GENETIC STUDIES FOR SOME AGRO-MORPHOLOGICAL AND QUALITY TRAITS IN GRASSPEA [*Lathyrus sativus* L.]

THESIS

By

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(A-2009-30-31)

Submitted to

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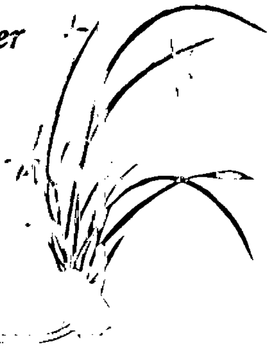
Is there anything I can say,
anything I can give
or do for you…..
Because all that I'm
all that I have
I owe to you…..

Affectionately Dedicated
to my
Revered Parents

Who sacrificed
their present
to make my future better



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CERTIFICATE – I

This is to certify that the thesis entitled "**Genetic studies for some agro-morphological and quality traits in grasspea (*Lathyrus sativus* L.)**" submitted in partial fulfillment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding and Genetics** of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, is a bonafide research work carried out by **Ms. Pallavi Mehra (A-2009-30-31)** daughter of **Shri. Sanjeev Mehra**, 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.

2.7.2011

(K.C. Sood)
Major Advisor

Place: Palampur
Dated: 2, July, 2011

CERTIFICATE – II

This is to certify that the thesis entitled **"Genetic studies for some agro-morphological and quality traits in grasspea (*Lathyrus sativus* L.)"** submitted by **Ms. Pallavi Mehra (A-2009-30-31)** daughter of **Shri. Sanjeev Mehra** to CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfillment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding and Genetics**, has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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Needless to say, all errors and omissions are mine.

Pallavi

Place : Palampur (Pallavi Mehra)

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TABLE OF CONTENTS

LIST OF TABLES

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Title of the thesis : Genetic studies for some agromorphological and quality traits in grasspea (*Lathyrus sativus* L.)
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ABSTRACT

The present investigation entitled "Genetic studies for some agro-morphological and quality traits in grasspea (*Lathyrus sativus* L.)" was undertaken during *rabi* 2009-10, to assess the nature of genetic variability and associations among various traits including their direct and indirect effects on seed yield. Data were recorded on seed yield per plant and other agro-morphological traits and crude protein content for different genotypes and analysed as per the standard statistical procedures. Sufficient genetic variability was observed for all the traits. High PCV and GCV values (>25%) were observed for seed yield per plant indicating wide range of observed and genetic variability for this trait. Heritability in broad sense was high (>80%) for days to 50% flowering, days to maturity, plant height,100-seed weight, biological yield per plant, harvest index, crude protein content and seed yield per plant. Whereas high heritability coupled with high genetic advance was observed for biological yield per plant, harvest index and seed yield per plant. Seed yield per plant exhibited positive and significant correlations with days to maturity, plant height, number of branches per plant, number of pods per plant, seeds per pod, biological yield per plant and harvest index indicating that the selection would be effective for these traits. Biological yield per plant and harvest index were observed as the best selection indices in grasspea because of their high direct contribution towards seed yield per plant.

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Introduction

1. INTRODUCTION

Pulses are the basic ingredient in the diets of a vast majority of Indian population because higher amount of quality protein in its seeds provide a perfect mixture of high biological value when supplemented with cereals (Kumar and Ali 2001). Pulses belong to the family Leguminosae and are endowed with the capacity of adequately using the atmospheric nitrogen, the most wanted plant nutrient. The pulse crops have been the mainstay of Indian agriculture through the centuries, enabling the land to turn out reasonable quantities of foodgrains without appreciable addition of manure or chemical fertilizers. Pulses contain 20-30 per cent protein which is nearly three times more than found in cereals.

Grasspea (*Lathyrus sativus* L.) is a legume crop belonging to tribe Vicieae and is a member of the large genus *Lathyrus*, which contains about 150 species (Kupicha 1983). The chromosome complement 2n=14 is common with most of the species of this genus. The crop is self-pollinated. It is under cultivation since ancient period. It's cultivation as agricultural crop may date back to 6000 B.C. In India, it is commonly known as *Khesari*, Chikling Vetch, Teoda, Lakhodi or Lakh and nutritionally is very rich as it contains about 28.2 per cent protein, 56.6 per cent carbohydrates and is also rich in calcium and iron. Bold-grained genotypes are called Lakh while the small-seeded are categorized as Lakhodi. *Lathyrus sativus* L. can grow wild in the form of weed.

Grasspea is endemic to the region from Caucasus to north of India. Though indigenous to Southern Europe and West Asia, it is principally grown in India in the Gangetic plains comprising states of Madhya Pradesh, Bihar, Uttar Pradesh, Orissa and West Bengal as well as in the hills upto a height of 4000'. It is grown on the area of approximately 1.5 million hectares with the annual production of 0.8 million tones (Anonymous 2008). It is largely grown as catch crop/relay crop known locally as Paira cultivation. It is sown 15 days before harvest of paddy in paddy fields under rainfed conditions. It is also grown as mixed crop with rainfed barley, wheat, gram and linseed. It is an important pulse crop due to its high seed protein and performs well even under extreme drought and rainfall conditions. In Himachal Pradesh, grasspea is a traditional pulse crop grown in Kangra and Mandi districts but now this hardy crop is almost at the verge of extinction.

The association of ill effects with consumption of pulses is rare. However, the consumption of khesari grains/ plant fodder in large quantities for prolonged periods has been known to be associated with the disease *lathyrism*, which is endemic in certain parts of India (Ganpathy and Dwivedi 1961). The factor causing neuroparalytic symptoms is an amino acid referred to as β-N-Oxalyl L-α,β-diaminopropionic acid (ODAP) or β-N-Oxalyl amino alanine (BOAA). Human lathyrism is hence, a sign of great public health importance. This crippling disease is known to result in the paralysis of lower limbs. In India, this pulse is otherwise a boon to the poor people as an article of diet, especially in times of famine when *Lathyrus* is the only available food in certain regions of country.

India's population grew at an estimated compound annual growth rate of 2% between 1970-71 and 2007-08, while production of pulses increased at 0.7%, thus widening the gap between supply and demand and it is visualized that it may add to chronic shortage of pulses due to further increase in demand and shortage of production. To reduce this gap country is importing about 2-3 million tonnes of pulses annually (Nadarajan 2010). Therefore, concerted efforts are needed to increase the productivity through various breeding techniques to evolve improved varieties which act as a catalyst for crop improvement.

The success of any breeding programme depends upon the nature and magnitude of genetic variability in the germplasm stock which provides better chances of selecting desired types. Therefore, the chances to initiate any breeding programme increase when the genetic variability is greater. The studies of genetic variability parameters like phenotypic and genotypic variances, heritability and genetic advance are of paramount importance. Correlation studies provide the degree but, not the cause of associations, whereas path-coefficient analysis permits a critical examination of specific forces acting to produce a given correlation and measure the relative importance of each factor contributing towards seed yield. Thus, knowledge of association among seed yield and its related traits and their direct and indirect contributions toward seed yield being a complex polygenic trait is of prime importance in formulating suitable breeding methodology.

Keeping in view the above considerations and genetic amelioration of *Lathyrus sativus* L., the present investigation was undertaken with the following objectives:

a. To study the nature and extent of variability for various agro-morphological and quality traits,
b. to study the nature of associations among these traits and identify potential genotypes.

Review of Literature

2. REVIEW OF LITERATURE

The chief objective of breeding programme remains higher yield to meet the food requirements of people. Superior varieties with improved agronomic traits have been the major factor in increased food production. An insight into the magnitude of variability present in a crop is of utmost importance as it provides the basis for effective selection. Numerous studies have been conducted to estimate the magnitudes of various components of the genetic variance. The efficiency of selection largely depends on the extent of genetic variability present in the population and the heritability of the concerned character. The information about the relative contributions of the various component traits to yield is provided by correlation studies and path analysis which helps in the isolation of potential genotypes.

A review of literature pertaining to various aspects included in the present study is given hereafter in the following sub-heads:

2.1 Parameters of genetic variability

2.2 Correlation studies

2.3 Path coefficient analysis

2.1 Parameters of genetic variability

Genetic variability, as an index of genetic architecture of a population and a pre-requisite for crop improvement programmes, has been widely used in evolving high yielding varieties in various crops. Fisher (1918) was the first to divide the genetic variance into three components, *i.e.*, additive, dominance and epistatic variances; also partitioned the continuous variation exhibited by a quantitative character into heritable and non-heritable components, the former being a consequence of genotypic while the later, a result of environmental factors. In crop improvement, only the genetic component of variation is important as only this component is transmitted to the next generation and is the main concern of plant breeders. Lush (1940) classified heritability into broad sense and narrow sense. Heritability in broad sense is the proportion of genetic variance to the total variance, whereas the narrow sense heritability is the proportion of additive genetic variance to the total variance. Expected genetic gain gives a measure of effectiveness of selection. Burton and De Vane (1953) suggested that a combination of genetic gain and heritability estimates gives a reliable indication of amount of improvement to be expected from selection and further remarked that expected genetic advance under particular system supplies practical information that is needed by a breeder.

Vavilov (1951) was the first to realize that a wide range of variability in any crop provides chances of selecting the desirable types. High amount of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) along with *per se* performance of individual genotypes are the indicators of desirable genetic variability. However, these estimates alone are not much helpful in determining the heritable portion therefore, the heritability and genetic advance along with PCV and GCV would be essential for crop improvement. Burton (1952) also suggested that GCV, heritability and genetic advance would give better information about efficiency of selection.

