was calculated.

Amount of carbohydrates in sample:

Absorbance corresponds to 0.1 ml of test = X mg of glucose

100 ml of the sample solution contains = $\frac{X}{0.1} \times 100$ mg of glucose = % of total sugars present.

5. Reducing sugars (%)

Reducing sugar was estimated by following the method of Miller (1972).

Reagents

- DNS (dinitrosalicylic acid) reagent- 1 g of DNS, 200 mg of crystalline phenol and 50 ml of sodium sulphite were dissolved in 100 ml of 1% NaOH solution by stirring it.
- 2. 40% of Rochelle salt (Sodium potassium tartrate).
- 3. Standard Glucose Solution :
 - (a) Stock solution 100 mg in 100 ml distilled water.
 - (b) Working standard solution 10 ml of stock diluted to 100 ml with distilled water.

Procedure

Extraction of the samples was done in similar way as for the total sugars. The supernatant was collected and 0.5 ml aliquots were taken for analysis. Three ml of DNS was added to it and was boiled for 5 minutes on boiling water bath up to colour development. One ml of 40% Rochelle salt was added, while the content was still warm. Test tubes were cooled under the running tap water and absorbance was taken at 510 nm. Amount of reducing sugar contents were recorded in similar way as it is prescribed for total sugars.

6. Starch content (%)

The starch contents were calculated according to the method given by Sadasivam and Manickam (1996).

Procedure

0.5 g of grain sample was taken in hot 80% ethanol to remove sugars. Then it was centrifuged and the residue was retained. Again, Washed the residue repeatedly with 80% ethanol till the washings had not given colour with anthrone reagent. The residue was dried well over a water bath. To the residue, 5 ml of water and 6.5 ml of 52% perchloric acid was added and extracted it at 0^oC for 20 minutes. Again it was centrifuged and the supernatant was saved. The extraction was repeated using fresh perchloric acid. The supernatant was pooled and made up the volume to 1 ml with distilled water.

Primary glucose standard (1000 ppm): Dissolved 100 mg glucose in 100 ml water.

Working glucose standard: 10 ml of primary standard diluted to 100 ml with distilled water.

Prepared the standards by taking 0.2, 0.4, 0.6, 0.8 and 1.0 ml of working standard and made up the volume to 1 ml in each tube with distilled water. To each tube of sample and standards, added 4 ml of anthrone reagent and heated them for eight minutes in a boiling water bath. Cooled rapidly and the intensity of green colour was read at 630 nm wavelength.

Calculation

Calculated the glucose content in the sample using the standard graph and multiplied the value by a factor 0.9 to arrive at the starch content.

3.4 Statistical analysis

3.4.1 Analysis of variance

The data for different characters was analyzed as per Gomez and Gomez (1983) and presented in the form of analysis of variance given in the table as follows :

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F ratio
Replications(r)	(r-1)	Sr	Mr=Sr/(r-1)	Mr/Me
Genotypes (t)	(t-1)	St	Mt=St/t-1	Mt/Me
Error (e)	(r-1) (t-1)	Se	Me=Ve	
Total	(rt-1)	-		

Where,

Mr = Mean sum of squares due to replication

Mt = mean sum of squares due to treatment

Me = Mean sum of squares due to error

The standard error of mean (SEm) and critical different (CD) for comparing the means of any two genotypes were computed as follows :

 $SE(m) = \pm (Me/r)^{1/2}$ $SE(d) = \pm (2Me/r)^{1/2}$

Critical difference (CD) = SE (d) x t (5%) value at error degree of freedom.

The calculated 'F' value was compared with the tabulated 'F' value at 5% level of significance. If the calculated 'F' value was higher than the tabulated, it was considered to be significant. All the characters which showed significant differences among genotypes were further subjected to the analysis for the different parameters.

3.4.2 Estimation of parameters of variability

The genotypic, phenotypic and environmental coefficients of variation were estimated by following method of Burton and De Vane (1953), as follows:

Genotypic coefficient of variation (GCV %)	$= \frac{\sigma_g}{\overline{x}} \times 100$
Phenotypic coefficient of variation (PCV %)	$= \frac{\sigma_p}{\overline{x}} \times 100$
Environmental coefficient of variation (ECV %)	$= \frac{\sigma_{e}}{\frac{1}{x}} \times 100$

W	here,
---	-------

σ_{g}	=	Genotypic standard deviation
σ _p	=	Phenotypic standard deviation
σ _e	=	Environment standard deviation
x	=	Grand mean

3.4.3 Heritability (h^2_{bs})

Heritability in broad sense (h_{bs}^2) was calculated as per the following formula given by Burton and De Vane (1953) and Johnson et al. (1955 a).

Heritability (%) =
$$\frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} \times 100$$

where,

σ_g^2	=	genotypic variance
σ_e^2	=	environmental variance
$\sigma_{g}^{2} + \sigma_{e}^{2}$	=	phenotypic variance

3.4.4 Genetic advance

The expected genetic advance (GA) resulting from the selection of 5% superior individuals was calculated as per Burton and De Vane (1953) and Johnson *et al.* (1955 a).

$$GA = k. \sigma_p.h^2$$

Where,

K = 2.06 (selection differential at 5% selection index) $\sigma_p = Phenotypic \text{ standard deviation}$

 h^2 = Heritability (broad sense)

Genetic advance as percentage of mean = $\xrightarrow{\text{Expected GA}}$ \times 100 Grand mean

3.4.5 Combined analysis of variance over environments

The combined analysis of variance over the environments was computed as per the procedure given by Verma *et al.* (1987).

The analysis was based on the following model:

 $Y_{ijk} = m + \alpha_i + \beta_j + \alpha \beta_{ij} + r_k + e_{ijk}$

Where

 Y_{ijk} = Phenotype of the ith genotype grown in jth environment in the kth block

m = General population mean

 α_i = Effect of ith genotype

 β_j = Effect of jth environment

 $\alpha\beta_{ij}$ = Effect of interaction of ith genotype with jth environment

 $r_k = k^{th}$ replication effect

 $e_{ijk} = Random error$

Source of variation	Degree of freedom	Mean Sum of Squares	F-Value	Expected Mean Squares
Replications	(r-1)	Mr	Mr/Me	$\sigma_e^2 + gy\sigma_r^2$
Environments	(y-1)	Му	My/Me	$\sigma_e^2 + rg\sigma_e^2 + r\sigma_{gy}^2$
Replication × environments	(r-1)(y-1)	Mry	Mry/Me	$\sigma_e^2 + g\sigma_{ry}^2$
Genotypes	(g-1)	Mg	Mg/Me	$\sigma_e^2 + r\sigma_{gy}^2 + yr\sigma_g^2$
Genotype × environments	(g-1)(y-1)	Mgy	Mgy/Me	$\sigma_e^2 + r\sigma_{gy}^2$
Pooled error	y(r-1)(g-1)	Me		σ_e^2

Analysis of variance combined over environments

Where,

r = Number of replications

g = Number of genotypes

y = Number of environments

 σ_e^2 = Error variance = Me

 σ_g^2 = Variance due to genotypes = Mg

 σ_r^2 = Variance due to replication = Mr

 σ_y^2 = Variance due to environments = My

 σ_{ry}^{2} = Variance due to replication × environments = Mry

 σ_{gy}^{2} = Variance due to genotype × environments = Mgy

Standard Errors

Standard Error of mean SE (m) = $\pm (Me/ry)^{1/2}$

Standard Error of difference between two genotypic means SE (d) = $\pm (2 \text{ Me/ry})^{1/2}$

Critical Difference

- For comparing the means of any two genotypes
- $CD = SE(d) \times t'$ value at 5% level of significance at combined error degrees of freedom.

Coefficient of Variation

 $CV(\%) = [(Me)^{1/2} / \overline{x}] \times 100$

Estimation of parameters of variability in combined over environments

Phenotypic Coefficient of Variation (PCV %) = $[(\sigma_g + \sigma_{gy} + \sigma_e) / \bar{x}] \times 100$

Genotypic Coefficient of Variation (GCV %) = $(\sigma_g / \vec{x}) \times 100$

Heritability (h_{bs}^2) in broad sense $(\%) = [\sigma_g^2/(\sigma_g^2 + \sigma_{gy}^2 + \sigma_e^2)] \times 100$

Genetic advance (GA) at 5% selection intensity = K ($\sigma_g + \sigma_{gy} + \sigma_e$) × h² (bs)

Genetic advance expressed as (%) of mean (GA %) = (GA/ \bar{x}) × 100

Where

 σ_g = Genotypic standard deviation

 σ_{gy} = Genotypic environmental standard deviation

 σ_e = Error standard deviation

For convenience, following classifications were used for describing various parameters in the text.

PCV and GCV:	>30 % - high; 10 – 30 % - moderate; <10 % – low
Heritability in broad sense:	>60 % - high; 30 – 60 % - moderate; <30 % - low
Genetic advance:	>30 % - high; 10 – 30 % - moderate; <10 % - low

Test of Homogeneity

The F-test (Test of Homogeneity) or the 'variance ratio' test was used to test the significance whether error variances are homogeneous or not. In order to carry the test of significance, F-ratio was calculated as:

$$F = \frac{S_1^2}{S_2^2}$$

Where

 S_1^2 = Large estimate of variance

 S_2^2 = Smaller estimate of variance

and $S_1^2 > S_2^2$

at $v_1 = n_1-1$ and $v_2 = n_2-1$ degrees of freedom

Where

 v_1 = degrees of freedom for sample having larger variance

 v_2 = degrees of freedom for sample having smaller variance

The calculated value of F was compared with the table value for v_1 and v_2 degrees of freedom at 5% level of significance. If calculated value of F was greater than the tabulated value, the F-ratio was considered as significant. If the calculated value of F was less than the table value, F-ratio was considered as non significant and it was inferred that both the samples have come from the population having same variance.

3.4.6 Correlation coefficients

For computing phenotypic, genotypic and environmental correlation coefficients, analysis of co-variance were carried out in all pairs of combinations of the characters.

Source of variation	df	Mean sum of product	Expected mean sum of product		
Replication(r)	(r -1)	Mr _{xy}	$\sigma_{exy} + g \sigma_{rxy}$		
Genotypes (g)	(g-1)	Mg _{xy}	σ_{exy} +r σ_{gxy}		
Error (e)	(r-1)(g-1) Me _{xy}	σ _{exy}		

Analysis of co-variance

Where,

 $\sigma_{exy} = \text{Error co-variance of character x and character y}$ $\sigma_{gxy} = \text{Genotypic co-variance of character x and character y}$ The genotypic, phenotypic, and error co-variances were calculated as follows: Genotypic co-variances (σ_{gxy}) = Mg_{xy} - Me_{xy}/r Phenotypic co-variances (σ_{pxy}) = $\sigma_{gxy} + \sigma_{exy}$ Environmental co-variances (σ_{exy}) = Me_{xy}

The phenotypic, genotypic and environmental coefficients of correlation were calculated as suggested by Al-Jibouri *et al.* (1958).

Phenotypic coefficient of correlation
$$(r_{pxy}) = \frac{\sigma_{pxy}}{\sqrt{\sigma_{px}^2 \times \sigma_{py}^2}}$$

where,

 σ_{pxy} = Phenotypic covariance between character x and y σ_{px}^{2} = Phenotypic variance of character x σ_{px}^{2} = Phenotypic variance of character y

Genotypic coefficient of correlation (rg_{xy}) = $\frac{\sigma_{gxy}}{\sqrt{\sigma_{gx}^2 \times \sigma_{gy}^2}}$

where,

 $\sigma_{gxy} =$ Genotypic co-variance between character x and y $\sigma_{gx}^2 =$ Genotypic variance of character x $\sigma_{gy}^2 =$ Genotypic variance of character y

Environmental coefficient of correlation (re_{xy}) = $\frac{\sigma_{exy}}{\sqrt{\sigma_{ex}^2 \times \sigma_{ey}^2}}$

where,

 σ_{exy} = Environmental co-variance between character x and y

 σ_{ex}^{2} = Environmental variance of character x

 σ_{ey}^2 = Environmental variance of character y

The significance of the phenotypic and genotypic coefficient of correlation were tested against the 'r' value as given by Fisher and Yates (1963) at ($n \times r$)-2 degree of freedom, where 'n' is the number of genotypes and 'r' is the number of replication.

3.4.7 Estimates of direct and indirect effects

Path analysis helps in partitioning of genotypic correlation into directs and indirect effects. Estimates of direct and indirect effects of component traits on green pod yield per plant and seed yield per plant were done through path analysis. The path coefficient analysis of different traits with green pod yield per plant and seed yield per plant were carried out by following Dewey and Lu (1959) as follows:

$py_{1+}py_{2}r_{12}+py_{3}r_{13}$	$\dots + py_n r_{in} = ry_i$
$py_1r_{12}+py_2+py_3r_{23}+\dots$	$\dots + py_n r_{2n} = ry_2$
$py_1r_{13}+py_2r_{23}+py_3+\dots$	$+py_nr_{3n}=ry_3$

$$py_1r_{n1}+py_2r_{n2}+py_3r_{n3}+...+py_n=ry_n$$

Where,

 py_1 , py_2 , py_3 ------, py_n are the directs path effects of 1, 2, 3-----, n variables on the dependent variable "y"

 r_{12} , r_{13} , ------, $r_{(n-1)n}$, are the possible coefficients of correlation between various independent variables with dependent variables "y"

The variation in the dependent variables which remained undetermined by including the other variables was assumed to be due to the variable (s) not included in the present investigation. The degree of the determination $(P^2 \times R)$ of such variables was calculated as follows:

Residual effects = $(1-R^2)^{1/2}$

:

Where, $R^2 = py_1ry_1 + py_2ry_2 + \dots + py_nry_n$ $K^{RISH} = 105282$ R^2 is the square multiple correlation coefficient and is the amount of variation in effect component that can be accounted by the causal component characters.

3.5 Genetic diversity analysis

A measure of group distance based on multiple characters was given by Mahalanobis (1936) and Rao (1952).

With x_1, x_2, x_3 x_p as the multiple measurements available on each individual and d_1, d_2, d_3 d_p as $x_1^{-1} - x_1^{-2}, x_2^{-1} - x_2^{-2}$ $x_p^{-1} - x_p^{-2}$, respectively, being the difference in the means of two populations, Mahalanobis D² statistic is defined as:

$$pD^2 = b_1d_1 + b_2d_2 + \dots + b_pd_p$$

Here, the b_i values are to be estimated such that the ratio of variance between the populations to the variance within the populations is maximized. In terms of variances and covariances, the D^2 value is obtained as follows:

$$pD^{2} = W_{ij} (x_{i}^{-1} - x_{i}^{-2}) (x_{j}^{-1} - x_{j}^{-2})$$

Where

W_{ij} is the inverse of estimated variance covariance matrix.

Test of significance

Using 'V' statistic which, in turn, utilizes Wilk's criteria, simultaneous test of difference mean values of a number of correlated variables/characters at 'pq' df (where, p = Number of characters and q = Number of genotypes-1) done as suggested by Rao (1952).

3.5.1 Grouping of genotypes into various clusters

Using D^2 values, different genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1952).

3.5.2 Average intra- and inter-cluster distances

Average intra- cluster $D^2 = \sum D_i^2/n$

Where,

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

Average inter- cluster distance $D^2 = \sum D_{ij}^2/n_i.n_j$

Where,

 $\sum D_{ij}^2$ = sum of all distances between all possible combinations (n_i.n_j) of the genotypes between the clusters.

 n_i = Number of genotypes in ith cluster

 n_j =Number of genotypes in jth cluster

3.5.3 Cluster mean

Character means of *Pisum sativum L*. falling under different clusters were calculated.

3.5.4 Contribution of individual character towards divergence

In all combinations, each character was ranked on the basis of $d_i = Y_i^j - Y_i^k$ values. Rank 1 was given to the highest mean difference and rank 'p' to the lowest mean difference where 'p' is the total number of characters. The contribution of individual character to the divergence was worked out in terms of 'n' number of times it appeared first.



RESULTS AND DISCUSSION

The results of the present investigation "Genetic variability for yield and horticultural traits in garden pea (*Pisum sativum* L.)" have been presented and discussed here under the following heads:

- 4.1 Genetic variability studies
- 4.2 Correlation coefficient analysis
- 4.3 Path coefficient analysis
- 4.4 Genetic divergence studies

4.1 Genetic variability studies

4.1.1 Analysis of variance

The analysis of variance revealed that mean squares due to genotypes were significant for all the morphological, yield and yield contributing, and quality traits during both the years (2009-10 and 2010-11) except days to first picking in the year 2010-11 (Table 4.1) exhibiting thereby the presence of sufficient genetic variability in the genotypes. Earlier workers namely, Singh and Saklani (1973), Kaur *et al.* (1976), Kalia (1985), Ramesh *et al.* (2002 b), Sharma *et al.* (2003), Singh and Dhillon (2004), Gupta *et al.* (2006), Sirohi *et al.* (2006), Jan *et al.* (2007), Kumar (2008), Nawab *et al.* (2008) and Sharma *et al.* (2009) have also reported variability in the genetic material of pea in different sets of environments.

The pooled analysis of variance over the years (Table 4.2) exhibited that mean squares due to genotypes were significant when tested against mean squares due to $G \times E$ interaction for all the traits except first flower node, number of branches, shelling (%), total sugars and reducing sugars. Significant variations among genotypes over the years were also observed by Sharma *et al.* (2006) and Sharma *et al.* (2007). The $G \times E$ interactions were also found to be significant for all the characters excluding days to first picking indicating that performance of genotypes was greatly influenced by environments.

Source Mean sum of squares						
Characters	Replication		Treatment		Error	
	2009-10	2010-11	2009-10	2010-11	2009-10	2010-11
df	2	2	4)	8	0
Morphological traits						
Days to first flower	29.20	14.44	9.90*	34.58*	4.16	8.61
First flower node	0.07	10.41	0.64*	2.79*	0.24	0.90
Days to 50% flowering	129.82	37.69	36.98*	38.50*	5.97	7.37
Days to first picking	26.81	70.63	23.30*	13.83	6.55	9.04
Number of branches	0.07	0.46	0.12*	0.82*	0.03	0.11
Internodal length (cm)	1.60	0.03	1.80*	2.25*	0.09	0.10
Nodes per plant	2.95	9.95	2.86*	6.25*	1.52	0.20
Plant height (cm)	52.15	17.71	274.51*	290.04*	9.88	8.79
Powdery mildew incidence (%)	634.65	-	3213.61*	-	164.53	-
Yield and yield contributing	traits					
Pod length (cm)	1.05	1.82	4.64*	3.75*	0.13	0.29
Seeds per pod	0.68	1.29	2.55*	2.69*	0.14	0.20
Shelling (%)	17.14	46.55	27.30*	17.13*	5.46	5.31
Pods per plant	6.34	3.42	16.42*	34.64*	1.90	1.28
Pod yield per plant (g)	21.76	2.94	296.77*	676.69*	15.43	16.01
Total biomass (g)	1.63	9.20	183.49*	127.57*	5.99	3.81
Seed yield per plant (g)	0.30	1.29	29.22*	23.99*	0.72	1.30
Harvest index (%)	3.46	23.65	137.07*	154.13*	0.22	13.36
100-seed weight (g)	11.56	0.98	24.44*	18.95*	1.41	1.79
Quality traits						
Total soluble solids (^o brix)	10.31	5.68	2.80*	1.55*	1.19	0.22
Ascorbic acid (mg)	17.27	1.09	3.14*	12.56*	0.28	1.12
Protein content (%)	1.67	23.09	7.93*	11.76*	0.29	2.19
Total sugars (%)	5.07	3.53	1.50*	1.74*	0.08	0.15
Reducing sugars (%)	0.35	0.10	0.84*	0.57*	0.06	0.14
Starch content (%)	9.71	4.95	34.17*	36.97*	2.83	3.52

Table 4.1	Analysis of variance for different characters in garden pea during the
	years 2009-10 and 2010-11

Characters			F-Test (Test			
Source		Genotypes	Environments	Genotype x	Pooled	of Userseenists)
				Environment $(G \times E)$	error	Homogeniety)
	df	40	1	40	160	
Morphologic	al traits					
Days to first f	lower	32.87*	15648.13	11.61*	6.39	4.28*
First flower ne	ode	1.97	0.03	1.46*	0.57	13.50*
Days to 50% t	flowering	62.40*	4122.00	13.09*	6.67	1.52
Days to first p	icking	28.60*	8301.00	8.55	7. 79	1.90*
Number of bra	anches	0.55	61.09	0.39*	0.07	13.44*
Internodal len	gth (cm)	3.04*	7.68	1.01*	0.09	1.23
Nodes per pla	nt	6.37*	512.30	2.74*	0.86	57.75*
Plant height (c	cm)	470.00*	1615.75	94.56*	9.33	1.26
Yield and yie	ld contributing	traits				
Pod length (cr	n)	7.89*	1.56	0.50*	0.21	4.98*
Seeds per pod		4.60*	6.81	0.64*	0.17	2.04*
Shelling (%)		26.69	112.63	17.74*	5.39	1.05
Pods per plant		37.15*	1358.72	13.90*	1.59	2.20*
Pod yield per	plant (g)	759.10*	20509.84	214.37*	15.72	1.07
Total biomass	(g)	221.58*	830.50	89.48*	4.90	2.47*
Seed yield per	plant (g)	43.84*	105.71	9.37*	1.01	3.25*
Harvest index	(%)	179.82*	31.22	111.39*	6.79	3687.81*
100-seed weig	sht (g)	39.14*	197.64	4.25*	1.60	1.61
Quality traits	ł					
Total soluble solids (°brix)		3.06*	46.29	1.29*	0.70	29.34*
Ascorbic acid	(mg)	14.13*	2.45	1.57*	0.70	16.02*
Protein conten	ıt (%)	16.56*	112.13	3.12*	1.24	57.14*
Total sugars (%)	1.74	0.60	1.50*	0.11	3.52*
Reducing suga	ars (%)	0.59	2.72	0.82*	0.10	5.44*
Starch content	(%)	44.08*	23.83	27.07*	3.17	1.55

Table 4.2Pooled analysis of variance over years for different characters in
garden pea

* Significance at $P \le 0.05$

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The F-test of homogeneity over years (Table 4.2) showed significant differences for majority of the traits *i.e.* 16 out of 23, thereby suggesting that interpretation of the results on the basis of pooled over years would not provide clear picture. Hence, the results of the individual years along with pooled over years have been discussed in this chapter. Gupta *et al.* (1992) also stressed the importance of $G \times E$ interactions while pooling over environments.

4.1.2 Mean performance of genotypes

The variation in the performance of 41 genotypes for different traits during 2009-10, 2010-11 and pooled over years, respectively (Appendix I), ranged from 73-82, 88-101 and 81-90 days to first flower; 13.20-14.18, 11.40-16.60 and 12.30-15.70 for first flower node; 82-96, 92-106 and 89-100 days to 50% flowering; 112-124, 126-135 and 119-129 days to first picking; 1.00-1.73, 1.47-3.33 and 1.27-2.53 for number of branches; 2.72-6.64, 2.59-6.77 and 2.66-6.52 cm for internodal length; 13.87-17.80, 16.07-22.07 and 15.47-19.87 for nodes per plant; 30.07-82.07, 38.26-85.43 and 34.51-81.67 cm for plant height; 6.18-13.25, 6.67-13.44 and 6.59-13.35 cm for pod length; 3.87-8.10, 3.97-8.63 and 3.92-8.37 for seeds per pod; 36.76-49.98, 35.89-47.87 and 39.10-48.93 for shelling (%); 2.91-15.03, 6.86-18.01 and 4.89-16.52 for pods per plant; 10.27-52.33, 18.00-80.17 and 14.13-66.25 g for pod yield per plant; 8.67-40.33, 11.00-41.33 and 9.83-40.83 g for total biomass; 1.57-15.62, 3.80-16.67 and 2.68-16.14 g for seed yield per plant; 18.08-43.76, 19.40-54.63 and 21.04-49.02% for harvest index; 12.33-26.33, 13.33-24.33 and 12.83-25.33 g for 100-seed weight; 14.53-19.60, 15.13-18.47 and 15.03-18.93° brix for total soluble solids; 13.14-17.43, 11.62-20.19 and 12.38-18.82 mg for ascorbic acid; 11.24-18.85, 10.06-18.51 and 10.65-18.68% for protein content; 5.80-8.40, 5.50-9.01 and 5.93-8.57% for total sugars; 2.28-4.61, 2.54-4.14 and 2.84-4.03% for reducing sugars; and 18.15-30.15, 18.30- 30.60 and 18.90-30.15% for starch content while powdery mildew incidence varied from 0.91-89.09% (resistant to susceptible) during 2009-10. It has also been observed that performance of majority of the genotypes for different traits varied during 2009-10 and 2010-11 indicating thereby the role of environment in that particular season in determining the performance of a particular genotype for different traits.



2010-11 (Initial stage after seed germination and plant growth)

Plate 1: General view of the crop
Earliness is a highly desirable trait in garden pea as the market prices are invariably high early in the season. The days to flower, first flower node and days to first picking of a particular genotype are the indicators of earliness. Accordingly, the standard check 'Punjab-89' observed to be the earliest on the basis of days to 50% flowering and first picking during both the years and pooled over years. However, the performance of different genotypes varied over the years indicating the role of environment in determining the inheritance of these traits. The lines 'DPPMFWR-20', 'DPPM-64' and 'VP-215' during 2009-10, 'DPPMFWR-1', 'DPPMFWR-5', 'DPPMFWR-11', 'DPPMFWR-12', 'DPPMFWR-20', 'DPPMFWR-27', 'DPPMFWR-30-1', 'DPPM-73', 'DPPM-74', 'DPPM-64', 'DPPMR-09-9', 'DPP-89' and 'VP-215' during 2010-11, and 'DPPMFWR-20', 'DPPMR-09-9' and 'DPP-89' in pooled over years took statistically similar number of days to flowering and first picking to that of 'Punjab-89'. The differences in the genotypes for days to flowering and first picking have also been reported by Singh and Saklani (1973), Singh (1985), Ramesh et al. (2002 b), Chaudhary and Sharma (2003), Singh and Dhillon (2004), Mehta et al. (2005), Gupta et al. (2006), Rana and Jamwal (2007), Kumar (2008) and Nawab et al. (2008) in the respective genetic material and locations of studies.

'DPPM-72' produced maximum number of branches which were significantly higher over all the four standard checks during 2009-10 and pooled over years and at par with the best performing check 'Punjab-89' during 2010-11. In addition, the genotypes 'DPPMFWR-4', 'DPPMFWR-11', 'DPPMFWR-29', 'DPPM-64', 'DPPM-65', 'DPPM-74', 'DPPM-07-4', 'DPPM-07-9', 'DPPMR-09-9', 'DPP-3-1' and 'DPP-11-2' were statistically at par with checks 'Lincoln', 'Palam Priya' and 'Punjab-89' for number of branches during both the years and with the best check 'Punjab-89' in pooled over years. Singh and Dhillon (2004) and Rathi and Dhaka (2007) have also observed wide variation for branches per plant.

Internodal length determines the height and nodes per plant. Besides having minimum internodal length, it is important to have more number of pod bearing nodes per plant. The significant minimum internodal length was observed for 'DPP-25G' over all the genotypes irrespective of years and pooled over years. Besides, 'DPPMFWR-2',



Plate 2: Genotypes with different plant characteristics

'DPPMFWR-12', 'DPPM-07-9' and 'DPP-3-1' which also revealed significantly short internodal length in comparison to the best check 'Palam Priya' during both the years while in addition to these, 'DPPMR-09-1' and 'DPPMR-09-9' also had short internodal length in pooled over years. Variation for internodal length has also been observed by Sureja and Sharma (2000) and Singh and Dhillon (2004). None of the genotypes could surpass the best check 'Palam Priya' for nodes per plant during 2009-10. However, the genotypes 'DPPMR-09-1', 'DPPMFWR-12', 'DPPMFWR-8', 'DPPMFWR-3' and 'DPP-89' during 2010-11 and 'DPPMR-09-1', 'DPPMFWR-12' and 'DPPMFWR-8' in pooled over years had significantly more number of nodes per plant over the best check 'Palam Priya'.

The desirable plant type in garden pea is the one that has dwarf growth habit which does not need staking and results in saving resources both in terms of money and labour. On the basis of plant height, 'DPP-25G' and 'DPPMFWR-29' were observed to be the dwarfest and the tallest genotypes, respectively during both the years and pooled over years. 'DPPMFWR-2' showed plant height at par with 'DPP-25G' while 'DPP-3-1' and 'DPPM-72' had plant height similar to that of 'DPPMFWR-29' during 2010-11. On the same line, 'DPPMFWR-1', 'DPPMFWR-3', 'DPPMFWR-12', 'DPPMFWR-30-2', 'DPPM-22', 'DPPM-74', 'DPPMR-09-2', 'DPPMR-09-3', 'DPPMR-09-5' and 'DPP-89' revealed plant height at par with the best check 'Palam Priya' in pooled over the years. It has been observed that plant height of majority of the genotypes during 2010-11 was comparatively more which may be due to favorable temperature and prolonged growing season. High temperature, particularly, at flowering and pod development stage during Feb-March, 2009-10 resulted in early cessation of growth. Amongst the check varieties, 'Azad P-1' had the maximum plant height while 'Punjab-89' and 'Palam Priya' showed the minimum plant height during 2009-10 and 2010-11, respectively. Further, genotypes namely, 'DPPMFWR-12', 'DPPM-22', 'DPPM-74', 'DPPMR-09-3', 'DPPMR-09-5', 'DPP-89' and 'DPP-168' showed statistically similar plant height to that of 'Punjab-89' and 'Palam Priya' during the respective years of 2009-10 and 2010-11. Wide variation in plant height of different genotypes has also been noticed by Singh and Dhillon (2004), Kalloo et al. (2005) and Mehta et al. (2005).



Under Indian conditions, consumers prefer well filled long and green pods and accordingly the genotype 'DPPM-64' (13.25, 13.44 and 13.35 cm) found to have significantly the maximum pod length during both the years and pooled over years in comparison to all other genotypes including checks. Amongst the checks, 'Punjab-89' (10.81, 9.98 and 10.40 cm) had the maximum pod length which was statistically at par with the lines 'DPP-3-1' and 'DPP-17-2' during 2009-10, 'DPPM-07-4', 'DPPM-73', 'DPP-3-1', 'DPPM-1', 'DPPMFWR-1', 'DPPMFWR-20', 'DPPM-72', 'DPPM-65', 'DPP-17-2' and 'Green Pearl' during 2010-11 and 'DPP-3-1' and 'DPPM-07-4' in pooled over years. Both 'DPPM-64' and 'Punjab-89' contained significantly **highezz** number of seeds per pod during both the years and pooled over years than rest of the genotypes, though 'DPPM-73' also exhibited similar performance to these lines for seeds per pod during 2009-10.

The highest shelling (%) was observed for 'DPPMFWR-12' which was statistically at par with the best check variety 'Punjab-89' during both the years and pooled over years. Besides, the genotypes 'DPPMFWR-4', 'DPPMFWR-5', 'DPPMFWR-8', 'DPPMFWR-11', 'DPPMFWR-20', 'DPPMFWR-27', 'DPPM-64', 'DPPM-72', 'DPPM-73', 'DPPM-74', 'DPPMR-09-9' and 'DPP-100' also had shelling (%) at par with the best check during both the years and pooled over years. In general, a wide range of variability for the performance of different genotypes for pod length, seeds per pod and shelling (%) was observed, which substantiated the findings of Sharma *et al.* (2003), Mehta *et al.* (2005), Jan *et al.* (2007) and Nawab *et al.* (2008) for pod length and seeds per pod and that of Mehta *et al.* (2005) and Jan *et al.* (2007) for shelling (%).

High yield is the basic objective of all crop improvement programmes. It is of immense importance to develop a genotype which has a potential to surpass a commercially adopted/adapted cultivar(s) otherwise the genotype will be of no significance even if it has excellent performance for other traits. Number of pods per plant has a direct bearing on the total productivity of garden pea crop. Keeping this in view, the highest number of pods per plant were found in 'DPPM-74' (15.03, 18.01 and 16.52) which was significant over rest of the genotypes including checks during 2009-10 and pooled over years though at par with the best check 'Palam Priya' and lines

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Plate 5: Pod characteristics of the best performing genotypes



'DPPMFWR-11', 'DPPMFWR-12', 'DPPMFWR-5' and 'DPPM-72' during 2010-11. Likewise, 'DPPM-74' produced significantly maximum pod yield per plant (52.33, 80.17 and 66.25 g) over all the four recommended check varieties over the years and pooled over years. In addition, 'DPPM-1', 'DPPM-64', 'DPPM-07-9' and 'VP-215' also performed statistically at par with those of 'Palam Priya' and 'Punjab-89' during 2009-10 whereas the performance of 'DPPMFWR-11', 'DPPM-64', 'DPPMFWR-20', 'DPPMFWR-5', 'DPPM-72' and 'DPPM-07-4' during 2010-11and 'DPPM-64', 'DPPMFWR-11' and 'DPPM-72' in pooled over years was statistically similar to the best check variety 'Punjab-89'. Singh and Dhillon (2004), Mehta *et al.* (2005), Gupta *et al.* (2006), Rana and Jamwal (2007), Chaddha *et al.* (2008) and Nawab *et al.* (2008) have also observed significant differences for pods per plant and pod yield per plant with different sets of genotypes and environmental conditions.

