Genetic analysis for yield, maturity and protein content in field pea (*Pisum sativum* var. arvense)

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Certificate-I

This is to certify that the thesis entitled **"Genetic analysis for yield, maturity and protein content in field pea (*Pisum sativum* var. arvense)"** submitted in partial fulfillment of the requirements for the award of the degree **of Master of Science in Agriculture (Plant Breeding and Genetics)**, to the **Faculty of Post-graduate Studies, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir** is a record of bonafide research work carried out by **Mr. Mushtaq Ahmad Malik (Registration No. 2003-A-706-M)** under my supervision and guidance. No part of the thesis has been submitted for any degree or diploma.

It is further certified that information received during the course of investigation have been duly acknowledged.

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ABSTRACT

The experimental material comprising of fifteen F_1s generated by crossing six diverse lines of field pea (*Pisum sativum* var. arvense) in a half diallel fashion and their six parents were evaluated in Randomized Complete Block Design with 3 replications at SKUAST-K, Shalimar campus, Srinagar during *rabi*, 2004-05.

Observations on various quantitative traits were recorded and the data subjected to diallel analysis of Griffing (1956) and Hayman (1954a,b). The estimates of genetic components of variance revealed significance of both additive and non-additive gene action for plant height, primary branches plant^{-1}, 100-seed weight and harvest index whereas, there was preponderance of non-additive gene action for other traits studied. Non-additive genetic variances were relatively greater than corresponding estimates of additive component of variance. The analysis of various

proportions of genetic components revealed that average degree of dominance was in the range of overdominance for all traits except plant height where dominance was complete. There was assymetrical distribution of positive and negative alleles in parents with preponderance of dominant alleles. The heritability estimates were moderate for all the traits.

None of the parents/crosses was found to be good general/specific combiner for all traits. The parents FP_2-80, FP_2-82 and Rachna were found to be good general combiners for most of the traits. The best crosses for most of the important traits were FP_2-80 x Rachna, FP_2-60 x Rachna and FP_2-60 x VL-1.

Recurrent selection is suggested as an effective procedure for exploitation of both additive and non-additive gene action bringing about sizeable improvement in population performance and simultaneously maintaining adequate variation in the population. Moreover, due to lower heritability values, indirect selection using component breeding can be a suitable approach for seeking improvement in grain yield of pea.

Signature of Student
Dated : _____

Signature of Major Advisor
Dated :_____

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Place : Shalimar, Srinagar **Mushtaq Ahmad Malik**

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Chapter-1

INTRODUCTION

Food legumes are important crops for food security worldwide, and are important to the livelihood of millions of people, especially in the developing countries, wherefrom their production households derive food, animal feed and income. Global pulse production estimated at some 58 million tonnes in 2002-04 remains to be dominated by the developing countries, accounting for about three forth of the total (Belhassen, 2005). Legumes such as chickpea, cowpea, dry beans, dry peas, faba beans, lentil, pigeon pea and other pulse crops are a good source of dietary protein, to complement the cereal-based diet, particularly for vegetarians in the developing world. Whereas, their by-products provide nutritious fodder for livestock. Because of their ability to fix atmosphere nitrogen, they play a key role in maintaining soil fertility and ensuring sustainability of production systems, particularly in low-input small scale agriculture. (Sakina, 2005). However, the global production of food legumes has not kept pace with increase, in global production. Therefore, there is general decline in per capita availability of pulses. This should obviously have nutritional consequences for the societies that primarily depend on pulses for enriching their daily food. The major factors responsible for poor growth in production of the food legumes is their low productivity and real challenge lies in raising productivity through widening the genetic base of these crops.

Indian sub-continent contributes about 37 per cent of the global area under pulse crops(21.1 m ha) with a production share of 26.62 (12.55 m

tonnes) per cent and productivity of about 600 kg ha^{-1} which is much below the world average of 846 q ha^{-1} (Singh and Kochar, 2005).

Field pea (*Pisum sativum* L.) or dry pea is an important *rabi*, pulse crop in India. Among rabi pulses it is most widely grown because of its higher yield potential. In Jammu and Kashmir State the pulses occupy an area of 27.45 thousand hectares with a production of 125 thousand quintals and a productivity of 4.55 q ha^{-1}. (Anonymous, 2003). However, maximum area under pulses is occupied under cultivation of pea crop.

Though there have been extensive genetic studies on field pea but the pace of development of cultivars with higher yield potential, besides possessing resistance to biotic and abiotic stresses has not been encouraging. The major constraints in this direction have been lack of promising cultivars adapted to high input agriculture, because pulses have evolved to adapt themselves for the purpose of survival, fixing their genetic potential at lower yields. Besides, pulses in general have a lower harvest index as compared to cereals. These factors coupled with incidence of diseases/abiotic stresses have rendered pulses unable to compete with cereals in order to be a major component of agricultural economy of India. It is therefore, imperative to develop a broader spectrum of high yielding genotypes by manipulation of yield components using both conventional breeding and biotechnological approaches. There are also opportunities by remodelling the structure of pea plant for higher productivity and sustainability.