Johnson *et al.* (1955) also found it more useful to estimate heritability values together with genetic advance in predicting the expected progress to be achieved through selection. Wright (1921) reported that the heritability component comprised of additive and non-additive portion and it was the former which responds to selection. However, high heritability alone does not necessarily mean high genetic gain therefore, is not sufficient to make improvement through selection. Thus, the genetic advance which has an added edge over heritability was also considered while making selection. Estimation of expected genetic advance is important to have an idea of effectiveness of selection.

Singh and Chaturvedi (1990) evaluated seeds for protein content along with five yield related characters and reported variability for all characters and a further enhancement was observed for most of the characters.

Dixit *et al.* (1995) reported that range and mean for protein content were higher in the exotic lines, while coefficient of variability was higher in the indigenous lines. Protein content was not significantly correlated to 100-seed weight, days to flowering and days to maturity.

Kumari *et al.* (1995) reported that genetic variability occurred for seed yield and its components. Yield per plot was in the range 115-560 g for low- and 80-450 g for high toxic genotypes. Heritability values were generally higher in the low toxic genotypes.

Tiwari *et al.* (1995) reported that harvest index was the highest and biomass production was the lowest in the Bio 164. Bio L08 gave the highest seed yield. The results showed differences in leaf characteristics and seed yield among somaclones and the P-24 parent.

Kumar and Dubey (1997) evaluated phenotypic and genotypic coefficients of variability in 25 grasspea genotypes and reported that yield per plant, pods per plant and seeds per plant were more variable than the other traits studied.

Kumari and Mehra (1997) reported significant differences among populations for seed yield and its component characters. Seed yield per plant, pods per plant and 100-seed weight showed considerable variation as revealed by high phenotypic and genotypic coefficients of variation. High narrow sense heritability accompanied by high genetic advance was observed for pods per plant. For seed yield per plant, both the heritability and genetic advance were low and the character was much influenced by environmental factors.

Pandey *et al.* (1997) conducted study on 13 yield components which indicated that a very wide range of variability for all the yield traits, presenting opportunities for selection.

Chowdhury and Slinkard (2000) evaluated 348 accessions and subaccessions of grasspea from 10 geographical regions. The lowest variability was found in accessions and subaccessions from South America, followed by those from Sudan-Ethiopia.

Pandey *et al.* (2000) reported a wide range of variation among 126 accessions of grasspea. High magnitude of GCV was noted for grain yield, pod and seed number per plant. High heritability coupled with high genetic gain was found for branches per plant, pods per plant and 100-seed weight.

Waghmare and Mehra (2000) reported mutagenic treatments with different doses of gamma rays (5-40 kR) and ethyl methanesulfonate (0.5 or 1.0% for 2 or 4 h) generated a substantial magnitude of genetic variability for economic characters. Grain yield per plant followed by number of pods per plant, number of seeds per pod and plant height showed significant variability in both. For days to flowering, days to maturity, number of primary branches, pod length and number of seeds per pod variability was less.

Sharma *et al.* (2001) reported that higher magnitude of genetic variability was present among 270 genotypes for most of the traits studied. The coefficients of variation for pods per plant, seed yield per plant, plant height, 100-seed weight and branches per plant were high. Maximum variability was observed for seed yield per plant followed by pods per plant, plant height and 100-seed weight indicating that selection for these traits may lead to development of desirable genotypes of grasspea.

Wuletaw and Endashaw (2002) recorded higher mean and coefficient of variation values for most of the agronomic traits indicating the presence of high genetic diversity. Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all the characters studied signifying that genotypic factors exerted reasonable effect in estimating the variation. The wide difference between PCV (22.4%) and GCV (13.0%) for seed yield per plant indicated the complexity of this trait and the important role of environment in influencing yield potential in addition to the genetic factors.

Kumari and Prasad (2003) evaluated 24 landraces of grasspea and analysis of variance revealed the presence of considerable genetic variability for all other yield related characters, except for days to maturity.

Tadesse and Bekele (2003) evaluated 50 grasspea populations for variations of five morphological traits and much variability was observed within populations.

Wuletaw and Endashaw (2003) evaluated 50 grasspea land race populations to determine variability for morphological characters. Highly significant differences were observed among the populations for most of the morphological characters.

Kumari and Prasad (2005) evaluated 24 diverse and determinate khesari germplasm lines and reported the presence of substantial variability for all characters under study, except for days to maturity.

Sammour *et al.* (2007) reported high variability of seed yield and its components at both inter-specific and intra-specific levels. This variability was attributed to genetic and environmental factors.

Sammour *et al.* (2007) evaluated 18 genotypes for variations of seed weight and seed protein content and reported that environmental factors may not be most appropriate for explaining variations in seed weight.

Ranjan *et al.* (2007) reported that the genetic variation among the genotypes was significant only for number of days to maturity, number of branches per plant, and seed yield per plant. The genetic and phenotypic coefficients of variation were highest for seed yield per plant followed by number of branches per plant and number of days to maturity. The estimates of heritability in the broad sense were high for number of days to maturity, number of branches per plant and seed yield per plant. The expected genetic advance was greatest for number of days to maturity followed by seed yield per plant and number of branches per plant. Seed yield was characterized by high levels of genetic advance and heritability, suggesting that selection based on phenotype is effective for the improvement of this trait.

Bhosle *et al.* (2008) reported significant variability for all the morphological characters except for days to 50 per cent flowering. The analysis of variance for the yield traits revealed that mean sum of squares due to genotypes were significant for days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per plant, seed index, harvest index and seed yield per plant. The genotype Prateek shows the significant result for the characters viz., branches per plant, pods per plant, seeds per plant, harvest index and seed yield per plant.

Kozak *et al.* (2008) evaluated 22 grasspea genotypes, two cultivars (Derek and Krab) and 20 mutants from those cultivars. Seed yield per plant and seven yield related traits were studied. Plant height, number of branches per plant, pod length and number of seeds per plant determined seed yield; number of pods per plant influenced seed yield only.

Rybinski et al. (2008) reported that the coefficient of variation was highest for days to flowering, plant height, number of pods per plant, number of seeds per plant and seed weight per plant whereas lowest for pod length and number of seeds per pod.

Talukdar and Biswas (2008) reported considerable amount of genetic variability for plant height, number of primary branches, pods per plant, 100-seed weight, seed yield per plant, biological yield per plant and harvest index in grasspea. High heritability coupled with high genetic advance (as percentage of means) estimated for yield related components offer scope for selection.

2.2 Correlation studies

Correlation coefficient is a key measure of the degree of association between two characters worked out at same time (Hays *et al.* 1955). The correlations are important and are of practical value in the selection of two or more traits simultaneously. The extent of observed inter-relationship between two characters is known as phenotypic correlation. 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 the basis for selection. For selection of several characters simultaneously, the knowledge of character association is helpful to avoid undesirable correlated changes in other characters.

For studying genetic variation in different characters and the manner in which environmental variation affects the expression of such variation, understanding of genotypic correlation is essential. Genotypic correlations are due to genetic causes through the pleiotropic effect of genes though, linkage is also a cause of transient correlation. The degree of genetic correlation arising from pleiotropy is the overall effect of all the segregating genes that affect both characters (Falconer 1961). Johnson *et al.* (1955) have stressed the importance of both phenotypic and genotypic correlations among the characters in planning and evaluating breeding programme. Correlation coefficients for a given trait vary with the genotypes studied and the environment where the test is carried out.

Kumari *et al.* (1995) reported that the correlation analysis from pooled data showed seed toxin content was positively correlated with biomass per plant, plant height, flowers per plant, pod length and seed size and was negatively correlated with yield per plant.

Waghmare *et al.* (1996) reported that number of pods per plant had a close positive association with seed yield. Plant height, number of seeds per pod and 100-seed weight also had significant and positive correlations with seed yield whereas days to 50% flowering had a negative correlation with seed yield.

Kumar and Dubey (1997) reported that the seed yield showed significant positive correlations with pods per plant, seeds per pod and seeds per plant. Length of main branch, number of primary branches, nodes on main branch and internode length also showed positive correlations with yield, while 100-seed weight showed significant positive correlation with yield at the genotypic level only. Days to flowering was negatively correlated with yield at all levels. Genotypic and phenotypic correlations between all the traits were in the same direction and similar in magnitude, while environmental correlations showed a different trend. Most genotypic correlations were higher than the respective phenotypic and environmental correlations. There were significant positive environmental correlations of yield with pods per plant, seeds per plant and seeds per pod. Various yield contributing traits also showed significant positive associations among themselves.

Sharma *et al.* (1997) reported that 100-seed weight expressed additive genetic variance and showed positive correlation with days to maturity.

Tadesse (1997) evaluated 335 landraces for six yield components and landraces with high toxin contents had good yield performance indicating a positive correlation between the two traits.

Mitra and Mehra (1999) reported that the single seed descent method resulted in a higher number of significant correlations when compared with the random bulk and pedigree methods. Only the correlation between pods per plant and yield per plant was consistent over breeding methods and generations.

Pandey *et al.* (2000) reported that grain yield was positively associated with days to maturity, plant height, branches per plant, pods per plant, seeds per plant and harvest index.

Zode et al .(2000) reported information on correlation coefficients derived from data on morphophysiological, biochemical and yield related traits in 10 genotypes of *Lathyrus sativus*. Seed yield was negatively associated with protein content and positively related with other yield related characters.