'DPPM-74' outperformed all the genotypes including checks in the respective years and pooled over years for total biomass (40.33, 41.33 and 40.83 g) and seed yield per plant (15.62, 16.67 and 16.14 g). Also, the genotypes 'DPPM-73' (39.67 g), 'DPPM-72' (36.67 g), 'DPPM-07-4' (36.00 g), 'DPPM-22' (35.67 g), 'DPPMR-09-9' (34.67 g), 'DPPMFWR-30-2' (34.00 g), 'DPPM-1' (33.00 g) and 'VP-215' (33.00 g) in 2009-10, 'DPPMR-09-2' (39.67 g), 'Green Pearl' (38.33 g), 'DPPMFWR-3' (37.33 g) and 'DPPMFWR-12' (37.33 g) in 2010-11 and 'DPPMFWR-12'(37.00 g), 'DPPM-73'(35.50 g) and 'DPPM-72' (35.17 g) on pooling of data were statistically at par with the best check 'Palam Priya' (36.00, 39.00 and 37.50 g) for total biomass. Further, it was observed that 'Punjab-89' had significantly less total biomass than 'Palam Priya' but resulted in maximum seed yield per plant at par with 'Palam Priya'. The genotypes 'DPPMFWR-30-2', 'DPPM-07-4', 'DPPM-1' and 'DPPM-73' during 2009-10 and 'DPPM-07-4' in pooled over years significantly outperformed 'Punjab-89' for seed yield per plant. In addition, the performance of 'DPPM-64', 'VP-215', 'DPPMFWR-30-1', 'DPPMR-09-1' and 'DPPMFWR-27', 'DPPMR-09-2', 'DPPM-07-4' and 'DPPM-64', and 'DPPM-64', 'DPPM-73' and 'DPPMFWR-30-2' was at par with that of 'Punjab-89' and 'Palam Priya' for seed yield per plant in the respective years and pooled over years. The differences in performance of genotypes for fresh and seed yield per plant in the present study might be attributed to pods per plant, seeds per pod and 100-seed weight.

'Punjab-89' along with 'DPPMFWR-11' during 2009-10 and 'DPPM-07-4' during 2010-11 outperformed all other genotypes for harvest index. The significant highest 100-seed weight was observed for 'DPPMR-09-2' over all the genotypes and check varieties over the years and pooled over years. Besides 'DPPMFWR-3', 'DPPM-22', 'DPPM-64', 'DPPM-74', 'DPPMR-09-1', 'DPPMR-09-3', 'DPPMR-09-5', 'DPPMR-09-9' and 'VP-215' during both the years and pooled over years, 'DPPMFWR-27' and 'Green Pearl' during 2009-10, and 'DPPM-07-4', 'DPP-100', 'Lincoln' and 'Punjab-89' during 2010-11 had statistically similar 100-seed weight to that of the best check 'Palam Priya'. These findings are in consonance with those of earlier workers who have also revealed wide variation in their breeding material for seed yield per plant (Sureja and Sharma 2000; Rathi and Dhaka 2007; Kumar 2008), for harvest index and 100-seed weight (Sharma *et al.* 2003; Rathi and Dhaka 2007; Kumar 2008).

Among the quality traits, 'DPP-3-1' and 'DPP-17-2' had significantly maximum total soluble solids over all four checks during 2010-11 and pooled over years along with 'DPP-168' during 2010-11. However, it was observed that majority of the genotypes had total soluble solids statistically at par with the best check 'Lincoln' except 'DPPMFWR-3' and 'DPPMFWR-29' during 2009-10, and 'DPPMFWR-4' and 'DPPMFWR-29' during pooled over years. The genotypes 'DPPMFWR-1', 'DPPM-73', 'DPPM-64', 'DPPM-07-4' and 'DPP-100' had also similar total soluble solids to that of the best performing genotypes 'DPP-3-1' and 'DPP-17-2' during 2010-11. On the other hand, all the genotypes, irrespective of year had significantly low ascorbic acid than that of check varieties 'Lincoln', 'Azad P-1' and 'Punjab-89'. The genotypes 'DPPM-64', 'DPPM-74' and 'DPPMFWR-27' contained significantly higher protein content over all the genotypes and checks during 2009-10. Similarly, 'DPPM-64' showed protein content at par with those of 'DPPMFWR-29', 'Punjab-89', 'DPPMFWR-27', 'DPPMFWR-30-2' and 'Green Pearl' during 2010-11, and 'DPPMFWR-20' in pooled over years.

Genotype 'DPPM-64' significantly resulted in maximum total sugars over the four check varieties in the respective years and pooled over years. In addition, 'DPPM-07-9' during 2009-10 and 'DPPM-72', 'DPPM-22', 'DPPMFWR-30-2' and 'DPPMFWR-27' during 2010-11 also had significant high total sugars than the checks.

With respect to reducing sugars, 'DPPM-74', 'DPPMR-09-3', 'DPP-25G', 'DPPM-72', 'DPPM-07-9' and 'DPPMFWR-27' had significantly higher reducing sugars than the check varieties during 2009-10, whereas 'Punjab-89' recorded maximum reducing sugars at par with 'DPPMFWR-4', 'Palam Priya', 'DPP-89', 'DPPM-07-4', 'Lincoln', 'DPP-100', 'Green Pearl', 'DPPMFWR-30-2', 'DPPMFWR-11', 'DPPM-22' and 'DPPM-64' during 2010-11. On the other hand, pooling of data revealed that 'DPPMFWR-4' contained maximum reducing sugars then checks though at par with 'DPPMFWR-4', 'DPP-25G', 'DPP-89', 'DPPMFWR-11', 'DPP-100', 'DPPM-22', 'DPPMR-09-2' and 'DPPMFWR-11', 'DPP-100', 'DPPM-22', 'DPPMR-09-2' and 'DPPMR-09-3'. The significant minimum starch content over the check varieties was found in 'DPPMR-09-2' and 'Green Pearl' during 2009-10, 'DPP-3-1', 'DPPMFWR-1', 'DPPMFWR-29', 'DPPMFWR-29', 'DPPMFWR-29', 'DPPMFWR-12', 'DPPMFWR-12', 'DPPMFWR-12', 'DPPMFWR-1', 'DPPMFWR-29', 'DPPMFWR-3' in pooled over years.

A wide variation in the performance of different genotypes for quality traits was also observed by earlier workers for total soluble solids (Mehta *et al.* 2005), ascorbic acid (Avakimova 1972; Kaur *et al.* 1976), protein content (Kaur *et al.* 1976; Krarup 1977), total sugars (Kaur *et al.* 1976; Haeder 1989; Ramesh *et al.* 2002a; Nair and Khare 2009), reducing sugars (Ramesh *et al.* 2002a; Mehta *et al.* 2005; Nair and Khare 2009) and starch content (Hybl *et al.* 1998).

Powdery mildew disease is one of the major constraints in pea production which affect total yield and pod quality. In this regard, the genotypes namely, 'DPPM-64', 'DPPMR-09-1', 'DPPMR-09-2', 'DPPMR-09-9', DPP-25G' were found to be resistant, whereas 'DPPMR-09-3', 'DPP-11-2', 'VP-215', 'Punjab-89', 'DPP-3-1' and 'DPP-17-2' were moderately resistant to powdery mildew disease during 2009-10. However, disease escaped during 2010-11 on account of prevailing low temperature conditions in the months of March and April. Earlier workers have also reported different genotypes resistant to powdery mildew disease (Tyagi *et al.* 1978; Kalia 1985; Thakur and Verma 1988; Thakur *et al.* 1996).

It can be concluded that the genotypes 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPM-72', 'DPPMFWR-11' and 'DPPM-07-4' appear to be promising on the basis of pod characters and yield.

4.1.3 Parameters of genetic variability

The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful in predicting the amount of variation present in the given genetic stock which in turn helps in formulating an efficient breeding programme. The estimates of PCV were higher than corresponding GCV for all characters studied (Tables 4.3 and 4.4) which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. Singh and Dhillon (2004), Sirohi *et al.* (2006) and Chadha *et al.* (2008) also found high PCV than the corresponding GCV.

PCV and GCV were high for pods per plant, pod yield per plant, total biomass and seed yield per plant during 2009-10, and for pod yield per plant during 2010-11. These high estimates indicated that there is substantial variability ensuring ample scope for improvement of these traits through selection. Kumar *et al.* (1998), Gupta *et al.* (2006), Kumar (2008), Nawab *et al.* (2008), Guleria *et al.* (2009), Sharma *et al.* (2009) and Kumar *et al.* (2010) have also reported high PCV and GCV for pods per plant and pod yield per plant whereas Sharma *et al.* (2003), Rathi and Dhaka (2007) and Guleria *et al.* (2009) reported the same for total biomass and/or seed yield per plant. Contrary to these reports, Sharma *et al.* (2007) reported moderate PCV and GCV for pods per plant and pod yield per plant which could be due to differences in genetic material and growing conditions. High PCV and moderate GCV were recorded for seed yield per plant during 2010-11, and pod yield and seed yield per plant in pooled over years.

The moderate estimates of PCV and GCV were recorded for number of branches, internodal length, plant height, pod length, seeds per pod, harvest index, 100-seed weight, protein content and starch content in both the years and pooled over years, pods per plant, total biomass and ascorbic acid during 2010-11 and pooled over years, and total sugars and reducing sugars during 2009-10. The moderate estimates suggest that direct selection

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18.89 52.99 23.48 20.19 16.63 24.64 14.72 53.69 42.77 37.09 25.16 2009-10 2010-11 2009-10 2010-11 36.32 32.24 29.80 22.82 28.89 60.21 6.56 GCV, PCV and ECV represent genotypic, phenotypic and environmental coefficients of variations, respectively; h²bs: Heritability in Broad sense; 7.56 5.15 0.77 5.97 4.62 GA (%) 23.66 20.28 19.02 26.81 60.10 11.89 18.70 26.59 31.17 27.53 27.78 51.79 58.24 71.52 42.25 27.80 4.67 4.07 2.77 9.71 2.08 5.84 3.21 85.29 67.04 77.32 59.25 78.17 76.03 58.49 12.56 93.22 91.55 77.83 49.81 50.12 41.12 67.64 87.97 90.93 91.43 80.39 76.14 15.01 79.87 89.7 $h_{h_s}^2$ 80.03 78.70 31.06 63.39 45.39 86.20 22.66 92.99 77.26 89.93 85.92 31.50 35.46 46.04 89.93 92.32 85.43 57.14 71.84 85.87 99.52 84.48 90.8 10.56 11.37 14.68 11.55 10.89 2.74 5.52 7.70 2.76 2.29 6.24 2.36 5.16 9.33 8.16 6.59 7.83 7.02 3.16 6.83 4.63 ECV (%) 7.68 6.21 10.37 11.44 13.72 2010-1 16.69 15.13 30.27 27.85 14.00 12.96 12.73 21.44 7.49 12.39 15.64 27.52 21.7 20.41 3.89 3.27 0.96 4.45 PCV (%) 5.72 3.17 16.54 11.73 15.73 17.79 29.06 31.35 22.68 30.16 23.13 14.74 16.21 26.06 15.82 17.45 16.04 (%) (%) 4.28 2.49 7.86 13.87 6.81 4.75 4.48 8.92 13.75 18.58 12.77 7.68 5.40 4.09 7.00 6.74 2.14 5.52 5.34 9.44 9.91 6.06 3.56 3.50 °S €C 3.52 2.71 4.09 6.08 1.43 6.29 2.65 12.95 2009-10 15.95 36.00 10.38 10.00 14.55 13.47 13.90 4.15 14.59 29.66 31.48 29.67 20.56 14.68 S S S C 3.56 1.98 13.91 6.23 4.07 6.57 2.62 1.80 14.59 19.99 16.82 35.00 33.97 31.13 37.34 10.95 10.75 16.26 14.97 14.47 5.79 20.61 15.97 7.30 GCV (%) 4.47 2.92 8.73 8.25 7.47 4.40 3.21 31.02±1.74 13.88±0.55 [4.02±0.85 24.35±1.08 98.50±1.57 8.95±0.26 17.14 ± 0.27 **92.78**±1.69 2.26±0.19 14.64±1.33 2.12±0.65 29.60±1.13 33.57±2.11 7.08±0.77 15.07±0.61 5.07±0.18 63.99±1.71 5.82 ± 0.26 19.02±2.31 **9.87±0.66** 7.01±0.22 3.29±0.22 8.67±0.31 2010-11 Population Mean 24.97±0.97 76.83±1.18 [3.90±0.28] 90.32±1.41 119.401.48 5.43±0.17 43.29±1.35 30.76±2.27 8.87±0.69 18.01±0.63 1.26±0.10 25.93±1.41 32.85±0.27 14.87±0.31 15.37±0.31 6.92±0.16 6.06±0.71 58.87±1.81 7.42 ± 0.80 8.56±0.49 3.50±0.14 **6.15±0.22** 2009-10 8.82±0.21 15.13-18.47 11.62-20.19 18.30-30.60 11.40-16.60 6.07-22.07 8.00-80.17 10.06-18.51 38.26-85.43 35.89-47.87 1.00-41.33 9.40-54.63 3.33-24.33 6.67-13.44 3.80-16.67 1.47-3.33 2.59-6.77 3.97-8.63 6.80-18.01 5.50-9.01 2.54-4.14 88-101 92-106 126-135 2010-11 Range GA (%): Genetic advance (%) of mean 13.20-14.18 36.76-49.99 14.53-19.60 13.14-17.43 11.24-18.85 8.15-30.15 13.87-17.80 0.27-52.33 8.08-43.76 30.07-82.07 6.18-13.25 2.33-26.33 8.67-40.33 1.57-15.62 3.87-8.10 2.91-15.03 5.80-8.40 2.72-6.64 1.00-1.73 2.28-4.61 2009-10 112-124 82-96 73-82 **Yield and yield contributing traits** Days to 50% flowering Seed yield per plant(g) Internodal length (cm) Pod yield per plant (g) Morphological traits Days to first picking Reducing sugars (%) Number of branches 100-seed weight (g) Days to first flower **Total soluble solids** Protein content (%) Ascorbic acid (mg) Starch content (%) Total biomass (g) Harvest index (%) First flower node Plant height (cm) Fotal sugars (%) Nodes per plant Pod length (cm) Pods per plant Seeds per pod **Ouality traits** Shelling (%) Traits (°brix)

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Estimates of different parameters of vari
Table 4.4

Traits	Range	Population Mean	GCV (%)	PCV (%)	ECV (%)	h^{2}_{bs}	GA (%)
Morphological traits							
Days to first flower	81-90	84.80 ± 1.03	2.48	3.88	2.98	40.85	3.26
First flower node	12.30-15.70	13.89±0.31	3.48	6.45	5.44	29.05	3.86
Days to 50% flowering	89-100	94.41±1.05	3.23	4.23	2.74	58.20	5.07
Days to first picking	119-129	125.21±1.14	1.49	2.68	2.23	30.81	1.70
Number of branches	1.27-2.53	1.76 ± 0.11	16.07	22.01	15.03	53.33	24.18
Internodal length (cm)	2.66-6.52	5.25±0.13	13.36	14.53	5.71	84.53	25.30
Nodes per plant	15.47-19.87	17.51±0.38	5.47	7.62	5.30	51.64	8.10
Plant height (cm)	34.51-81.67	61.43±1.25	14.26	15.11	4.97	89.16	27.75
Yield and yield contributing tr	raits						
Pod length (cm)	6.59-13.35	8.74 ± 0.19	12.94	13.97	5.24	85.91	24.72
Seeds per pod	3.92-8.37	5.98±0.17	14.37	15.94	6.89	81.28	26.69
Shelling (%)	39.10-48.93	43.96±0.95	4.29	6.80	5.28	39.71	5.56
Pods per plant	4.89-16.52	9.77±0.51	24.92	28.06	12.91	78.85	45.58
Pod yield per plant (g)	14.13-66.25	39.89±1.62	27.90	30.00	9.94	88.74	54.15
Total biomass (g)	9.83-40.83	27.76±0.90	21.65	23.07	7.97	88.05	41.85
Seed yield per plant (g)	2.68-16.14	9.22±0.41	28.98	30.96	10.90	87.60	55.87
Harvest index (%)	21.04-49.02	33.21±1.06	16.17	17.97	7.85	80.94	30.00
100-seed weight (g)	12.83-25.33	17.98 ± 0.52	13.91	15.59	7.04	79.64	25.57
Quality traits							
Total soluble solids (^o brix)	15.03-18.93	17.58 ± 0.34	3.57	5.95	4.76	35.98	4.41
Ascorbic acid (mg)	12.38-18.82	14.97±0.34	10.00	11.45	5.59	76.18	17.97
Protein content (%)	10.65-18.68	14.70±0.45	10.87	13.25	7.58	67.31	18.37
Total sugars (%)	5.93-8.57	6.97±0.14	7.48	8.86	4.76	71.18	13.00
Reducing sugars (%)	2.84-4.03	3.40±0.13	8.41	12.54	9.30	44.95	11.61
Starch content (%)	18.90-30.15	24.66±0.73	10.59	12.82	7.22	68.26	18.02
GCV, PCV and ECV represent gen GA (%): Genetic advance (%) of m	otypic, phenotypic lean	and environmental	coefficients of v	ariations, respect	tively; h ² bs: Heri	tability in B	oad sense;

for these traits should be considered cautiously. These moderate estimates have also been reported by Kuksal *et al.* (1983) and Guleria *et al.* (2009) for pod length and seeds per pod, Ramesh *et al.* (2002 b) and Guleria *et al.* (2009) for internodal length and plant height, and Kumar (2008) for seeds per pod and 100-seed weight. On the other hand, Sharma *et al.* (2007) reported high PCV and GCV for plant height. The rest of the traits namely days to first flower, first flower node, days to 50% flowering, days to first picking, nodes per plant, shelling (%), total soluble solids showed low PCV and GCV over the years and pooled over years in addition to ascorbic acid and total sugars during 2009-10 and pooled over years, respectively. The low estimates for days to first picking were also observed by Pathak and Jamwal (2002) and Sharma *et al.* (2007).

4.1.4 Heritability and genetic advance

The coefficient of variation alone cannot be used to partition the heritable components of variation (Burton 1952). This suggested that genetic coefficient of variation together with heritability estimates would give the best picture of the amount of advance to be expected from selection. The information on heritability estimates is helpful in studying the inheritance of quantitative characters as well as for planning breeding programmes with desired degree of expected general progress. Heritability in broad sense is of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression (Lush 1940).

In the present study, high heritability estimates (>60%) were observed for internodal length, plant height, pod length, seeds per pod, pods per plant, pod yield per plant, total biomass, seed yield per plant, harvest index, 100-seed weight, ascorbic acid, total sugars and starch content during both the years and pooled over years, protein content during 2009-10 and pooled over years, nodes per plant and total soluble solids during 2010-11 and days to 50% flowering during 2009-10 (Tables 4.3 and 4.4). The high heritability estimates for these characters revealed the lesser influence of environment and greater role of genetic component of variation. Earlier workers also revealed high heritability estimates for days to 50% flowering (Singh 1985; Sharma *et al.* 2003), internodal length (Sureja and Sharma 2000; Ramesh *et al.* 2002b), plant height (Dev *et al.* 1993; Sureja and Sharma 2000; Ramesh *et al.* 2002b; Sharma *et al.* 2003), seeds per

pod (Dev et al. 1993; Sharma et al. 2003; Chadha et al. 2008), pods per plant (Sureja and Sharma 2000; Pathak and Jamwal 2002; Sharma et al. 2003; Chadha et al. 2008), pod yield per plant (Korla and Singh 1988; Dev et al. 1993; Sureja and Sharma 2000), total biomass (Sharma et al. 2003), seed yield per plant (Sureja and Sharma 2000; Sharma et al. 2003), harvest index (Sharma et al. 2003; Kumar 2008), 100-seed weight (Chaudhary and Sharma 2003; Sharma et al. 2003; Nawab et al. 2008) and ascorbic acid (Pathak and Jamwal 2002).

Heritability was moderate for the characters namely, days to first flower, first flower node and shelling (%) during both the years, days to first picking, number of branches, total soluble solids during 2009-10, and days to 50% flowering, protein content and reducing sugars during 2010-11. Pooling of data revealed moderate heritability estimates for days to first flower, days to 50% flowering, days to first picking, number of branches, nodes per plant, shelling (%), total soluble solids and reducing sugars. Nodes per plant, days to first picking and first flower node exhibited low heritability estimates during 2009-10, 2010-11 and pooled over years, respectively. Low heritability indicated that the character is highly influenced by environmental factors and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effects.

For an effective selection programme, knowledge of estimates of heritability alone is not sufficient and it is therefore useful to study genetic advance along with heritability. Genetic advance may or may not be in proportion to genetic variability and heritability estimates because both high heritability and high genetic variability are important to obtain higher genetic gain (Kumari 2010).

In the present study, the results revealed that the response to selection for different characters which showed high heritability need to be given due emphasis for effective selection as these characters were under genetic control. However, the high heritability does not necessarily mean high genetic gain and is insufficient alone to make improvement through simple phenotypic selection. The heritability estimates become more beneficial when used to estimate genetic advance (Johnson *et al.* 1955 a) and hence, the genetic advance provides an edge over heritability as a guiding factor to breeders in various selection programmes (Guleria *et al.* 2009).

The high expected genetic advance expressed as % of mean (>30%) was observed for pods per plant, pod yield per plant, total biomass, seed yield per plant and harvest index during both the years and pooled over years, plant height during both the years, and number of branches and internodal length during 2010-11 (Tables 4.3 and 4.4). Earlier workers have also reported high genetic advance for plant height (Kumar *et al.* 1998; Chaudhary and Sharma 2003; Gupta *et al.* 2006; Sharma *et al.* 2007), pods per plant (Kumaran *et al.* 1995; Kumar *et al.* 1998; Ramesh *et al.* 2002b; Chaudhary and Sharma 2003; Sharma *et al.* 2003; Kumar *et al.* 2010), pod yield per plant (Dev *et al.* 1993; Kumaran *et al.* 1995; Kumar *et al.* 1998; Gupta *et al.* 2006), total biomass (Sharma *et al.* 2003; Gupta *et al.* 2006; Rathi and Dhaka 2007), seed yield per plant (Sureja and Sharma 2000; Sharma *et al.* 2003; Rathi and Dhaka 2007; Kumar 2008), number of branches (Sureja and Sharma 2000; Singh and Dhillon 2004; Gupta *et al.* 2006), and internodal length (Sureja and Sharma 2000; Ramesh *et al.* 2002b).

These estimates were moderate for pod length, seeds per pod, 100-seed weight, ascorbic acid, protein content, total sugars, reducing sugars and starch content over the years and pooled over years, number of branches and internodal length during 2009-10 and pooled over years, nodes per plant during 2010-11, and plant height during pooled over years. Singh and Saklani (1973) and Chadha *et al.* (2008) for seeds per pod, Rathi and Dhaka (2007) for 100-seed weight, and Ramesh *et al.* (2002 b) for reducing sugars have also reported moderate estimates of genetic advance. All the remaining characters *viz.*, days to first flower, first flower node, days to 50% flowering, days to first picking, shelling (%) and total soluble solids during both the years and pooled over years along with nodes per plant during 2009-10 and pooled over years exhibited low estimates for genetic advance. The low estimates of genetic advance have also been reported by earlier workers for days to flowering (Srivastava *et al.* 1972; Singh 1985), days to first picking (Singh and Saklani 1973; Korla and Singh 1988).

Based on the present study, high heritability coupled with high genetic advance was observed for pods per plant, pod yield per plant, total biomass, seed yield per plant and harvest index during both the years and pooled over years along with plant height over the years, and number of branches and internodal length during 2010-11 (Tables 4.3 and 4.4). The results suggested the importance of additive gene action for the inheritance of these characters and improvement could be brought about by phenotypic selection. The earlier researchers have also reported similar findings for plant height (Chaudhary and Sharma 2003; Kumar *et al.* 2004; Gupta *et al.* 2006; Sharma *et al.* 2007; Guleria *et al.* 2009), pods per plant (Chaudhary and Sharma 2003; Sharma *et al.* 2003; Kumar *et al.* 2004; Nawab *et al.* 2008), pod yield per plant (Chaudhary and Sharma 2003; Kumar *et al.* 2004; Singh and Dhillon 2004; Gupta *et al.* 2006; Chadha *et al.* 2008; Nawab *et al.* 2008), total biomass/biological yield (Sharma *et al.* 2003; Kumar 2008), seed yield per plant (Sharma *et al.* 2003; Kumar 2008), number of branches (Singh and Dhillon 2004; Gupta *et al.* 2008), number of branches (Singh and Dhillon 2004; Gupta *et al.* 2009). However, Sharma *et al.* 2009) observed moderate heritability and genetic advance for pods per plant and pod yield per plant.

High heritability along with moderate genetic advance was observed for pod length, seeds per pod, 100-seed weight, ascorbic acid, total sugars and starch content during both the years and pooled over years, internodal length, protein and reducing sugars during 2009-10, nodes per plant during 2010-11, and internodal length and plant height during pooled over years, which may be attributed to non-additive gene effects. High heritability coupled with moderate genetic advance was reported by Ramesh *et al.* (2002 a) for reducing sugars, and for pod length and 100-seed weight by Singh *et al.* (2011).

On the other hand, days to first flower and shelling (%) over the years and pooled over years, days to first picking, nodes per plant and total soluble solids during 2009-10 and pooled over years, first flower node over the years, and days to 50% flowering in pooled over years had shown moderate heritability coupled with low genetic advance. Korla and Singh (1988) also reported similar findings for shelling (%). While days to first picking and protein content revealed these estimates in the range of low and moderate, respectively during 2010-11. Moderate estimates of heritability and genetic advance were also noticed for reducing sugars in pooled over years. These estimates indicated the role of dominance and epistasis and hence these traits could be improved through hybridization/recombination breeding. Rana and Jamwal (2007) also suggested improvement through recombinant breeding for days to flowering and first harvest.

Besides this, the breeder's interest lies in assessing the performance of an individual genotype with respect to economic traits under selection. In the present investigation, genotypes 'DPPM-74', 'DPPM-64', 'DPPM-07-4', 'DPPM-72' and

'DPPMFWR-11' were found to have high yield potential and other desirable economic traits. The superior performance of these genotypes for pod length, pods per plant, 100-seed weight, total biomass and harvest index might have resulted in high yield since these traits also exhibited high to moderate PCV and GCV along with high heritability and high genetic advance. Hence, these traits can be improved by selection (Kumaran *et al.* 1995; Sureja and Sharma 2000; Sharma *et al.* 2003; Jan *et al.* 2007).

4.2 Correlation coefficient analysis

After understanding the nature of variation for pod yield and related traits, it would be desirable to know the nature and magnitude of associations among these characters in order to bring out improvement in a complex character like yield. Knowledge of association between traits serves two main purposes for breeders, *i.e.*, (1) selection of characters which are not easily observed or genotypic values of which are modified by environment effects, and (2) provides information about the nature and extent, and direction of selection pressure among different traits.

The effectiveness of any breeding or selection programme depends upon the nature of association between yield and other component characters, as more directly a character is associated with yield in the desirable direction, more will be the success of the selection programme. Therefore, after getting the knowledge on the nature and magnitude of genetic variation, it is also important to gather information on association of yield with other characters and among themselves, and their basis to identify characters for increasing the efficiency of both direct and indirect selection and thereby defining an ideal plant type.

In the present study, in general, the genotypic correlation coefficients were of higher magnitude than the corresponding phenotypic ones (Tables 4.5, 4.6 and 4.7) which revealed that though there is a strong inherent association between various characters, the phenotypic expression of the correlation gets reduced under the influence of environment. Pathak and Jamwal (2002), Chaudhary and Sharma (2003), Kumar *et al.* (2004), Singh and Singh (2005), Patel *et al.* (2006), Singh (2007) and Dhama *et al.* (2010) also reported that genotypic correlation coefficients were higher than their respective phenotypic correlation coefficients for most of the characters. The effective

Table 4.	2	Estima	tes of]	pheno	typic (P) and	genot	ypic (1	G) cor	relatic	n coef	ficient	s for d	lifferei	ıt pair	s of h	orticul	tural tr	aits in	garder	_
		pea au	ring 20	01-60	_																
T mit	Days to first flower	First flower node	Days to 50% flowcri ng	Days to first picking	Number of branches	Internoda I length (cm)	Nodes per plant	Plant height (cm)	Pod length (cm)	Seeds per pod	Shelling (%)	Pods per plant	Pod vield per plant (g)	Fotal E biomass y g) I	Seed H rield / in blant (3	arvest 10 dex sec (a) we (g)	- Tota d solu ight solu	I Ascorbi Ne acid (л s(°	ic Proteir ng) conten (%)	Total t sugars (%)	Reducing sugars (%)
First flower node	P 0.01 G 0.09																				
Days to 50%	P 0.71*	-0.05																			
Days to first	P 0.57*	10.0	0.74*																		
picking	G 0.75*	-0.06	*16.0	:																	
Number of branches	P -0.22* G -0.31*	0.05	-0.25	-0.09 -0.15																	
Internodal	P -0.11	0.20*	-0,18*	-0.20	0.02																
length (cm)	G -0.18*	0.36	-0.21*	-0.27*	0.03														•		
plant	G 0.47*	0.40- 1.03*	61.0 • 16.0	0.25*	-0.05	0.14															
Plant height	P -0.02	0.41*	-0.02	0.00	0.07	0.70*	0.38*														
(cm)	G 0.09	0.64*	0.03	-0.03	0.03	0.77	0.65*														
Pod length	P -0.21*	0.11	-0.28*	-0.33*	0.04	0.43	0.00	0.40*													
(сш)	P -0.27*	0.10	-0.30	-0.48	0.01	0.48*	-0.04 -0.03	0.33	0.65*												
Seeds per pod	G -0.45*	0.02	-0.57*	-0.72*	0.05	0.53*	-0.08	0.39*	0.74*												
Shelling (%)	P -0.06	0.13	-0.17	-0.16	0.05	0.07	0.17	0.08	11'0	0.37*											
	P 0.03	0.16	-040-	0.00	0.17	0.19*	0.20*	0.18*	90.0	- 0C-0	0.28*										
Pods per plant	G 0.16	0.31*	0.08	0.02	0.38*	0.17	0.48*	0.26*	0.14	0.22	0.41*										
Pod yield per	P -0.03	0.03	-0.07	-0.11	0.26*	0.28*	0.14	0.28*	0.34*	0.39*	0.32*	0.71*									
Total biomass	P -0.13	0.14	90.0- -0.16	-010 •010	- c£.U	0.30*	-67.0	0.35*	0.37*	0.50*	0.17	0.76* 0.36*	0 12								
(8)	G -0.22*	0.25*	-0.21	-0.27*	-0.16	0.40*	0.14	0.37*	0.39*	0.53*	0.22*	0.42*	0.12								
Seed yield per nlant (a)	P -0.12	0.05	-0.21*	-0.20*	0.14	0.25*	-0.05	0.19*	0.38*	0.25*	-0.08	0.18*	0.45*	0.22*							
Harvest index	P -0.01	-0.24	0.07	0.03	0.01	0.07	0.10	-0.03	0.16	10.0	-0.07	0.01	0.13	-0.06	-0.01						
(%)	G 0.19*	-0.51*	0.23*	0.07	-0.10	0.11	-0.15	-0.18*	0.30*	0.03	-0.16	-0.08	0.20*	-0.11	-0.13						
100-seed weight (g)	P 0.03 G 0.01	-0.07	-0,13 -0.19	-0.05	-0.06	0.15	0.00	0.05	0.13	0.29* 0.37*	0.11	0.08	10.0	0.33*	0.20* 1.25*	0.08 0.25*					
Total soluble	P -0.04	0.25*	-0.10	-0.09	-0.12	0.03	0.06	-0.02	0.18*	0.13	0.16	-0.04	0.02	0.08	0.19*	0.11	+61				
solids ("brix)	0.01	0.44*	-0.12	-0.13	-0.16	0.03	60.0	-0.02	0.19*	0.13	0.23*	-0.08	0.03	0.08	0.17	0.27* 0.	21*				
Ascorbic acid (mg)	10.0- 0-0-0-0	0.05	-0.02	-0.04	0.09	0.02	-0.0 -0.0	6 6 6 7	0.00	-0.08 0.08	-0.05	0.19*	-0.21*	0.05	0.09 0.09	5 8	.06 14 0.1	×			
Protein	P -0.08	60.03	-0.03	-0.03	0.22*	-0.17	01.0	-0.18*	-0.15	-0.20*	0.16	0.02	0.12	-0.24*	0.22* 0	.14 -0	33* 0.1	2 0.13			
content (%) Total success	G -0.23*	0.11	-0.12	-0.13	0.34*	-0.18*	-0.04	-0.18*	-0.16	-0.27*	0.08	0.05	0.13	-0.26*	0.27* 0	• 10 [5]	.49* 0.1 16 0.0	4 0.17 9 -0.13	013		
(%)	G -0.15	0.35*	-0.19	-0.23*	0.39*	-0.14	-0.01	-0.03	0.01	0.05	0.15	0.08	0.06	-0.06	-0.18* 0	10	.16 0.0	6 -0.14	0.23		
Reducing	P -0.11	0.13	-0.21*	-0.25*	0.23*	0.31*	0.20*	0.28*	0.46*	0.51*	0.28*	0.72*	0.72*	0.55*	0.45* 0	0.10	21* 0.0	9-0.10	0.06	0.06	
Sugars (%) Starch content	G -0.05	0.27*	-0.24*	-0.44*	0.16	0.33*	0.25*	0.28*	0.51*	0.59*	0.45*	0.83*	0.76*	0.59* 0.62*	0.50* 0	0 0	26* 0.0 14 0.0	7 -0.14 8 -0.18	0.06	0.08	0.85*
(%)	G -0.12	0.26*	-0,16	-0.25*	0.16	0.40*	0.29*	0.42*	0.49*	0.59*	0.45*	0.81*	0.82*	0.65*	0.48* 0	0.07	15 0.0	7 -0.21	-0.0	0.05	0.91*
*Signific	ant at I	≤ 0.05		[ļ		1					[