Das and Kundagrami (2002) reported that pods per plant and seeds per pod showed consistent high positive correlations both at phenotypic and genotypic levels with seed yield per plant. However, 100-seed weight showed negative association with seed yield. Significant positive correlations were observed between pods per plant and seeds per pod, and days to flowering and days to maturity, while negative correlations were observed between pods per plant and 100-seed weight, pods per plant and days to flowering, and pods per plant and days to maturity. Seed protein content showed a negative association with seed yield. A negative correlation was also observed between 100-seed weight and protein content. Days to flowering and days to maturity maintained a positive correlation with seed protein content.

Kundagrami and Das (2002) evaluated nine genotypes and reported that exotic bold produced very large and bold seeds, followed by P-90 and P-505, which had 100-seed weight of ~9 g. The 100-seed weight of Midnapur local, Hoogly local and P-24 was ~6 g, which was the lowest among the genotypes. Differences in seed protein content were recorded for different genotypes, which ranged from 25 to 30%. Sel 1276 displayed 30% seed protein content; P-505 and P-28 had ~30% and 28%, respectively. The seed protein content of P-90, Nirmal and P-24 was ~25% showing relatively lesser amount of protein content compared to others. The correlation between seed size and protein content showed that 100-seed weight was significantly and positively correlated with protein content, indicating that large and bold seeds has high protein content.

Wuletaw and Endashaw (2002) recorded the strong positive association of pods per plant, 100 seed weight and primary branches per plant with seed yield indicated the possibility of selecting lines for yield improvement based on these characters at the early stage of the grasspea breeding programme

Geda *et al.* (2005) conducted study on low toxin lines and results indicated that the the protein content of low toxin genotypes ranged from 24.41 to 30.23%.

Kumari and Prasad (2005) reported that the seed yield was positively and significantly associated with plant height, days to flowering, days to podding, pods per plant and seeds per pod. Seed weight was negatively but, non-significantly correlated with seed yield. Plant height had a significant positive correlation with days to flower. Further, days to flower and days to podding were strongly positively correlated.

Polignano *et al.* (2005) reported some high yielding lines could be used directly for cultivation as new varieties or as parental lines in crossing programmes and no significant correlation was observed between toxin and other morphological traits.

Urga *et al.* (2005) reported that the correlation coefficient for 100-seed weight was positively correlated ($P<0.05$) with crude protein.

Sammour *et al.* (2007) reported significant and negative correlation between protein content and 100 seed weight. The most promising accession for breeding programs was *L. sativus* from Tunisia. This accession has good grain quality due to high protein content.

Bhosle *et al.* (2008) reported that the correlation coefficient for single plant yield had positive correlation with the harvest index, seed number per plant and pod number per plant at genotypic and phenotypic levels under both conditions. The days to 50% flowering showed positive correlation with plant height in E1, whereas negative correlation with the days to maturity under E2.

2.3 Path coefficient analysis

Although the correlations are helpful in understanding the complex traits like yield, but, when more variables are included, the associations between various characters do not provide the true picture of the relative importance of direct and indirect influences of each of the component traits because these give the degree but not the cause. Under such complex situations, the total correlation, is insufficient to explain the real cause of association for an effective manipulation of the character. For finding a suitable and reliable selection index, correlations must be analysed further and partitioned into direct and indirect effects through path analysis.

Path coefficient is a standardized partial regression coefficient and as such, measures the direct influence of one variable upon others. Wright (1921) originally devised the tool of path coefficient analysis to measure the direct influence of one variable upon the other and permit the partitioning of the correlation coefficients into components of direct and indirect effects. Dewey and Lu (1959) have opened the way for plant breeders by using for the first time, the path coefficient analysis in breeding programme.

Kavuncu et al. (1985) studied seed yield and eight related traits in 10 ecotypes and found that plant weight, pod weight, number of primary branches and harvest index were all significantly correlated with yield, but, only plant weight and harvest index had a significant direct effect on yield in path analysis.

Islam et al. (1989) assessed 23 strains for seven yield related characters and the highest phenotypic and genotypic coefficients of variation were obtained for pods per plant followed by seed yield per plant and branches per plant. Pods per plant, 100-seed weight and branches per plant were estimated to have a high heritability and pods per plant gave the highest potential for genetic advance.

Waghmare *et al.* (1996) reported that path analysis revealed that number of pods per plant and 100-seed weight had large positive and direct effects on seed yield while the remaining characters had direct negative effects on seed yield.

Pandey *et al.* (2000) reported that among all the yield attributes pods per plant had the highest positive effect towards grain yield.

Das and Kundagrami (2002) reported that pods per plant registered high positive effects on seed yield for three years at the phenotypic level, whereas pod length, seeds per pod, 100-seed weight recorded positive direct effects on seed yield.

Kumari and Prasad (2005) reported that pods per plant, plant height, days to podding and seeds per pod had direct positive effects on seed yield. Pods per plant had the highest contribution to seed yield followed by plant height. The effect of number of branches and seed weight was via pods per plant and plant height, respectively. A comparison of correlations and path analysis showed that plant height, days to podding, pods per plant and seeds per pod were the principal yield components. The number of days to flower also contributed to seed yield but, mainly via pods per plant. Path coefficient analysis revealed that pods per plant followed by plant height contributed the most towards seed yield.

Kozak et al. (2008) studied seed yield per plant and seven yield related traits. Among these, plant height, number of branchesper plant, pod length and number of seeds per plant determined seed yield; number of pods per plant influenced seed yield only.

Materials and Methods

3. MATERIALS AND METHODS

The present investigation entitled "Genetic studies for some agro-morphological and quality traits in grasspea (*Lathyrus sativus* L.)" was carried out at the Experimental Farm of the Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur during *rabi* 2009-10. The biochemical analysis was carried out in the Quality Lab of the Department. The experimental farm is situated at 32°6' N latitude and 76°3' E longitude at an elevation of 1290.8m above mean sea level and represents the mid-hill zone of Himachal Pradesh.

The present investigation was carried out to study the nature and extent of variability for various agro-morphological and quality traits in locally adapted germplasm lines along with the released varieties procured from Indira Gandhi Agricultural University, Raipur and to analyse the associations among the traits.

3.1 Experimental material and methods

The experimental material for the present study consisted of 42 genotypes of grasspea (*Lathyrus sativus* L.) including 37 local collections and 5 varieties *viz.*, Mahateora, Pusa-24, Prateek, Ratan and Nirmal from Indira Gandhi Agricultural University, Raipur. All the genotypes were evaluated in a Randomized Block Design with three replications. The plot size consisted of two rows of each entry in each replication with the row length of 2m and spacing of 20cm between the rows and 10cm within the rows. Sowing was done on 27th October, 2009. Recommended package of practices were followed to raise the crop. The details of the experimental material are given in Table 3.1.

Table 3.1 List of 42 genotypes of grasspea under study

Sr. No.	Genotype	Source
1	HPLa-1	Mohanghatti, Jogindernagar
2	HPLa-2	Chattar, Palampur
3	HPLa-3	Biara, Palampur
4	HPLa-4	Paprola, Baijnath
5	HPLa-5	Chobu, Baijnath
6	HPLa-6	Bodhal
7	HPLa-7	Bhattiyat, Chamba
8	HPLa-8	Bahli, Shahpur
9	HPLa-9	Arth, Palampur
10	HPLa-10	Darati, Nagri
11	HPLa-11	Lahla, Palampur
12	HPLa-12	Trehal, Paprola
13	HPLa-13	Deol, Baijnath
14	HPLa-14	Deol, Baijnath
15	HPLa-15	Sagoor, Panchrukhi
16	HPLa-16	Upper Dattal, Pahra
17	HPLa-17	Angloh, Lahla, Palampur
18	HPLa-18	Trind, Nagrota
19	HPLa-19	Ghartholi, Palampur
20	HPLa-20	Baldhar, Kangra
21	HPLa- 21	Roonchar, Kangra
22	HPLa-22	Lahla, Palampur
23	HPLa-23	Angloh, Palampur
24	HPLa-24	Aaiju, Jogindernagar
25	HPLa-25	Sukhbag, Jogindernagar
26	HPLa-26	Padhiyarkhar, Jandpur
27	HPLa-27	Kothi Biara, Panchrukhi
28	HPLa-28	Jolan, Chamba

29	HPLa-29	Gopalpur, Palampur
30	HPLa-30	Arth, Palampur
31	HPLa-31	Raipur, Chamba
32	HPLa-32	Lower Romehar, Kangra
33	HPLa-33	Bahru, Panchrukhi
34	HPLa-34	Upper Dattal, Pahra
35	HPLa-35	Bhattiyat, Chamba
36	HPLa-36	Pathiar, Kangra
37	HPLa-37	Arth, Palampur
38	Mahateora	IGKV, Raipur
39	Pusa-24	IGKV, Raipur
40	Prateek	IGKV, Raipur
41	Ratan	IGKV, Raipur
42	Nirmal	IGKV, Raipur

3.2 Observations recorded

Observations were recorded for 13 characters *viz*., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield, seed yield per plant, harvest index, crude protein content and disease data on five competitive plants from each genotype in each replication to study various genetic parameters, correlations and path analysis.

The morphological characters which are expected to contribute towards the seed yield were recorded at appropriate stages and their mean values were used for the statistical analysis. The procedure followed in recording observations for these characters is described in detail as under:

i. **Days to 50% flowering:** The total number of days taken from the date of sowing to 50% flowering were recorded.

ii. **Days to maturity:** The total number of days taken from the date of sowing to date of maturity were recorded.

iii. **Plant height (cm):** The height of the randomly selected plants was measured from the ground level to the apex of the main stem at the time of maturity.

iv. **Number of branches per plant:** The total number of branches were recorded for each randomly selected plant at the time of harvest.

v. **Number of pods per plant:** The total number of pods were counted for each randomly selected plant at the time of maturity.

vi. **Pod length (cm):** The length of the five randomly selected mature pods from each plant was measured.

vii. **Seeds per pod:** Randomly selected five mature pods from each plant were threshed manually and total number of seeds per pod were counted.

viii. **100-seed weight (g):** A random sample of one hundred seeds was taken from each genotype in each replication and weight was recorded in grams.

ix. **Biological yield (g):** Randomly selected sun dried plants were weighed and biological yield was recorded in grams.

x. **Seed yield per plant (g):** Randomly selected competitive plants were threshed manually and seed yield for each plant was recorded in grams.

xi. **Harvest index (%):** Harvest index was calculated as-

$$\text{HI (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

xii **Crude protein content (%):** Semi-micro Kjeldahl method was adopted to determine per cent nitrogen content and conversion factor of 6.25 was used to calculate crude protein content (AOAC 1970).

$$\text{N (\%)} = \frac{\text{Titre value} \times 0.014 \times \text{Volume of digest} \times \text{Normality of acid used}}{\text{Aliquot taken} \times \text{Weight of sample (g)}} \times 100$$

$$\text{Crude Protein (\%)} = \text{N (\%)} \times 6.25$$

xiii **Disease data (if any):** As such no major disease incidence was observed.

3.3 Statistical analysis

The data were recorded for various characters and the statistical analysis was carried out under the following sub heads:

3.3.1 Analysis of variance

The data recorded for different characters for each genotype was statistically analysed to test their significance as per the procedure given by Panse and Sukhatme (1984). The analysis of variance (ANOVA) was constructed based on the linear model given by Fisher (1954):

$$Y_{ij} = m + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of i^{th} genotype in the j^{th} replication

m = general population mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

e_{ij} = random error associated with i^{th} genotype in the j^{th} replication

On the basis of linear model, the analysis of variance would be as follows:

Analysis of Variance

Source	Degrees of freedom	Mean sum of squares	F-value	Expected mean square
Replications	r-1	Mr	Mr/Me	$\sigma^2e + g\sigma^2r$
Genotypes	g-1	Mg	Mg/Me	$\sigma^2e + r\sigma^2g$
Error	(r-1) (g-1)	Me	---------	σ^2e
Total	(rg-1)			

Where,

r = number of replications

g = number of genotypes

$\sigma^2 r$ = variance due to replications

$\sigma^2 g$ = variance due to genotypes

$\sigma^2 e$ = error variance

The replication and genotype mean squares were tested against error mean squares by 'F' test for (r-1), (r-1)(g-1) and (g-1), (r-1)(g-1) degrees of freedom, respectively at 5 per cent level of significance (P = 0.05) and 1 per cent level of significance (P=0.01).

The genotypic and phenotypic variances were calculated as below:

Genotypic variance ($\sigma^2 g$) = (Mg-Me)/r

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Error variance ($\sigma^2 e$) = Me

The standard error mean SE(m), standard error of difference SE(d), and critical difference (CD) for comparing the means of any two genotypes were computed as follows:

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

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

CD = SE(d) x 't' value (5%) at error degrees of freedom

Where, 'Me' is the error mean square and 't' is the table value at 5 per cent level of significance at error degree of freedom.

Coefficient of variation (CV) was calculated as per the following formula:

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

Where, $\bar{x}$ = grand mean

3.3.2 Estimation of parameters of variability

Coefficients of variation:

The various coefficients of variation were calculated as per the formula suggested by Burton and De Vane (1953) and Johnson *et al.* (1955).

i. Phenotypic coefficient of variation (PCV %) = $(\sigma p / \bar{x}) \times 100$

ii. Genotypic coefficient of variation (GCV %) = $(\sigma g / \bar{x}) \times 100$

iii. Environmental coefficient of variation (ECV %) = $(\sigma e / \bar{x}) \times 100$

Where,

σp = phenotypic standard deviation

σg = genotypic standard deviation

σg = environmental standard deviation

$\bar{x}$ = grand mean

Heritability in broad sense (h^2bs):

$$\text{Heritability } [h^2bs\%] = \frac{\sigma^2 g}{(\sigma^2 g + \sigma^2 e)} \times 100$$

Expected Genetic advance (per cent of mean):

Genetic advance (GA) = $K \times \sigma p \times h^2$ (bs)

Where,

K = Selection differential at 5% selection intensity i.e. 2.06

σp = phenotypic standard deviation

h^2 (bs) = heritability in broad sense

GA% of mean = $(GA/ \bar{x}) \times 100$

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

PCV and GCV : >25% - High; 10-25% - moderate; <10% - low

Heritability : >80% - high; 40-80% - moderate; <40% - low

Genetic advance : >30% - high; 20-30% - moderate; <20% - low

3.3.3 Estimation of correlation coefficients

Phenotypic, genotypic and environmental coefficients of correlation were worked out following Analysis of covariance involving all possible paired combinations among the characters studied.

Analysis of covariance

Source	Degrees of freedom	Mean sum of products	F-value	Expected mean sum of products
Replications	r-1	Mr_{xy}	Mr_{xy} / Me_{xy}	$\sigma e_{xy} + \sigma r_{xy}$
Genotypes	g-1	Mg_{xy}	Mg_{xy} / Me_{xy}	$\sigma e_{xy} + \sigma g_{xy}$
Error	(r-1) (g-1)	Me_{xy}	---------	σe_{xy}

The genotypic, phenotypic and environmental covariances were calculated as follows:

$\sigma g_{xy} = (Mg_{xy} - Me_{xy})/r$

$\sigma p_{xy} = \sigma g_{xy} + \sigma e_{xy}$

$\sigma e_{xy} = Me_{xy}$

where,

r = number of replications

g = number of genotypes

σg_{xy} = genotypic covariance between traits x and y

σp_{xy} = phenotypic covariance between traits x and y

σe_{xy} = environmental covariance between traits x and y

Mg_{xy} = mean sum of squares due to genotypes from the analysis of covariance between traits x and y

Me_{xy} = mean sum of square due to error from the analysis of covariance between traits x and y

The phenotypic, genotypic and environmental coefficients of correlation were computed as per the methods suggested by Al- Jibouri *et al.* (1958) as under:

Phenotypic coefficient of correlation (rp_{xy})

$$rp_{xy} = \frac{\sigma p_{xy}}{(\sigma^2 p_x . \sigma^2 p_y)^{1/2}}$$

Where,

σp_{xy} = phenotypic covariance between two traits x and y

$\sigma^2 p_x$ = phenotypic variance of trait x

$\sigma^2 p_y$ = phenotypic variance of trait y

Genotypic coefficient of correlation (rg_{xy})

$$rg_{xy} = \frac{\sigma g_{xy}}{(\sigma^2 g_x . \sigma^2 g_y)^{1/2}}$$

Where,

σg_{xy} = genotypic covariance between two traits x and y

$\sigma^2 g_x$ = genotypic variance of trait x

$\sigma^2 g_y$ = genotypic variance of trait y

Environmental coefficient of correlation (re_{xy})

$$re_{xy} = \frac{\sigma e_{xy}}{(\sigma^2 e_x . \sigma^2 e_y)^{1/2}}$$

Where,

σe_{xy} = environmental covariance between two traits x and y

$\sigma^2 e_x$ = environmental variance of trait x

$\sigma^2 e_y$ = environmental variance of trait y

Test of significance

The significance of phenotypic coefficient of correlations at (g-2) degree of freedom where, g is the number of genotypes, were tested at 5 per cent level of significance against the table values of correlation coefficient (Fisher and Yates 1963).

3.3.4 Path coefficient analysis

Path coefficient is a standardized partial regression coefficient. It permits the partitioning of the correlation into direct and indirect effects. Path coefficient analysis of various growth parameters, yield and quality traits including crude protein content with seed yield was worked out as per method suggested by Dewey and Lu (1959):

$Py_1 + Py_2.r_{12} + Py_3.r_{13} +$ -- $+ Py_n.r_{1n} = ry_1$

$Py_1.r_{12} + Py_2 + Py_3.r_{23} +$ -- $+ Py_n.r_{2n} = ry_2$

$Py_1.r_{13} + Py_2.r_{23} + Py_3 +$ -- $+ Py_n.r_{3n} = ry_3$

:

:

$Py_1.r_{n1} + Py_2.r_{n2} + Py_3.r_{n3} +$ -- $+ Py_n = ry_n$

Where,

Py_1, Py_2, Py_3 ------------ Py_n are the direct 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 and ry_1, ry_2, ry_3, ------------- ry_n are the correlation coefficients of independent variables with dependent variable 'y'.

The residual factor (i.e. the variation in yield unaccounted for the association) was calculated from the following formula:

Residual effect (P x R) = $(1-R^2)$

Where,

$$R^2 = Py_1ry_1 + Py_2ry_2 + \text{-----------} + Py_nry_n$$

R^2 is the squared multiple correlation coefficient and the amount of variation in yield that can be attributed to the variable/variables not included in the present study.