Table 4.(Estim nea di	ates of a	phenot	ypic (F) and	genot	ypic (1	G) cor	relati	on coe	officien	its for	differe	ent pair:	s of ho	rticult	ural t	raits i	n gard	en
		pra u	17 Sm m	11-010					:												
T rait	Days (first flov	to First ver flower node	Days to 50% flowcring	Days to first picking	Number of branches	Intermodal length (cm)	Nodes per plant	Plant height (cm)	Pod length (cm)	eds per She pod (lling Pods %) plar	per Total i biomass (Harvest g) index (%)	100-seed weight (g)	Total solubic solids ("brix)	Ascorbic acid (mg)	Protein content (%)	Total sugars (%)	Reducing sugars (%)	Starch content (%) p	Pod yield er plant (g)
First flower node	P 0.24																				
Days to 50%	P 0.88	• 0.30*																			
flowering	G 1.03 ⁴	0.68*																			
Days to first	P 0.25	-0.01	*15,0																		
picking	G 0.70'	0.44	0.89*																		
Number of branches	P 0.01	-0.10	-0.02	-0.03																	
Internodal	0.0- -0.0- -0.0-	-0.08	-0.02	-0.30	0.24*																
length (cm)	G 0.03	-0.25*	0.01	-0.19*	0.29*																
Nodes per plant	P 0.16	0.20*	0.16	0.19*	-0.15	0.01															
	G 0.21	• 0.35*	0.23*	0.51*	-0.17	0.02															
Plant height	P -0.06	0.10	-0.03	-0.08	0.39*	0.58*	0.18*														
	G -0.01	0.13	-0.05	-0.12	0.52*	0.63*	0.20*														
Pod length (cm)	P -0.03	-0.06	-0.07	-0.18*	0.19*	0.27*	-0.25	0.32													
Cando nos nod	0.0	70'0	-0.0	-96.0-	.87.0	0.30	-15.0-	0.35													
nod ind snape	F -0.28	-0.55	-0.32	-0.61*	0.16	0.27	-0 •01 •01 •01 •01	0.21	0.63*												
Shelling (%)	P -0.33	-0.13	-0.30	-0.25*	0.03	0.20*	0.08	0.18*	0.08	31*											
	G -0.38	* -0.46*	-0.42*	-0.29*	0,10	0.25*	0.12	0.29*	0.19* (.46*											
Pods per plant	P -0.22	• -0.11	-0.30*	-0.20*	0.31	0.26*	-0.01	0.25*	0.00	0.25* 0.	32*										
	G -0.33	• -0.09	-0.37	-0.66	0.35*	0.29*	-0.03	0.28*	0.01	0.28* 0.	52*										
Total biomass	P -0.05	0.03	-0.11	0.01	0.17	0.38*	0.13	0.31*	0.15	0.19* 0	02 0.4	*									
University index	0 0 0 0	0.07	-0.15	-0.11	0.16	0.39*	0.14	0.32	0.17	0.19* 0	07 0.4										
(%)		70.0	-0.0	-0.63	4120	60.0-	- C7'0-	10.0-	10.45*		7 0 00	100									
100-seed weight	P 0.18*	0.37*	0.18*	-0.05	0.07	-0.04	-0.10	-0.04	0.26*	0.14	28* -0.1	4 0.19*	0.33*								
(B)	G 0.18 ⁴	• 09.0	0.17	-0.10	0.04	-0.01	-0.10	-0.08	0.33*	0-18+ -0	48* -0.2	0* 0.20*	0.40*								
Total soluble	P 0.02	-0.06	0.00	0.03	-0.03	0.02	-0.19	0.08	0.23*	0.05 0	.07 -0.	12 -0.21*	• 0.09	0.09							
	0.0 0	-0.14	-0.03	0.35	0.07	0.01	-0.27	0.10	0.35*	0.09 0	.16 -0.	16 -0.25	0.05	0.10							
Ascorbic acid (mg)	P 0.13	-0.07	0.06	-0.14	0.16	0.35	-0.15	0.08	0.13	0.28* 0	.05 0.1	4 0.12	0.19*	0.15	-0.0 -0.0						
Protein content	P 0.02	60 ^{.0}	60.0-	-0.22*	0.14	0.17	-0.16	0.08	0.23*	0.28* -(500	01.0 90	0.07	-0.01	•61.0-	0.28*					
(%)	G 0.06	-0.27*	0.01	-0.41*	0.21*	0.19*	-0.20*	0.06	0.30*	0.32* 0	0.0	0.12	0.21*	0.07	-0.23*	0.39*					
Total sugars (%)	P 0.05	-0.17	0.04	-0.16	0.18*	0.31*	-0.11	0.25*	0.48*	0.33* 0	.14 0.1	1 0.26*	0.15	0.11	0.11	0.16	0.22*				
	G 0,14	-0.23*	0.07	-0.41*	0.17	0.39*	-0.12	0.31*	0.62*	0.47* 0.	23* 0.1	4 0.31*	0.25*	0.18*	0.17	0.15	0.30*				
Keducing sugars	P 0.05	0.12	0.04	0.02 -0.06	0.12	-0.02	0.03	-0.20	0.0 7	0.20* 0	.10	3 0.05	0.18*	0.06	-0.12	0.16	0.13	01.0			
Starch content	P 0.13	0.03	0.17	0.04	-0.13	-0.05	-0.10	-0.27*	-0.11	90.0-	0.0	0.12	0.20*	0.02	-0.20*	0.17	60 ^{.0} -	-0.08	0.22*		
(%)	G 0.36 ⁴	-0.08	0.36*	0.21*	-0.08	-0.04	-0.14	-0.32*	-0.15	-0.09	0.07 -0.0	0.13	0.26*	0.05	-0.25*	0.17	-0.16	-0.11	0.30*		
Pod yield per plant (a)	P -0.20	-0.08	-0.28*	-0.26	0.34	0.35*	-0.22*	0.29*	0.41*	0.44* 0.	24* 0.8	l* 0.49*	0.42*	0.16	-0.03	0.25*	10.0	0.34	0.20	0.04	
Send with a set	G -0.25	-0.00 -0.00	-0.34*	-0.79	0.37	0.37*	-0.24	0.30*	0.46*	0.48* 0.	36* 0.8	3* 0.51*	0.48*	0.16	0 ⁰	0.28*	0.0 5 5	0.40	0.26	c0.0	0.68*
plant (g)	G0.06	10'0	-0.13	-0.51	0.34*	0.31*	-0,13 -0,13	0.24*	0.48*	0.42* 0	0.0 0.5 0.5 0.5	• 0.69* 0* 0.69*	0.64*	0.46*	-0.13	0.26*	0.24*	0.41	0.27*	0.0	0.73*
*Signific	ant at	P ≤ 0.0.	5																		

Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different pairs of horticultural traits in garden

		pea	in poole	ia ovei	r years																	
Trait	Days to first flowc	First I flower node	Days to 50% flowering	Days to first picking	Number of branches	Internodal length (cm)	Nodes per plant	Plant height (cm)	Pod S Icngth (cm)	cods por Spod	helling Pc (%)	ds per 7 plant bi	otal H mass ind (g)	arvest 1 lex (%) w	00-seed T cight (g) se	otal soluble olids (° brix)	Ascorbic acid (mg)	Protcin content (%)	Total sugars (%)	Roducing augars (%)	Starch content (%)	Pod yield Ser plant (g)
First flower 1 node	P 0.19*																-					
Days to 50% F	0.80*	0.18*																				
flowering	±1011 €	0.53*																				
Days to first F	0.36*	0	0.53*																			
9	0.84	0.36	0.96																			
branches		-0.07	-0.08	-0.05																		
Internodal	-0.07	0	-0.12	-0.15*	0.18*																	
length (cm)	-0.09	-0.12	-0.15*	-0.28*	0.28*																	
Nodes per plant F	0.14*	0.25*	0.15*	0.20*	-0.11	0.07																
	5 0.37*	0.64*	0.38*	0.37*	-0.31*	0.06																
Plant height }	-0.04	0.19*	-0.03	-0.04	0.28*	0.63	0.28*															
Bod booth 7	0.03	0.30*	0.05	-0.1	0.32*	0.76*	0.32*	47.00														
(cm) (cm)		0 0	-0.18	-07.0-	0.13	1.35	-0.12	0.36*														
Seeds per pod F	-0.21	-0.23	0.36	-0.38	0.12	0.36*	577 O-	0.40	0.64*													
	1 -0.39*	-0.35*	-0.54*	-0.71	0.23*	0.49*	-0.25*	0.39*	0.72*													
Shelling (%) p	-0.21	-0.03	-0.23*	-0.20*	0.03	0.13*	0.13*	0.13*	0.1	0.34*												
5	3 -0.47*	-0.24	-0.51*	-0.55*	0.35*	0.13*	0.02	0.28*	0.29*	0.62*												
Pods per plant F	• -0.14	-0.03	-0.15*	-0.11	0.28*	0.23*	0.08	0.22*	0.03	0.21* (0.29*											
	-0.09	0.05	-0.19	-0.32	0.46*	0.36*	0.30*	0.28*	0.06	0.35* (3.81*											
Total biomass F	-0.04	0.03	-0.09	-0.06	0.18*	0.32*	0.13*	0.29*	0.25*	0.29*	0.19* 0	.55*										
inder of	20.0	• 61 .0 • 2 2 2	-0.04	-0.24	0.23	0.42	0.14	0.39*	0.33	0.35*	0.41° 0	.70	;									
	0.0 2	-0.17	-0.11	-0.53	0.21*	0.15	1.0	0.15* 0.25*	•/? • 20	0.40*	0.07	138* 0	36*									
100-seed	0.06	0.24*	-0.02	-0.13*	0.08	0.11	-0.07	0.08	0.32*	0.06	0.17*	000	34* 0	.28*								
weight (g) C	3 0.12	0.52*	-0.03	-0.25*	0.08	0.14*	-0.18*	0.04	0.41*	0.07	0.31* -	0.04 0	45* 0	.35*								
Total soluble F	0.01	-0.12	0.04	0.03	-0.01	0.05	-0.13*	0.01	0.18*	0.02	-0.02	0.05 (10.	0	0.02							
Ascorbic acid p	6.0	0.36	0.12	0.14*	-0.25*	0.1	-0.32*	-0.04 0.04	0.42	0.1	0.12		0.08 202	0.08	-0.02	10.0-						
(am)	0 16*	000	-0.04	-0.1	2 1 2 1 2 4	0.25	-0.16	6 T C	12#	0.28	13*	71.0		*07	0.10	-0.0-						
Protein content p	0.00	0	-0.06	-0.16	0.08	0.11	-0.07	0.04	0.20*	0.22*	0.05	0.07	38	0.07	0.08	-0.14*	0.25*					
c (%)	0.00	0.12	-0.08	-0.29*	0.07	0.14*	-0.11	0.07	0.26*	0.22*	0.26*	0.06	08	.21*	0.13*	-0.36*	0.32*					
Total sugars F	0.03	-0.1	0.01	-0.08	0.13*	0.16*	-0.06	0.12	0.24*	0.15*	0.04	0.01 (.02	0.11	0.1	0.07	0.09	0.18*				
5	9-0.05	-0.06	-0.09	-0.15	-0.02	0.35*	0.00	0.21*	0.50*	0.37* (0.24* 0	0,13* 0	31* 0	17*	0.23*	0.40*	0.02	0.30*				
Reducing F	0.0	-0.07	0.00	0.00	0.14*	-0.09	0.06	-0.19*	-0.06	0	0.13*	0.08	60	0.02	0.15*	0.04	-0.01	0.12	0.11			
) (o/) emane	0.0	0.14*	-0.08	-0.31*	-0.1	-0.36	-0.30	-0.46*	-0.12	-0.12	- - -	0.04	90	.15*	0.30	-0.08	-0.25 *	0.21*	0.1	+01 0		
(%)	0.02	-0.0/	10.0	/0.0- 0-0-	10:0-	-0.04 *1 C 0-	-0.0/ +0C 0-	-0.13	-0.0- 13*	10.0	50.0	7 T T T T T T T T T T T T T T T T T T T	1.04	• 15*	90.0 90.0	/0.0-	00'0 10 0-	70.0	- 00 0-	0 53*		
Pod yicld per P	-0.17*	-0.03	-0.25*	-0.25*	0.31*	0.33*	-0.05	0.28*	0.42*	0.46*	0.25* 0	.78* 0	57* 0	47*	0.27*	0.04	0.24*	0.03	0.17*	0.14*	0.04	
plant (g) C	i -0.15*	0.01	-0.35*	-0.63*	0.37*	0.49*	-0.03	0.28*	0.53*	0.66* (0.70* 0	.80* 0	77* 0	*69'	0.36*	0.1	0.30*	0.11	0.37*	0.21*	0.05	
Seed vield per F plant (g) G	-0.06	0.06 0.05	-0.13* -0.16*	-0.19* -0.44*	0.23* 0.27*	0.32* 0.45*	0 0.02	0.30* 0.37*	0.42 * 0.53 *	0.46*	0.16* 0 0.47* 0).58* 0).65* 0	75* 0 86* 0	.78*	0.44 * 0.49 *	0.02 -0.01	0.18 * 0.22 *	0.11 0.19*	0.07 0.27*	0.06 0.17*	0.05 0.02	0.74* 0.87*
*Signific	ant at	P ≤ 0.	05						-													

Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different pairs of horticultural traits in garden

Table 4.7

yield improvement would be achieved through the characters which have significant and positive/desirable correlation with each other. Genotypic correlation provides measures of genetic association between characters and is more reliable than phenotypic correlation and thus, helps to identify the characters to be utilized in breeding programmes.

In the present study, pod yield per plant had shown a positive and significant correlation at both phenotypic and genotypic levels with pods per plant, seeds per pod, pod length, internodal length, plant height, shelling (%) and ascorbic acid during both the years and also with nodes per plant during 2009-10, and with number of branches, total sugars and reducing sugars during 2010-11(Tables 4.5 and 4.6). Pooling of data over years also revealed positive associations of pod yield per plant with all these characters except nodes per plant (Table 4.7). Selection on the basis of these traits might lead to higher yield. Earlier reports of many research workers have also indicated significant and positive association for pod yield per plant with pods per plant (Katiyar and Ram 1987; Sharma and Kalia 1998; Bhardwaj and Kohli 1999; Ramesh and Tewatia 2002; Kumar et al. 2003; Mehta et al. 2005; Kumar and Sharma 2006; Singh 2006; Sharma et al. 2007; Sharma et al. 2009), seeds per pod (Katiyar and Ram 1987; Sharma and Kalia 1998; Ramesh and Tewatia 2002; Kumar et al. 2003; Mehta et al. 2005; Sharma et al. 2007), harvest index (Katiyar and Ram 1987), pod length (Ramesh and Tewatia 2002; Kumar et al. 2003; Kumar et al. 2004; Mehta et al. 2005; Singh 2006; Kaur et al. 2007; Sharma et al. 2007), 100-seed weight (Kumar et al. 2004), shelling percentage (Bhardwaj and Kohli 1999, Chaudhary and Sharma 2003; Mehta et al. 2005; Kaur et al. 2007), plant height (Sharma and Kalia 1998; Ramesh and Tewatia 2002; Kumar et al. 2003; Kumar and Sharma 2006; Sharma et al. 2009), first flower node (Bhardwaj and Kohli 1999; Kumar and Sharma 2006; Sharma et al. 2009) and number of branches (Kumar et al. 2003; Kaur et al. 2007) with different breeding materials at different locations thereby, suggesting improvement of yield by giving special focus to these traits.

Pod yield per plant had revealed negative association at both genotypic and phenotypic levels with days to 50% flowering and days to first picking during both the years and pooled over years and that of with nodes per plant and days to first flower during 2010-11. Days to first flower also showed negative association with pod yield in pooled over years. Teotia *et al.* (1983) and Gupta and Singh (2006) have also reported negative correlation of pod yield per plant with days to first picking and days to first flower, respectively.

Seed yield per plant also revealed positive association with internodal length, plant height, pod length, seeds per pod, pods per plant, pod yield per plant, total biomass, harvest index and 100-seed weight during both the years at phenotypic and genotypic levels while it had positive association with first flower node and nodes per plant at genotypic level during 2009-10, and shelling (%) and number of branches at both levels in the respective years (Tables 4.5 and 4.6). A significant positive correlation for all these characters with seed yield per plant except first flower node and nodes per plant had also been observed on pooling of data over years at both genotypic and phenotypic levels (Table 4.7). In addition, total sugars at both levels over the years and pooled over years, ascorbic acid during 2010-11 and pooled over years, and protein content and reducing sugars at genotypic level during 2010-11 and pooled over years also showed positive associations with seed yield per plant. Many research workers have also reported positive association of seed yield per plant with various traits (Singh et al. 1987; Tiwari et al. 2001; Singh and Mishra 2002; Arya et al. 2004a; Singh and Singh 2005; Singh and Yadav 2005; Patel et al. 2006; Mahajan et al. 2007; Singh 2007; Usmani and Dubey 2007; Singh et al. 2008; Togay et al. 2008; Guleria et al. 2009; Devi et al. 2010; Dhama et al. 2010; Kumar et al. 2010; Awasthi et al. 2011; Singh et al. 2011).

Among the growth parameters, days to first flower had significant positive association with days to 50% flowering and days to first picking at phenotypic and genotypic levels during both the years; with nodes per plant and total soluble solids at genotypic level during 2009-10; with first flower node and 100-seed weight at phenotypic level during 2010-11; and with first flower node, starch content, ascorbic acid, reducing sugars, nodes per plant and 100-seed weight at genotypic level during 2010-11. Kumar and Sharma (2006) also reported significant positive correlation of days to first flower with days to first picking. Also, it showed negative association with pod length, seeds per pod and number of branches during 2009-10 and seeds per pod, pods per plant and shelling (%) during 2010-11 at both phenotypic and genotypic levels. Pooled data over

years revealed significant positive association of days to first flower with first flower node, days to 50% flowering, days to first picking and nodes per plant at both levels, and ascorbic acid at genotypic level while, it had negative association with seeds per pod and shelling (%) at both levels along with pods per plant and number of branches at phenotypic and genotypic levels, respectively.

First flower node revealed significant positive association with plant height, nodes per plant, protein content and internodal length at phenotypic level, and with nodes per plant, plant height, protein content, shelling (%), internodal length, starch content, pods per plant and harvest index at genotypic level during 2009-10 whereas, it showed positive association with 100-seed weight, days to 50% flowering and nodes per plant, and days to 50% flowering, 100-seed weight and days to first picking at phenotypic and genotypic levels, respectively during 2010-11. Pooling of data over years revealed positive association of first flower node with days to 50% flowering, nodes per plant, plant height and 100-seed weight at both the levels and days to first picking, total biomass and reducing sugars at genotypic level only. Kalloo *et al.* (2005) also noticed positive and significant correlation of first flower node with days to 50% flowering and plant height.

Days to 50% flowering and days to first picking had significant positive association with days to first picking and nodes per plant, respectively at both phenotypic and genotypic levels over the years. While, both these characters besides having positive association between themselves had also shown positive association with nodes per plant in pooled over years at both genotypic and phenotypic levels. Earlier workers namely, Kumar *et al.* (2003), Kumar *et al.* (2004) and Sirohi *et al.* (2006) have also reported positive and significant correlation of days to 50% flowering with days to first picking. On the contrary, days to 50% flowering showed negative association with seeds per pod, pod length, number of branches, internodal length and 100-seed weight during 2009-10, and seeds per pod, shelling (%) and pods per plant during 2010-11 at both levels, whereas days to first picking had negative correlation with seeds per pod, pod length, internodal length during 2009-10 and 2010-11, respectively at phenotypic level. A negative association with days to first picking and

seed yield per plant has also been noticed by Rathi and Dhaka (2007). Contrary to the present findings, positive association of days to 50% flowering with pod length has been noticed by Srivastava *et al.* (1972). Similar association of days to first picking has also been reported by earlier workers with various characters namely, pod length (Korla and Rastogi 1977; Teotia *et al.* 1983; Srivastava and Singh 1989), seeds per pod (Korla and Rastogi 1977; Teotia *et al.* 1983; Kumar *et al.* 2003), shelling percentage (Korla and Rastogi 1977), and 100-seed weight (Kumar *et al.* 2003).

Number of branches exhibited positive association with total biomass, pods per plant, starch content and reducing sugars during 2009-10, with plant height, pods per plant, internodal length, harvest index and pod length during 2010-11, and internodal length, plant height, pod length, pods per plant, total biomass and harvest index in pooled over years at both phenotypic and genotypic levels. However, total sugars and reducing sugars at phenotypic level and seeds per pod, shelling (%), ascorbic acid and starch content at genotypic level also showed positive association with number of branches in pooled over years. A positive association of branches per plant have been reported earlier by various researchers with plant height (Sirohi et al. 2006), pod length and pods per plant (Kumar et al. 2003; Sirohi et al. 2006), seed yield per plant (Singh et al. 1987), and seeds per pod and 100-seed weight (Kumar et al. 2003). Significant positive correlation of internodal length was observed with plant height, seeds per pod, pod length, harvest index, total biomass and pods per plant at both phenotypic and genotypic levels during both the years except harvest index during 2010-11, and pods per plant at genotypic level during 2009-10, although all these characters showed positive association at both levels on pooling of data over years. In addition, positive correlation of ascorbic acid and total sugars at both levels, and 100-seed weight and protein content at genotypic level with internodal length was also found. Similarly, nodes per plant was positively associated with plant height at both levels and years, besides had positive association with pods per plant at both levels and that with shelling (%) and total biomass at genotypic level during 2009-10. In pooled over years, plant height and total biomass had positive associations with nodes per plant at both the levels, while, it showed the same association with shelling (%) and pods per plant at phenotypic and genotypic levels, respectively.

A positive association of plant height was recorded with pod length, harvest index, seeds per pod, total biomass, pods per plant and shelling (%) at phenotypic and genotypic levels over the years and pooled over years except shelling (%) and harvest index at phenotypic level during 2009-10 and 2010-11, respectively. Earlier reports of various workers with their respective genetic materials and locations have also revealed similar association of plant height with pod length (Kumar *et al.* 1998; Sirohi *et al.* 2006), shelling percentage (Kumar *et al.* 2004), pods per plant (Pandey and Gritton 1975; Narsinghani *et al.* 1978; Kumar *et al.* 2003; Sirohi *et al.* 2006). In contrary, Nandpuri *et al.* (1973) reported negative correlation of plant height with seeds per pod.

Pod length showed positive association with seeds per pod, 100-seed weight, harvest index, and protein content during both the years at genotypic and phenotypic levels; with total biomass and total sugars during 2009-10 and 2010-11, respectively at both the levels; with shelling (%) over the years and total soluble solids during 2009-10 at genotypic level alone. Similarly, on pooling of data over the years, it revealed positive association with seeds per pod, total biomass, harvest index, 100-seed weight, total soluble solids, protein content and total sugars at both the levels, along with shelling (%) and ascorbic acid at genotypic level. Earlier workers have also found similar association of pod length with seeds per pod (Srivastava *et al.* 1972; Teotia *et al.* 1983; Kumar *et al.* 2003), shelling percentage (Korla and Rastogi 1977) and 100-seed weight (Kumar *et al.* 2004).

Similarly, seeds per pod had positive association with harvest index, total biomass, shelling (%), ascorbic acid and pods per plant over the years and pooled over years except pods per plant at phenotypic level during 2009-10, and that with 100-seed weight during 2009-10, and total sugars and protein content during 2010-11 and pooled over years at both genotypic and phenotypic levels. Contrary to 2010-11, reducing sugars showed negative association with seeds per pod during 2009-10. Shelling (%) revealed positive correlation with pods per plant and total biomass during both the years and pooled over years except total biomass during 2009-10 at both genotypic and phenotypic levels. In addition, it had positive association with reducing sugars at phenotypic level,

and harvest index, ascorbic acid, protein content and total sugars at genotypic level in pooled over years. However, negative association between seeds per pod and protein content have been observed by Peshin (1975) and that of shelling (%) and pods per plant by Nandpuri *et al.* (1973) and Kumar and Sharma (2006).

A significant positive association was noticed for pods per plant with total biomass and harvest index, and total biomass with 100-seed weight during 2009-10, 2010-11 and pooled over years at both phenotypic and genotypic levels. Besides, a positive association of pods per plant with ascorbic acid and total sugars, and total biomass with harvest index and total sugars was also found on pooling of data over the years at genotypic level. These findings are in consonance with those of earlier workers who found positive association of pods per plant with total biomass (Kumar and Sharma 2006) and harvest index (Kumar *et al.* 2003). Besides, both these traits had shown negative association with total sugars during 2009-10. Contrary, total biomass had positive association with total sugars during 2010-11.

A positive association at both genotypic and phenotypic levels was also observed for traits *viz.*, harvest index with ascorbic acid and 100-seed weight, ascorbic acid with protein content, and reducing sugars with starch content (except at phenotypic level, 2009-10) during both the years and pooled over years; 100-seed weight with reducing sugars and ascorbic acid during 2009-10 and pooled over years, and that of protein content with total sugars during 2010-11 and pooled over years, and harvest index with starch content and reducing sugars during 2010-11. Moreover, positive correlations were also found for harvest index with protein content and total sugars during 2010-11 and pooled over years along with 100-seed weight with protein content and total sugars, total soluble solids with total sugars, and protein content with reducing sugars in pooled over years at genotypic level. A negative association was noticed for ascorbic acid with reducing sugars during 2009-10 and that of total soluble solids with protein content in 2010-11 and pooled over years at both genotypic and phenotypic levels. Total soluble solids also revealed negative association with protein content and ascorbic acid during 2009-10 and with ascorbic acid in pooled over years at genotypic level. On the basis of correlation studies and their coefficients of determination, it can be concluded that the selection for pods per plant, pod length, seeds per pod, plant height, total biomass and harvest index will be effective for isolating plants with higher fresh pod yield and seed yield. A significant and positive correlation between seed yield and fresh pod yield per plant is of significance as it indicated the possibility of development of dual purpose pea variety.

4.3 Path coefficient analysis

Yield is a complex character with polygenic inheritance and depends upon series of processes *viz.*, phenological, canopy development, biomass production etc. that are driven by environment influences. The performance of a genotype is ultimately determined by the integrated effect of genotype and environment. The end product, yield has often been described as the product of its component traits which show interdependence (Wilson 1987). The path coefficient analysis allows partitioning of correlation coefficients into direct and indirect effects of various traits towards dependent variable and thus, helps in assessing the cause-effect relationship as well as effective selection. It plays an important role in determining the degree of relationship between yield and its component effects and also permits critical examination of specific factors that provide a given correlation. The effects of yield components via path analysis were examined only for significant correlated traits with yield (fresh and seed).

The present study revealed that the direct effects obtained at genotypic level were markedly different from those at phenotypic level. These differences might be due to varying degree of influence of environment on various traits studied, which were also observed from the results of component variance analysis and correlation studies. In few cases, the direct effects were observed to be of opposite sign (positive to negative and vice-versa) at corresponding phenotypic and genotypic levels like first flower node, days to first picking, plant height, pod length, protein content and total sugars on fresh pod yield (Table 4.8) and that of days to first flower, days to 50% flowering, internodal length, pod length, seeds per pod, shelling (%), pods per plant, 100-seed weight, total soluble solids and reducing sugars on seed yield per plant during 2009-10 (Table 4.11) while the same contrasting effects were revealed for days to first flower, nodes per plant, plant height and total soluble solids on fresh pod yield and that of first flower node, days to 50% flowering, days to first picking, number of branches, nodes per plant, plant height, pod length, pods per plant, pod yield per plant and 100-seed weight on seed yield per plant during 2010-11(Table 4.9).

Pooling of data over years at genotypic and phenotypic levels also revealed contrasting effects with positive to negative and vice-versa on the direct effects of days to first picking, number of branches, seeds per pod, shelling (%) and reducing sugars on pod yield per plant (Table 4.10) and that of days to first flower, days to 50% flowering, days to first picking, internodal length, plant height, pod length, seeds per pod, pods per plant, pod yield per plant, ascorbic acid, reducing sugars and starch content on seed yield per plant (Table 4.13). Such a change in direction and magnitude of direct and indirect effects might be due to environmental factors influencing various traits. This indicates that the path analysis at the phenotypic level may not provide a true picture of direct and indirect traits towards the fresh pod yield and seed yield per plant, respectively at the genotypic level. Fresh pod yield per plant and seed yield per plant were taken as dependent variable and all other traits used for correlation were used as causal variables.

Direct and indirect effects of different traits on pod yield per plant

Pods per plant and pod length had maximum positive direct effects on fresh pod yield per plant during both the years at phenotypic level and only at genotypic level during 2010-11 (Table 4.8 and 4.9). At genotypic level during 2009-10, the high positive direct effects on pod yield per plant were due to seeds per pod followed by nodes per plant, pods per plant, days to first picking, first flower node and ascorbic acid. Besides, seeds per pod, ascorbic acid, nodes per plant, number of branches and plant height at phenotypic level during 2009-10, and reducing sugars, nodes per plant, ascorbic acid, internodal length and total sugars at genotypic level during 2010-11 had also appreciable direct contribution to the total association with fresh pod yield per plant. At phenotypic level during 2010-11, reducing sugars, total sugars, ascorbic acid, internodal length and days to first flower had also contributed directly to some extent on the total association

Table 4.8	Estimates of direct and indirect effects of different traits on pod yield per plant at phenotypic (P) and genotypic (G) level
	in garden nea during 2009-10

		D	-		D															
T rait	ñ	ays to Fi	irst wer	Days to	Days to first	Number	Interno	Nodes	Plant heicht	Pod Ienoth	Seeds per pod	Shelling	Pods	Total	Ascorbi	Protein	Total	Reducin	Starch	L
	ú	ower no	ode	flowering	picking	branches	length (cm)	plant	(cm)	(cm)	hot hot	(67)	plant	solids (^o brix)	(mg)	(%)	(%)	(%)	(%)	
Days to first	Ь	0.067 0	000.0	-0.054	-0.054	-0.010	110.0	0.014	-0.001	-0.057	-0.047	0.005	0.022	0.000	0.003	100'0	0.000	-0.012	0.003	-0.11
tiower	5	0.217 0	0.026	-0.838	0.325	-0.083	0.096	0.308	-0.021	0.028	-0.543	0.251	060'0	0.083	0.000	-0.001	0.004	-0.037	0.045	-0.05
First flower	Ь	0,001 -0	1.012	0.004	-0.001	0.002	-0.020	0.042	0.018	0.029	-0.002	-0.011	0.108	-0.015	-0.009	-0.003	0.001	0.005	-0.003	0.13
node	c	0.020 0	0.274	0.007	-0.024	0.018	-0.189	0.669	-0.157	-0.017	0.028	-0.263	0.178	-0.222	-0.001	0.035	-0.002	0.017	-0.101	0.27*
Days to 50%	4	0.047 0	100.0	-0.076	-0.070	-0.011	0.019	0.014	-0.001	-0.076	-0.094	0.014	0.031	0.004	-0.015	0.001	0.000	-0.005	0.003	-0.21*
flowering	U	0.209 -0	7.002	-0.870	0.420	-0.072	0.111	0.198	-0.007	0.032	-0.683	0.260	0.044	0.101	-0.005	-00:00	0.002	-0.019	0.055	-0.24*
Days to first	٩	0.038 0	000.0	-0.056	-0.095	-0.004	0.021	0.022	0.000	-0.090	-0.100	0.014	0.001	0.002	-0.006	0.001	0.000	-0.004	0.003	-0.25*
picking	U	0.162 -0	2.015	-0.842	0.434	-0.041	0.140	0.162	0.008	0.050	-0.867	0.297	0.009	0.031	-0.004	-0.010	0.001	-0.021	0.066	-0.44*
Number of	۔	-0.015 -0	0.001	0.019	0.008	0.043	-0.002	-0.005	0,003	0.011	0.011	-0.004	0.139	0.000	-0.007	0.001	100'0	0.034	-0.005	0.23*
branches	U U	-0.068 0	0.019	0.237	-0.067	0.265	-0.014	-0.244	-0.007	-0.001	0.062	-0.111	0.216	-0.044	-0.002	-0.013	-0.003	0.053	-0,113	0.17
Internodal	ч.	-0.007 -0	7.002	0.014	0.019	0.001	-0.104	0.015	0:030	0.117	0.105	-0.006	0.126	0.005	0.018	0.000	0.000	-0.026	0.003	0.31*
length (cm)	U	-0.040 0	0.099	0.184	-0.116	0.007	-0.522	0.257	-0.189	-0.051	0.634	-0.095	0.098	0.047	0.004	0.003	0.001	-0.029	0.039	0.33
Nodes per	с.	0-0000	0.005	-0.010	-0.020	-0.002	-0.015	0.104	0.016	0.001	-0.006	-0.014	0.135	-0.006	0.000	-0.001	0.000	0.015	0.001	0.20*
plant	Ċ	0.103 0	7.283	-0.266	0.109	-0.100	-0.207	0.648	-0.160	0.004	-0.092	-0.281	0.272	-0.066	-0.002	0.007	0.001	-0.006	0.003	0.25*
Plant height	۰.	-0.001 -0	0.005	0.002	0.000	0.003	-0.072	0.040	0.043	0.108	0.076	-0.007	0.119	-0.002	0.006	0.000	-0.001	-0.027	0.001	0.28*
(cm)	5	0.019 0.	2.174	-0.025	-0.014	0.008	-0.402	0.420	-0.246	-0.042	0.465	-0.126	0.147	-0.078	0.002	-0.002	0.002	-0.029	0.010	0.28*
Pod length	٩	-0.014 -0	1001	0.022	0.032	0.002	-0.045	0.001	0.017	0.270	0.149	-0.010	0.037	0.010	0.015	-0.002	0.000	-0.022	0.000	0.46*
(cm)	ن	-0.058 0	0.045	0.261	-0.208	0.003	-0.253	-0.027	-0.099	-0.105	0.890	-0.134	0.078	0.132	0.004	0.015	0.000	-0.025	-0.004	0.51*
Seeds per pod	ط	0.014 0.	000'(0.031	0.041	0.002	-0.048	-0.003	0.014	0.176	0.228	-0.032	0.111	0000	0.035	-0.002	-0.001	-0.030	-0,001	0.51*
	5	0.098 0	006	0.494	-0.313	0.014	-0.275	-0.050	-0.095	-0.078	1.204	-0.324	0.128	0.011	0.009	0.010	0.003	-0.042	-0.014	0.59*
Shelling (%)	L	-0.004 -0	0.002	0.013	0.016	0.002	-0.007	0.018	0.004	0.030	0.086	-0.085	0.184	-0.004	0.013	-0.002	100'0-	0.025	-0.002	0.28*
	5	0.083 0.	111	0.347	-0.198	0.045	-0.076	0.278	-0.047	-0.022	0.598	-0.653	0.231	-0.071	100'0	0.018	0.000	0.013	-0.044	0.45*
Pods per plant	Ч	0.002 -0.	0.002	-0.004	0.000	0.009	-0.020	0.021	0.008	0.015	0.038	-0.023	0.664	0.000	0.010	0.001	-0.003	0.003	-0.001	0.72*
	σ	0.034 0.	0.086	-0.068	0.007	0.101	060'0-	0.310	-0.064	-0.014	0.270	-0.265	0.569	-0.033	0.002	-0.007	0.009	0.002	-0.023	0.83*
Total soluble	Ъ	0.000	003	-0.006	-0,003	0.000	-0.008	-0.010	100'0-	0.044	0.002	0.006	0.003	0.061	-0.010	0.001	0.001	0.021	0.000	0.10
solids (- Drix)	σ	0.041 -0.	0.139	-0.201	0.031	-0.027	-0.057	-0.097	0.044	-0.032	0.031	0.106	-0.043	0.439	-0.006	-0.021	0.000	0.034	-0.010	0.09
Ascorbic acid	٩	0.002 0.	1001	0.010	0.005	-0.003	-0.016	0.000	0.002	0.034	0.067	-0.009	0.054	-0.005	0.119	-0.002	100'0-	-0.050	0.003	0.21*
(mg)	U	0.002 -0.	013	0.162	-0.072	-0.020	-0.084	-0.056	-0.020	-0.016	0.448	-0.029	0.054	-0.109	0.025	0.016	0.005	-0.076	0.045	0.26*
Protein	۰	0.003 -0.	003	0.008	0.008	-0.005	-0.003	0.006	-0.001	0.049	0.029	-0.014	-0.030	-0.007	0.023	-0.012	0.002	0.018	-0.002	0.06
content (%)	5	0.002 0.),121	0.103	-0.056	-0.043	-0.017	0.057	0.005	-0.020	0.153	-0.150	-0.048	-0.118	0.005	0.078	-0.004	0.022	-0.018	0.07
Total sugars	ч. ,	0- 100'0	1.00.1	0.001	-0.001	0.002	0.003	-0.001	-0.001	-0.001	-0.012	0.004	-0.127	0.002	-0.007	-0.002	0.017	0.020	0.002	-0.10
(%)	U	0.021 0.	0.012	0.047	-0.016	0.023	0.020	-0.025	0.010	0.001	-0.096	0.003	-0.132	-0.001	-0.003	600'0	-0.037	0.027	0.041	-0.14
Reducing	م	0.005 0.	000'	0.003	0.002	0.010	0.018	010.0	-0.008	-0,040	-0.046	-0.014	0.014	0.008	-0.039	-0.002	0.002	0.152	-0.002	0.06
sugars (%)	5	0.051 0.	0.029	0.107	-0.058	0.089	0.096	-0.023	0.045	0.017	-0.323	-0.052	0.006	0.094	-0.012	0.011	-0.006	0.157	-0.067	0.06
Starch content	ч.	0.011 -0.	0.002	0.014	0.016	0.012	0.016	-0.004	100.0-	0.004	0.012	-0.008	0.033	0.001	-0.019	-0.001	-0.002	0.020	-0.019	0.06
(%)	ט	0.033 0.	096	0.165	-0.099	0.103	0.071	-0.006	0.008	-0.001	0.057	-0.098	0.046	0.016	-0.004	0.005	0.005	0.036	-0.290	0.08
Inevnlained	variatio	n (P) · 0 23	1. (U) -1	1 NR																

Unexplained variation (P) : 0.23; (U) : 0.08 *Significant at P \leq 0.05; r-correlation coefficient with pod yield per plant; bold values indicate direct effects

tes of direct and indirect effects of different traits on pod yield per plant at phenotypic (P) and genotypic (G) levels	en pea during 2010-11
.9 Estimates o	in garden p
Table 4.	