Results and Discussion

4. RESULTS AND DISCUSSION

The present investigation entitled "Genetic studies for some agro-morphological and quality traits in grasspea (*Lathyrus sativus* L.)" was undertaken during *rabi* 2009-10 in Randomized Block Design with three replications at the Experimental Farm of the Department of Crop Improvement, CSK HPKV Palampur, to assess the extent of genetic variability, associations between yield and its components and their causes among forty two genotypes of grasspea. The biochemical analysis for the estimation of crude protein content was carried out in the Quality Lab of the Department. The results on various aspects of present study have been presented and discussed as below:

4.1 Nature and magnitude of variation for seed yield and its related traits

The success of any crop improvement programme depends on the nature and magnitude of genetic variability present in the germplasm. Therefore, germplasm serves as the most valuable natural reservoir in providing needed attributes for developing improved varieties. The germplasm resources will be of little value unless these are properly evaluated under target situations. Genetic improvement of quantitative traits can be achieved through a clear understanding of the nature and amount of variability present in the germplasm and the extent to which the desirable traits are heritable.

The information on the parameters such as variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance and influence of environment on these traits help the breeders to evolve suitable cultivars within a short time. Vavilov (1951) opinioned that a wide range of variability present in any crop species provides a better chance of selecting the desired types. Most of the traits of interest to plant breeders are quantitative in nature which exhibit continuous variation. The continuous variation comprises of heritable and non-heritable components (Fisher 1918). The heritable component is a consequence of genotypic and non-heritable of environmental factors. As it is difficult to assess the genotypes directly, it is possible only through the assessment of phenotypic expression (which is an interplay of genotype and environment interaction). Therefore, the study of genotypes for various agro-morphological traits under investigation is of utmost importance.

4.1.1 Analysis of variance

The analysis of variance (Table 4.1) revealed significant differences among the genotypes under study for all the characters viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, seeds per pod, 100-seed weight, seed yield per plant, biological yield per plant, harvest index and crude protein content, thereby indicating a wide range of genetic variability and scope of selection for these traits. Kumari *et al.* (1995) also reported genetic variability for seed yield and its components in grasspea. Kumar and Dubey (1997) reported higher variability for yield per plant, pods per plant and seeds per plant. A wide range of variability was observed for various traits, presenting opportunities for selection by some earlier workers *viz.*, Pandey *et al.* (1997), Sharma *et al.* (2001), Talukdar and Biswas (2008) and Bhosle *et al.* (2008) in grasspea.

4.1.2 Estimates of parameters of variability

The estimates of parameters of variability *viz.,* grand mean (x), range, phenotypic coefficient of correlation (PCV), genotypic coefficient of correlation (GCV), environmental coefficient of variation (ECV), heritability in broad sense (h^2bs) and genetic advance (GA) expressed as percentage of mean for different traits studied (Appendix-I and Table 4.2) are described in detail as below:

4.1.2.1 Mean performance and Range

Genotype HPLa-28 was found to be superior for seed yield per plant followed by HPLa-13 and HPLa-26. Genotype HPLa-28 was also found to be superior for other traits like plant height, pods per plant, seeds per pod, biological yield per plant and harvest index, however, its 100-seed weight (8.30g) was less and therefore need improvement through hybridization and selection.

Table 4.1 Analysis of variance for various traits in grasspea

Source of variation	df	Characters											
		Mean sum of squares (MS)											
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Crude protein content (%)	Seed yield per plant (g)
Replications	2	5.45	0.22	10.56	4.73*	13.21*	0.07*	0.03	1.11*	1.70	26.35*	0.26	0.07
Genotypes	41	82.42*	52.94*	137.34*	4.76*	34.68*	0.07*	0.27*	0.81*	21.66*	145.69*	8.58*	5.32*
Error	82	0.16	1.78	1.17	10.14	0.46	2.75	0.01	0.07	0.06	0.57	8.30	0.17

*** Significant at $P \leq 0.05$**

Potential genotype identified for days to 50% flowering was variety Prateek and that for days to maturity were Nirmal and Prateek. HPLa-13 was found to be superior for number of branches per plant. Genotypes HPLa-4, HPLa-14, HPLa-26, HPLa-30, HPLa-33, HPLa-37 and variety Ratan were found to be superior for pods per plant: HPLa-10, HPLa-14, HPLa-20, HPLa-23, HPLa-29, HPLa-33 and HPLa-34 were identified as potential genotypes for both plant height and seeds per pod.

For crude protein content, genotypes HPLa-3, HPLa-18, HPLa-21 and HPLa-30 were found to be superior. HPLa-34, Prateek and Ratan were identified as the potential genotypes for 100-seed weight. For harvest index HPLa-2, HPLa-5, HPLa-19, HPLa-24 and HPLa-26 were identified as the potential genotypes.

Maximum range was found for harvest index (17.79-45.54) followed by plant height (29.33-56.47) and days to 50% flowering (97.67-122.67) indicating the wide range of genetic variability for these traits.

4.1.2.2 Coefficients of variation

The PCV and GCV are the indicators of observed and genetic variability. PCV values were found higher than their corresponding GCV values for all the traits. Wuletaw and Endashaw (2002) also reported slightly higher PCV values than GCV values for all the characters signifying that genotypic factors exerted reasonable effect in estimating the variation. The results from the present study indicated high PCV and GCV values (>25%) for seed yield per plant indicating wide range of observed and genetic variability for this trait. Ranjan *et al.* (2007) reported highest PCV and GCV values for seed yield per plant. There is not a wider gap of PCV and GCV values thus, indicating lesser role of environmental fluctuations.

The present study revealed low PCV and GCV values for characters such as days to 50% flowering, days to maturity, pod length, seeds per pod, 100-seed weight and protein content thereby indicating low genetic variability for these characters. The PCV and GCV values were moderate for the remaining characters. The PCV and GCV are of little importance if some other parameters like heritability and genetic advance are not calculated, because of their difficult characterization for comparison of population with desired precision when expressed in absolute values.

4.1.2.3 Heritabilty in broad sense (h^2 bs)

A useful measure of considering the ratio of genetic variance to the total variance is heritability. The information on heritability estimates are useful in studying the inheritance of quantitative traits as well as for rational planning of breeding programmes with desired degree of expected genetic progress. It may be observed as a measure of relative importance of heredity and environment.

The present study revealed that heritability in broad sense was high (>80%) for days to 50% flowering, days to maturity, plant height, 100-seed weight, biological yield per plant, harvest index, crude protein content and seed yield per plant. Ranjan *et al.* (2007) reported that heritability estimates in broad sense were high for days to maturity and seed yield per plant. High heritability for these traits revealed less influence of environment and greater role of genetic component of variation. Thus, the selection for these traits on the basis of phenotypic expression would be more effective and can be relied upon.

Moderate heritability (40-80%) estimates were observed for number of branches per plant, number of pods per plant, pod length and seeds per pod. Similar results for moderate heritability estimates have also been reported earlier by Ranjan *et al. (2007)* and Talukdar and Biswas (2008) for various characters in grasspea.

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

4.1.2.4 Genetic advance (GA)

For an effective selection programme, knowledge of the estimates of heritability alone is not sufficient and genetic advance if studied along with heritability is more useful. Genetic advance may or may not be in proportion to genetic variability and heritability estimates, because both heritability and high genetic variability are important to obtain higher genetic gain.

Based on this consideration, high heritability coupled with high genetic advance was observed for biological yield per plant, harvest index and seed yield per plant. It indicated predominance of additive gene action in the inheritance of these traits and selection would be most effective. Higher value of additive gene effects is indication of high breeding value. High heritability coupled with high genetic advance for some of these traits have also been reported by Kumari and Mehra (1997), Ranjan *et al.* (2007) and Talukdar and Biswas (2008). High heritability coupled with high genetic advance estimated for important yield components offer scope for selection.

High heritability with moderate genetic advance was observed for plant height indicating predominance of both additive and non additive gene action in the inheritance of these traits, suggesting hybridization coupled with selection to exploit both types of gene action.

High heritability with low genetic advance for days to 50% flowering, days to maturity, 100-seed weight and crude protein content indicated non additive gene action which revealed the importance of dominance and epistatic effects in the inheritance of these traits and selection for these traits would be less effective.

4.2 Correlation and path coefficients for seed yield and other traits

After understanding the nature of variation for seed yield per plant and other traits, it would be desirable to know the nature and magnitude of

Table 4.2 **Mean performance and parameters of variability for various traits in grasspea**

Traits	Mean	Range	PCV (%)	GCV (%)	ECV (%)	h^2bs	Genetic advance (%) of mean
Days to 50% flowering	118.67+0.77	97.67 - 122.67	4.51	4.37	1.12	93.8	8.72
Days to maturity	164.37+0.63	151.33 – 169.33	2.61	2.53	0.66	93.6	5.04
Plant height (cm)	47.32+1.84	29.33 – 56.47	15.32	13.76	6.73	80.7	25.47
No. of branches per plant	10.12+0.39	7.6 – 13.87	13.60	11.82	6.72	75.6	21.17
No. of pods per plant	19.35+0.96	7.33 – 24.07	18.92	16.86	8.58	79.4	30.96
Pod length (cm)	2.56+0.05	2.19 – 2.8	6.62	5.76	3.27	75.6	10.32
Seeds per pod	3.69+0.15	2.87 – 4.13	9.91	6.96	7.06	49.3	10.07
100-seed weight (g)	8.46+0.14	7.51 – 9.71	6.58	5.92	2.88	80.9	10.97
Biological yield per plant (g)	12.13+0.44	6.27 – 19.2	22.73	21.86	6.24	92.5	43.29
Harvest index (%)	34.24+1.66	17.79 – 45.54	21.48	19.76	8.41	84.7	37.46
Crude protein content (%)	27.30+0.20	23.23 – 29.79	6.28	6.15	1.25	96	12.42
Seed yield per plant (g)	4.18+0.23	1.13 – 8.32	32.76	31.36	9.47	91.6	61.85

PCV: Phenotypic Coefficient of Variation (%)
GCV: Genotypic Coefficient of Variation (%)
ECV: Environmental Coefficient of Variation (%)
h^2bs: Heritability in broad sense (%)
GA : Genetic Advance (%) of mean

associations existing among these traits in order to bring about improvement in a complex trait like seed yield. Grafius (1956) has also opinioned that the improvement of complex triats such as seed yield per plant may be accomplished better through component breeding, thus, a better understanding of the contribution of each trait in building the genetic make-up of the crop can be obtained through correlation studies.

In order to understand the nature and magnitude of correlations among seed yield per plant and other traits along with their causal factors, estimates of correlation coefficients at phenotypic, genotypic and environmental levels and their direct and indirect effects through path coefficient analysis were computed and the results obtained are discussed as under :

4.2.1 Correlation coefficients at phenotypic, genotypic and environmental levels

The effectiveness of any breeding or selection programme depends upon the nature of associations between yield and other component characters, as more directly and positively a character is associated with seed yield, the more will be the success of the selection programme. Therefore, besides getting information on the nature and magnitude of variation, it is also imperative to have knowledge on the associations of seed yield with other traits and among themselves and there causation to identify characters for defining an ideal plant type as well for increasing deficiency of both direct and indirect selection.

Estimates of phenotypic and genotypic coefficients of correlation and that of direct and indirect effects provide the base necessary for identification of traits for an ideal plant type and effective selection. Based on the estimates of genotypic and phenotypic correlations, the breeder will be able to decide the method of breeding to be followed to exploit the useful correlations.

The results on correlations computed at phenotypic, genotypic and environmental levels for all possible paired combinations are presented in Table 4.3. In present investigation, the phenotypic correlation estimates were higher than that of their corresponding environmental correlations except between pod length and days to maturity, pod length and number of pods per plant, biological yield per plant and pod length, biological yield per plant and 100-seed weight, harvest index and days to 50% flowering, crude protein content and number of pods per plant, crude protein content and seeds per pod and seed yield per plant and days to 50% flowering.

The genotypic correlation estimates were generally similar and observed to be higher than their corresponding phenotypic correlations which indicated the inherent associations among various traits studied except between number of branches per plant and days to 50% flowering, pod length and number of pods per plant and crude protein content and number of pods per plant. It has been well established that yield is one of the most important economic character which is influenced to a great extent by the interaction of the several morphological traits.

At both phenotypic and genotypic levels, seed yield per plant exhibited positive and significant correlations with days to maturity, plant height, number of branches per plant, number of pods per plant, seeds per pod, biological yield per plant and harvest index, whereas, it showed negative and significant correlation with crude protein content. seed yield per plant exhibited non-significant positive correlation with days to 50% flowering and pod length while negative correlation with 100-seed weight.

Positive and significant correlations also existed between days to 50% flowering and days to maturity, plant height, number of pods per plant, seeds per pod, biological yield per plant, harvest index and crude protein content; between days to maturity and plant height, number of branches per plant, number of pods per plant, seeds per pod, biological yield per plant, harvest index and crude protein content; between plant height and number of pods per plant, seeds per pod, biological yield per plant, harvest index and crude protein content; between number of branches per plant and number of pods per plant and biological yield per plant; between number of pods per plant and seeds per pod, biological yield per plant and harvest index; between pod length and seeds per pod and harvest index; between biological yield and harvest index and between seeds per pod and biological yield per plant and harvest index. Positive association of seed yield per plant with pods per plant and seeds per pod was also reported by Waghmare *et al.* (1966), Kumar and Dubey (1977). Similarly, Das and Kundagrami (2002) reported positive correlation of seed yield per plant with pods per plant and seeds per pod both at the genotypic and phenotypic levels. Wuletaw and Endashaw (2002) also reported positive correlation of seed yield with pods per plant and branches per plant. Kumari and Rajendra (2005) reported positive association of seed yield per plant with plant height, days to flowering, pods per plant and seeds per pod. Bhosle *et al.* (2008) reported that harvest index, seeds per pod, pods per plant were positively correlated with seed yield per plant both at genotypic and phenotypic levels.

Negative and significant correlations existed between seed yield per plant and crude protein content; between 100-seed weight and days to 50% flowering, days to maturity, plant height, number of pods per plant, seeds per pod and harvest index; between crude protein content and number of branches per plant, biological yield per plant and harvest index. Rest of the character combinations exhibited non-significant positive or negative associations. Negative and significant association of seed yield per plant with crude protein content was also observed by Das and Kundagrami (2002) and Kumari and Rajendra (2005). Kumar and Dubey (1997) reported that various yield contributing traits also showed significant and positive associations among themselves. Kumari and Rajendra (2005) and Bhosle *et al.* (2008) reported positive association of days to 50% flowering and plant height. Das and Kundagrami (2002) reported significant and positive association between days to flowering and days to maturity; days to flowering and protein content. In the present study the results obtained in respect of associations are in conformity to the studies of Das and Kundagrami (2002).The strong positive associations between seed yield per plant and other yield contributing traits indicated the possibility of selecting lines for yield improvement.

At genotypic level, the estimates of correlation coefficients were generally similar to that observed at the phenotypic level for most of the traits. However, the magnitude of genotypic correlation coefficients was generally higher than their corresponding phenotypic values for most of the characters which indicated the inherent associations among various characters studied. Kumar and Dubey (1997) also reported higher genotypic correlation coefficients than their respective phenotypic correlation coefficients for most of the traits studied. This indicated that phenotypic estimates of correlation coefficients represent the genotypic correlation coefficients, therefore, yield improvement through these traits which were significantly and positively correlated would be effective. Genotypic correlations provide measures of genetic association between traits and are more reliable than phenotypic correlations. Genetic correlations along with observed correlations help to identify the traits to be considered in breeding programmes.

At environmental level, estimates of correlation coefficients were comparatively lower for most of the traits studied. Positive and significant association existed between days to 50% flowering and days to maturity and number of pods per plant; between days to maturity and 100-seed weight, biological yield per plant and seed yield per plant; between number of branches per plant, number of pods per plant and biological yield per plant; between number of pods per plant and biological yield per plant, seed yield per plant; between biological yield per plant and seed yield per plant and between harvest index and seed yield per plant.

On the other hand, negative and significant associations existed between days to 50% flowering and harvest index, seed yield per plant; between 100-seed weight and harvest index; between harvest index and crude protein content and between crude protein content and seed yield per plant. Kumar and Dubey (1997) also reported positive association of seed yield with pods per plant and seeds per pod. Waghmare *et al.* (1996) reported negative association of seed yield with days to 50% flowering.

Table 4.3 Estimates of correlation coefficients at phenotypic (P), genotypic (G) and environmental (E) levels among various traits in grasspea

Traits		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Crude protein content (%)
Days to maturity	P	0.785*										
	G	0.826										
	E	0.176*										
Plant height (cm)	P	0.571*	0.687*									
	G	0.649	0.773									
	E	0.057	0.138									
No. of branches per plant	P	-0.044	0.182*	0.101								
	G	-0.042	0.195	0.137								
	E	-0.076	0.145	-0.025								
No.of pods per plant	P	0.289*	0.444*	0.361*	0.663*							
	G	0.361	0.493	0.453	0.711							
	E	0.203*	0.162	-0.010	0.499*							
Pod length (cm)	P	0.169	0.063	0.105	-0.155	0.062						
	G	0.222	0.089	0.156	-0.179	0.042						
	E	-0.148	-0.104	-0.077	-0.083	0.129						
Seeds per pod	P	0.333*	0.413*	0.391*	0.171	0.454*	0.332*					
	G	0.479	0.633	0.691	0.299	0.703	0.492					
	E	0.035	-0.093	-0.144	-0.033	0.044	0.089					
100-seed weight (g)	P	-0.367*	-0.374*	-0.313*	0.065	-0.250*	-0.121	-0.353*				
	G	-0.432	-0.458	-0.383	0.077	-0.327	-0.136	-0.542				
	E	0.080	0.226*	-0.019	0.024	0.061	-0.068	-0.036				
Biological yield (g)	P	0.178*	0.353*	0.255*	0.624*	0.684*	-0.015	0.311*	-0.049			
	G	0.197	0.363	0.285	0.707	0.739	-0.031	0.436	-0.069			
	E	-0.082	0.212*	0.076	0.249*	0.402*	0.076	0.084	0.084			
Harvest index(%)	P	0.237*	0.327*	0.309*	0.163	0.406*	0.175*	0.379*	-0.225*	0.193*		
	G	0.302	0.356	0.370	0.234	0.463	0.229	0.613	-0.233	0.237		
	E	-0.327*	0.103	0.015	-0.128	0.150	-0.040	-0.059	-0.186*	-0.159		
Crude protein content (%)	P	0.386*	0.309*	0.269*	-0.249*	-0.014	-0.074	0.008	-0.233	-0.247*	-0.269*	
	G	0.400	0.329	0.297	-0.286	-0.005	-0.095	-0.012	-0.258	-0.253	-0.277	
	E	0.118	-0.051	0.091	-0.043	-0.105	0.072	0.113	-0.061	-0.163	-0.251*	
Seed yield per plant (g)	P	0.212	0.394*	0.328*	0.539*	0.666*	0.089	0.414*	-0.140	0.773*	0.740*	-0.429*
	G	0.252	0.411*	0.383*	0.619*	0.713*	0.105	0.607*	-0.154	0.797*	0.751*	-0.439*
	E	-0.299*	0.177	-0.009	0.163	0.440*	0.016	0.028	-0.061	0.501*	0.693*	-0.318*

*Significant at 5 per cent level

Based on correlation studies, it can be concluded that seed yield per plant is positively and significantly correlated with days to maturity, plant height, number of branches per plant; number of pods per plant, seeds per pod, biological yield per plant and harvest index both at the phenotypic and genotypic levels and selection through these traits would be effective.