T rait		lays to first lower	First flower node	Days to 50% flowering	Days to first picking	Number of branches	Interno dal length	Nodes per plant	Plant height (cm)	Pod length (cm)	Seeds per pod	Shelling (%)	Pods per plant	Total soluble solids (^o brix)	Ascorbi c acid (mg)	Protein content (%)	Total sugars (%)	Reducin g sugars (%)	Starch content (%)	-
Days to first	Ч	0.039	0.018	-0.091	-0.004	0.000	-0.003	-0.020	0.001	-0.012	0.008	0.019	-0.171	-0.001	0.008	-0.002	0.005	0.005	0.003	-0.20*
flower	IJ	-0.093	0.076	-0.220	-0.083	0.001	0.002	0.022	-0.001	0.035	0.060	0.085	-0.270	-0.007	0.017	-0.001	0.009	0.036	0.088	-0.25*
First flower	ፈ	0.010	0.075	-0.031	0.000	0.002	-0.005	-0.026	-0.001	-0.023	0.013	0.007	-0,081	0.003	-0.004	0.008	-0.014	-0.012	0.001	-0.08
node	c	-0.069	0.102	-0.145	-0.052	0.007	-0.016	0.037	0.001	0.009	0.119	0.101	-0.074	-0.015	-0.005	0.005	-0.014	-0.033	-0.021	-0.06
Days to 50%	٩	0.035	0.022	-0.103	-0.005	0.000	-0.004	-0.020	0.000	-0,028	0.012	0.017	-0.228	0.000	0.004	0.003	0.003	0.004	0.005	-0.28*
flowering	G	-0.096	0.069	-0.214	-0.106	0.001	0.001	0.025	0.000	-0.015	0.076	0.092	-0.304	-0.003	0.009	0.000	0.004	0.034	060'0	-0.34
Days to first	ď	0.010	-0.001	-0.032	-0.017	0.001	-0.006	-0.024	100.0	-0.067	0.012	0.014	-0.150	100.0-	600.0-	0.018	-0.013	0.002	100.0	-0.26*
picking	ŋ	-0.065	0.045	-0.191	-0.119	0.024	-0.012	0.054	-0.001	-0.219	0.132	0.065	-0.533	0.037	-0.034	0.008	-0.025	-0.010	0.053	-0.79*
Number of	٩	0.000	-0.007	0.002	0.001	-0.015	0.014	0.019	-0.004	0.070	-0.006	-0.002	0.240	0.001	0.011	-0.011	0.015	0.012	-0.004	0.34*
branches	ŋ	0.001	-0.009	0.004	0.036	-0.079	0.018	-0.017	0.005	0.159	-0.046	-0.022	0.286	0.008	0.015	-0.004	0.010	0.023	-0.021	0.37*
Internodal	ď	-0.002	-0.007	0.007	0.002	-0.004	0.056	-0.001	-0.005	0.099	-0.010	-0.011	0.200	-0.001	0.022	-0.014	0.026	-0.002	-0.001	0.35*
length (cm)	U	-0.003	-0.025	-0.002	0.023	-0.023	0.063	0.002	0.006	0.172	-0.065	-0.055	0.239	0.001	0.031	-0.004	0.023	-0.006	-0.010	0.37*
Nodes per	ď	0.006	0.015	-0.016	-0.003	0.002	100'0	-0.126	-0.002	-0.091	0.006	-0.004	-0.007	0.008	-0.010	0.013	-0.009	0.003	-0.003	-0.22*
plant	Ċ	-0.019	0.036	-0.050	-0.061	0.013	0.001	0.105	0.002	-0,176	0.041	-0.027	-0.027	-0.028	-0.014	0.004	-0.008	0.002	-0.035	-0.24*
Plant height	ď	-0.002	0.008	0.004	0.001	-0.006	0.032	-0.023	-0.009	0.120	-0.008	-0.010	0.191	-0.003	0.006	-0.007	0.020	-0.019	-0.007	0.29
(cm)	G	0.007	0.013	0.010	0.014	-0.041	0.040	0.021	0.009	0.202	-0.047	-0.065	0.226	0.010	0.008	100.0-	0.019	-0.049	-0.078	0.30*
Pod length	Ь	-0.001	-0.005	0.008	0.003	-0.003	0.015	0.031	-0.003	0.371	-0.023	-0.004	0.001	-0:010	0.008	-0.019	0.040	0.004	-0.003	0.41*
(cm)	G	-0.006	0.002	0.006	0.046	-0.022	0.019	-0.032	0.003	0.570	-0.145	-0.041	0.009	0.036	0.014	-0.006	0.037	0.008	-0.036	0.46*
Seeds per pod	٩	-0.008	-0.026	0.033	0.005	-0.003	0.015	0.019	-0.002	0.233	-0.037	-0.017	0.192	-0.002	0.018	-0.023	0.027	0.019	-0.002	0.44*
	U	0.026	-0.056	0.076	0.073	-0.017	0.019	-0.020	0.002	0.384	-0.215	-0.101	0.228	0.010	0.025	-0.006	0.028	0.047	-0.022	0.48*
Shelling (%)	Р.	-0.013	-0.010	0.031	0.004	-0.001	0.011	-0.010	-0.002	0.028	-0.012	-0.056	0.244	-0.003	0.003	0.003	0.011	0.009	-0.001	0.24*
	U	0.036	-0.047	0.089	0.035	-0.008	0.016	0.013	0.003	0.106	-0.099	-0.220	0.420	0.017	0.011	0.000	0.014	0,000	-0.019	0.36*
Pods per plant	P	-0.009	-0.008	0.031	0.003	-0.005	0.015	0.001	-0.002	0.001	-0.009	-0.018	0.768	0.005	0.00	0.007	0.009	0.012	0.000	0.81*
	U	0.031	-00.00	0.080	0.078	-0.028	0.019	-0.003	0.003	0.006	-0.060	-0.114	0.812	-0.017	600.0	0.001	0.009	0.026	-0.007	0.83*
Total soluble	Ь	0.001	-0.004	0.001	0.000	0.000	0.001	0.024	-0.001	0.084	-0.002	-0.004	-0.089	-0.045	100.0-	0.015	0.009	-0.011	-0.006	-0.03
solids ("brix)	U	0.007	-0.014	0.006	-0.042	-0.006	0.001	-0.028	0.001	0.197	-0.020	-0.035	-0.129	0.106	-0.003	0.004	0.010	-0,022	-0.063	-0.03
Ascorbic acid	٩.	0.005	-0.005	-0.006	0.002	-0.003	0.019	0.019	-0.001	0.047	-0.010	-0.003	0.107	0.000	0.065	-0.023	0.013	0.016	0.005	0.25*
(mg)	υ	-0.022	-0.007	-0.027	0.058	-0.017	0.028	-0.021	0.001	0.111	-0.076	-0.034	0.107	-0.004	0.070	-0.008	0.009	0.067	0.042	0.28*
Protein	Ч	0.001	-0.007	0.003	0.004	-0.002	0.010	0.020	-0.001	0.084	-0.010	0.002	-0.068	0.008	0.018	-0.081	0.018	0.013	-0.002	0.01
content (%)	Ċ	-0.006	-0.028	-0.002	0.049	-0.016	0.012	-0.021	0.001	0.169	-0.070	-0.004	-0.057	-0.024	0.027	-0.019	0.018	0.051	-0.038	0.04
Total sugars	۵.	0.002	-0.013	-0.004	0.003	-0.003	0.017	0.014	-0.002	0.179	-0.012	-0.008	0.087	-0.005	0.010	-0.018	0.082	0.009	-0.002	0.34*
(%)	c	-0.013	-0.023	-0.015	0.048	-0.014	0.024	-0.013	0.003	0.352	-0.101	-0.050	0.114	0.018	0.011	-0.006	0,060	0.031	-0.028	0.40*
Reducing	۵	0.002	-0.009	-0.004	0.000	-0.002	-0.001	-0.004	0.002	0.014	-0.008	-0.005	0.099	0.005	0.011	-0.011	0.008	0.095	0.006	0.20*
sugars (%)	U	-0.020	-0.021	-0,044	0.007	-0.011	-0.002	0.001	-0.003	0.026	-0.060	0.000	0.124	-0.014	0.028	-0.006	0.011	0.166	0.075	0.26*
Starch content	ď	0.005	0.002	-0.018	-0.001	0.002	-0.003	0.012	0.003	-0.042	0.002	0.002	0.001	0.009	0.011	0.007	-0.007	0.021	0.027	0.04
(%)	Ċ	-0.033	-0.008	-0.078	-0.025	0.007	-0.002	-0.015	-0.003	-0.083	0.019	0.016	-0.022	-0.027	0.012	0.003	-0.007	0.050	0.248	0.05
Inevnlained	variatic	0 · (d) uc	- 13- (U)	-0.01																

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Unexplained variation (r) : 0.13; (U) : -0.01 *Significant at P \leq 0.05; r-correlation coefficient with pod yield per plant; bold values indicate direct effects

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		n B	arden	pea in p	oolea (over ye	ars													
T rait		Days to first flower	First flower node	Days to 50% flowering	Days to first picking	Number of branches	Interno dal length	Nodes per plant	Plant height	Pod length	Seeds per pod	Shelling (%)	Pods per plant	Total soluble solids ("brix)	Ascorbi c acid (mg)	Protein content (%)	Total sugars (%)	Reducin g sugars (%)	Starch content (%)	L
Days to first	•	0.035	0.011	-0.076	-0.006	0.000	0.000	-0.008	0.000	-0.032	-0.011	0.010	-0.106	0.000	0.010	0.000	0.002	0.000	0.000	-0.17*
flower	U	0.637	0.282	-1.258	0.635	0.103	-0.056	-0.348	-0.006	-0.068	0.306	-0.269	-0.082	-0.035	0.012	-0.001	-0.008	0.000	0.007	-0.15*
First flower	٩	0.007	0.056	-0.017	0.000	-0.001	0.000	-0.014	0.000	-0.001	-0.013	0.001	-0.025	0.000	-0.006	0.000	-0.008	-0.007	0.001	-0.03
node	G	0.422	0.425	-0.663	0.274	0.007	-0.073	-0.610	-0.057	0.072	0.276	-0.136	0.044	0.255	-0.006	-0.051	-0.009	-0.002	-0.155	0.01
Days to 50%	Ч	0.028	0.010	-0.095	-0.008	-0.001	100.0-	-0.008	0.000	-0.060	-0.020	0.011	-0.114	0.000	0.000	0.004	0.001	0.000	0.000	-0.25
flowering	G	0.641	0.225	-1.251	0.720	0.110	-0.093	-0.362	-0.009	-0.233	0.424	-0.296	-0.167	-0.087	-0.003	0.037	-0.015	0.001	0.003	-0.35
Days to first	Ч	0.013	0.000	-0.050	-0.016	0.000	-0.001	-0.011	0.000	-0.087	-0.021	0.010	-0.079	0.000	-0.010	0.009	-0.006	-0.001	-0.001	-0.25*
picking	σ	0.537	0.154	-1.195	0.754	0.230	-0.174	-0.355	0.019	-0.519	0.556	-0.316	-0.280	-0.096	-0.018	0.129	-0.024	0.004	-0.031	-0.63*
Number of	d.	-0.001	-0.004	0.008	0.001	0,008	100'0	0.006	0,000	0.044	0.007	-0.002	0.208	0.000	0.011	-0.005	0.010	0.015	0.000	0.31*
branches	υ	-0.081	-0.004	0.170	-0.215	-0.807	0.173	0.291	-0.062	0.276	-0.177	0.200	0.398	0.177	0.011	-0.032	-0.003	0.001	0.056	0.37*
Internodal	đ	-0.003	0.000	0.012	0.002	0.001	0.004	-0.004	-0.001	0.115	0.020	-0.006	0.171	0.000	0.026	-0.007	0.013	-0.010	-0.002	0.33
length (cm)	5	-0.057	-0.050	0.188	-0.211	-0.224	0.622	-0.059	-0,145	0.530	-0.384	0.073	0.314	-0.067	0.026	-0.061	0.059	0.005	-0.071	0.49*
Nodes per	٩.	-0.005	0.014	-0.014	-0.003	-0.001	0.000	-0.056	0.000	-0.040	-0.005	-0.006	0.058	0.000	-0.009	0.004	-0.005	0.007	-0.002	-0.05
plant	U	0.233	0.273	-0.477	0.282	0.248	0.039	-0.949	-0.061	-0.250	0.195	0.010	0.258	0.225	-0.012	0.050	0.001	0.004	-0.098	-0.03
Plant height	Ч	-0.002	0.011	0.003	0.001	0.002	0.003	-0.015	-0.002	0.121	0.015	-0.006	0.161	0000	0.007	-0.002	0.009	-0.020	-0.003	0.28*
(cm)	Ċ	0.020	0.126	-0.057	-0.075	-0.260	0.472	-0.304	-0.192	0.509	-0.303	0.160	0.248	0.025	0.007	-0.030	0.034	0.006	-0.103	0.28*
Pod length	4	-0.003	0.000	0.017	0,004	0.001	0.001	0.007	100:0-	0.334	0.035	-0.005	0.019	0.000	0.011	-0.012	0.019	-0.007	-0.001	0.42*
(cm)	U	-0.039	0.028	0.261	-0.351	-0.200	0.296	0.214	-0.088	1.113	-0.568	0.168	0.055	-0.295	0.012	-0.114	0.083	0.002	-0.043	0.53*
Seeds per pod	ď	-0.007	-0.013	0.034	0.006	0.001	0.002	0.005	0.000	0.213	0.055	-0.016	0.158	0.000	0.025	-0.013	0.012	0,000	0.000	0.46*
	U	-0.248	-0.149	0.677	-0.534	-0.182	0.305	0.236	-0.074	0.806	-0.784	0.358	0.302	-0.068	0.028	-0.097	0.062	0.002	0.018	0.66*
Shelling (%)	d.	-0.007	-0.002	0.022	0.003	0.000	0.001	-0.007	0.000	0.032	0.019	-0.048	0.216	0.000	0.006	-0.003	0.003	0.014	0.001	0.25*
	G	-0.297	-0.100	0.640	-0.413	-0.279	0.079	-0.017	-0.053	0.323	-0.487	0.578	0.705	0.083	010.0	-0.116	0.041	0.001	0.005	0.70*
Pods per plant	Ь	-0.005	-0.002	0.015	0.002	0.002	0.001	-0.004	0.000	0.008	0.012	-0.014	0.741	0.000	0.011	0.004	-0.001	0.009	0.000	0.78*
	G	-0.059	0.022	0.239	-0.242	-0.367	0.223	-0.280	-0.054	0.070	-0.271	0.465	0.875	0.102	0.010	0.028	0.021	-0.001	0.018	0.80*
Total soluble	۵.	0.000	-0.007	-0.004	-0.001	0.000	0.000	0.007	0.000	0.061	0.001	0.001	-0.034	-0.001	-0.003	0.008	0.005	0.005	-0.001	0.04
SOLIDS (DELX)	G	0.032	-0.154	-0.155	0.103	0,203	0.060	0.304	0.007	0.468	-0.076	-0.068	-0.127	-0.702	-0.012	0.156	0.067	0.001	-0,004	0.10
Ascorbic acid	e.	0.004	-0.004	0.000	0.002	0.001	0.001	0.005	0.000	0.040	0.015	-0.003	0.090	0.000	0.093	-0.015	0.007	-0.001	0.001	0.24*
(mg)	С	0.102	-0.037	0.056	-0.186	-0.124	0.218	0.154	-0.019	0.187	-0.298	0.076	0.120	0.113	0.073	-0.139	0.004	0.003	-0.002	0.30
Protein	ፈ	0.000	0.000	0.006	0.003	0.001	100'0	0.004	0.000	0.068	0.012	-0.003	-0.054	0.000	0.024	-0.059	0.014	0.013	0.000	0.03
content (%)	G	0.002	0.049	0.105	-0.221	-0.059	0.086	0.108	-0.013	0.288	-0.174	0.152	-0.055	0.249	0.023	-0.439	0.050	-0.003	-0.037	0.11
Total sugars	4	0.001	-0.006	-0.001	0.001	0.001	0.001	0.004	0.000	0.081	0.009	-0.002	-0.006	0.000	0.008	-0.011	0.078	0.012	-0.002	0.17*
(%)	0	-0.032	-0.024	0.111	-0.110	0.012	0.221	-0.004	-0.039	0.554	-0.291	0.141	0.110	-0.281	0.002	-0,131	0.166	-0.001	-0.032	0.37*
Reducing	ч	0.000	-0.004	0.000	0.000	0.001	0.000	-0,004	0.000	-0.020	0.000	-0.006	0.059	0.000	-0.001	-0.007	0.009	0.107	0.004	0.14*
sugars (%)	σ	-0.007	0.060	0.104	-0.230	0.081	-0.227	0.284	0.088	-0.133	0.095	-0.061	0.031	0.054	-0.018	-0.094	0.016	-0.013	0.176	0.21*
Starch content	4	100.0	0.004	-0.001	0.001	0.000	0.000	0.004	0.000	-0.016	0.000	-0.002	0.016	0.000	0.006	0'001	-0.008	0.019	0.021	0.04
(%)	IJ	0.012	-0.196	-0.009	-0.069	-0.134	-0.131	0.277	0.059	-0.142	-0.042	0.008	0.047	0.009	0.000	0.048	-0.016	-0.007	0.336	0.05
Unexplained *Significant	variat at P ≤	tion (P) :0 0.05; r-cc).19; (G) : prrelation (0.014 coefficient	with pod	yield per I	plant; bolc	l values in	dicate dir	ect effect	s									
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with pod yield per plant. The direct effects of remaining traits were low. Pooled data over years (Table 4.10) indicated the maximum direct effects of pods per plant and pod length at phenotypic level and that of pod length followed by pods per plant, days to first picking, internodal length and shelling (%) at genotypic level on pod yield per plant. Earlier researchers have also reported direct and positive effects of pods per plant (Wakankar *et al.* 1974; Kalloo and Dhankar 1977; Singh and Singh 1985; Kumar *et al.* 1995; Ramesh and Tewatia 2002; Chaudhary and Sharma 2003; Singh *et al.* 2005; Kaur *et al.* 2007; Rathi and Dhaka 2007; Sharma *et al.* 2007; Nawab *et al.* 2008), pod length (Singh and Ram 1988; Kumar *et al.* 2007; Rathi and Dhaka 2007; Rathi and Dhaka 2007; Nawab *et al.* 2008), first flower node (Kaur *et al.* 2007), days to first picking (Narsinghani *et al.* 1978; Ramesh and Tewatia 2002), number of branches (Kaur *et al.* 2007), nodes per plant (Ramesh and Tewatia 2002), plant height (Chandel and Joshi 1976; Narsinghani *et al.* 1978; Nawab *et al.* 2008), and total sugars (Ramesh and Tewatia 2002) on the total association with pod yield per plant.

Further, it was also observed that indirect effect of pods per plant substantially enhanced the magnitude of total correlation of number of branches, internodal length, nodes per plant, plant height and shelling (%) at phenotypic level during both the years, and at genotypic level during 2010-11 except nodes per plant at both levels during 2010-11 (Table 4.8 and 4.9). At genotypic level during 2009-10, indirect effects via seeds per pod and nodes per plant canceled the negative direct effects of internodal length, plant height and shelling (%) and resulted in positive association with fresh pod yield per plant, and also enhanced the extent of association of pods per plant. Indirect contributions of both pod length and seeds per pod to each other at phenotypic level during 2009-10 and that of pod length to seeds per pod at genotypic and phenotypic levels during 2010-11, and seeds per pod to pod length at genotypic level during 2009-10 build up their correlation levels with pod yield per plant. Indirect contribution of pods per plant further added to increase the magnitude of total association of seeds per pod at both levels over the years and also resulted in significant association of ascorbic acid and reducing sugars with fresh pod yield per plant at both levels during 2010-11. Joshi and Narsinghani (1992) also suggested pods per plant as the most reliable component in breeding programme in pea for increased yield potential. Pod length had also contributed indirectly to the total association of plant height and total sugars both at phenotypic and genotypic levels and that of internodal length, number of branches, shelling (%) and ascorbic acid only at genotypic level during 2010-11.

Similarly, pooled data over years indicated that the indirect contribution of pods per plant and pod length increased the total association of number of branches, internodal length, plant height, seeds per pod and ascorbic acid at both phenotypic and genotypic levels (Table 4.10). The magnitude of these characters was so high that they nullified the negative direct contribution of number of branches, seeds per pod and plant height at genotypic level. In addition, internodal length, nodes per plant and shelling (%) also added substantially through their indirect contribution to number of branches, pod length and seeds per pod along with contribution of shelling (%) and internodal length to pods per plant at genotypic level.

Direct and indirect effects of different traits on seed yield per plant

Path analysis for seed yield per plant revealed that total biomass and harvest index had maximum positive direct effects at both genotypic and phenotypic levels during 2010-11 and pooled over years (Tables 4.12 and 4.13) and only at phenotypic level during 2009-10 (Table 4.11). The direct contribution of pods per plant at genotypic level in pooled over years was also of high magnitude followed by pod length. On the other hand, pod yield per plant and total biomass had the maximum positive direct effects on seed yield per plant at genotypic level during 2009-10 (Table 4.11). In addition, internodal length, plant height, shelling (%), harvest index, pod length, days to first picking and total sugars during 2009-10 and that of pods per plant, pod length, protein content, seeds per pod and internodal length during 2010-11 had also contributed directly to some extent towards seed yield per plant at genotypic level. On the other hand, at phenotypic level, pods per plant, plant height, pod yield per plant, days to first picking, seeds per pod and 100-seed weight during 2009-10 and that of pod yield per plant, 100seed weight, seeds per pod, internodal length and plant height during 2010-11 had also Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in garden pea during 2009-10 Table 4.11

raít	Days to first flowe	First flower sr node	Days to 50% flowering	Days to first picking	Numbcr of branches	Internodal length (cm)	Nodes per plant	Plant height (cm)	Pod S length (cm)	eeds per Si pod	helling 1 (%)	Pods per plant yi	Pod cld/plant bi (g)	Total iomass in (g)	tarvest 11 dex (%) we	00-sced sight (g)	Total soluble olids (° brix)	Ascorbic acid (mg) c	Protcin ontent (%) s	Total ugars (%)	Reducing sugars (%) c	Starch ontent (%)	-
tys to first P	0.004	0.000	-0.045	0.018	0.010	0.008	-0.005	-0.001	0.004	-0.003	0.002	0.003	-0.005 -(0.024	-0.066	0.002	0.000	-0.001	-0.002	0.001	-0.002	-0.003	-0.11
	-0.476	-0.017	0.522	0.042	0.095	-0.046	-0.160	0.020	-0.024	0.239 -	0.072	-0.051	-0.055 -(0,014	-0.041	0.024	-0.072	0.000	0.000	-0.004	100'0	-0.033	-0.12
rst flower P	0.000	-0.015	0.003	0.000	-0.002	-0.014	-0.015	0.026	-0.002	- 000.0	0.004	0.013	0.006 C	0.024	0.074	100.0	-0.006	0.003	010.0	-0.002	0.001	0.003	0.10
D 20% D	C#0.0-	1000	CUU.U-	500.0-	170.0-	160.0	-0.348	0.146	0.015	-0.012	0.076	-0.101	0.283 (0.073	0.046	-0.015	161.0	100.0-	-0.007	0.002	0.000	0.075	0.26*
wering G	-0.458	0.002	0.542	10.055	0.087	C10.0	CON:0-	200.0-	0.000		200.0 200.0	0.004	- 600'0-	0.048	-0.086	-0.003	0.002	0.006	-0.004	100.0	-0.00	-0.004	9.19 2.19
tys to first P	0.002	0.000	-0.047	0.032	0.004	0.015	-0.008	0.000	0.007	- 105.0	5/0/C	C70.0-	- 242	0.078	0.005	1000	180.0-	-0.004	-0.004	70070	000.0	-0.041	01.0
king G	-0.356	0100	0.525	0.057	0.047	-0.068	-0.085	-0.007	-0.044	0.382	0.086	-0.005	-0.461 -1	0.084	-0.050	0.055	0.027	-0.004	0.002	-0.002	0000	0.040	-0.25*
umber of P	100.0-	-0.001	0.016	-0.003	-0.045	-0.001	0.002	0.005	-0.001	0.001	0,002	0.017	0.010 0	0.173	-0.054	0.002	0.000	0.003	-0.005	-0.002	0.005	0.005	0.12
anches G	0.150	-0.013	-0.148	-0.009	-0.302	0.007	0.127	0.007	0.001	-0.028	0.032	-0.122	0.174 0	0.223	-0.029	0.041	0.038	-0.002	0.003	0.004	-0.001	0.084	0.16
ternodal P	0.000	-0.003	0.012	-0.007	-0.001	-0.072	-0.005	0.044	-0.009	0.007	0.002	0.015	0.013 0	0,191	0.195	0.003	0.002	-0.007	0.001	0.001	-0.004	-0.003	0.37*
ngtn (cm) G	0.088	-0.067	-0.115	-0.015	-0.008	0.252	-0.134	0.177	0.044	-0.279	0.027	-0.055	0.349 (0.191	0.074	-0.057	-0.041	0.003	100.0-	-0.002	0.000	-0.029	0.40*
odes per P	0.001	-0.006	-0.008	0.007	0.002	010.0-	-0.037	0.024	0.000	0.000	0.006	0.016	0.009 (0.092	0.036	-0.001	-0.002	0.000	0.002	0.001	0.002	-0.001	0.12
5	-0.226	-0.191	0.166	0.014	0.114	0.100	-0.338	0 149	-0.004	0.041	0,081	-0.154	0.264 (0.186	0.026	0.011	0.057	-0.002	100'0-	-0.002	0.000	-0.002	0.29*
lant height P	0.000	-0.006	0.002	0.000	-0.003	-0.050	-0.014	0.064	-0.008	0.005	0.003	0.014	0.012 0	0.187	0.181	0.002	-0.001	-0.002	-0.001	0.002	-0.004	100'0-	•38*
	-0.041	-0.118	0.015	-0.002	-0.009	0.194	-0.219	0.229	0.037	-0.205 (0.036	-0.083	0.298 (0.199	0.068	-0.040	0.067	0.002	0.000	-0.002	0.000	-0.007	0.42*
od length P	100.0-	-0.002	0.018	-0.011	-0.002	-0.031	0.000	0.025	-0.021	0.010	0.004	0.005	0.020 (0.229	0.193	0.005	0.004	-0.006	0.007	0.000	-0.003	0.000	0.44*
9 .	0.126	-0.030	-0.163	-0.027	-0.003	0.122	0.014	0.093	160'0	-0.392 (0.039	-0.044	0.540 (0.247	0.071	-0.081	-0.113	0.003	-0.003	0.000	0.000	0.003	0.49*
eeds per pod P	100'0-	0.000	0.026	-0.014	-0.002	-0.033	0.001	0.021	-0.014	0.016 -	0.012	0.013	0.022 (0.263	0.260	0.003	0.000	-0.013	0.005	0.003	-0.005	100.0	0.54*
، ت : :	0.215	-0.004	-0.308	-0.041	-0.016	0.132	0.026	0.089	0.067	-0.531 (0.094	-0.072	0.623 (0.270	860.0	-0.056	-0.010	0.008	-0.002	-0.004	0.001	0.010	0.59*
helling (%) P	0.000	-0.002	0.011	-0.005	-0.002	-0.005	-0.006	0.005	-0.002	0.006	0,033	0.022	0.012 (0.214	0.087	-0.001	-0.002	-0.005	0.007	0.003	0.004	0.002	•16.0
ט ט - -	0.183	-0.075	-0.216	-0.026	-0.051	0.036	-0.145	0.044	0.019	-0.264 (0.188	-0.130	0.472 (0.285	0.040	0.002	0.061	0.001	-0.004	0.000	0.000	0.032	0.45*
ods per plant P	0.000	-0.003	-0.003	0.000	600'0-	-0.014	-0.008	0.011	-0.001	0.003	0.009	0.080	0.031 (0.479 •	0.190	0.002	0.000	-0.004	-0.002	0.011	100'0	0.001	0.76*
	9/0/0-	-0.058	0.042	100.0	-0.115	0.043	-0.162	0.059	0.013	-0.119	0.076	-0.321	0.869 (0.480	0.078	-0.042	0.029	0.002	0.001	-0.011	0.000	0.017	•18.0
od yleid/P	100'0-	-0.002	0.014	-0.008	-0.010	-0.022	-0.007	0.018	-0.010	0.008	600'0	0.057	0.043 (0.488	0.287	0.006	0.002	-0.009	0.003	0.006	100'0	100.0	0.85*
	0,000	000.0-	271.0-	C70.0-	0.00-0-	0.084	-0.085	0.065	0.047	-0.314	0.084	-0.265	1.052	0.480	0.108	-0.098	-0.035	0.006	-0.001	-0.006	0.000	0.016	•16.0
	0000	100.0-	200.0	+00.0-	110.0-	07070-	-0.00 -	810.0	-0.007	0.006	0100	0.056	0.031	0.679	0.061	0.006	0.003	0.000	0.001	0.011	0.003	0,001	0.82*
annet index D	110'0	170'0-	-0.050	2000	-0.107	0.076	-0,100	0.072	0.036	-0.226	0.085	-0.244	0.799	0.632	0.022	-0.093	-0.077	100'0-	0.000	-0.011	0.000	0.013	0.82*
() () () () () () () () () () () () () (-0.046	110.0	000.0-	CUU.U	170.0-	-0.002	0.022	800.0-	- 800.0	0.005	0.029	0.023 (0.079	0.522	0.003	-0.00	-0.015	0.003	-0.003	-0.005	-0.001	0.63
D_eerd D	100 0-	100.0-	100	2000	1000	101.0	0.000	C00/0	0,000	-0.282	0.041	0(1.0-) 179'0	0.0/6	0.183	-0.046	0.043	0.008	-0.001	0.003	100.0	-0.012	0.65
cight (g) G	0.059	-0.015	-0.142	-0.016	-0.064	0.074	0.020	210.0	000.0-	- 155 L	200.0	-0.060	0 430 0	0.505 0	0.044	0.013	0.000	-0.00	0.008	-0.004	C00.0	-0.003	0.46" 0.49*
otal P	0.000	0.004	-0.005	0.001	0.000	-0.005	0.004	-0.002	-0.003	0.000	1.002	0000	0.004	0.088	- 0 0-	0.000	0.03	0.004	500.0-	-0.002	100.02	0000	0.08
elublesolids (" G	060.0-	0.094	0.125	0.004	0.031	0.027	0.051	-0.041	0.027	-0.014 -	0.031	0.024) 860.0	0.129	-0.021	0.025	-0.377	-0.005	0.004	0.000	-0.001	0.008	0.07
scorbic acid P	0.000	0.001	0.008	-0.002	0.003	-0.011	0.000	0,003	-0.003	0.005	0.004	0 006	500.0	0 007	0 177	0.001	-0 002	-0.044	0 008	0 003	-0.007	-0 003	0.14
ig) G	-0.003	0.009	101.0-	-0.010	0.023	0.040	0.029	0.018	0.014	-0.198 (0.009	-0.030	0.275 -1	0.017	0.069	-0.049	0.094	0.021	-0.003	-0.006	0.001	-0.034	0.15
otcin content P	0.000	-0.004	0.006	-0.003	0.005	-0.002	-0.002	-0.001	-0.004	0.002	0.005	-0.004	0.003	0.016	0.040	0.002	-0.003	-0.009	0.041	-0.007	0.003	0.002	0.08
ۍ و	0.004	-0.082	-0.064	-0.007	0,049	0.008	-0.030	-0.005	0.017	-0.067	0.043	0.027	0.073 (0.016	0.014	-0.033	0.101	0.004	-0.015	0.005	0.000	0.014	0.07
otal sugars P	0.000	-0.001	0.001	0.000	-0.002	0.002	0.000	-0.002	0.000	100'0-	0.002	-0.015	-0.004	0.141	0.028	0.001	0.001	0.003	0.005	-0.055	0.003	-0.003	-0.18*
D I	0.045	-0.008	-0.029	-0.002	-0.026	-0.010	0.013	-0.009	0.000	0.042 -	0.001	0.075	-0.144 -	0.157	0.011	-0.018	100'0	-0.003	-0.002	0.045	0.000	-0.031	-0.21*
colucing P	0.000	-0.001	0.002	100.0-	-0.010	0.012	-0.004	-0.011	0.003	-0.003	0.005	0.002	0.003 (0.082	-0.123	0.003	0.003	0.015	0.005	-0.007	0.022	0.003	-0.01
D (ac) cmg	0.111	-0.020	-0.067	-0.008	-0.101	-0.046	0.012	-0.042	-0.015	0.142 (0.015	-0.003	0.061 (0.083	-0.048	-0.053	-0.081	-0.010	-0.002	0.008	-0.002	0.050	-0,02
Karch content P	0.073	-10.065	-0103	-0.013	-0.117	110.0	0.002	-0.002	0.000	0.001 ·	0.003	0.004	0.003	0.024	-0.022	-0.002	0.000	0.007	0.004	0.007	0.003	0.019	0.05
, - -				0000		+CD.D	cuu.u	-0.006	100.0	C70'0-	0.028	070.0-	0.080	0.057	110.0-	0.035	-0.013	-0.005	100'11-	000.0-	-0.001	0.216	6.0
Unexplaitieu 'Sionificant :	variation of $P < 0.6$	ו (ד') : ט.ט. איי ד-כחדדפ	2; (U) : lation c	-0.UUZ Aefficier	nt with n	بالمزيد ليد	tucla roa	" hold "	ما معدام	dinota di													
	ジリ T m	11, 1-1011		~~~~	יוו איווו אי	טם אובות	per prair	r; vuu v	Alucs III	ID DICALC UL	rect env	ects											
Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in garden pea during 2010-11 Table 4.12

T rait	Days to	First flower	Days to	Days to 1	Vumber of 1	Internodal	Nodes per	Plant	Pod Sc	cds pcr Sh	cling Pc	ds pcr	Pod T	otal Ha	rvest 10t)-seed	Total A	scorbic	Protein	Total F	teducing	Starch	.
	first flow	cr node	50% flowering	first picking	branches	length (cm)	plant	height (cm)	length (cm)	pod	。 (%)	plant yic	ild/plant bic (g)	(g) (g)	dex wei %)	ght (g) s	oluble ac blids (° brix)	id (mg) co	ntent (%) su	gars (%) sı	igars (%) cc	ntent (%)	
Days to first	0.0	-00 ⁻ 00	1 0.025	0.000	0.000	100.0-	-0.002	0.000	0.000	-0.005	0.003	0.005	-0.013	-0.034	600.0	0.008	0.000	-0.003	0.00	-0.001	-0.002	0.001	-0.03
flower	G 0.0	20 0.01	3 -0.084	-0.017	0.000	0.001	110'0	0.001	0.005	-0.005	0.041	-0.029	0.012	-0.061	-0.005	-0.005	-0.006	-0.006	0.003	-0.006	-0.007	0.025	-0.06
First flower	0.0 4	10.0- 0015	600 ^{.0}	0.000	0.000	-0.001	-0.003	0.000	0.000	-0.008	0.001	0.003	-0.005	0.023	0.017	0.017	0.000	0.002	100.0-	0.003	0.005	0.000	0.04
abou	0.0	44 0.01	-0.055	-0.010	0.002	-0.005	0.018	-0.001	0.001	010.0-	0.049	-0.008	0.003	0.051	-0.060	-0.015	-0.012	0.002	-0.013	0.009	0.006	-0.006	0.01
Days to 50%	0.0	00 -0.00	0.029	0.000	0.000	-0.001	-0.002	0.000	0.000	-0.007	0.003	0.007	-0.019	-0.081	-0.042	0.008	0.000	-0.001	0.000	-0.001	-0.002	0.001	-0.11
tiowering	0.0	51 0.012	-0.081	-0.021	0.00	0.000	0.012	0.000	-0.002	-0.007	0.044	-0.032	0.016	-0.115	0.021	-0.004	-0.003	-0.003	0.001	-0.003	-0.006	0.026	-0.13
Days to first	0.0	00.00	600.0 (0.001	0.000	100.0-	-0.003	0.000	0.000	-0.008	0.002	0.005	-0.017	. 600.0	-0.185	-0.002	0.000	0.003	-0.003	0.003	0.001	0.000	-0.19
picking (00 00	12 0.00	7 -0.073	-0.024	0.007	-0.004	0.026	0.001	-0.028	-0.011	0.031	-0.057	0.037	-0.081	-0,441	0.003	0.031	0.011	-0.020	0.017	0.002	0.015	-0.51
Number of	0.0	00.0	100:0-	0.000	0.000	0.002	0.002	0.001	0.000	0.004	0.000	-0.008	0.022	0.121	0.170	0.003	0.000	-0.004	0.002	-0.003	-0.005	100.0-	0.31
branches (0.0	100'0- 10	0.002	0.007	-0.024	0.005	-0,008	-0.004	0.020	0.004	-0.011	0.031	-0.017	0.125	0.216	-0.001	0.006	-0.005	0.010	-0.007	-0.004	-0.006	0.34
Internodal	0.0	0.00%	-0.002	0.000	0.000	0.009	0.000	0.001	-0.001	0.006	-0.002	-0.006	0.023	0.268 -	0.022	-0.002	0.000	-0.008	0.002	-0.006	0.001	0.000	0.26*
length (cm) (G 0.0	72 -0.004	100.0- 1	0.005	-0.007	0.018	0.001	-0.004	0.022	0.006	-0.027	0.026	-0.017	0.298	0.006	0.000	0.001	-0.010	0.009	-0.016	0.001	-0.003	0.31
Nodes pcr 1	0.0(0.004	0,005	000'0	0.000	0.000	-0.013	0.000	100.0	-0.004	100.0-	0.000	-0.014	0.092	0.180	-0.004	0.000	0.004	-0.002	0.002	100.0-	-0.001	-0.12
plant (G 0.0	12 0.00	910.0- 9	-0.012	0.004	0.000	0.051	100'0-	-0.023	-0.004	-0.013	-0.003	0.011	0.106	0.215	0.003	-0.023	0.005	-0.009	0.005	0.000	-0.010	-0.13
Plant height	0.0	200.0- 00	100'0-	0.000	0.000	0.005	-0.002	0.002	-0.001	0.005	-0.002	-0.006	0.019	0.216	010.0	-0.002	0.000	-0.002	0.001	-0.005	0.008	-0.001	0.22*
(cm) (-0.0	0.002	0.004	0.003	-0.013	0.012	0.010	-0.007	0.026	0.004	-0.031	0.024	-0.014	0.245	0.004	0.002	0.009	-0.003	0.003	-0.012	0.009	-0.022	0.24
Pod length 1	0.00	0.001	-0.002	0.000	0.000	0.002	0.003	0.001	-0.002	0.015	-0.001	0.000	0.027	0.104	0.259	0.012	0,000	-0.003	0.003	-0,009	-0.002	-0.001	0.41*
(cm)	G 0.00	14 0.000	0.002	0.009	-0.007	0.006	-0.016	-0.002	0.073	0.013	-0.020	0.001	-0.022	0.128	0.319	-0.008	0.030	-0.005	0.014	-0.025	100.0-	-0.010	0.48*
1 Free strange	0.0	0.006	600.0-	0.000	0.000	0.002	0.002	0.000	-0.002	0.023	-0.003	-0.006	0.029	0.133	0.229	-0.007	0.000	-0.001	0.004	-0.006	600'0-	0.000	0.38*
) pod rad snaac	0.0- E	17 -0.005	0.029	0.015	-0.005	0.006	-0.010	-0.002	0.049	0.019	-0.049	0.024	-0.023	0.143	0.268	0.005	0.008	-0.008	0.016	610.0-	-0.009	-0.006	0.42*
Challing (9/)	0.0(00.0	-0.009	0.000	0.000	0.002	-0.001	0.000	0.000	0.007	-00.00	-0.008	0.016	0.013	-0.021	-0.013	0.000	-0.001	-0.001	-0.003	-0.004	0.00	-0.03
) (w) functions	-0.0	13 -0.008	0.034	0.007	-0.002	0.005	0,006	-0.002	0.014	0.009	-0.107	0.045	-0.017	0.053	0.062	0.012	0.014	-0.004	0.001	600.0-	0.000	-0.005	0.08
1 million bed	0.00	0.002	-0.009	0.000	0.000	0.002	0.000	0.001	0.000	0.006	-0.003	-0.024	0.053	0.307	0.146	-0.007	0.000	-0.003	100.0-	-0.002	-0.006	0.000	0.46*
Lous per prant	G.00.02	0.002	0.030	0.016	-0,009	0.005	-0,002	-0.002	0.001	0.005	-0.055	0.087	-0.039	0.355	0.155	0.005	-0.014	-0.003	-0.003	-0.006	-0.005	-0.002	0.50*
Pod yield F	0.00	0,001	-0.008	0.000	0.000	0.003	0.003	0.001	-0.001	010.0	-0,002	-0.019	0.065	0.347	0.299	0.007	0.000	-0.006	0.000	-0.006	-0.008	0.000	0.68*
/plant (g) (G.00.01	15 -0.001	0.027	0.019	-0.009	0.007	-0.012	-0.002	0.034	0.009	-0.039	0.072	-0.047	0.386	0.336	-0.004	-0.003	-0.007	0.002	-0.016	-0.008	0.004	0.73*
Total biomass F	0.0	100.0- 00	-0.003	0.000	0.000	0.003	-0,002	0.001	0.000	0.004	0.000	-0.010	0.032	0.706	-0.076	0.009	0.000	-0.003	0.001	-0,005	-0,002	-0.001	0.65*
(g)	G.0.	100.0 20	0.012	0.003	-0.004	0.007	0.007	-0.002	0.012	0.004	-0.007	0.040	-0.024	0.763	-0.069	-0.005	-0.022	-0.003	0.006	-0.012	-0.003	-0.009	•69*0
Harvest index 1	0.00	0.000	-0.002	0.000	0.000	0.000	0.003	0.000	-0.001	0.008	0.000	-0.005	0.028	-0.075	0.708	0.015	0.000	-0.005	0.001	-0.003	-0.008	0.001	•99.0
) (%)	.0.0	100.0- 00	0.002	0.015	-0.007	0.000	-0.015	0.000	0.033	0.007	-0.010	0.019	-0.022	-0.075	0.703	-0.010	0.005	-0,006	0.010	-0.010	-0.011	0.019	0.64*
100-seed	0.00	0.006	0.005	0.000	0.000	0000	0.001	0.000	-0.001	-0.003	0.003	0.003	010.0	0.132	0.236	0.046	0.000	-0.004	0.000	-0.002	-0.003	0.000	0.42*
weight (g) (10:0	0.010	-0.014	0.002	-0.001	0.000	-0.005	0.001	0.024	-0.003	0.052	-0.017	-0.008	0.153	0.280	-0.025	0.009	-0.005	0.003	-0.007	-0.005	0.004	0.46*
Total soluble	0.00	100'0 0	0.000	0.000	0.000	0.000	0.002	0.000	-0.001	0.001	100.0-	0.003	-0.002	-0.151	0.063	0.004	0.000	0.000	-0.003	-0.002	0.005	-0.001	-0.08
solids ("brix) (-0.0	-0.002	0.002	-0.008	-0.002	0.000	-0.013	-0.001	0.025	0.002	-0.017	-0.014	0.001	-0.191	0.036	-0.003	0.087	0.001	-0.011	-0.007	0.004	-0.018	-0.13
Ascorbic acid	0.00	0.001	0.002	0.000	0.000	0.003	0.002	0.000	0.000	0.007	0.000	-0.003	0.016	0.085	0.136	0.007	0.000	-0.024	0.004	-0.003	-0.007	0.001	0.22*
(mg) (0.01	4 -0.001	-0.010	0.012	-0.005	0.008	-0.010	-0.001	0.014	0.007	-0.016	0.011	-0.013	0.099	0.172	-0.006	-0.003	-0.023	0.018	-0.006	-0.013	0.012	0.26*
Protein content F	0.00	0 0.002	-0.001	0.000	0,000	0.002	0.002	0.000	-0.001	0.007	0.000	0.002	0.001	0.073	0.049	0.000	0,000	-0,007	0.014	-0.004	-0.006	100.0-	0.13
) (%)	G.0C	14 -0.005	-0.001	0'010	-0.005	0.004	-0.010	0.000	0.022	0.006	-0.002	-0.006	-0.002	0.092	0.145	-0.002	-0.020	-0.009	0.048	-0.012	-0.010	-0.011	0.24*
Total sugars F	0.00	0 0.003	0.001	0.000	0.000	0.003	0.001	0.001	100'0-	0.008	100.0-	-0.003	0.022	0.185	0.108	0.005	0.000	-0.004	0.003	-0.019	-0.004	0.000	0.31*
) (%)	0.00	8 -0.004	-0.006	0.010	-0.004	0.007	-0.006	-0.002	0.045	0.009	-0.024	0.012	-0.019	0.236	0.178	-0.005	0.015	-0.004	0.014	-0.040	-0.006	-0 008	0.41*
Reducing F	0.00	0 0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.005	-0.001	-0.003	0.013	0.032	0.128	0.003	0.000	-0.004	0.002	-0.002	-0.043	0.001	0.13
sugars (%) (0.0	3 -0.003	-0.017	0.002	-0.003	-0.001	0.001	0.002	0.003	0.005	0.000	0.013	-0.012	0.061	0.239	-0.004	-0.012	-0.009	0.015	-0.008	-0.031	0.021	0.27*
Starch content P	0.00	100'0- 0	0.005	000 0	0'00'0	0.000	0.001	-0.001	0.000	-0.001	0.000	0.000	0.002	-0.084	0.139	0.001	0.000	-0.004	-0.001	0.002	-0.010	0.005	0.05
) (%)	0.02	100.0- 1	-0.030	-0.005	0.002	-0.001	-0.007	0.002	-0.011	-0.002	0.008	-0.002	-0.002	-0.102	0.186	100.0-	-0.022	-0.004	-0.007	0.005	-0.009	0.070	0.09
Unexplained	1 variatio,	<u>n (P)</u> : 0.0	2 (G)	0.005																			

*Significant at $P \le 0.05$; r-correlation coefficient with pod yield per plant, bold values indicate direct effects

Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in garden pea in pooled over years Table 4.13

T mit Days to first flow the first flow to be a fir	First flowc rr node 12 -0.00 27 -0.01 18 -0.01 18 -0.01	r Days to 50% flowcring	Days to first picking	Number of branches	Internodal 1 iength (cm)	Nodes per plant	Plant height (cm)	Pod length (cm)	eds pcr SI pod	helling Pod (%) pl	s per Pod	yicld To	tal Har nass index	cst 100-sc t (%) weight	(g) Solu	al Asc ble acid	orbic P I (mg) con	rotein To tent (%)	otal sugars 1 (%) s	Reducing sugars (%) cr	Starch ontent (%)	-
Days to first P 0.0 Days to first P 0.0 Days to 50% P 0.0 Days to 50% P 0.0 Days to 50% P 0.0 Days to 10% P 0.0 Days to 10% P 0.0 Days to 10% P 0.0 Days to 200 P 0.0 Days to 2	2 -0.00 17 -0.01 12 -0.06 18 -0.01											т (8)	(6		3ē	8 (R				•		
Rower G -0.0 First Rower P 0.0 Days to 50% P 0.0 Rowering G -0.0 Days to first P 0.0 Days to first P 0.0 nicking G -0.0	7 -0.01 22 -0.00 18 -0.01		0.000	0.000	0.002	-0.003	-0.001	0.001	0.002	0.005	0.002 -	0.012 -0	0- 0-0	.032 0.	100	000'(-0.002	0.000	100.0-	0.000	0.000	-0.06
First flower P 0.0 mode C 0.0.0 Days to 50% P 0.0 flowering G 0.0 Days to first P 0.0 nickine C 0.0	2 -0.00	0.130	-0.138	0.007	0.000	-0.015	-0.002	-0.014	-0.032	0.032 -	0.052	0.109 (0- 610.0	.046 0.	600	0.004	0.004	0.000	0.003	-0.001	-0.001	-0.02
Days to 50% P 0.0 Days to 50% P 0.0 Days to first P 0.0 Days to first P 0.0	-0.01	100.001	0.000	0.000	0.000	-0.006	0.004	0.000	0.003	0.001	0.000	0.002 0).022 C	.036 0.	002	0.002	0.001	0.000	0.002	0.000	100.0	0.06
Days to 50% F 0.0. Days to first P 0.0. bicking C 0.0	000	1 0.069	-0.060	100:0	0.000	-0.026	-0.019	0.015	-0.029	0.016	0.028	0.010 (0.096	037	0:030	-0.002	0.004	0.004	0.018	0.019	0.05
Days to first P 0.0			0.000	0.000	200.0	500.0-	100.0-	200.0	0.004	0.006	- 200.0	0.017 -4).065 -C	.066	000	100.0	0.000	-0.002	0.000	0.000	0.000	-0.13
nicking C 22	14 0.00	671-0 0- 0	0000	0000	0.004	910.0-	-0.003	-0.048	-0.045	0.005	901.0	9 2100)- 050.0	0 0 0	2007	010.0	100.0-	-0.003	0.006	010.0-	0.000	-0 -0
	00.0-	6 0.124	-0.164	0.017	100.0-	-0.015	0.006	-0107	-0.059	0.037	0 177	0.017 -1 0.456 -1			100	100	200.0	000.0-	0.010	-0.038	0.00	-0.46*
Number of P -0.0	0.00	0.001	0.000	-0.003	-0.004	0.003	0.006	-0.001	100.0-	100 0	0.003	0.201 6	1129 0	086 0.	100	000'0	-0.002	0.002	-0.003	100'0-	000.0	0.23*
branches G 0.0	0.00	0 -0.018	0.047	-0.059	0.001	0.013	-0.020	0.057	0.019	-0.023	0.251	0.272 0	0 0 0	.118 0.	900	1.021	0.004	0.003	0.001	-0.013	-0.007	0.27*
Internodal P -0.0	0.00	0.001	0.000	-0.001	-0.025	-0.002	0.013	-0.004	-0.004	-0.003	0.003	0.023 (0 235 0	.0 160.	100	100'(-0.005	0.003	-0.003	0.000	-0.002	0.32*
length (cm) G 0.0	0.00	2 -0.019	0.046	-0.016	0.002	-0.003	-0.047	0.109	0.041	-0.009	0.198 -	0.354 (0.315 6	.207 0.	010	3.008	0.009	0.005	-0.024	-0.046	0.009	0.45*
Nodes per plant	12 -0.00	100'0- 10	000.0	0.000	-0.002	-0.023	0.006	0.001	0.001	-0.003	- I00.0	0.004 0)- 960.(.067 -0.	F 100	2007	0.002	-0.002	100'0	000.0	100'0-	00.0
000 000	10.0- 0.01	0 0.049	-0.061	0.018	0,000	-0.041	-0.020	-0.052	-0.021	-0.001	0.163	0.022 (), 106 -(049 -0.	- 013	0.026	-0.004	-0.004	000'0	-0.037	0.012	0.02
Plant height P -0.0	0.0- 10	00000	0.000	-0.001	-0.016	-0.007	0.021	-0.004	-0.003	-0.003	0.003	0.019 ().209 C	0.094 0.	001	000.0	-0.001	0.001	-0.002	0.001	-0.003	0.30*
(clin) G -0.0	0.0 . I(5 0.006	0.016	610'0-	0.002	-0.013	-0.063	0.105	0.032	-0.019	0.157 -	0.207 (0.290 0	.141 0.	- 6003	0.003	0.003	0.003	-0.014	-0.057	0.013	0.37*
Pod length (cm)	0.00	0.001	0.000	0.000	-0,009	0.003	0.007	-0.010	-0.007	-0.002	0.000	0.029 (0.184 C	.226 0.	.003	2.002	-0.002	0.006	-0.005	0.000	-0.001	0.42*
0.0	12 -0.00	-0.027	0.077	-0.015	0.001	0.009	-0.029	0.230	0.060	-0.020	0.035 -	0.387 (),246 C	.311 0.	030	0.034	0.004	010.0	-0.034	-0.015	0.005	0.53*
Seeds per pod P -0.0	13 0.00	1 0.002	0.000	0.000	-0.009	0.002	0.006	-0.007	-0.011	-0.008	0.003	0.031 (0,212 6	249 0.	100	000.0	-0.005	0.006	-0.003	0.000	0.000	0.46*
0.0	0.00	-0.070	0.116	-0.013	0.001	0.010	-0.024	0.167	0.083	-0.042	0.191	0.477 ().264 (.385 0.	.005	0.008	0.010	0.009	-0.026	-0.015	-0.002	0.59*
Shelling (%) P -0.0	13 0.00	0.001	0.000	0.000	-0.003	-0.003	0.003	-0.001	-0.004	-0.024	0.004	0.017 () 139 (043 -0	.002	000.0	-0.001	0.002	100'0-	100.0-	0.001	0.16*
0.0	2 0.00	4 -0.066	060.0	-0.020	0.000	-0.001	-0.017	0.067	0.015	-0.068	0.445	0.511 (),307 (.222 -0.	- 022	010.0	0.003	0.010	-0.017	-0.013	-0.001	0.47*
Pods per plant0.0	12 0.00	0.001	0.000	-0.001	-0.006	-0.002	0.005	0.000	-0.002	-0.007	0.012	0.053 (), 395 (165 0.	000	0.001	-0.002	-0.002	0.000	0.000	0.000	0.58*
0.0	13 -0.00	-0.025	0.053	-0.027	0.001	-0.012	-0.018	0.014	0.029	-0.055	0.552 -	0.580 (1,528 C	.209 -0.	- 500.	0.012	0.004	-0.002	-0.009	0.005	-0.002	0.65*
Pod yicld per P -0.0	12 0.00	0.001	0.000	100'0-	-0.008	0.001	0.006	-0.004	-0.005	-0.006	0.010	0.068 (1,413 (.288 0.	.003	0.001	-0.005	0.001	-0.004	-0.001	0.001	0.74*
plant (g) G 0.0	4 0.00	0 -0.046	0.103	-0.022	0.001	0.001	-0.018	0.122	0.054	-0.048	0.440	0.727 () 579 (.379 0.	.026	3.008	0.008	0.004	-0.026	0.026	-0.002	0.87*
Total biomass P -0.0	0.00	100'0 0	0.000	-0.001	-0.008	-0.003	0.006	-0.003	-0.003	-0.005	0.007	0.039 (0.724 0	005 0.	.003	000.0	-0.001	0.002	0.000	0.000	-0.001	0.75*
(B) G -0.0	-0.00	3 -0.005	0.040	-0.014	0.001	-0.006	-0.024	0.075	0.029	-0.028	0.389 -	0.561 (0.751 0	.199 0.	- 032	7.007	0.001	0.003	-0.021	0.007	0.005	0.86*
Harvest index P -0.0	1 0.00	0 0.001	0.000	0'00	-0.004	0.003	0.003	-0.004	-0.004	-0.002	0.003	0.032 (3,005 (.618 0.	.003	0.000	-0.005	0.002	-0.002	0.000	0.002	0.64*
(24) C 0.0	0.00	3 -0.036	0.088	-0.013	0.001	0.004	-0.016	0.129	0.057	-0.027	0.209 -	0.498 (1.270 6	.553 0.	.025	0.007	0.011	0.008	-0.012	0.019	-0.006	0.78*
100-seed weight P 0.0	0.00	0.000	0.00	0.000	-0.003	0.002	0.002	-0.003	100.0-	0.004	0.000	0.019 (),244 (171 0.	.010	0,000	-0.003	0.002	-0.002	100.0-	-0.001	0.44*
18/ C -0:0	-0.00	8 -0.004	0.040	-0.005	0.000	0.008	-0.003	0.094	0.006	0.021	0.025 -	0.261 (),334 (192 0.	- 210.	0,002	0.006	0.005	-0.161	0.038	0.002	0.49*
solublesolids (° _ 0.0	00.00	0.000	0.000	0000	-0.001	0.003	0.000	-0.002	0.000	0.001	100'0	0.003 () 600.0	0 1001	000	0.013	100.0	-0.004	-0.00	0.000	-0.001	0.02
briv) C -0.0	1 0:00	6 0.016	-0.022	0.015	0.000	0.013	0.022	0.097	0.008	0.008	0.080 -	0.047 -C) 063 (0.044 -0.	.002	010	-0.004	-0.014	-0.028	-0.010	0.001	-0.01
Ascorbic acid P 0.0	0.00	0.000	0.000	0.000	-0.007	0.002	100.0	-0.001	-0.003	-0.002	0.002	0.016 (1.047 (140 0.	- 200.	100.0	-0.020	0.007	-0.002	0.000	0.001	0.18*
(mg) G -0.0	4 0.00	1 -0.006	0.041	-0.009	0.001	0.007	-0.006	0.039	0.031	-0.009	0.076 -	0.218 (),038 (1231 0.	- 810	0.013	0.025	0.012	-0.002	-0.031	0.00	0.22*
Protein content P 0.0	0.00	0.000	0.000	0.000	-0.003	0.002	100'0	-0.002	-0.002	100.0-	0.001	0.002 (),047 (0.044 0.	100.	0.002	-0.005	0.029	0.004	100.0-	0.000	0.11
(%) G 0.0	0.00	2 -0.011	0.048	-0.004	0.000	0.005	-0.004	0.060	0.018	-0.018	0.035 -	0.081 () 029 (114 0	· 600	0.029	0.008	0.038	-0.021	0.027	0.005	•61.0
Total sugars P 0.0	0.00	1 0.000	0.000	0.00	-0.004	0.002	0.002	-0.003	-0.002	-0.001	0.000	0.011 (0.013 (0.068 0.	100	0.001	-0.002	0.005	-0.021	100'0-	-0.002	0.07
(%) G 0:0	0.00	1 -0.011	0.024	100'0	0.001	0.000	-0.013	0.114	0.031	-0.017	0.070 -	0.270 (1,232 C	0 260	.017	0.033	0.001	0.011	-0.069	0.012	0.004	0.27*
Reducing P 0.0	00.0	00000	0.000	0.000	0.002	-0.002	-0.004	0.001	0.000	0.003	0.001) 600.0),064 -0	013 0.	.002	100'0	0,000	0.004	-0.002	-0.005	0.004	0.06
	0.00.0	2 -0.011	0.050	0.006	-0.001	0.012	0.029	-0.027	-0.010	0.007	0.020 -	0.149 (),043 (0.084 0.	.022	0.006	-0.006	0.008	-0.007	0.125	-0.021	0.17*
Starch content P 00	0 0.00	0.000	0.000	000	0.002	0.002	-0.003	0.001	0.000	-0.001	0.000	0.003 -().026 C	0.054 -0.	. 100.	0.001	-0.001	-0.001	0.002	-0.001	0.020	0.05
I Inavnlainad wariatis		100.0 1	c10.0	-0.010	-0.00	0.012	0.019	-0.029	0.004	-0.001	0.029	0.035 -() 099 (0.083 -0	004	0.001	0.000	0.004	0.007	0.066	-0.041	0.02

Unexplained variation (P) :0.03; (c) : 0.005 * (c) : 0.005 * Significant at P \leq 0.05; r-correlation coefficient with pod yield per plant; bold values indicate direct effects

.

92

direct contribution to certain extent towards seed yield per plant. Earlier reports have also indicated the importance of direct effects of biological yield (Togay *et al.* 2008), harvest index (Singh and Mishra 2002; Singh 2007), pods per plant (Singh and Mishra 2002; Arya *et al.* 2004a; Singh *et al.* 2005; Singh and Yadav 2005; Singh 2007; Singh *et al.* 2008; Togay *et al.* 2008; Esposito *et al.* 2009; Guleria *et al.* 2009; Sharma *et al.* 2009; Awasthi *et al.* 2011; Singh *et al.* 2011), seeds per pod (Joshi and Narsinghani 1992; Singh 2007; Esposito *et al.* 2009), pod length (Singh and Yadav 2005; Singh 2007) and plant height (Arya *et al.* 2004a) on the total association of seed yield per plant and were suggested as the most reliable components in pea breeding programmes.

The maximum indirect contribution via total biomass resulted in the significant positive association with seed yield per plant for the characters viz., plant height, pod length, seeds per pod, shelling (%), pods per plant, pod yield per plant and 100-seed weight during 2009-10 at phenotypic level, and internodal length, plant height, pods per plant, pod yield per plant and total sugars at both phenotypic and genotypic levels during 2010-11 (Table 4.11 and 4.12). The total biomass at phenotypic level had also nullified the negative direct effects of pod length and shelling (%) during 2009-10 and that of pods per plant and total sugars during 2010-11, whereas at genotypic level during 2010-11, it had negated the negative direct effects of plant height, pod yield per plant and total sugars. Contrary to total biomass, maximum indirect effect via pod yield per plant resulted in the total association of first flower node, internodal length, nodes per plant, plant height, pod length, seeds per pod, shelling (%), pods per plant, total biomass, harvest index and 100-seed weight with seed yield per plant at genotypic level during 2009-10 and had also canceled the negative direct effects of first flower node, nodes per plant, seeds per pod, pods per plant and 100-seed weight. In addition, harvest index had maximum indirect contribution on internodal length at phenotypic level during 2009-10, and number of branches, pod length, seeds per pod, 100-seed weight and ascorbic acid at phenotypic and genotypic levels during 2010-11 along with protein content and reducing sugars at genotypic level during 2010-11.

Pooled data over years showed the significance of total biomass and harvest index by their maximum indirect contribution to the total association of number of branches, internodal length, plant height, pod length, seeds per pod, shelling (%), pods per plant, pod yield per plant, 100-seed weight and ascorbic acid on seed yield per plant at both phenotypic and genotypic levels (Table 4.13). Both these traits also had significant indirect contribution for quality traits *viz.*, protein content, total sugars and reducing sugars at genotypic level. The negative direct effect of pod yield on seed yield per plant was cancelled by the high magnitude of indirect contribution of total biomass and harvest index. In addition, pods per plant had also contributed indirectly to total biomass, shelling (%), harvest index, plant height, ascorbic acid and internodal length at genotypic level to increase the magnitude of total association with seed yield per plant. Indirect contribution of plant height, branches per plant, seeds per pod, pod length and harvest index on seed yield per plant had also been observed by Singh and Singh (2005) and that of biological yield and harvest index by Usmani and Dubey (2007).

The low magnitude of unexplained variation in the respective years of 2009-10, 2010-11 and pooled over years at genotypic levels (0.08, -0.01 and 0.01 for fresh pod yield and -0.002, 0.005 and 0.005 for seed yield per plant) indicated that the traits included in the present investigation accounted for the greater part of the variation present in the dependent variable (Tables 4.8-4.13).