4.2.2 Estimation of path coefficients

Path coefficient analysis elucidates the intrinsic nature of observed association between yield and its attributes. It also reveals the magnitude of contribution made by different plant traits towards yield, thereby imparting confidence in selection of important yield attributes. The data pertaining to path coefficient analysis (Table 4.4) revealed that biological yield per plant had the highest direct effect on seed yield per plant followed by harvest index both at phenotypic and genotypic levels.. Number of branches per plant, plant height and days to maturity also showed positive direct effect with very low magnitude. High negative direct effect on seed yield per plant was exhibited by crude protein content.

The characters exhibiting low positive direct effects or negative direct effects contributed indirectly towards yield per plant mainly via biological yield per plant or harvest index or both. Kavuncu *et al.* (1985) reported that harvest index and branches per plant were the major direct contributors toward seed yield per plant. Kumari and Rajendra (2005) also observed positive direct effects of pods per plant, plant height and seeds per pod on seed yield per plant. Therefore, the results from the present study clearly indicated that biological yield per plant and harvest index would be the best selection indices for increasing seed yield per plant in grasspea.

Table 4.4 Estimates of direct and indirect phenotypic and genotypic effects of various traits on seed yield

		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Crude protein content (%)	Seed yield per plant (g)
Days to 50% flowering	P	**-0.003**	-0.002	-0.002	0.000	-0.001	-0.001	-0.001	0.001	-0.001	-0.001	-0.001	0.212
	G	**-0.093**	-0.077	-0.060	0.004	-0.034	-0.021	-0.045	0.040	-0.018	-0.028	-0.037	0.252
Days to maturity	P	0.013	**0.017**	0.012	0.003	0.007	0.001	0.007	-0.006	0.006	0.006	0.005	0.394*
	G	0.072	**0.088**	0.068	0.017	0.043	0.008	0.055	-0.040	0.032	0.031	0.029	0.411*
Plant height (cm)	P	0.012	0.015	**0.021**	0.002	0.008	0.002	0.008	-0.007	0.005	0.006	0.006	0.328*
	G	0.083	0.099	**0.128**	0.018	0.058	0.020	0.089	-0.049	0.037	0.048	0.038	0.383*
No. of branches per plant	P	-0.003	0.010	0.006	**0.057**	0.038	-0.009	0.010	0.004	0.035	0.009	-0.014	0.539*
	G	-0.001	0.006	0.004	**0.032**	0.023	-0.006	0.010	0.003	0.023	0.008	-0.009	0.619*
No.of pods per plant	P	-0.015	-0.024	-0.019	-0.035	**-0.053**	-0.003	-0.024	0.013	-0.036	-0.022	0.000	0.666*
	G	0.003	0.004	0.003	0.005	**0.008**	0.000	0.005	-0.003	0.006	0.004	0.000	0.713*
Pod length (cm)	P	-0.001	-0.000	-0.000	0.000	-0.000	**-0.003**	-0.001	0.000	0.000	-0.000	0.000	0.089
	G	0.018	0.007	0.013	-0.014	0.003	**0.080**	0.039	-0.011	-0.003	0.018	-0.008	0.105
Seeds per pod	P	-0.002	-0.002	-0.002	-0.001	-0.002	-0.002	**-0.005**	0.002	-0.002	-0.002	0.000	0.414*
	G	-0.117	-0.155	-0.169	-0.073	-0.172	-0.120	**-0.245**	0.133	-0.106	-0.149	0.003	0.607*
100-seed weight (g)	P	0.004	0.004	0.004	-0.000	0.003	0.001	0.004	**-0.011**	0.000	0.003	0.003	-0.140
	G	0.033	0.035	0.029	-0.006	0.025	0.010	0.041	**-0.076**	0.005	0.018	0.019	-0.154
Biological yield (g)	P	0.111	0.219	0.159	0.388	0.425	-0.009	0.193	-0.031	**0.622**	0.119	-0.154	0.773*
	G	0.126	0.233	0.183	0.453	0.474	-0.020	0.279	-0.044	**0.641**	0.152	-0.162	0.797*
Harvest index(%)	P	0.140	0.193	0.182	0.096	0.239	0.104	0.224	-0.133	0.114	**0.590**	-0.159	0.740*
	G	0.185	0.218	0.227-	0.144	0.283	0.140	0.375	-0.143	0.145	**0.612**	-0.169	0.751*
Crude protein content (%)	P	-0.045	-0.036	0.031	0.029	0.002	0.009	-0.009	0.270	0.029	0.031	**-0.116**	-0.429*
	G	-0.057	-0.047	-0.042	0.041	0.000	0.014	0.002	0.037	0.036	0.039	**-0.142**	-0.439*

Residual effects (P) = 0.159; (G) = 0.092

The bold values indicate direct effects; P= Phenotypic level and G= Genotypic level

*Significant at 5 per cent level

Summary and Conclusions

5. SUMMARY AND CONCLUSIONS

The present investigation entitled "Genetic studies for some agro-morphological and quality traits in grasspea (*Lathyrus sativus* L.)" was undertaken to assess genetic variability, association of various traits with seed yield per plant and their direct and indirect effects. The biochemical analysis for the estimation of crude protein content was also carried out.

The experimental material comprising 42 genotypes of grasspea (37 local collections and 5 varieties procured from Raipur) was raised in Randomized Block Design with three replications, at the Experimental Farm of the Department of Crop Improvement, CSK HPKV, Palampur, during *rabi* 2009-10. Data were recorded on seed yield per plant and various other morphological traits *viz.,* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, seeds per pod, 100-seed weight, biological yield per plant, harvest index and crude protein content. Biochemical analysis for the estimation of crude protein content was also done in the Quality Laboratory of the Department of Crop Improvement, CSKHPKV, Palampur.

The data analysis for morphological and quality traits was done as per the standard statistical procedures for various parameters of genetic variability, correlation and path coefficients. As such no disease incidence was observed. The analysis of variance revealed significant differences among the genotypes for all the traits studied indicating existence of sufficient genetic variability. Wide genetic variation was exhibited by the character harvest index followed by characters plant height, days to 50% flowering, days to maturity, number of pods per plant, biological yield per plant, seed yield per plant, crude protein content and number of branches per plant whereas for 100-seed weight, seeds per pod and pod length variation was less.

PCV values were found higher than their corresponding GCV values for all the traits studied. Both PCV and GCV were high (>25%) for seed yield per plant. There was a little gap between PCV and GCV values thus indicating less role of environment. The low PCV and GCV values were observed for days to 50% flowering, days to maturity, pod length, seeds per pod, 100-seed weight and protein content. Rest of the traits exhibited moderate PCV and GCV values.

High heritability values (>80%) were observed for days to 50% flowering, days to maturity, plant height, 100-seed weight, biological yield per plant, harvest index, crude protein content and seed yield per plant. Moderate heritability values were observed for number of branches per plant, number of pods per plant, pod length and seeds per pod.

High heritability coupled with high genetic advance was observed for biological yield per plant, harvest index and seed yield per plant indicating the predominance of additive gene action and hence would be useful for effective selection in early segregating generations due to their high breeding values.

Correlation studies indicated the higher magnitude of genotypic correlations compared to their corresponding phenotypic correlations for most of the traits indicating the inherent association among the various traits studied. At both phenotypic and genotypic levels, seed yield per plant exhibited positive and significant correlations with days to maturity, plant height, number of branches per plant, number of pods per plant, seeds per pod, biological yield per plant and harvest index.

Positive and significant correlations also existed between days to 50% flowering and days to maturity, plant height, seeds per pod, biological yield per plant, harvest index and crude protein content; between days to maturity and plant height, number of branches per plant, number of pods per plant, seeds per pod, biological yield per plant, harvest index and crude protein content; between plant height and number of pods per plant, seeds per pod, biological yield per plant, harvest index and crude protein content; between number of branches per plant and number of pods per plant and biological yield per plant; between number of pods per plant and seeds per pod, biological yield per plant and harvest index; between pod length and seeds per pod and harvest index; between biological yield per plant and harvest index and between seeds per pod and biological yield per plant and harvest index..

Negative and significant correlations existed between seed yield per plant and crude protein content; between 100-seed weight and days to 50% flowering, days to maturity, plant height, number of pods per plant, seeds per pod and harvest index; between crude protein content and number of branches per plant, biological yield per plant and harvest index. Rest of the character combinations exhibited non-significant positive or negative associations.