In view of the direct and indirect contribution of component traits, selection on the basis of pods per plant, pod length, seeds per pod and nodes per plant for fresh pod yield per plant and that of total biomass, pod yield per plant, pods per plant and harvest index for seed yield per plant would be a paying preposition for evolving high yielding genotypes. Patel *et al.* (2006) also emphasized the importance of pods per plant and harvest index in the improvement of seed yield of garden pea.

4.4 Genetic divergence studies

The extent of genetic diversity plays an important role in varietal improvement programme of a particular crop. D^2 statistic is a powerful tool for estimating genetic diversity among different genotypes and to identify the parents for hybridization to obtain desirable recombinants. The assessment of genetic divergence helps in reducing the number of breeding lines from the large germplasm and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants.

4.4.1 Test of significance

The technique of multivariate analysis was used for grouping of genotypes into clusters. Test of significance based on Wilk's criterion for each pair of population were found to be significant in 2009-10, 2010-11 and pooled over years which implies that the populations in the respective years differ significantly with respect to mean values. The 'D²' values obtained for a pair of population taken as the calculated value of χ^2 and were tested against the tabulated value of χ^2 . Most of the D² values, with a few exceptions were found to be significant in both the years and pooled over years.

4.4.2 Grouping of genotypes into clusters

On the basis of D^2 values for all possible pairs, 41 genotypes of garden pea were arranged into 8, 13 and 5 clusters in 2009-10, 2010-11 and pooled over years, respectively (Table 4.14) following Tocher's procedure (Rao 1952) and also depicted through dendrograms (Figures 2, 3 and 4), indicating thereby different clustering patterns over the years. Different clustering patterns in garden pea were also reported by earlier workers *viz.*, Kumar *et al.* (1994), Sureja and Sharma (2001), Singh and Singh (2003), Arya *et al.* (2004 b), Tiwari *et al.* (2004), Yadav *et al.* (2004), Gupta and Singh (2006), Kumar *et al.* (2006), Singh and Singh (2006), Kumar *et al.* (2007), Singh *et al.* (2007), Singh and Mishra (2008), Sharma *et al.* (2009), Yadav *et al.* (2009) and Devi *et al.* (2010). The composition of clusters on the basis of D² statistic differed between years which showed inconsistent clustering behaviour of some of the genotypes due to the influence of environmental variations. Such differences in clustering pattern over years have also been reported by Gupta *et al.* (1992), Partap *et al.* (1992) and Vikas and Singh (1999).

In both the years and pooled over years, cluster I was the largest one. Vikas and Singh (1999), Arya *et al.* (2004 b), Gupta and Singh (2006)), Kumar *et al.* (2006), Kumar *et al.* (2007), Singh and Mishra (2008) and Devi *et al.* (2010) also arranged genotypes into different clusters and reported cluster I as the largest one. In the year 2009-10, out of the 8 clusters of 41 genotypes, the largest cluster I comprising of 53.66% genotypes ('DPPMFWR-20', 'DPPMR-09-9', 'DPPMFWR-1', 'DPP-89',

Table 4.14Cluster compositions in garden pea following multivariate analysis in
2009-10, 2010-11 and pooled over years

2009-10 I 22 DPPMFWR-20, DPPMR-09-9, DPPMFWR-1, DPP-89, DPPMI DPP-3-1, DPPM-07-30, DPPMFWR-5, DPPMR-09-5, Palam Priv 100, DPPM (D) 00, 2, DPD 11, 2, VP 215, DPPM (D) VP 2, 4, 4, 4, 5, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7,	WR-12, /a, DPP- 1, DPP-
I 22 DPPMFWR-20, DPPMR-09-9, DPPMFWR-1, DPP-89, DPPMI DPP-3-1, DPPM-07-30, DPPMFWR-5, DPPMR-09-5, Palam Prij	WR-12, /a, DPP- 1, DPP-
DPP-3-1, DPPM-07-30, DPPMFWR-5, DPPMR-09-5, Palam Pri	/a, DPP- 1, DPP-
	1, DPP-
100, DPPMK-09-2, DPP-11-2, VP-215, DPPMFWR-3, Azad P	
168, DPP-17-2, Lincoln, DPPM-65, DPPMFWR-8, DPPMFWR-2	
II 1 DPPMR-09-1	
III 1 DPPMFWR-27	
IV 1 DPPMFWR-30-1	
V 9 DPPM-1, DPPM-07-4, DPPMFWR-30-2, DPPMFWR-4, D	PPM-74,
Green Pearl, Punjab-89, DPPMFWR-11, DPPM-64	
VI 5 DPPM-22, DPPM-72, DPPM-07-9, DPPMR-09-3, DPPMFWR-29)
VII 1 DPPM-73	
VIII 1 DPP-25G	
2010-11	
1 26 DPPM-65, DPPM-72, DPPM-73, DPPMFWR-11, DPPMFWR-5,	Azad P-
1, DPPMFWR-30-1, DPPM-1, DPPMFWR-4, Green Pearl, DPF	MFWR-
27, DPP-100, DPPMFWR-30-2, Palam Priya, DPPM-22, DPP-17	-2, DPP-
168, DPPMR-09-3, DPPMR-09-3, DPPM-07-30, DPP-89, DPP	'M-0/-4,
Lincoln, DPPMF WR-1, DPPMF WR-8, DPP-3-1	
$II \qquad I \qquad DPPMFWK-12$	
$\begin{array}{cccc} III & I & DPPMF W K-20 \\ IV & 2 & DPPM 07.0 DPPM D 00.0 DPPM D 00.2 \\ \end{array}$	
IV 3 DPPM-07-9, DPPMR-09-9, DPPMR-09-2	
$V = 1 \qquad \text{DPPW-}/4$	
VI I PUNJAO-09 VII I VID 215	
$VII \qquad 1 \qquad VF-213$ $VIII \qquad 1 \qquad DDDMEWD 2$	
$\frac{1}{2} \frac{1}{2} \frac{1}$	
$X = 2 \qquad DI I WI W K-2, DI I -250$ $XI = 1 \qquad DPDMEWR 20$	
$\begin{array}{ccc} XI & I & DI I WI W K-29 \\ XII & I & DPPM_64 \end{array}$	
$XIII 1 DPP_{11,2}$	
Pooled over veers	
I 0000 000 years I 37 DPPM-1 DPPM-65 DPPM-72 DPP-17-2 DPPM-07-30 I	1 5.DD
DPPMFWR-5 DPPMFWR-4 DPPMFWR-20 DPPMFWR-11	VP_{215}
DPPMFWR-30-1 DPP-168 DPPMFWR-27 DPPM- 07-4 DPF	$MEWR_{-}$
30-2 DPP-100 DPP-89 Azad P-1 DPPMR-09-9 DPPN	IR_00_1
DPPMFWR-8 DPPMFWR-3 DPPMFWR-1 DPPMR-09-5 Gre	on Pearl
DPPM-22 Lincoln Palam Priva DPPMR-09-3 DPF	M_07_0
DPPMFWR-12 DPPM-74 DPP-11-2 DPPM-73 DPPMR-09-2	Puniah_
89	i ulija0-
II 1 DPPMFWR-2	
III 1 DPP-25G	
IV 1 DPPMFWR-29	
V 1 DPPM-64	



Fig. 2 Dendrogram showing grouping of 41 garden pea genotypes generated using D² cluster analysis (Tocher's method) during 2009-10



Fig. 3 Dendrogram showing grouping of 41 garden pea genotypes generated using D² cluster analysis (Tocher's method) during 2010-11



Fig. 4 Dendrogram showing grouping of 41 garden pea genotypes generated using D² cluster analysis (Tocher's method) in pooled over years

'DPPMFWR-12', 'DPP-3-1', 'DPPM-07-30', 'DPPMFWR-5', 'DPPMR-09-5', 'Palam Priya', 'DPP-100', 'DPPMR-09-2', 'DPP-11-2', 'VP-215', 'DPPMFWR-3', 'Azad P-1', 'DPP-168', 'DPP-17-2', 'Lincoln', 'DPPM-65', 'DPPMFWR-8' and 'DPPMFWR-2') followed by cluster V with 9 genotypes ('DPPM-1', 'DPPM-07-4', 'DPPMFWR-30-2', 'DPPMFWR-4', 'DPPM-74', 'Green Pearl', 'Punjab-89', 'DPPMFWR-11' and 'DPPM-64') and cluster VI with 5 genotypes ('DPPM-22', 'DPPM-72', 'DPPM-07-9', 'DPPMR-09-3' and 'DPPMFWR-29'). The remaining five clusters namely, II ('DPPMR-09-1'), III ('DPPMFWR-27'), IV ('DPPMFWR-30-1'), VII ('DPPM-73') and VIII ('DPP-25G') were monogenotypic, *i.e.* contained only one genotype.

On the other hand, in the year 2010-11, all these 41 genotypes were grouped into 13 clusters (Table 4.14). Similar to previous year, the cluster I was the largest consisting of 26 genotypes with 63.41% constitution ('DPPM-65', 'DPPM-72', 'DPPM-73', 'DPPMFWR-11', 'DPPMFWR-5', 'Azad P-1', 'DPPMFWR-30-1', 'DPPMFWR-4', 'Green Pearl', 'DPPMFWR-27', 'DPP-100', 'DPPMFWR-30-2', 'Palam Priya', 'DPPM-22', 'DPP-17-2', 'DPP-168', 'DPPMR-09-3', 'DPPMR-09-5', 'DPPM-07-30', 'DPPM-97, 'DPPM-07-4', 'Lincoln', 'DPPMFWR-1', 'DPPMFWR-8' and 'DPP-3-1') followed by cluster IV with 3 genotypes ('DPPM-07-9', 'DPPMR-09-9' and 'DPPMR-09-2') and cluster X with 2 genotypes ('DPPMFWR-2' and 'DPP-25G'). Clusters II, III, V, VI, VII, VIII, IX, XI, XII and XIII contained one genotype each *viz.*, 'DPPMFWR-12', 'DPPMFWR-20', 'DPPM-74', 'Punjab-89', 'VP-215', 'DPPMFWR-3', 'DPPMFWR-29', 'DPPM-64' and 'DPP-11-2', respectively suggesting that these genotypes diverged most from others.

Pooling of data showed that the genotypes were arranged into 5 clusters with cluster I representing 90.24% *i.e.* 37 genotypes (Table 4.14). Clusters II, III, IV and V were monogenotypic, comprising of genotypes 'DPPMFWR-2', 'DPP-25G', 'DPPMFWR-29' and 'DPPM-64', respectively. Partap *et al.* (1992), Vikas and Singh (1999), Arya *et al.* (2004 b), Singh and Singh (2006), Singh and Mishra (2008) also observed clusters with one genotype only and also suggested that such genotypes diverged most from others.

The clustering of the genotypes was random and indicating that there was no parallelism between clustering pattern and geographical diversity as different clustering patterns were formed during the respective years and pooled over years. However, 14 genotypes from cluster I ('DPPM-65', 'DPPMFWR-5', 'Azad P-1', 'DPP-100', 'Palam Priya', 'DPP-17-2', 'DPP-168', 'DPPMR-09-5', 'DPPM-07-30', 'DPP-89', 'Lincoln', 'DPPMFWR-1', 'DPPMFWR-8' and 'DPP-3-1') and the best performing genotype 'DPPM-74' from cluster V showed consistency in clustering pattern by remaining in the same group over both the years. Beside, 'DPPMR-09-1' also showed consistency by maintaining monogenotypic cluster over the years. Similarly, Gupta *et al.* (1992) and Vikas and Singh (1999) also observed consistency in clustering pattern of genotypes over environments. Pooled data over years implies that all the 14 genotypes which showed consistency to some extent by maintaining monogenotypic cluster in one of the year and pooled over years.

The clustering pattern revealed that the genotypes of same geographical distribution fall into different clusters which indicated the influence of genetic constitution of the genotypes in the clustering pattern. This suggests that genetic diversity is not always related to geographical diversity (Partap *et al.* 1992; Kumar *et al.* 1994; Sureja and Sharma 2001; Tiwari *et al.* 2004; Kumar *et al.* 2006; Kumar *et al.* 2007).

4.4.3 Average intra and inter-cluster distances

The intra-cluster distance ranged from 0 to 3.46 with the highest in cluster VI (3.46) followed by cluster I (3.32) and cluster V (3.22) in the year 2009-10. The clusters II, III, IV, VII and VIII were constituted by a single genotype each and hence, their intracluster distance was zero (Table 4.15). In the year 2010-11, the intra-cluster distances were comparable in cluster IV (2.90), cluster I (2.76) and cluster X (2.63), while for clusters II, III, V, VI, VII, VIII, IX, XI, XII and XIII, the intra-cluster divergence was zero (Table 4.16). Similarly, the intra-cluster distance varied from 0 to 1.75 with the highest in cluster I and the remaining monogenotypic clusters had zero distance in pooled over years (Table 4.17). Vikas and Singh (1999), Singh and Singh (2003), Yadav *et al.* (2004), Kumar *et al.* 2006, and Sharma *et al.* (2009) also observed maximum intra-cluster variation among genotypes. Since the intra-cluster distance was low, the chances of developing good segregants by hybridization among parents within cluster would be low. Therefore, it is logical to attempt crosses between genotypes falling in different clusters based on inter-cluster distance.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	11.05	12.84	13.83	13.56	18.20	17.04	13.11	24.29
	(3.32)	(3.58)	(3.72)	(3.68)	(4.27)	(4.13)	(3.62)	(4.93)
II		0.00	6.04	6.20	9.77	23.53	11.22	32.29
		(0.00)	(2.46)	(2.49)	(3.13)	(4.85)	(3.35)	(5.68)
III			0.00	7.62	9.52	24.34	11.68	32.68
			(0.00)	(2.76)	(3.09)	(4.93)	(3.42)	(5.72)
IV				0.00	9.94	24.89	13.88	32.55
				(0.00)	(3.15)	(4.99)	(3.73)	(5.71)
V					10.39	29.40	16.21	37.63
					(3.22)	(5.42)	(4.03)	(6.13)
VI						11.95	19.03	15.90
						(3.46)	(4.36)	(3.99)
VII							0.00	28.29
							(0.00)	(5.32)
VIII								0.00 (0.00)

Table 4.15Average intra and inter-cluster distances in garden pea during 2009-10

Values in bold figures are intra-cluster distances Values in parenthesis are $\sqrt{D^2} = D$ values

The inter-cluster distance ranged from 6.04-37.63, 7.18-16.43 and 3.02-8.35 during 2009-10, 2010-11 and pooled over years, respectively (Tables 4.15, 4.16 and 4.17). The maximum inter-cluster genetic divergence was recorded between clusters V and VIII (37.63) followed by clusters III and VIII (32.68), clusters IV and VIII (32.55) and clusters II and VIII (32.29) suggesting wide diversity among genotypes of the two clusters due to different genetic constitution in 2009-10. Therefore, genotypes within

Clusters	I	II	III	IV	v	VI	VII	VIII	IX	X	XI	XII	XIII
I	7.60	9.68	8.79	8.97	8.88	10.59	8.80	9.24	9.39	10.85	10.31	10.86	11.94
	(2.76)	(3.11)	(2.96)	(2.99)	(2.98)	(3.25)	(2.97)	(3.04)	(3.06)	(3.29)	(3.21)	(3.30)	(3.46)
II		0.00	8.81	11.27	8.21	15.75	13.10	7.27	10.76	12.02	9.56	15.45	15.80
		(0.00)	(2.97)	(3.36)	(2.87)	(3.97)	(3.62)	(2.70)	(3.28)	(3.47)	(3.09)	(3.93)	(3.97)
III			0.00	8.21	7.18	11.92	10.55	11.15	12.38	11.51	12.72	12.32	16.32
			(0.00)	(2.87)	(2.68)	(3.45)	(3.25)	(3.34)	(3.52)	(3.39)	(3.57)	(3.51)	(4.04)
IV				8.40	10.03	12.33	10.64	10.06	11.36	10.45	12.55	12.15	15.36
				(2.90)	(3.17)	(3.51)	(3.26)	(3.17)	(3.37)	(3.23)	(3.54)	(3.49)	(3.92)
v					0.00	10.93	9.99	10.22	11.71	13.57	12.81	11.07	15.18
	•				(0.00)	(3.31)	(3.16)	(3.20)	(3.42)	(3.68)	(3.58)	(3.33)	(3.90)
VI						0.00	7.76	15.27	13.24	14.75	15.13	7.99	12.35
_						(0.00)	(2.79)	(3.91)	(3.64)	(3.84)	(3.89)	(2.83)	(3.51)
VII							0.00	11.74	10.97	12.43	12.07	10.74	9.99
							(0.00)	(3.43)	(3.31)	(3.55)	(3.47)	(3.28)	(3.10)
VIII								0.00	9.24	10.99	9.16	14.66	13.64
								(0.00)	(3.04)	(3.32)	(3.03)	(3.83)	(3.69)
IX									0.00	9.72	10.48	13.64	10.04
									(0.00)	(3.12)	(3.24)	(3.69)	(3.17)
Х										6.94	12.80	15.87	15.03
										(2.63)	(3.58)	(3.98)	(3.88)
XI											0.00	16.43	11.24
											(0.00)	(4.05)	(3.35)
XII												0.00	14.82
												(0.00)	(3.85)
XIII													0.00 (0.00)

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 Table 4.16
 Average intra and inter-cluster distances in garden pea during 2010-11

Values in bold figures are intra-cluster distances Values in parenthesis are $\sqrt{D^2} = D$ values

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Clusters	I	Π	III	IV	v
Ι	3.08 (1.75)	4.16 (2.04)	5.10 (2.26)	4.72 (2.17)	5.30 (2.30)
II		0.00 (0.00)	3.02 (1.74)	5.06 (2.25)	7.74 (2.78)
III			0.00 (0.00)	5.51 (2.35)	8.35 (2.89)
IV				0.00 (0.00)	7.80 (2.79)
V					0.00 (0.00)

Table 4.17Average intra and inter-cluster distances in garden pea in pooled over
years

Values in bold figures are intra-cluster distances Values in parenthesis are $\sqrt{D^2}=D$ values

clusters might not be selected rather selected from different clusters for further hybridization among themselves. The cluster II and III (6.04) had the minimum intercluster distance. On the other hand, in 2010-11, the highest genetic divergence at intercluster level was observed between clusters XI and XII (16.43) followed by clusters III and XIII (16.32), clusters X and XII (15.87), clusters II and XIII (15.80) and clusters II and VI (15.75). The inter-cluster proximity was the maximum between clusters III and V (7.18). Similarly, in pooled over years, the highest inter-cluster genetic divergence was found in clusters III and V (8.35) followed by clusters IV and V (7.80), and clusters II and V (7.74) while clusters II and III (3.02) showed maximum inter-cluster proximity.

This clearly indicates that the genotypes included in the clusters with high intercluster distance showed sufficient genetic diversity and selection of parents from these diverse clusters would be useful in hybridization programme for improving yield and other desirable horticultural traits. The crosses involving the diverse genotypes would be expected to manifest maximum heterosis and release of desirable recombinants in segregating generations. Based on inter-cluster distance, the earlier workers also suggested selection of parents from diverse clusters for utilization in hybridization programme to obtain desirable transgressive segregants (Gupta *et al.* 1992; Partap *et al.* 1992; Vikas and Singh 1999; Singh and Singh 2003; Arya *et al.* 2004b; Tiwari *et al.* 2004; Kumar *et al.* 2006; Singh and Singh 2006; Singh *et al.* 2007; Singh and Mishra 2008; Yadav *et al.* 2009).

4.4.4 Cluster means and contribution of individual character towards genetic divergence

The composition of cluster means for different characters showed considerable differences among the clusters for each character during both the years and pooled over years (Tables 4.18, 4.19 and 4.20). In 2009-10, cluster I was observed to be important for desirable minimum internodal length while had moderate to low values for the remaining characters (Table 4.18). The cluster II exhibited the highest nodes per plant (17.67) and 100-seed weight (21.33 g), while cluster VI had maximum number of branches (1.49). Maximum ascorbic acid (15.47 mg) and protein content (17.98%) were represented by cluster III along with genotypes for early maturity manifested by days to first flower (76.00) and days to first picking (117.00). The cluster IV showed maximum mean values for pods per plant (10.77) and total sugars (7.38%) along with genotypes for dwarf plant growth habit (less plant height) and desirable low starch content (22.35%). The most economic traits viz., pod yield per plant (41.32 g) and harvest index (41.48%) were represented with higher means by cluster V along with earliness for days to 50% flowering. Cluster VII represented maximum cluster means for six characters namely, pod length (9.85 cm), seeds per pod (7.61), shelling percentage (46.50%), total biomass (39.67 g), seed yield per plant (13.00 g) and total soluble solids (19.07°brix), whereas cluster VIII had maximum cluster mean for reducing sugars (4.44%).

In 2010-11, cluster V was observed to be important with maximum cluster means for the most valuable traits (Table 4.19) *viz.*, pods per plant (18.01), pod yield per plant (80.17 g), total biomass (41.33 g) and seed yield per plant (16.67 g), while cluster III had maximum mean values for harvest index (54.63%), ascorbic acid (20.14 mg) and

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Table 4.18 Clu	ster means	for dif	fferent c	haracters	in garder	n pea duri	ng 2009-1(
Clu Traits	sters I		II	III	IV	Λ	VI	VII	VIII	Mean	Max.	Min.
Morphological tra	its											
Days to first flower	. 77.1		77.67	76.00	76.33	76.00	76.73	77.00	78.67	76.94	78.67	76.00
First flower node	13.7	62	14.80	14.53	13.80	14.06	13.93	13.33	13.87	14.01	14.80	13.33
Days to 50% flowe	ring 90.7	76	94.00	88.33	91.33	88.26	90.67	92.67	92.33	91.04	94.00	88.26
Days to first pickin	g 119.	62 1	22.00	117.00	118.67	117.96	120.33	120.33	122.33	119.78	122.33	117.00
Number of branche	s 1.2	n	1.13	1.10	1.13	1.30	1.49	1.13	1.13	1.21	1.49	1.10
Internodal length (c	:m) 5.3	5	5.47	5.51	5.45	5.75	5.51	6.50	2.72	5.28	6.50	2.72
Nodes per plant	16.0	10	17.67	17.43	17.47	15.75	15.94	15.53	15.43	16.41	17.67	15.43
Plant height (cm)	57.5	52	56.32	69.23	52.31	61.86	60.48	71.00	30.07	58.60	71.00	30.07
Yield and yield co	ntributing	traits										
Pod length (cm)	8.6	1	9.61	9.00	7.88	9.70	8.52	9.85	6.18	8.67	9.85	6.18
Seeds per pod	6.0	5	5.66	6.79	5.58	6.93	5.41	7.61	3.87	5.99	7.61	3.87
Shelling (%)	42.5	59 4	40.70	46.18	42.47	44.98	43.21	46.50	41.18	43.48	46.50	40.70
Pods per plant	6.9	-	8.80	7.92	10.77	8.95	6.68	6.77	2.91	7.46	10.77	2.91
Pod yield per plant	(g) 27.8	86	33.97	36.03	37.90	41.32	26.31	26.60	10.27	30.03	41.32	10.27
Total biomass (g)	23.5	55	28.67	27.33	28.33	29.48	29.40	39.67	8.67	26.89	39.67	8.67
Seed yield per plan	t (g) 7.3	8	10.64	10.55	10.81	12.04	6.74	13.00	1.57	9.09	13.00	1.57
Harvest index (%)	31.6	20	37.09	38.59	38.16	41.48	22.52	32.74	18.08	32.54	41.48	18.08
100-seed weight (g) 18.2	25	21.33	21.00	18.00	20.15	19.80	17.67	14.00	18.78	21.33	14.00
Quality traits												
Total soluble solids	18.0	00	17.07	18.27	18.67	17.87	18.20	19.07	17.47	18.08	19.07	17.07
	0 7 7	, y			1 4 1 1	15 10			7 1 7 1	74 46	15 17	12 14
Ascoroic acia (mg)	7.4.	ς :	14.12	17.41	14.11	61.01	I4.09	10.61	10.14	14.40	10.47	+1.01
Protein content (%)	14.8	68	14.13	17.98	14.04	16.02	15.63	16.67	17.43	15.85	17.98	14.04
Total sugars (%)	6.9	0	6.66	7.27	7.38	6.82	7.23	6.87	6.05	6.90	7.38	6.05
Reducing sugars (%	6) <u>3.3</u>	3	3.79	4.05	3.71	3.45	3.95	3.58	4.44	3.79	4.44	3.33
Starch content (%)	24.6	51 2	24.90	29.25	22.35	25.17	24.54	26.55	30.00	25.92	30.00	22.35
Max-Maximum; Min-Mir	imum											

106

						D	•	D								
Clusters Traits	I	Π	III	IV	>	ΙΛ	IIV	VIII	XI	×	XI	IIX	XIII	Mean	Max.	Min.
Morphological traits					ľ											
Days to first flower	92.83	90.00	89.00	93.44	93.00	91.00	88.33	88.00	101.33	93.50	93.00	94.33	95.00	92.52	101.33	88.00
First flower node	13.79	13.93	13.53	14.31	14.33	12.13	13.40	14.10	16.60	13.07	15.07	14.67	13.60	14.04	16.60	12.13
Days to 50% flowering	98.58	94.33	94.33	98.67	98.67	95.00	94.33	93.67	106.00	100.33	100.00	99.67	103.00	98.20	106.00	93.67
Days to first picking	131.01	130.67	129.33	130.78	129.33	126.33	130.00	133.33	131.33	134.17	130.00	130.00	134.33	130.82	134.33	126.33
Number of branches	2.21	2.13	1.53	2.58	2.53	3.07	1.87	2.40	1.80	1.73	3.13	2.60	2.87	2.34	3.13	1.53
Internodal length (cm)	5.17	4.75	4.90	4.26	5.80	5.80	6.74	4.52	3.87	3.20	5.42	5.80	6.77	5.15	6.77	3.20
Nodes per plant	19.03	22.00	17.33	16.64	20.00	17.53	17.40	20.93	22.07	18.23	19.93	18.00	20.53	19.20	22.07	16.64
Plant height (cm)	65.12	69.09	55.54	57.74	62.76	67.03	64.15	64.90	66.12	38.61	81.26	72.28	85.43	64.74	85.43	38.61
Yield and yield contributin	g traits															
Pod length (cm)	8.73	7.64	9.48	8.54	8.76	9.98	8.13	8.08	8.19	6.99	6.67	13.44	8.34	8.69	13.44	6.67
Seeds per pod	5.93	5.90	6.53	4.89	6.03	8.03	4.93	4.53	4.60	5.13	5.33	8.63	4.83	5.79	8.63	4.53
Shelling (%)	44.91	47.87	46.23	41.37	43.86	47.03	43.61	46.50	42.38	42.72	43.01	45.81	46.63	44.76	47.87	41.37
Pods per plant	12.36	17.71	15.67	11.43	18.01	13.35	11.63	9.20	8.06	7.50	13.38	11.44	7.78	12.12	18.01	7.50
Pod yield per plant (g)	49.96	58.50	66.17	51.83	80.17	69.20	49.10	36.50	29.30	19.55	28.90	68.50	30.00	49.05	80.17	19.55
Total biomass (g)	30.38	37.33	34.33	30.00	41.33	26.33	25.00	37.33	17.33	14.83	34.33	31.33	20.67	29.27	41.33	14.83
Seed yield per plant (g)	9.85	11.33	11.67	10.11	16.67	14.33	10.67	10.67	5.67	4.40	8.83	13.67	6.67	10.35	16.67	4.40
Harvest index (%)	32.73	30.52	34.02	33.38	40.24	54.63	42.77	28.53	32.71	30.65	24.30	43.83	32.24	35.43	54.63	24.30
100-seed weight (g)	16.65	17.67	15.00	20.44	20.33	17.67	19.00	20.67	19.33	14.17	14.00	22.00	15.00	17.84	22.00	14.00
Quality traits																
Total soluble solids (^o brix)	17.31	16.27	15.13	17.53	16.47	16.67	17.27	17.53	16.53	16.77	15.53	17.87	17.33	16.79	17.87	15.13
Ascorbic acid (mg)	15.33	12.11	12.86	14.46	14.95	20.04	14.57	12.46	14.77	13.59	15.44	16.71	14.57	14.76	20.04	12.11
Protein content (%)	13.69	13.04	12.51	13.18	15.90	17.59	13.89	14.26	13.28	15.09	17.59	18.51	12.84	14.72	18.51	12.51
Total sugars (%)	7.19	6.64	6.22	6.66	7.05	7.40	7.01	6.91	6.36	5.97	5.72	9.01	6.64	6.83	9.01	5.72
Reducing sugars (%)	3.31	3.23	3.10	3.26	3.36	4.14	2.93	2.67	2.89	3.49	2.97	3.58	3.23	3.24	4.14	2.67
Starch content (%)	24.35	19.95	28.50	23.87	26.42	29.10	24.90	19.05	26.55	26.13	18.90	21.45	26.40	24.27	29.10	18.90
Max-Maximum; Min-Minimum																

Table 4.19Cluster means for different characters in garden pea during 2010-11

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Clusters	I	II	III	IV	٨	Mean	Max.	Min.
Morphological traits								
Days to first flower	84.74	84.17	87.17	85.33	84.83	85.25	87.17	84.17
First flower node	13.87	12.30	14.30	14.97	14.53	13.99	14.97	12.30
Days to 50% flowering	94.32	95.17	97.83	96.50	91.67	95.10	97.83	91.67
Days to first picking	125.13	127.83	128.00	126.50	121.33	125.76	128.00	121.33
Number of branches	1.76	1.33	1.57	2.27	1.85	1.76	2.27	1.33
Internodal length (cm)	5.34	3.80	2.66	5.48	5.87	4.63	5.87	2.66
Nodes per plant	17.55	15.87	17.02	18.52	17.02	17.20	18.52	15.87
Plant height (cm)	62.03	37.86	34.51	81.67	69.58	57.13	81.67	34.51
Yield and yield contributing traits								
Pod length (cm)	8.79	6.59	6.61	6.64	13.35	8.40	13.35	6.59
Seeds per pod	6.01	5.63	3.92	4.97	8.37	5.78	8.37	3.92
Shelling (%)	44.02	42.81	41.40	43.67	45.94	43.57	45.94	41.40
Pods per plant	10.00	6.47	4.88	10.20	8.79	8.07	10.20	4.88
Pod yield per plant (g)	41.20	17.82	14.13	21.87	57.33	30.47	57.33	14.13
Total biomass (g)	28.56	14.17	9.83	28.17	29.33	22.01	29.33	9.83
Seed yield per plant (g)	9.51	3.95	2.68	6.93	12.66	7.15	12.66	2.68
Harvest index (%)	33.49	28.54	26.14	24.71	43.22	31.22	43.22	24.71
100-seed weight (g)	18.15	12.83	14.50	15.67	22.67	16.76	22.67	12.83
Quality traits								
Total soluble solids (^{obrix})	17.65	17.87	16.77	15.03	17.83	17.03	17.87	15.03
Ascorbic acid (mg)	14.99	15.34	12.38	15.25	16.20	14.83	16.20	12.38
Protein content (%)	14.50	14.42	16.19	16.87	18.68	16.13	18.68	14.42
Total sugars (%)	6.97	6.71	6.10	6.29	8.57	6.93	8.57	6.10
Reducing sugars (%)	3.39	3.32	3.99	3.00	3.64	3.47	3.99	3.00
Starch content (%)	24 61	26.65	20 18	20.02	2115	20 10	00 10	20.02

108

Max-Maximum; Min-Minimum

reducing sugars (4.04%) along with minimum days to first picking (126.33). Cluster II, IX and XI represented the highest cluster means for shelling percentage (47.87%), nodes per plant (22.07) and number of branches (3.13), respectively. Similarly, cluster XII symbolized six characters with maximum cluster means for pod length (13.44 cm), seeds per pod (8.63), 100-seed weight (22.00 g), total soluble solids (17.87°brix), protein (18.51%) and total sugars (9.01%). Cluster X represented with minimum desirable internodal length (3.20 cm) and plant height (38.61 cm), while cluster VIII had the minimum days to first flower (88.00) and days to 50% flowering (93.67), respectively.

Pooled data over years (Table 4.20) indicated that cluster V observed to be the most imperative with the highest cluster means for majority of the traits namely, pod length (13.35 cm), seeds per pod (8.37), shelling percentage (45.94%), pod yield per plant (57.33 g), total biomass (29.33 g), seed yield per plant (12.66 g), harvest index (43.22%), 100-seed weight (22.67 g), ascorbic acid (16.20 mg), protein content (18.68%) and total sugars (8.57%) followed by cluster IV with maximum cluster means for number of branches (2.27), nodes per plant (18.52) and pods per plant (10.20) along with minimum starch content (20.03%). Cluster II and cluster V showed importance for earliness with minimum cluster means for days to first flower (84.17) and first flower node (12.30), and days to 50% flowering (91.67) and first picking (121.33), respectively. While, cluster III had minimum cluster means for internodal length (2.66 cm) and plant height (34.51 cm) exhibiting desirable bush type growth habit along with maximum cluster means for reducing sugars (3.99%). Cluster II had also revealed maximum cluster mean for total soluble solids (17.87° brix) whereas cluster I represented with moderate cluster means for all the traits. Hence, different clusters of genotypes on the basis of means revealed divergence for different characters and can be utilized as indicators for selecting diverse parents for hybridization programmes (Singh and Singh 2003; Yadav et al. 2004; Gupta and Singh 2006; Sharma et al. 2009; Devi et al. 2010).

The contribution of individual characters to divergence has been worked out in terms of number of times it appeared first (Table 4.21). Harvest index (73.17%) contributed maximum towards total genetic divergence in 2009-10 followed by total sugars (6.59%), pod length (3.17%), protein content (3.17%), total biomass (2.93%),

Characters	Times ranked Ist	Contribution (%)	Times ranked Ist	Contribution (%)	Times ranked Ist	Contribution (%)
	2005	-10	201	0-11	Po	oled
Morphological traits						
Days to first flower	0	0.00*	0	0.00*	8	0.98
First flower node	0	0.00*	0	0.00*	5	0.24
Days to 50% flowering	0	•00.0	0	0.00*	1	0.12*
Days to first picking	0	. *00.0	0	0.00*	1	0.12*
Number of branches	0	0.00*	7	0.24	8	0.98
Internodal length (cm)	່ຕ	0.37	61	7.44	44	5.37
Nodes per plant	0	0.00*	115	14.02	8	0.98
Plant height (cm)	15	1.83	75	9.15	35	4.27
Yield and yield contributing	traits					
Pod length (cm)	26	3.17	33	4.02	135	16.46
Seeds per pod	1	0.12	5	0.61	47	5.73
Shelling (%)	1	0.12	0	0.00*	7	0.24
Pods per plant	ς	0.37	102	12.44	47	5.73
Pod yield per plant (g)	4	0.49	73	8.90	50	6.10
Total biomass (g)	24	2.93	119	14.51**	15	1.83
Seed yield per plant (g)	13	1.59	13	1.59	22	2.68
Harvest index (%)	600	73.17**	2	0.24	1	0.12*
100-seed weight (g)	11	1.34	26	3.17	138	16.83**
Quality traits						
Total soluble solids (^o brix)	0	• • 00.0	21	2.56	m	0.37
Ascorbic acid (mg)	9	0.73	72	8.78	131	15.98
Protein content (%)	26	3.17	4	0.49	59	7.20
Total sugars (%)	54	6.59	43	5.24	18	2.20
Reducing sugars (%)	17	2.07	7	0.85	2	0.24
Starch content (%)	16	1.95	47	5.73	43	5.24

reducing sugars (2.07%), starch content (1.95%), plant height (1.83%), seed yield per plant (1.59%) and 100-seed weight (1.34%). On the other hand, total biomass (14.51%), nodes per plant (14.02%), pods per plant (12.44%), plant height (9.15%), pod yield per plant (8.90%), ascorbic acid (8.78%), internodal length (7.44%), starch content (5.73%), total sugars (5.24%), pod length (4.02%), 100-seed weight (3.17%), total soluble solids (2.56%) and seed yield per plant (1.59%) contributed more towards genetic divergence in 2010-11. On the basis of pooled analysis of data, 100-seed weight (16.83%), pod length (16.46%) and ascorbic acid (15.98%) contributed maximum towards total genetic divergence followed by protein content (7.20%), pod yield per plant (6.10%), pods per plant (5.73%), seeds per pod (5.73%), internodal length (5.37%), starch content (5.24%), plant height (4.27%) and seed yield per plant (2.68%). Therefore, it could also be used as parameters based on specific trait (s) in selecting genetically diverse parents for hybridizing to create variability in the population. On the other hand, earlier reports revealed that early yield per plant (Gupta and Singh 2006), plant height (Tiwari et al. 2004; Kumar et al. 2007) and pods per plant (Sharma et al. 2009) contributed maximum towards total genetic divergence.

The critical study of cluster means for different characters indicated that cluster VII was desirable for pod length, seeds per pod, shelling (%), total biomass and seed yield per plant, cluster V for pod yield per plant and harvest index, and cluster IV for pods per plant during 2009-10, while clusters V (pods per plant, pod yield per plant, total biomass and seed yield per plant), XII (pod length and seeds per pod) and VI (harvest index) during 2010-11, and cluster V for majority of the traits in pooled over years were desirable. It is, therefore, suggested that the genotypes namely, 'Punjab-89', 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPMFWR-4', 'DPPMFWR-30-2' and 'DPP-25G' will show greater potentiality as a breeding stock by virtue of desirable characters as well as maximum inter-cluster distance and could be used as parents in hybridization for expecting transgressive segregants for further exploitation in garden pea improvement programme (Kumar *et al.* 1994; Kumar *et al.* 2006; Kumar *et al.* 2007).



SUMMARY AND CONCLUSIONS

5. SUMMARY AND CONCLUSIONS

The present investigation entitled, "Genetic variability for yield and horticultural traits in garden pea (Pisum sativum L.)" was undertaken at the Experimental Farm of the 'Department of Vegetable Science and Floriculture', College of Agriculture, CSKHPKV, Palampur during winters 2009-10 and 2010-11. The experimental material comprising of 41 genotypes of garden pea including four checks namely, 'Lincoln', 'Azad P-1', 'Palam Priya' and 'Punjab-89' was evaluated in randomized complete block design with three replications to assess the nature of genetic variability, association of various traits with yield and their direct and indirect effects for effective selection, and to study the extent of genetic diversity among genotypes through multivariate analysis. Data were recorded on 23 characters viz., days to first flower, first flower node, days to 50% flowering, days to first picking, number of branches, internodal length (cm), nodes per plant, plant height (cm), pod length (cm), seeds per pod, shelling (%), pods per plant, pod yield per plant (g), total biomass (g), seed yield per plant (g), harvest index (%), 100-seed weight (g), total soluble solids (°brix), ascorbic acid (mg), protein content (%), total sugars (%), reducing sugars (%) and starch content (%) in addition to powdery mildew disease incidence (%). The observations were recorded on 10 competitive plants taken at random in each entry over the replications. The data analysis was done as per the standard statistical procedures for parameters of genetic variability, correlation and path-coefficients, and genetic diversity in the respective years.

The analysis of variance revealed the presence of sufficient genetic variability for all morphological, yield and yield contributing, and quality traits during both the years 2009-10 and 2010-11 except for days to first picking in the year 2010-11. The pooled analysis over the years exhibited the presence of $G \times E$ interactions for all the traits except days to first picking indicating that performance of genotypes was greatly influenced by environments. On the basis of mean performance, 'DPPM-74' was significantly superior for fresh pod yield per plant over all the four recommended check varieties during both the years and pooled over years. In addition, 'DPPM-1', 'DPPM-64', 'DPPM-07-9' and 'VP-215' also performed statistically at par with best performing checks 'Palam Priya' and 'Punjab-89' during 2009-10 whereas the performance of 'DPPMFWR-11', 'DPPM-64', 'DPPMFWR-20', 'DPPMFWR-5', 'DPPM-72' and 'DPPM-07-4' during 2010-11 and 'DPPM-64', 'DPPMWFR-11' and 'DPPM-72' in pooled over years was statistically similar to the best performing check variety 'Punjab-89'. The superior performance of these genotypes for fresh pod yield per plant was mainly attributed to number of branches, plant height, pod length and pods per plant. Similarly, 'DPPM-74' outperformed all the genotypes including checks for total biomass and seed yield per plant over the years and pooled over years. Also, genotypes 'DPPMFWR-30-2', 'DPPM-07-4', 'DPPM-1' and 'DPPM-73' during 2009-10 and 'DPPM-07-4' in pooled over years significantly outperformed 'Punjab-89' for seed yield per plant. On the other hand, 'DPPM-64', VP-215', 'DPPMFWR-30-1', 'DPPMR-09-1' and 'DPPMFWR-27', 'DPPMR-09-2', 'DPPM-07-4' and 'DPPM-64', and 'DPPM-64', 'DPPM-73' and 'DPPMFWR-30-2' performed at par with 'Punjab-89' and 'Palam Priya' for seed yield per plant in the respective years and pooled over years. The superior performance of these genotypes for number of branches, plant height, pod length, pods per plant, total biomass, harvest index and 100-seed weight might have resulted in higher seed yield.

The estimates of PCV and GCV were high for pods per plant, pod yield per plant, total biomass and seed yield per plant during 2009-10, and for pod yield per plant during 2010-11 indicating substantial variability and ensuring ample scope for improvement through selection. High PCV and moderate GCV were recorded for seed yield per plant during 2010-11 and for pod yield and seed yield per plant in pooled over years. On the other hand, moderate estimates of PCV and GCV were recorded for number of branches, internodal length, plant height, pod length, seeds per pod, harvest index, 100-seed weight, protein content and starch content over the years and pooled over years; pods per plant, total biomass and ascorbic acid during 2010-11 and pooled over years; and reducing sugars and total sugars during 2009-10, suggesting that direct selection for these traits should be considered cautiously.

High heritability coupled with high genetic advance was observed for pods per plant, pod yield per plant, total biomass, seed yield per plant and harvest index during both the years and pooled over years along with plant height over the years, and number of branches and internodal length during 2010-11 suggesting the importance of additive gene action for the inheritance of these characters and improvement could be brought about by phenotypic selection. High heritability along with moderate genetic advance was observed for pod length, seeds per pod, 100-seed weight, ascorbic acid, total sugars and starch content over the years and pooled over years; internodal length, protein content and reducing sugars during 2009-10 and pooled over years; nodes per plant during 2010-11; and ascorbic acid, total sugars and starch content in pooled over years, which may be attributed to non-additive gene effects.

In general, the genotypic correlation coefficients were of higher magnitude than the corresponding phenotypic ones indicating the inherent association among the various traits. Fresh pod yield per plant showed a positive and significant correlation at both phenotypic and genotypic levels with pods per plant, seeds per pod, pod length, internodal length, plant height, shelling (%) and ascorbic acid during both the years and pooled over years. Similarly, seed yield per plant had positive association with internodal length, plant height, pod length, seeds per pod, pods per plant, pod yield per plant, total biomass, harvest index and 100-seed weight over the years and pooled over years at phenotypic and genotypic levels. Selection on the basis of these traits might lead to higher yield.

Path coefficient analysis revealed high positive direct effects of pods per plant and pod length on fresh pod yield per plant during both the years and pooled over years at phenotypic level and only at genotypic level during 2010-11. Seeds per pod, nodes per plant and pods per plant during 2009-10 and that of pod length, pods per plant, days to first picking, internodal length and shelling (%) in pooled over years had the maximum direct effects on pod yield per plant at genotypic level. On the other hand, total biomass and harvest index had maximum positive direct effects on seed yield per plant at both levels during 2010-11 and pooled over years, and only at phenotypic level during 2009-10 whereas, pod yield per plant and total biomass had contributed maximum positive direct effects on seed yield per plant at genotypic level during 2009-10. Pods per plant, seeds per pod, pod length and nodes per plant had maximum indirect contribution for enhancing the magnitude of association for majority of the traits with fresh pod yield per plant while total biomass, harvest index, pods per plant and pod yield per plant had the same indirect contribution for seed yield per plant. Therefore, pods per plant, pod length, seeds per pod and nodes per plant for fresh pod yield per plant, and total biomass, pod yield per plant and harvest index for seed yield per plant could be considered reliable selection parameters for evolving high yielding genotypes.

The multivariate analysis revealed considerable genetic diversity present in the genotypes. All the 41 genotypes of garden pea were arranged into 8, 13 and 5 clusters in 2009-10, 2010-11 and pooled over years, respectively. Maximum genotypes were placed in cluster I over the years and pooled over years. However, 14 genotypes from cluster I showed consistency in clustering pattern while the best performing genotype 'DPPM-74' along with 'DPPM-64', 'DPPMR-09-1' and 'DPP-25G' showed uniformity to certain extent on the basis of monogenotypic clusters in one of the years and pooled over years. The clustering pattern revealed that the genotypes of same geographical distribution fall into different clusters which indicated that the clustering pattern and geographical distribution were independent of each other. The maximum intra-cluster distance were observed in cluster VI, cluster IV, and cluster I in 2009-10, 2010-11 and pooled over years, respectively. The maximum inter-cluster genetic divergence was recorded between clusters V and VIII, clusters XI and XII, and clusters III and V in 2009-10, 2010-11 and pooled over years, respectively suggesting wide diversity among genotypes of the two clusters due to different genetic constitution. Harvest index, total biomass, and 100-seed weight contributed maximum towards total genetic divergence in 2009-10, 2010-11 and pooled over years, respectively. Selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters and accordingly genotypes 'Punjab-89', 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPMFWR-4'. 'DPPMFWR-30-2' and 'DPP-25G' offer promise as a breeding stock to be used in hybridization for obtaining transgressive segregants for further exploitation in garden pea improvement programme.

Conclusions:

Sufficient genetic variability was observed for all morphological, yield and yield contributing, and quality traits during both the years of 2009-10 and 2010-11. Genotypes 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPM-72', 'DPPMFWR-20' and 'DPPM-07-4' were observed to be promising on the basis of pod characters and yield. High heritability coupled with high genetic advance was observed for pods per plant, pod yield per plant, total biomass, seed yield per plant and harvest index which revealed the importance of additive gene action and phenotypic selection would be effective for improvement in the early generations (Jan et al. 2007). Based upon correlation and path coefficient analysis, pods per plant, pod length, seeds per pod and nodes per plant for fresh pod yield per plant, and total biomass, pod yield per plant and harvest index for seed yield per plant could be considered as the reliable selection parameters for evolving high yielding genotypes (Sharma et al. 2007). The multivariate analysis revealed considerable genetic diversity present in the 41 genotypes studied. The genotypes viz., 'DPPM-64', 'DPPM-74', 'DPP-25G' and 'DPPMR-09-1' showed consistency in clustering pattern to certain extent along with 14 other genotypes. On the basis of genetic divergence, genotypes 'Punjab-89', 'DPPM-74', 'DPPM-64', 'DPPM-73', 'DPPMFWR-4', 'DPPMFWR-30-2' and 'DPP-25G' offer greater potentiality as a breeding stock to be used in hybridization for the isolation of transgressive segregants in garden pea (Kumar et al. 2007).



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APPENDICES

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Genotypes	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled
DPPMFWR-1	76,67	88.67	82.67	14.00	14.00	14.00	87.00	92.00	89.50	118.33	126.33	122.33	1.00	2.07	1.53	5.68	4.86	5.27
DPPMFWR-2	77.00	91.33	84.17	13.20	11.40	12.30	93.00	97.33	95.17	121.00	134.67	127.83	1.20	1.47	1.33	3.79	3.80	3.80
DPPMFWR-3	76.33	88.00	82.17	14.07	14.10	14.08	89.67	93.67	91.67	118.67	133.33	126.00	1.07	2.40	1.73	5.05	4.52	4.79
DPPMFWR-4	74.67	92.00	83.33	14.00	13.20	13.60	88.67	97.67	93.17	118.00	132.33	125.17	1.60	2.93	2.27	5.38	5.06	5.22
DPPMFWR-5	76.67	88.67	82.67	14.27	14.40	14.33	89.33	94.00	91.67	118.67	128.00	123.33	1.33	1.87	1.60	5.80	4.92	5.36
DPPMFWR-8	79.00	61.67	85.33	14.20	13.47	13.83	92.67	97.67	95.17	120.00	133.00	126.50	1.07	1.47	1.27	6.64	5.04	5.85
DPPMFWR-11	74.67	88.67	81.67	14.00	13.47	13.73	84.67	94.33	89.50	117.33	130.67	124.00	1.39	2.53	1.96	6.15	5.14	5.65
DPPMFWR-12	77.00	90.00	83.50	13.80	13.93	13.87	92.00	94.33	93.17	121.33	130.67	126.00	1.18	2.13	1.66	4,16	4.75	4.45
DPPMFWR-20	75.00	89.00	82.00	14.20	13.53	13.87	84.67	94.33	89.50	114.33	129.33	121.83	1.30	1.53	1.41	6.25	4.90	5.58
DPPMFWR-27	76.00	88.67	82.33	14.53	13.00	13.77	88.33	95.00	91.67	117.00	129.00	123.00	1.10	1.67	1.38	5.51	5.11	5.31
DPPMFWR-29	77.67	93.00	85.33	14.87	15.07	14.97	93.00	100.00	96.50	123.00	130.00	126.50	1.40	3.13	2.27	5.53	5.42	5.48
DPPMFWR-30-1	76.33	92.00	84.17	13.80	13.93	13.87	91.33	96.33	93.83	118.67	131.00	124.83	1.13	2.20	1.67	5.45	5.86	5.65
DPPMFWR-30 -2	75.33	96.33	85.83	14.20	12.53	13.37	92.00	101.00	96.50	121.67	129.67	125.67	1.00	1.87	1.43	5.61	5.20	5.41
DPPM-1	78.33	95.00	86.67	13.93	13.60	13.77	91.33	100.67	96.00	123.67	133.00	128.33	1.27	2.13	1.70	6.19	5.65	5.92
DPPM-22	78.67	96.67	87.67	13.33	15.67	14.50	93.67	103.00	98.33	120.67	127.67	124.17	1.13	1.87	1.50	5.33	4.79	5.06
DPPM-64	75.33	94.33	84.83	14.40	14.67	14.53	83.67	99.67	91.67	112.67	130.00	121.33	1.10	2.60	1.85	5.94	5.80	5.88
DPPM-65	72.33	00.66	86.67	14.53	13.33	13.93	92.00	100.33	96.17	119.33	131.00	125.17	1.13	3.00	2.07	6.38	6.14	6.26
DPPM-72	55.17	79.94	86.00	14.20	12.60	13.40	92.00	100.00	96.00	120.00	130.33	125.17	1.73	3.33	2.53	6.41	6.22	6.32
DPPM-73	00.77	79.19	84.33	13.33	13.53	13.43	92.67	97.67	95.17	120.33	130.00	125.17	1.13	2.07	1.60	6.50	5.24	5.87
DPPM-/4	00.77	00.54	00.08	14.47	14.33	14.40	90.00	98.67	94.33	118.67	129.33	124.00	1.60	2.53	2.07	5.11	5.80	5.46
DPPM-07-0	00.11	10.68	83.33 54 53	14.47	13.40	13.93	88.67	96.67	92.67	116.33	132.00	124.17	1.33	2.87	2.10	5.98	3.81	4.89
DFFIN-07-9	00.02	00.00	00.90	19.01	14.20	14.U3	00.06	79.67	94.33 20 00	118.67	55.151	00.621	1.47	3.00	2.23	4.01	4.40	4.48
	20.61	10.14	05.00	10.01	15.61	12.11	00.06	55.501	10.001	123.33	134.00	19.821	00.1	7.20	no.1	4.8/	4.83	C0.4
DFFINIK-09-1	10.11	66.101 00 22	00.48	14.80	10.00	0/.01	94.00	106.00	00.001	122.00	131.33	126.67	1.13	08.1	1.47	74.0	1.8.5	4.07
DPDMR-00-3	73.67	CC.77	00.07	00.01	C/.CI	14.07	00.64	CC.401	70.07	00.121	124.00	00.121	00.1	CI .7	10.1	0.12 5 75	4.00	04.0
DPPMR-09-5	78.67	93.33	86.00	13 40	C/ .CI	10.01	04.07	10.16	96 33	CC.611	CC.1C1	00 201	0,1	7.47 2.00	9C.1	C	14.0	00. 005
DPPMR-09-9	73.67	88.00	80.83	14 27	13.00	13.63	85.00	00.50	80.00	116.67	100 201	121.83	07-1	2 60	201 2012	5 8 5	1.5 6	4.67
DPP-25G	78.67	95.67	87.17	13.87	14.73	14.30	92.33	103.33	97.83	122.33	133.67	128.00	1.13	2.00	1.57	2.72	2.59	2.66
DPP-89	74.33	88.67	81.50	13.40	12.67	13.03	86.67	94,00	90.33	115.00	128.67	121.83	1.06	2.20	1.63	5.13	4.88	5.00
DPP-100	77.67	94.67	86.17	13.80	14.60	14.20	91.33	100.67	96.00	120.33	132.33	126.33	1.47	2.00	1.73	4.91	4.79	4.85
DPP-168	78.33	97.00	87.67	13.47	14.00	13.73	94.00	103.33	98.67	121.67	132.00	126.83	1.37	1.73	1.55	4.76	3.68	4.22
DPP-3-1	77.00	89.67	83.33	13.20	14.27	13.73	93.00	95.33	94.17	121.00	131.33	126.17	1.27	2.87	2.07	4.57	4.78	4.68
DPP-11-2	55.61 55.25	00.66	81.17	13.60	13.60	13.60	96.00	103.00	99.50 27.20	121.67	134.33	128.00	1.27	2.87	2.07	6.27	6.77	6.52
VP_215	73 23	22.42	50 03	00 21	12.40	12 20	10.24	55.101 55.101	00.16	10.221	132.00	CC./21	1.5.1	1.80	9C.1	2.47	10.0	/0.C
Green Pearl	78.33	95 33	86.83	13 73	00 11	13.87	00.50	25.001	64.40	29101	132.00	C0.771	00.1	160	1 40	5 50	5 46	55.5
Lincoln	76.33	97.00	86.67	13.67	13.67	13.67	88.33	101 67	95.00	10.121	00.001	1121	07.1	2 80	00 2	5 17	10.9	5.59
Azad P-1	77.00	92.00	84.50	13.40	14.07	13.73	90.67	97.67	94.17	121.00	132.00	126.50	107	2.47	1.77	5.39	5.74	5.57
Palam Priya	81.67	95.00	88.33	13.87	14.47	14.17	92.00	102.00	97.00	119.00	132.33	125.67	1.40	2.53	1.97	4.67	5.46	5.07
Punjab-89	73.33	91.00	82.17	13.33	12.13	12.73	82.33	95.00	88.67	111.67	126.33	119.00	1.20	3.07	2.13	5.76	5.80	5.79
Range	73-82	88-101	81-90	13.20-	11.40-	12.30-	82-96	92-106	89-100	112-124	126-135	119-129	1.00-1.73	1.47-3.33	1.27-2.53	2.72-6.64	2.59-6.77	2.66-6.52
2				14.18	16.60	15.70			:							•		
Mean	/0.83	97.78	84.80	13.90 2.0	13.88	13.89	90.32	98.50	94.41	119.40	131.02	125.21	1.26	2.26	1.76	5.43	5.07	5.25
SE(m) ±	2.18	60.1 21.0	1.03	0.28	0.55	0.31	1.41	1.57	1.05	1.48	1.74	1.14	0.10	0.19	0.11	0.17	0.18	0.13
CV (%)	200.7	01.0	2.98	3.53	6.85	5.44	2.71	2.76	2.74	2.14	2.30	2.23	14.77	14.83	15.40	5.50	6.17	5.80
CU at F 2 0.05	10.0	4.11	2.90	U.8U	1.24	0.87	3.97	4.41	2.90	4.10	4.88	3.20	0.30	0.54	15.0	0.49	10.0	cc.0

Definitives 200-10 2010-10 2010-11	Traits	z	odes per pla	nt	Ρlέ	ant height (c	(m	Po	d length (cm	()	Š	ceds per poo			shelling (%)		Pc	ds per plant	
PDFMEWK-1 157 173 1710 576 391 381 841 842 649 659 659 659 650 659 4130 420 4492 730 PDFMEWK-1 159 130 1320 1350 153 230 150 6413 653 730 653 643 654 459 736 659 659 659 659 659 659 659 659 659 737 759 759 759 759 759 759 759 759 759 75	Genotypes	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled
DPMANNA: List	DPPMFWR-1	16.47	17.73	17.10	57.63	59.19	58.41	8.42	9.48	8.96	6.83	6.87	6.85	42.62	44.97	43.80	4.40	9.10	6.75
Diperimeter, 12:10 10:1	DPPMEWR-2	15.8/ 16.12	17.8/	18.53	37.40 E2.20	38.25	37.80 50.60	67.0 0	979 0	9C.0	4.95 C 2 2	0.3U	50.5	41.80	43.82 AG ED	42.81 AA 77	4.8L	8.14 0.00	7.10
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPMFWR-4	15.87	18.60	CC.01	UC.2C	04.90 67 73	00.00	0.72	0.00 8 40	00.0 8 79	/ c.c	40.4 77 A	5.78	00 00	40.00	77 14	5.15 75 A	10.94	8 74
DPMMIRVR-1 173 747 577 547 577 547 577 547 577 547 547 666 666 673 DPMMIRVR-1 1733 2200 1976 661 666 673 675 673	DPPMFWR-5	17.00	19.20	18.10	64.10	68.42	66.26	60.8	94.2	7.94	2007 1987	6.00	5.93	44.59	47.78	46.19	6.40	17.09	11.75
DPMARVR-11 1591 1740 6131 6150 6573 845 875 861 653 653 654 770 DPMARVR-12 1530 1200 1740 661 553 550 651 653 673 653 673 663 770 DPMARVR-201 1530 1200 8241 553 664 573 653 <td< td=""><td>DPPMFWR-8</td><td>17.80</td><td>21.47</td><td>19.63</td><td>64.73</td><td>69.52</td><td>67.13</td><td>7.66</td><td>7.27</td><td>7.47</td><td>5.77</td><td>5.10</td><td>5.44</td><td>46.64</td><td>43.33</td><td>44.99</td><td>7.02</td><td>14.58</td><td>08.01</td></td<>	DPPMFWR-8	17.80	21.47	19.63	64.73	69.52	67.13	7.66	7.27	7.47	5.77	5.10	5.44	46.64	43.33	44.99	7.02	14.58	08.01
DPMARWR:1 173 200 19/5 646 600 54/7 849 74 809 747 809 747 DPMARWR:27 1743 1830 1812 6213 730 6717 500 557 554 559 557 654 567 654 567 654 563 653	DPPMFWR-11	15.91	19.07	17.49	. 63.13	69.64	66.39	8.45	8.76	8.61	6.82	6.80	6.81	46.45	47.70	47.08	7.80	17.81	12.80
Method 153<	DPPMFWR-12	17.33	22.00	19.67	48.64	60.69	54.67	8.49	7.64	8.07	6.45	5.90	6.18	49.98	47.87	48.93	9.87	17.71	13.79
$\begin{array}{llllllllllllllllllllllllllllllllllll$	DPPMFWR-20	16.50	17.33	16.92	65.41	55.54	60.48	9.08	9.48	9.28	6.83	6.53	6.68	44.58	46.23	45.41	5.50	15.67	10.58
$\begin{array}{llllllllllllllllllllllllllllllllllll$	DPPMFWR-27	17.43	18.80	18.12	69.23	70.30	69.77	9.00	8.63	8.82	6.79	6.27	6.53	46.18	44.70	45.44	7.92	8.34	8.13
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	DPPMFWR-29	17.10	19.93	18.52	82.07	81.26	81.67	6.60	6.67	6.64 • 01	4.60	5.33	4.97	44.33	43.01	43.67	7.02	13.38 15 01	10.20
DPPMA(1) 15.37 19.99 10.0 65.77 95.91 95.01 67.01 77.00 65.21 64.91 DPPMA(2) 16.30 13.00 11.00 13.27 70.29 13.33 13.41 13.35 85.0 6.20 6.20 6.21 6.23 7.24 73.37 13.41 13.35 81.0 6.57 6.53	DPPMFWR-30-1	16.83	20.33 18 53	17.68	16.20	08.4U 49.87	00.00	00.1 8 73	0.13 8.65	0.01 8 44	2000	5.2.5 1.60	0/.c	42.47	42.24 A3.63	0C.24	10.74	70.CL	96.6
DPPMA27 1630 1900 1700 52.7 52.61 77.94 8.84 5.96 4.90 5.37 6.23 6.33	DPPM-1	16.27	19.93	18.10	66.87	69.57	68.22	9.91	6.62	9.76	6.74	7.10	6.92	42.29	44.97	43.63	10.83	10.54	10.69
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPM-22	16.20	19.00	17.60	53.27	62.61	57.94	8.84	8.83	8.84	5.69	4.90	5.30	43.36	43.83	43.59	6.64	11.13	8.89
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-64	16.03	18.00	17.02	66.87	72.28	69.58	13.25	13.44	13.35	8.10	8.63	8.37	46.07	45.81	45.95	6.15	11.44	8.79
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-65	17.08	18.27	17.68	72.47	70.29	71.38	9.95	9.30	9.63	6.93	6.33	6.63	40.98	46.18	43.58	7.49	14.87	11.18
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-72	16.39	17.33	16.86	65.13	78.84	21.99	10.13	9.36	9.75	6.83	6.57	6.70	46.17	43.78	44.98	9.77	16.35	13.06
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-73	15.53	16.87	16.20	71.00	74.67	72.84	9.85	9.82 	9.84	7.61	6.57	7.09	46.50	46.81	46.65	6.77	14.00	10.38
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	DPPM-/4	15.51	20.00	17.72	55.27	62.76 70.75	20.60	8.25	8.76	8.51	6.33	6.03	6.18 6.61	47.87	43.86	13.64	15.03	10.01	70011
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	DPPM-07-9	14 87	12.21 16.07	15.47	45.50 A5.60	C7.U/	60.11	07.7 09.60	75.5 6.9 0	9.70 8.66	0.88	65.0 F7 N	10.0	40.43	41.29 12 20	44.04	9.04 5.77	10 97	8 17
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-07-30	16.80	20.67	18.73	61.78	60.63	61.21	8.61	60.6	8.82	4.01	5.40	5.15	38,88	44.00	41.44	3.27 8.15	8.58	8.37
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPMR-09-1	17.67	22.07	19.87	66.32	66.12	66.23	9.61	8.19	8.90	5.66	4.60	5.13	40.70	42.38	41.55	8.80	8.06	8.43
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPMR-09-2	15.86	17.60	16.73	58.97	61.44	60.20	8.79	8.83	8.81	5.52	4.50	5.01	42.68	35.89	39.29	5.60	8.03	6.81
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPMR-09-3	15.17	18.20	16.68	56.32	59.53	57.93	8.35	8.32	8.34	5.11 .	4.90	5.00	37.51	42.45	39.98	5.69	TT.T	6.73
DFPrivicus-099 15.87 16.27 16.07 5493 52.02 53.14 8.86 8.15 8.51 6.47 5.43 5.95 45.01 44.83 DPP-25G 15.43 18.60 17.02 33.07 38.95 34.51 6.18 8.15 5.37 5.97 5.97 4.39 46.60 DPP-168 15.53 19.07 17.30 66.07 56.6 8.20 8.34 8.37 5.96 6.50 6.20 4.39 46.61 DPP-168 15.53 19.07 17.30 66.07 56.6 8.20 8.37 5.96 6.57 6.38 4.51 DPP-168 15.53 19.07 17.30 66.07 56.6 8.20 8.37 5.96 6.57 6.38 4.51 DPP-172 15.07 18.34 64.71 68.56 66.64 10.47 9.12 8.31 8.46 8.37 4.96 6.67 4.66 DPP-172 15.87 17.40	DPPMR-09-5	14.66	18.73	16.69	53.11	55.16	54.14	8.61	8.76	8.69	6.70	5.53	6.12	37.61	40.58	39.10	5.86	7.49	6.67
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPMK-09-9	15.87	16.27	16.07	54.93	52.02	53.48	8.86	8.15	8.51	6.47	5.43	5.95	45.01	44.83	44.92	9.37	15.29 C 0C	12.35
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	DCZ-77U	14.45	18.6U	207/1	30.07	38.95 01.02	10.46 25 22	0.18 0.70	5.7	70.0	3.87	3.97	5.92 2 7 0	41.18	41.63	41.40	16.7	0.80	4.07 6.67
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	DPP-100	16.27	c/.02 18.40	16.11	49.20	57 87	51.04	07.00	8.54 7 40	16.0	22.0 7.2.7	1 8 U	0.20 5 09	40.70 42 20	46 90	45.15	8 90 0 8	15.61	12.26
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPP-168	15.53	19.07	17.30	66.07	56.29	61.18	8.49	8.05	8.27	5.96	6.20	6.08	42.91	46.61	44.76	7.66	9.59	8.62
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPP-3-1	15.07	18.53	16.80	52.20	79.17	65.68	10.33	69.6	10.01	6.37	5.17	5.77	42.92	47.62	45.27	6.60	14.03	10.31
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPP-11-2	15.00	20.53	17.77	60.84	85.43	73.14	8.66	8.34	8.51	5.09	4.83	4.96	36.76	46.63	41.70	7.68	7.78	7.73
VT-213 VT-213 V.7.2 V.2.2 V.2.2 S.13 S.09 b.81 V.4.35 V.2.41 4.5.61 Green Pearl 15.27 18.67 16.97 60.30 64.97 62.94 9.27 9.12 9.20 6.35 5.31 4.2.41 4.5.61 Lincein 15.23 18.67 17.25 52.23 60.32 56.28 7.84 8.34 8.09 6.35 5.35 5.36 42.94 45.95 Azad P-1 15.73 18.40 17.55 52.23 60.32 56.28 7.84 8.34 8.09 6.35 6.31 40.92 45.95 Palam Priya 16.84 20.13 18.40 7.57 59.28 72.49 65.87 8.38 6.47 58.9 42.96 Palam Priya 16.84 20.13 18.40 7.57 59.28 17.35 13.44 13.35 8.16 7.19 87.9 47.96 47.96 Palam Priya 16.69 55.73	DPP-17-2	16.68	20.20	18.44	64.71	68.56	66.64	10.47	9.15	9.81	5.69	5.93	5.81	40.79	47.16	43.98	4.76	10.22	7.49
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	Vr-213 Graan Doort	76.CT	1/.40	16.07	00.30 00.00	04.P0	C7.20	2.2 2.5	8.13	8.09 0.00	1 0 0 0	. 4.93	18.0	147.4T	43.61	40.01	10.2	10.01	7C'NI
Azad Pi Los Los <thlos< th=""> Los <thli> <thli< t<="" td=""><td>Lincoln</td><td>15.27</td><td>10.0T</td><td>12.01</td><td>50.5U</td><td>16.40 CC 03</td><td>96.20 56.38</td><td>12.6</td><td>71.6</td><td>07.4</td><td>6./9 C 35</td><td>2.83 2.83</td><td>10.0</td><td>75.04 V3.64</td><td>46.UL</td><td>43.47</td><td>6.15 0.7</td><td>10.01</td><td>0.00</td></thli<></thli></thlos<>	Lincoln	15.27	10.0T	12.01	50.5U	16.40 CC 03	96.20 56.38	12.6	71.6	07.4	6./9 C 35	2.83 2.83	10.0	75.04 V3.64	46.UL	43.47	6.15 0.7	10.01	0.00
Palametry Law Composition Co	Azad D.1	CO.CT	10.01	12.51	C7.7C	707 62	07.00	to ; o	0.04 0.40	0.07	CC.0	0.00 7 0 1	17. C	40.04	44.30	00.04	00.0 6 6 7	11 28	10.80
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	Palam Priva	16.84	20.13	18.49	55.73	58.64	57.19	8.23	8.10 8	8.17	6.37	5.83	6.08	42.14	46.79	44.47	11.06	16.36	13.71
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	Punjab-89	13.87	17.53	15.70	51.53	67.03	59.28	10.81	9.98	10.40	8.05	8.03	8.04	46.95	47.03	47.00	8.25	13.35	10.80
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	Range	13.87-	16.07-	15.47-	30.07-	38.26-	34.51-	6.18-	-6.67-	6.59-	3.87-	3.97-	3.92-	36.76-	35.89-	39.10-	2.91-	6.80-	4.89-
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Man	17.80	22.07	19.87	82.07	85.43	81.67	13.25	13.44	13.35	8.10	8.63	8.37	49.99	47.87	48.93	15.03	18.01	16.52
CV (%) 7.68 2.37 5.30 5.34 4.63 4.97 4.01 6.22 5.22 6.03 7.79 6.89 5.40 5.16 CD at P ≥ 0.05 2.00 0.73 1.06 5.10 4.82 3.50 0.57 0.88 0.52 0.60 0.73 0.47 3.79 3.74	SE(m) +	0.01	CK.01	85.0	181	7 1 1 1	01.45	0.21 0.21	8.0/	8./4 0.10	c1.0 CC 0	78.0	56.0	42.64	44.04 1 33	0.05	0.80	7177 0 65	0.51
CD at P ≤ 0.05 2.00 0.73 1.06 5.10 4.82 3.50 0.57 0.88 0.52 0.60 0.73 0.47 3.79 3.74	CV (%)	7.68	2.37	5.30	5.34	4.63	4.97	4.01	6.22	5.22	6.03	7.79	6.89	5.40	5.16	5.28	18.57	9.33	12.90
	<u>CD at P ≤ 0.05</u>	2.00	0.73	1.06	5.10	4.82	3.50	0.57	0.88	0.52	0.60	0.73	0.47	3.79	3.74	2.66	2.24	1.84	1.44