Path coefficient analysis revealed the high positive direct effect for biological yield per plant and harvest index towards seed yield per plant whereas high negative direct effect on seed yield per plant was exhibited by crude protein content and the direct effects of remaining traits were observed to be negligible.

Conclusions

Sufficient genetic variability was observed for all the traits studied. High heritability values were observed for days to 50% flowering, days to maturity, plant height, 100-seed weight, biological yield per plant, harvest index, crude protein content and seed yield per plant. High heritability coupled with high genetic advance was observed for biological yield per plant, harvest index and seed yield per plant indicating effective selection for these traits in early segregating generations.

Based on correlation studies, it can be concluded that seed yield per plant is positively and significantly correlated with days to maturity, plant height, number of branches per plant, pods per plant, seeds per pod, biological yield per plant and harvest index both at the phenotypic and genotypic levels and selection through these traits would be effective. Biological yield per plant and harvest index were observed as the best selection indices in grasspea because of their high direct contribution towards seed yield per plant.

Genotype HPLa-28 was found to be superior for seed yield per plant, pods per plant, plant height, seeds per pod, biological yield per plant and harvest index, whereas, its 100-seed weight was found to be less. For days to 50% flowering and days to maturity variety Prateek was identified as the potential genotype. Genotype HPLa-13 was found to be superior for number of branches per plant whereas, genotypes HPLa-4, HPLa-14, HPLa-26, HPLa-30, HPLa-33, HPLa-37 and variety Ratan were found to be superior for pods per plant. HPLa-10, HPLa-14, HPLa-20, HPLa-23, HPLa-29, HPLa-33 and HPLa-34 were identified as potential genotypes for both plant height and seeds per pod.

For crude protein content, genotypes HPLa-3, HPLa-18, HPLa-21 and HPLa-30 were found to be superior. HPLa-34, Prateek and Ratan were identified as the potential genotypes for 100-seed weight. For harvest index, genotypes HPLa-2, HPLa-5, HPLa-19, HPLa-24 and HPLa-26 were identified as the potential genotypes. The present study indicates a strong need for thorough testing of genotypes over the years and locations for their direct use as a variety or involvement in future grasspea improvement programme.

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Appendices

APPENDIX- I

Estimation of mean values for 42 genotypes of grasspea with respect to 12 characters

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Crude Protein content (%)	Seed yield per plant
HPLa-1	118.67	164.67	55.53	10.87	18.67	2.70	3.53	8.40	14.40	21.88	29.15	3.16
HPLa-2	119.67	166.00	53.40	9.60	9.20	2.55	3.67	8.96	10.73	44.89	27.62	4.62
HPLa-3	121.67	165.33	51.13	9.60	18.67	2.73	3.93	8.25	10.00	32.71	29.43	3.39
HPLa-4	119.67	166.67	56.47	11.07	21.53	2.45	3.40	8.32	11.87	34.16	28.46	4.03
HPLa-5	121.00	165.00	46.13	10.00	18.80	2.53	3.80	8.82	11.40	42.99	27.80	4.91
HPLa-6	119.00	165.00	46.73	10.00	19.53	2.67	3.87	8.68	12.60	39.46	27.73	4.95
HPLa-7	121.00	165.00	48.27	9.40	18.40	2.75	3.47	8.48	11.87	34.59	28.74	4.11
HPLa-8	120.67	165.67	46.73	9.80	20.27	2.77	4.00	8.05	15.00	22.77	28.81	3.43
HPLa-9	122.67	165.00	42.33	9.53	17.00	2.24	3.53	7.63	9.80	35.70	28.47	3.53
HPLa-10	118.67	161.33	53.20	9.47	18.93	2.67	3.80	8.53	10.20	39.17	28.21	3.99
HPLa-11	119.67	168.33	49.40	11.07	22.13	2.57	3.73	8.35	14.73	39.52	25.64	5.82
HPLa-12	120.67	169.33	47.13	11.40	21.27	2.51	3.67	8.64	15.00	32.32	25.81	4.84
HPLa-13	117.33	168.33	47.67	13.87	22.40	2.55	3.53	8.88	16.20	38.95	26.16	6.32

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Crude Protein content (%)	Seed yield per plant
HPLa-14	120.67	168.33	53.67	11.27	22.13	2.63	4.13	7.93	13.33	40.85	25.37	5.46
HPLa-15	122.00	166.33	47.80	8.93	23.87	2.63	3.73	8.14	14.00	25.48	27.93	3.77
HPLa-16	119.67	166.00	46.33	8.87	18.00	2.72	4.00	8.86	12.80	38.26	27.15	4.89
HPLa-17	120.00	168.67	44.60	0.07	19.27	2.52	3.67	8.18	12.33	37.89	27.09	4.66
HPLa-18	119.33	164.67	47.60	9.13	16.67	2.43	3.67	8.46	10.87	26.13	29.43	2.82
HPLa-19	119.67	166.33	48.57	8.40	17.67	2.75	4.00	7.53	11.73	44.82	25.03	5.23
HPLa-20	118.67	165.67	54.73	9.53	20.73	2.46	3.80	7.51	10.93	34.32	28.69	3.76
HPLa-21	118.67	165.00	50.67	8.73	16.93	2.58	3.73	7.59	9.60	33.52	29.69	3.22
HPLa-22	118.67	164.67	50.93	8.87	17.60	2.60	3.67	8.11	10.93	35.51	27.81	3.86
HPLa-23	118.67	169.00	52.07	10.27	20.13	2.35	4.07	8.21	13.07	28.39	28.82	3.71
HPLa-24	120.33	166.33	51.13	9.87	21.00	2.62	3.67	8.55	14.00	42.96	25.37	6.00
HPLa-25	121.00	165.33	49.13	8.93	19.20	2.56	3.67	7.75	11.33	36.46	28.55	4.13
HPLa-26	115.33	159.33	49.40	11.13	22.40	2.71	4.07	8.03	13.87	45.54	23.86	6.29
HPLa-27	121.67	165.67	48.53	10.87	21.00	2.76	4.20	8.38	10.80	40.61	28.30	4.38
HPLa-28	120.67	165.00	51.80	12.30	24.07	2.53	3.93	8.30	19.20	43.34	23.23	8.32
HPLa-29	122.00	166.67	51.47	10.80	17.80	2.52	4.00	8.29	13.27	34.17	25.60	4.53
HPLa-30	122.67	165.33	39.73	11.47	21.53	2.39	3.40	7.77	10.73	28.70	29.79	3.08

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Crude Protein content (%)	Seed yield per plant
HPLa-31	121.00	166.00	44.67	10.20	21.07	2.53	3.60	8.49	9.47	38.65	28.48	3.66
HPLa-32	119.00	161.67	47.73	9.80	19.27	2.44	3.53	8.63	12.87	27.23	29.09	3.50
HPLa-33	121.67	164.33	54.47	11.40	22.60	2.51	3.80	9.15	13.47	29.63	27.34	3.99
HPLa-34	121.33	167.00	52.50	10.47	21.20	2.70	4.00	9.32	11.07	38.33	27.26	4.24
HPLa-35	122.00	165.67	52.27	9.40	18.60	2.19	3.27	9.05	11.00	35.22	28.19	3.87
HPLa-36	120.00	166.33	48.47	9.07	17.60	2.77	3.73	8.59	11.07	33.51	28.79	3.69
HPLa-37	120.67	166.00	45.47	11.80	23.33	2.42	3.87	8.55	15.20	28.28	26.51	4.30
Mahateora	118.67	156.00	29.93	7.60	11.67	2.59	3.00	9.18	8.80	28.83	26.05	2.16
Pusa-24	116.33	157.33	34.67	8.27	9.73	2.80	3.07	9.11	6.27	19.09	25.26	1.19
Prateek	97.67	152.67	35.07	8.80	7.33	2.21	2.87	9.71	6.40	17.79	25.12	1.13
Ratan	105.33	155.00	30.40	12.20	22.40	2.33	3.33	9.38	18.60	31.53	26.26	5.87
Nirmal	100.33	151.33	29.33	10.93	20.93	2.65	3.67	8.56	8.60	34.06	24.69	2.93
$\overline{X}$	118.67	164.37	47.32	10.12	19.35	2.56	3.69	8.46	12.13	34.24	27.30	4.18
SE (m)+	0.77	0.63	1.84	0.39	0.96	0.05	0.15	0.14	0.44	1.66	0.19	0.23
C.D.at 5%	2.17	1.76	5.17	1.11	2.69	0.14	0.42	0.39	1.23	4.68	0.55	0.64
C.V.	1.12	0.66	6.73	6.72	8.58	3.27	706	2.88	6.24	8.41	1.25	9.47

Brief *Resume* of the Student

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Academic Qualifications

Qualification	Year	School/Board/University	Marks (%)	Division	Major Subject
10th	2003	Himachal Pradesh Board of School Education, Dharamshala	74.85	First	English, Mathematics, Hindi, Social Science, Science, Sanskrit, Economics
10+2	2005	Himachal Pradesh Board of School Education, Dharamshala	76.80	First	English, Biology, Physics, Chemistry, Information Technology
B.Sc. (Agriculture)	2009	CSK Himachal Pradesh Agricultural University, Palampur (H.P.), India	77.50	First	All Agriculture and Allied subjects
M.Sc. (Agri.) Plant Breeding and Genetics	2011	CSK Himachal Pradesh Agricultural University, Palampur (H.P.), India	73.30	First	Major Discipline: Plant Breeding and Genetics Minor Discipline: Plant Pathology