Traits	(pod	'ield per plan	t (g)	Tot	tal biomass (g)	Seed y	ield per plan	t (g)	Harv	est index (*	(%	100-s	eed weight	(g)	Total sol	ble solids (brix)
Genotypes	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled
DPPMFWR-1	21.73	39.50	30.62	18.00	23.33	20.67	5.04	7.67	6.35	27.91	33.14	30.53	16.33	15.67	16.00	17.40	17.93	17.67
DPPMFWR-2	14.53	21.10	17.82	9.67	18.67	14.17	2.89	5.00	3.95	29.96	27.11	28.54	12.33	13.33	12.83	18.27	17.47	17.87
DPPMFWR-3	23.23	36.50	29.87	18.33	37.33	27.83	6.08	10.67	8.37	33.09	28.53	30.81	21.00	20.67	20.83	16.07	17.53	16.80
DPPMFWR-4	30.90	42.97	36.93	22.33	35.67	29.00	9.21	10.67	9.94	41.30	29.99	35.64	19.33	17.00	18.17	16.53	16.67	16.60
DPPMFWR-5	26.83	66.10 17 27	46.47	20.67	32.67	26.67	6.48	12.00	9.24	31.39	36.73	34.06	17.33	15.67	16.50	18.60	17.33	17.97
DPPMFWK-8	27.43	47.97	37.70	15.67	32.67	24.17	5.53	6.33	5.94	35.31	19.40	27.35	13.50	14.00	13.75	18.67	17.07	17.87
DPPMFWK-11	37.10	71.73	24.42	22.67	26.33	24.50	9.92	10.00	9.96	43.76	38.01	40.88	19.33	14.00	16.67	17.60	17.47	17.53
DPPINIF W.K-12	32.10	58.50	45.50	36.67	37.33	37.00	9.12	11.33	10.23	24.87	30.52	27.70	14.33	14.67	14.50	17.60	16.27	16.93
DPPMFWK-20	25.20	66.17	45.68	27.00	34.33	30.67	7.25	11.67	9.46	26.83	34.02	30.43	19.33	15.00	17.17	18.20	15.13	16.67
DPPMFWK-27	36.03	35.30	35.67	27.33	30.33	28.83	10.55	9.33	9.95	38.59	30.81	34.70	21.00	17.00	19.00	18.27	16.47	17.37
DPPMFWR-29	14.83	28.90	21.87	22.00	34.33	28.17	5.53	8.33	6.93	25.12	24.30	24.71	17.33	14.00	15.67	14.53	15.53	15.03
DPPMFWR-30-1	. 37.90	59.57	48.73	28.33	35.33	31.83	10.81	9.33	10.07	38.16	26.35	32.25	18.00	15.33	16.67	18.67	16.87	17.77
DPPMFWK-30-2	46.23	36.43	41.33	34.00	33.00	33.50	14.30	9.33	11.81	42.04	28.30	35.17	17.67	14.67	16.17	18.73	17.33	18.03
	35./3	46.67	41.20	33.00	30.33	31.67	13.13	9.33	11.23	39.79	30.69	35.24	18.67	15.00	16.83	18.07	17.27	17.67
	31.45	56.67	cu. 44	35.67	30.00	32.83	7.81	12.00	9.90	21.89	39.95	30.92	20.67	21.67	21.17	19.60	16.33	17.97
DEFINI-04	17.04	06.80	CC./C	20.05	31.33 22.00	25.92 00.00	c 0. 0	13.67	00.21	42.61	43.83	45.22	23.33	22.00	19.77	1/.80	1/.8/	C2 L1
DPPM-77	41.62	70.03 65 50	53 57	25.67	79 65	26.00	0.30	00.11	40.4 10.60	30.45	55.54 26.74	66.90 CC 0C	10.53	15.00	16.00	10.71	77.1T	CC./1
DPPM-73	26.60	56.73	41.67	20.67	10.00	35 50	0.00	11 67	10.00	46.12	1/.00	20, 62	10.01	00.CT	16.00	10.01	CC'/T	19.50
DPPM-74	57 33	80.17	10.11	10.55	CC.TC	00°.00	15 63	10.11	00.21 N1 31	52./4	C7.1C	54.40 54.14	/0/ CC	14.33 20.33	21.67	10.61	CC./1	16.07
DPPM-07-4	44.90	63.53	54 22	00.95	79.80	10.01 55 CF	12 05	10.01	14.14	20.24	40.04	C4.14	10.00	18 22	10.12	10.00	14.01	18.47
DPPM-07-9	20.63	54.00	37 32	75 33	26.67	26.00	4 99	2014	5 50	10.68	10.04	2010	19.67	17 22	18.50	18.87	17.67	18.27
DPPM-07-30	31.03	34.67	32.85	24.33	31.67	28.00	7.43	11.33	9.38	30.54	35.70	33.12	18.67	16.33	17.50	18.80	16.73	17.77
DPPMR-09-1	33.97	29.30	31.63	28.67	17.33	23.00	10.64	5.67	8.15	37.09	32.71	34.90	21.33	19.33	20.33	17.07	16.53	16.80
DPPMR-09-2	28.17	41.73	34.95	25.67	39.67	32.67	8.12	14.67	11.40	31.63	36.93	34.28	26.33	24.33	25.33	17.87	17.47	17.67
DPPMR-09-3	23.03	33.33	28.18	27.33	24.00	25.67	6.55	6.33	6.44	23.96	26.46	25.21	22.67	19.33	21.00	19.27	17.67	18.47
DPPMR-09-5	32.60	38.33	35.47	29.00	28.00	28.50	9.15	9.33	9.24	31.56	33.32	32.44	23.33	19.33	21.33	18.40	17.53	17.97
DPPMR-09-9	33.93	59.77	46.85	34.67	23.67	29.17	9.39	9.67	9.53	27.02	40.79	33.91	20.33	19.67	20.00	16.73	17.47	17.10
DPP-25G	10.27	18.00	14.13	8.67	11.00	9.83	1.57	3.80	2.68	18.08	34.19	26.13	14.00	15.00	14.50	17.47	16.07	16.77
DPP-89	17.17	34.83	26.00	15.33	29.00	22.17	4.20	8.33	6.26	27.33	28.72	28.02	16.33	17.33	16.83	18.00	16.67	17.33
DPP-100	30.73	51.23	40.98	27.33	26.33	26.83	8.74	10.33	9.54	31.97	39.36	35.67	18.33	17.67	18.00	18.20	17.73	17.97
DPP-168	28.10	35.00	31.55	24.67	23.67	24.17	8.35	9.00	8.67	33.85	38.02	35.93	18.33	15.67	17.00	18.33	18.27	18.30
DPP-3-1	25.37	50.17	37.77	24.00	28.33	26.17	6.99	8.33	7.66	29.14	29.41	29.28	16.67	16.33	16.50	19.40	18.47	18.93
DPP-11-2	20.50	30.00	25.25	18.00	20.67	19.33	6.17	6.67	6.42	34.29	32.24	33.27	16.00	15.00	15.50	17.93	17.33	17.63
VD 715		57.75	70'67	10.07	23.67	20.00	38.5	6.00	5.94 5.05	35.20	25.39 11 11	50.29	17.67	16.67	1.11	19.33	18.47	18.90
Green Pearl	01.64	49.10	45.22	00.00	00.62	20.67	00.0	/9.0T	60.11	34.80	11.24	20.02	20.33	00.91	10.61	00./T	17.11	17 22
Lincoln	17.70	59.33	38.52	15.67	25.00	20.33	5.61	00 0	111	25 27	26.72	36.05	17.67	17 23	17.50	17.87	CC-01	17 57
Azad P-1	29.97	61.37	45.67	24.67	35.33	30.00	9.01	2.00 10.67	9.84	36.53	27.40	31.96	19.33	17.67	18.50	17.47	16.53	17.00
Palam Priya	47.33	60.33	53.83	36.00	39.00	37.50	11.13	12.67	11.90	30.88	35.87	33.38	21.67	19.67	20.67	17.47	16.80	17.13
Punjab-89	43.70	69.20	56.45	26.67	26.33	26.50	11.57	14.33	12.95	43.40	54.63	49.02	19.67	17.67	18.67	17.70	16.67	17.18
Range	10.27-	18.00-	14.13-	8.67-	11.00-	9.83-	1.57-	3.80-	2.68-	18.08-	19.40-	21.04-	12.33-	13.33-	12.83-	14.53-	15.13-	15.03-
;	52.33	80.17	66.25	40.33	41.33	40.83	15.62	16.67	16.14	43.76	54.63	49.02	26.33	24.33	25.33	19.60	18.47	18.93
Mean	30.76	49.02	39.89	25.93	29.60	27.76	8.56	9.87	9.22	32.85	33.57	33.21	18.87	17.08	17.98	18.01	17.08	17.58
SE(Ⅲ) ±	77.7	2.31	1.62	1.41	1.13	0.90	0.49	0.66	0.41	0.27	2.11	1.06	0.69	0.77	0.52	0.63	0.27	0.34
	17.11	8.16	9.94	9.44	6.59	1.6.1	9.88	11.57	10.90	1.42	10.89	7.85	6.29	7.84	1.04	6.06 21	2.73	4./8
	0.38	6.50	4C.4	3.98	3.1/	2.54	1.37	1.85	1.15	0.76	5.94	2.99	1.93	2.17	1.45	1.17	0./6	0.70

Classifier 200-10 Display Display <thdisplay< th=""> <</thdisplay<>	Traits	Asc	orbic acid ((mg)	Prote	ein content	(%)	To	tal sugars (%	(9)	Reduc	sing sugars	(%)	Starc	sh content ((%)	Powdery m	ildew incidence (%)
DPM-HYWI: 150 153 1	Genotypes	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled	2009-10	2010-11	Pooled		2009-10
Deprindence 1331 1336	DPPMFWR-1	15.60	16.54	16.07	16.58	15.38	15.98	6.36	5.50	5.93	3.36	2.67	3.02	20.55	18.30	19.43	95.82	(82.49)-S
Deprinvisi (12)	DPDMFWR-3	13.56	96.01	40.01 10.01	17.00	(7.C)	14.41	CO./	6/ 0	17.0	5.19 272	5.45 7.45	3.32	30.00	23.30	20.02	87.49	S-(08.7/)
DPMCNVAS 157 167 163 15	DPPMFWR-4	14.82	14.98	14.90	15.44	14.26	14.85	6.56	7.89	1 23	27.5 60 E	4 14	4.03	28.65	CU. 61	C5 LC	91.65	S-(62.60)
DPMERWAR: 113 136 73 651 711 356 355 35	DPPMFWR-5	15.77	16.87	16.32	13.25	12.58	12.91	6.71	6.95	6.83	3.23	3.19	3.21	25.80	26.40	26.10	91.66	(75.90)-S
DPMARWRA: 113 22.0 7.3 6.4 7.14 3.75 3.75 2.75 3.75 <	DPPMFWR-8	14.04	13.42	13.74	14.83	13.13	13.98	7.78	6.51	7.15	3.66	3,41	3.53	20.55	22.53	21.54	83.33	(69.70)-S
DPMARKR:1 137 137 149 139 70 645 655 315 319 3115 139 319 3115 139 319 3115 139 323 339 3315	DPPMFWR-11	14.26	13.86	14.06	13.69	11.11	12.40	7.53	6.74	7.14	3.92	3.58	3.75	27.75	23.10	25.42	91.66	(75.90)-S
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPMFWR-12	13.39	12.11	12.74	14.74	13.04	13.89	7.07	6.64	6.86	3.15	3.23	3.19	24.15	19.95	22.05	87.49	(72.80)-S
DPMMMRA23 153 174 173 173 173 173 173 173 173 173 173 173 173 173 173 173 173 173 173 173 173 1	DPPMFWR-20	13.76	12.86	13.31	14.91	12.51	13.71	6.10	6.22	6.16	3.66	3.10	3.38	28.04	28.50	28.27	91.65	(79.39)-S
	DPPMFWR-27	15.47	16.28	15.87	17.98	17.21	17.59	7.27	8.06	7.67	4.05	2.67	3.36	29.25	21.90	25.57	99.98	SH-(60'68)
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	DPPMFWR-29	15.05	15.44	15.25	16.14	17.59	16.86	6.87	5.72	6.29	3.02	2.97	3.00	21.15	18.90	20.02	99.98	SH-(60.68)
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	DPPMFWK-30-1	14.11	13.55	13.83	14.04	11.11	12.58	7.38	7.74	7.56	3.71	3.02	3.36	22.35	23.25	22.80	95.82	(82.49)-S
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPMFWK-30-2	40.CI	15.42	15.24	16.14	16.95	16.54	5.85	8.14	6.99	3.58	3.66	3.62	25.95	23.70	24.82	91.65	(79.39)-S
$ \begin{array}{llllllllllllllllllllllllllllllllllll$		11.01	37 31	45.CI	14.00	C0.51	14.15	0.20	26.7 21.9	10.7	2.28	3.41	2.84	24.30	20.25	22.27	95.82	(82.49)-S
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	DPPM-64	15.60	16.71	16.20	10.11	19 51	0C.CI	0.41	0.01	67.1	5.75	5.50 03 c	60.6 12 c	21.00	21.50	21.12	C0.17	C-(65.6/)
DPPMA77 150 153	DPPM-65	15.04	15.43	15 24	CC 11	12.61	13 80	0.14	10.2	10.5	5.11	01.5	9.04 5.04	C8.02	20.01	24.13	c0.0	N-(16.0)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-72	15.06	15 46	15 26	16.23	14.68	15.45	6.81	00''	(), (10.7	2.17	CK-7	24./4	11.02	21.15	70'C4	2H-(04.40)
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	DPPM-73	13.51	12.36	12.93	16.67	15.40	16.04	6.87	12.0	10.1	3 58	+ C C	3.25	20.12	29.05	08 20	05.87	CIT-(60.69)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-74	14.81	14.95	14.88	18.06	15.90	16.98	7.02	7 05	102	4.61	3.36	000	06 90	CP 9C	25,66	54 17	(47 41)-MS
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPM-07-4	13.61	12.55	13.08	14.48	14.35	14.41	6.10	6,90	6.50	3.36	3.88	3.62	28.50	21.15	24.83	62.50	(52.41)-MS
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPM-07-9	13.58	12.49	13.04	15.18	13.48	14.33	8.40	6.59	7.49	4.14	3.15	3.64	27.00	25.35	26.17	91.65	(79.39)-S
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPPM-07-30	14.58	14.50	14.54	14.04	13.10	13.57	7.02	6.92	6.97	3.45	2.63	3.04	23.25	29.70	26.47	91.65	(79.39)-S
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPPMR-09-1	14.72	14.77	14.75	14.13	13.28	13.70	6.66	6.36	6.51	3.79	2.89	3.34	24.90	26.55	25.72	0.03	(0.91)-R
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	DPPMK-09-2	14.96	15.26	15.12	14.91	13.63	14.27	6.51	6.27	6.39	3.92	3.41	3.66	18.30	23.47	20.88	0.03	(0.91)-R
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	DEPLAN 09.5	14.20	15.65	16.01	00.61	10.15	67.21	20. 20. 20.	0.92	05.7	4.53 5.5	2.80	3.66	23.40	27.00	25.20	c <u>c</u> .8	(10.01)-MK
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	DPPMR_09-9	C1.C1	CO.CI	14.01	14.30	C1.01	67.71	75.1	0.13 215	6.73 6 56	3.10	2.93	3.02	22.65	26.70	24.67	54.18	(43.40)-MS
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	DPP-25G	11.01	11 62	12.38	10.01	C#71	16.18	0.00 6 05	71.7	00.9	5.25 A A A	(7.5 5 5 5	67.6 00 5	20.00	20.05	C7.07	c0.0	N-(16.0)
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	DPP-89	13.97	13.28	13.62	15 18	14 50	14.84	6.76	7.03	6 00	175	101	2 2 2	25.65	01.92	75.87	CV.V	N-(12.0)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPP-100	15.04	15.42	15.23	16.05	15.20	15.63	7.63	6.48	7.05	3.71	3.71	3.71	21 00	26.10	23.55	62.50	(52.41)-MS
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	DPP-168	14.14	13.61	13.88	11.24	10.06	10.65	7.27	7.10	7.19	3.58	3.23	3.41	25.65	27.90	26.77	87.49	(72.80)-S
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	DPP-3-1	14.42	14.18	14.30	12.64	12.31	12.48	5.80	7.32	6.56	3.36	2.72	3.04	19.50	18.30	18.90	16.68	(20.30)-MR
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	DPP-11-2	14.62	14.57	14.60	15.44	12.84	14.14	6.10	6.44	6.27	2.84	3.23	3.04	26.85	26.40	26.62	8.35	(10.61)-MR
VP-215 14.62 14.57 14.52 14.62 14.57 14.52 13.86 7.07 7.01 7.04 3.58 2.72 25.50 24.90 25.20 Green Pearl 16.03 17.40 16.71 17.45 16.78 17.11 7.99 7.64 7.81 3.23 3.17 3.47 18.15 24.15 21.15 Creen Pearl 17.43 20.19 18.82 17.11 7.99 7.64 7.81 3.23 3.47 18.15 24.15 21.15 Azad P-11 17.14 19.61 18.38 15.26 13.33 14.54 6.30 6.41 6.35 3.19 4.09 3.64 29.70 30.60 30.15 Punjab-89 17.155 20.04 18.70 15.44 17.59 16.51 6.00 7.40 6.70 2.44 2.30 2.367 Raime 13.14-11.622-12.338 11.24+17.59 16.51 6.00 7.40 6.70 2.44	DPP-17-2	14.84	15.01	14.93	17.89	12.86	15.38	7.17	6.95	7.06	3.15	3.28	3.21	28.50	19.95	24.22	16.68	(20.30)-MR
Offeen Pearl 16.03 17.40 16.71 17.45 16.78 17.11 7.99 7.64 7.81 3.23 3.71 3.47 18.15 24.15 21.15 Lincoln 17.43 20.19 18.82 17.10 15.46 16.28 7.68 7.32 7.50 2.59 3.75 3.17 24.15 28.80 26.47 Azad 17.14 19.61 18.38 15.26 13.83 14.54 6.30 6.41 6.35 3.19 3.03 24.45 28.80 26.47 Azad 17.35 20.04 18.70 15.44 17.59 16.51 6.00 7.40 6.70 2.41 4.14 3.28 21.45 29.10 25.27 Runge 13.14 11.62 12.38 11.24 10.06 10.65 5.80-8.40 5.50-9.16 5.93-8.57 2.28.4.61 2.8.4.40 18.90 30.15 Runge 13.14 11.62 12.38 18.51 18.30 18.90	VP-215	14.62	14.57	14.59	13.86	13.89	13.88	7.07	7.01	7.04	3.58	2.93	3.25	25.50	24.90	25.20	8.35	(10.61)-MR
Luncoin 17.43 20.19 18.82 17.10 15.46 16.28 7.68 7.32 7.50 2.59 3.75 3.17 24.15 28.80 26.47 Azad P-1 17.14 19.61 18.38 15.26 13.83 14.54 6.30 6.41 6.35 3.33 3.43 29.76 23.87 Palam Priva 16.51 18.36 17.44 15.00 12.44 17.59 16.51 6.00 6.71 6.35 3.33 24.45 27.73 23.87 Punjab-89 17.33 10.04 15.44 17.59 16.51 6.00 6.71 6.35 3.32 24.43 29.70 23.47 29.70 23.77 Range 11.743 20.19 18.82 18.68 $58.0.8.40$ $55.64.61$ $52.44.14$ $28.4.66$ 30.15 Mean 17.43 20.19 18.82 18.85 18.68 $550.9.901$ 5	Ureen Pearl	16.03	17.40	16.71	17.45	16.78	17.11	7.99	7.64	7.81	3.23	3.71	3.47	18.15	24.15	21.15	99.98	SH-(60.68)
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$		17.43	20.19	18.82	17.10	15.46	16.28	7.68	7.32	7.50	2.59	3.75	3.17	24.15	28.80	26.47	99.98	(89.09)-HS
Tataun trya 10.51 18.50 17.44 15.00 12.43 15.71 0.00 6.71 6.35 3.19 4.09 3.64 29.70 30.60 30.15 Punjab-89 17.53 20.04 18.70 15.44 17.59 16.51 6.00 7.40 6.70 2.41 4.14 3.28 21.45 29.10 25.27 Punjab-89 17.43 20.19 18.82 18.51 18.65 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.34-4.14 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.85 18.51 18.68 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.84-4.14 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.85 18.51 18.68 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.84-4.14 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.85 18.51 18.68 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.85 18.51 18.68 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.85 18.51 18.68 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.85 18.51 18.68 5.80-8.40 5.50-9.01 5.93-8.57 2.28-4.61 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 18.82 18.53 18.51 18.68 5.90-8.01 5.90-9.01 5.93-8.57 2.28-4.61 2.84-4.03 18.15 18.30 15 Mange 17.43 20.19 10.87 24.0 20.13 0.116 0.22 0.14 0.14 0.12 0.13 0.15 0.05 0.15 0.15 0.13 0.15 0.15 0.13 0.15 0.13 0.15 1.008 0.13 0.15 0.15 0.15 0.10 0.14 0.14 0.14 0.12 0.13 0.13 0.15 1.08 0.13 0.15 0.15 0.15 0.15 0.13 0.15 0.13 0.15 0.13 0.15 0.13 0.15 0.13 0.15 0.13 0.13 0.13 0.13 0.13 0.13 0.13 0.13	Azad P-1	17.14	19.61	8.38	15.26	13.83	14.54	6.30	6.41	6.35	3.53	3.32	3.43	24.45	27.30	25.87	99.98	(89.09)-HS
Range 17.39 2.0.04 1.0.70 10.31 0.000 7.40 0.010 2.41 4.14 3.28 21.43 29.10 25.21 Range 13.14 11.62- 12.38 11.24+ 0.006 5.80.8.40 5.50-9.01 5.93-8.57 2.284.4.61 2.84.4.03 18.15- 18.30- 18.90- Range 17.43 20.19 18.82 18.85 18.51 18.68 0.065- 5.80.8.40 5.50-9.01 5.93-8.451 2.54.4.14 2.84.4.03 18.15- 18.30- 18.90- Mean 14.87 15.07 14.97 15.37 14.05 14.57 14.06 5.30- 10.31 0.31 0.315 0.3015 30.15 Mean 14.87 15.07 14.97 15.37 14.05 6.92 7.01 6.97 3.50 3.015 30.15 SE(m) \pm 0.31 0.61 0.34 0.14 0.14 0.22 0.13 0.97 1.08 0.73 CV (%) 3.56 7.02 5.59 3.47 11.98 7.57 4.03 <th< td=""><td>raiaii riiya Dunish.00</td><td>10.01</td><td>18.30</td><td>10.70</td><td>00.61</td><td>12.45</td><td>12.71</td><td>0.00</td><td>6.71</td><td>6.35</td><td>3.19</td><td>4.09</td><td>3.64</td><td>29.70</td><td>30.60</td><td>30.15</td><td>87.49</td><td>S-(08.7/)</td></th<>	raiaii riiya Dunish.00	10.01	18.30	10.70	00.61	12.45	12.71	0.00	6.71	6.35	3.19	4.09	3.64	29.70	30.60	30.15	87.49	S-(08.7/)
Near 17.43 20.19 18.82 18.85 18.51 18.66 9.005 9.005 19.744 1.044 1.05 16.30 16.30 30.15 Mean 14.87 15.07 14.97 15.37 14.05 14.97 15.37 14.05 15.37 14.07 5.30 30.15 30.15 SE(m) \pm 0.31 0.61 0.34 0.31 0.63 0.45 0.16 0.22 0.14 0.14 0.22 24.95 24.66 SE(m) \pm 0.31 0.61 0.34 0.31 0.85 0.45 0.16 0.22 0.14 0.14 0.22 0.13 0.97 1.08 0.73 CV (%) 3.56 7.02 5.59 3.47 11.98 7.57 4.03 5.48 4.82 7.27 11.48 9.48 6.74 7.70 7.22 CD at $P \leq 0.05$ 0.86 1.72 0.96 0.87 2.40 1.28 0.45 0.62 0.38 0.41 0.61 0.37 273 3.04 2.04	Range	13 14-	11 62	17 38.	11 24-	-20 01	10.01	0.00	7.40	0./0	2.41 1 7 7 0 1 2 1	4.14	5.28 2 1 1 17	21.01	01.62	17.07	CC.8	MM-(10.01)
$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$		17.43	20.19	18.82	18.85	-00.01	18.68	04.0-00.0	10.4-00.6	10.0-06.0	10.4-02.2	4.04-4.14	2.04-4.00	-015	-06.81 20.60	30.15		02.22-00.0
SE(m) ± 0.31 0.61 0.34 0.31 0.85 0.45 0.16 0.22 0.14 0.14 0.22 0.13 0.97 1.08 0.73 CV (%) 3.56 7.02 5.59 3.47 11.98 7.57 4.03 5.48 4.82 7.27 11.48 9.48 6.74 7.70 7.22 CD at P ≤ 0.05 0.86 1.72 0.96 0.87 2.40 1.28 0.45 0.62 0.38 0.41 0.61 0.37 2.73 3.04 2.04	Mean	14.87	15.07	14.97	15.37	14.02	14.70	6.92	7.01	6.97	3.50	3.29	3.40	24.97	24.35	24.66		58.04
CV (%) 3.56 7.02 5.59 3.47 11.98 7.57 4.03 5.48 4.82 7.27 11.48 9.48 6.74 7.70 7.22 CD at P ≤ 0.05 0.86 1.72 0.96 0.87 2.40 1.28 0.45 0.62 0.38 0.41 0.61 0.37 2.73 3.04 2.04	SE(m) ±	0.31	0.61	0.34	0.31	0.85	0.45	0.16	0.22	0.14	0.14	0.22	0.13	0.97	1.08	0.73		7.41
CU at P ≥ 0.05 0.86 1.72 0.96 0.87 2.40 1.28 0.45 0.62 0.38 0.41 0.61 0.37 2.73 3.04 2.04	CV (%)	3.56	7.02	5.59	3.47	11.98	7.57	4.03	5.48	4.82	7.27	11.48	9.48	6.74	7.70	7.22		(22.10)
	<u>CU at P ≤ 0.05</u>	0.86	1.72	0.96	0.87	2.40	1.28	0.45	0.62	0.38	0.41	19.0	0.37	2.73	3.04	2.04		(20.84)

Appendix-II

Mean weekly weather data 2009-10

	Tempera	ture (⁰ C)	Rainfall (mm)	Relative	Sunshine
	Max.	Min.		humidity (%)	hours
Nov 1-7	24.70	9.56	0.00	47.43	8.90
Nov 8-14	20.13	8.31	4.34	61.29	5.79
Nov 15-21	18.64	6.67	5.57	52.00	6.43
Nov 22-28	20.21	6.07	0.00	48.57	8.40
Nov 29-Dec 5	20.34	7.24	0.00	59.86	6.57
Dec 6-12	19.29	7.09	0.03	49.86	5.74
Dec 13-19	17.41	5.50	0.00	55.00	4.43
Dec 20-26	17.03	3.17	0.00	54.50	6.08
Dec 27-Jan 2	16.04	3.07	0.00	52.00	6.57
Jan 3-9	17.49	4.53	2.49	58.86	7.93
Jan 10-16	17.03	3.96	0.80	52.57	6.71
Jan 17-23	19.63	5.56	0.00	47.29	7.43
Jan24-30	18.86	6.49	0.31	40.71	5.50
Jan31-Feb 6	17.86	4.67	0.43	57.67	8.29
Feb 7-13	14.49	5.54	14.71	71.71	1.93
Feb 14-20	18.33	4.94	0.00	71.57	7.86
Feb 21-27	20.81	8.74	2.09	56.57	6.79
Feb 28-Mar 6	21.53	10.21	2.26	52.14	5.07
Mar 7-13	22.56	9.04	0.00	45.00	8.07
Mar 14-20	26.03	12.20	0.00	39.80	9.98
Mar 21-27	29.50	16.75	0.00	27.00	8.50
Mar 28-Apr 3	28.27	13.73	1.46	27.71	9.29
Apr 4-10	29.43	14.69	0.00	25.57	10.50
Apr 11-17	31.70	16.39	0.01	27.43	9.07
Apr 18-24	29.96	16.34	3.51	37.00	4.67
Apr 25-May 1	30.79	17.23	0.43	28.86	7.43

<u> </u>	Tempera	ture (⁰ C)	Rainfall (mm)	Relative	Sunshine
	Max.	Min.		humidity (%)	hours
Nov 5-11	24.51	10.59	0.00	50.29	9.37
Nov 12-18	23.94	9.76	0.17	37.14	9.46
Nov 19-25	21.17	8.40	0.57	50.57	7.03
Nov 26-Dec 2	20.26	7.17	0.00	57.57	8.43
Dec 3-9	19.60	5.77	0.00	40.57	8.71
Dec 10-16	17.70	4.74	0.00	55.00	7.00
Dec 17-23	18.91	4.14	0.00	37.57	8.64
Dec 25-31	16.80	4.60	13.03	52.57	6.14
Jan 1-7	15.70	2.93	0.83	50.71	8.53
Jan 8-14	17.14	4.67	0.00	44.14	7.03
Jan 15-21	12.00	2.44	8.31	60.14	4.17
Jan 22-28	16.09	3.51	0.00	48.57	8.64
Jan 29-Feb 4	18.06	6.49	0.14	50.29	5.00
Feb 5-11	19.11	7.64	3.29	48.83	4.00
Feb 12-18	14.29	6.53	15.54	70.57	2.00
Feb 19-25	16.83	5.86	0.14	58.57	4.50
Feb 26-Mar 4	15.07	6.06	5.54	71.71	2.29
Mar 5-11	19.46	7.56	1.10	43.71	7.14
Mar 12-18	24.41	11.24	0.00	42.29	8.79
Mar 19-25	24.79	11.66	0.00	35.00	8.00
Mar 26-Apr 1	25.89	12.20	0.77	39.57	8.21
Apr 2-8	22.73	10.50	0.71	45.17	6.14
Apr 9-15	24.43	12.64	0.80	50.71	5.86
Apr 16-22	24.03	11.83	11.44	49.71	7.14
Apr 23-29	28.67	17.01	0.00	45.71	10.50
Apr 30-May 6	31.61	19.21	1.43	46.14	9.71

Mean weekly weather data 2010-11

Brief Biodata of student

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Name	:	Ajay Bhardwaj
Father's Name	:	Sh. Ratan Chand
Mother's Name	:	Smt. Meera Devi
Date of Birth	:	15 th October, 1986
Permanent Address	:	Vill. Badhar, P.O. Tal, Teh. & Distt. Hamirpur (H.P.) Pin code: 177401

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Academic Qualifications:

Qualification	Year	School/Board/	Marks	Division	Major Subject
		University	(%)		
10 th	2002	CBSE, New Delhi	78.40	1 st	English, Math,
					Science, Social
					Science, Hindi
10+2	2004	CBSE, New Delhi	58.00	2 nd	English, Math,
					Biology,
					Physics,
					Chemistry
B.Sc.	2009	CSK Himachal Pradesh	72.60	1 st	All agriculture
(Agriculture)		Agricultural University,			and allied
		Palampur (H.P.), India			subjects
M.Sc.	2011	CSK Himachal Pradesh	76.70	1 st	Major
(Agriculture)		Agricultural University,			Discipline
Vegetable		Palampur (H.P.), India			Vegetable
Science	i i				Science
					Minor
					Discipline:
					Plant Breeding
					and Genetics