The choice of parents in a breeding programme based on planned hybridization is one of the most critical consideration as the selection on the basis of *per se* performance does not provide a clear inforamtion and the

results can sometimes be misleading. The genetic parameters such as combining ability of parents and nature and extent of gene action for yield and its component traits have been found to be useful tools in selection of parents which when used in a planned hybridization programme are likely to yield successful results. Various biometrical techniques to obtain a measure of such genetic parameters have been developed such as diallel and line x tester analysis which can be efficiently used for both inbreeders and outbreeders and provide a reasonable basis for predicting the performance of yet untested crosses. Since the assessment of parents can not be done on mare yield performance, the combining ability studies are an essential component of ant crop improvement programme based on hybridization.

Diallel analysis as developed by Jinks and Hayman (1953) and Griffing (1956) is an efficient technique for deriving basic information on parental combinations in terms of their combining ability besides elucidating the nature and magnitude of gene action. Such basic information is thus a prelude to any breeding programme aiming at speedy improvement and development of a broad spectrum of high yielding genotypes. The information on general and specific combining ability can thus be used to differentially classify the parents in terms of their ability to nick well when crossed with each other and can give desirable segregates provided the evaluation of segregating generations and selection techniques are based on sound scientific grounds.

Since there has undoubtedly been meager improvement in field pea especially in the state of Jammu and Kashmir more specifically due to lack of information of these critical genetic parameters, the present study entitled

“ Genetic analysis for yield, maturity and protein content in field pea (*Pisum sativum* var. arvense)” was therefore, undertaken with following objectives.

- To estimate the general and specific combining ability effects and identify superior general and specific combiners for future breeding programmes.
- To estimate the nature and magnitude of genetic variances for aiding in selection breeding programmes.
- To generate information for genetic component of variances on the control of yield, yield attributes, maturity and protein content.

Chapter-2

REVIEW OF LITERATURE

The workdone on various aspects in pea crop in India and abroad including combining ability, nature and extent of gene action has been reviewed in the present chapter.

2.1 Combining ability

Combining ability refers to the ability of parents to transmit superior performance to their progeny. General combining ability is the overall performance of a line in cross combinations whileas specific combining ability is used to designate the cross combinations that perform better or worse than would be expected on the basis of the performance of lines involved (Sprague & Tatum, 1942). The general combining ability (gca) is specific for a set of lines and testing environments and therefore is meaningful only when its value is considered in relation to at least one other line. In terms of genetic effects, general combining ability is a function of additive genetic variance and additive x additive epistatic component whileas specific combining ability is a function of non-additive gene effects.

The concept of combining ability, even though initially put forth by maize breeders, was later on used to elucidate information in both self-and cross pollinated crops with equal success. In pea a number of studies have been carried out to estimate the combining ability effects and variances for isolating superior parental lines that show better nicking ability in cross combinations. Besides the relative magnitude of such estimates help in

formulating a systematic breeding performance for effecting improvement in the performance of the crop species.

General combining ability (gca) is the average merit of an individual or a line with respect to some traits or weighed combination of traits of large number of progenies when mated with random sample from some specific population under a specified set of environmental conditions. Specific combining ability (sca) on the other hand is the deviation of an average of an indefinitely large number of progenies of two individuals or lines from the lines which would be expected on the basis of known gca of these lines or individuals and the maternal ability of the female parent (Henderson, 1952). In the presence of epistasis, Hayman (1956) expressed the view that both gca and sca involves epistatic effects : gca involving average epistasis of array and sca involving epistasis of a particular cross combination.

Singh and Jain (1970) in their studies on pea reported that gca accounted for most of the variation for yield and its components particularly pods plant^{-1}, seeds pod^{-1} and test weight (Singh and Jain, 1970). However, variances due to gca were higher in magnitude for pod length and that of sca for seed yield, pods plant^{-1}, 100 seed weight, primary branches plant^{-1} and days to flowering (Buttler, *et al*., 1975). Crevato *et al* (1977) reported the equal significance of both gca and sca variances for inheritance of important traits in pea crop, though magnitude of gca variances was relatively higher. Studies of Dahiya *et al*. (1977) also revealed similar results for seed yield, plant height and pods plant^{-1}. Contrarily, Singh *et al*. (1977) reported higher magnitude of sca variances for days to flower, pod width and number of seeds pod^{-1}.

Paccuci and Troccoli (1977) reported that gca variance was important in the expression of seeds pod^{-1} and 100-seed weight, whereas, estimates of sca variances were predominant in the expression of other traits studied. Equal importance of both the combining ability variances was suggested by Venkateshwarlu and Singh (1981) though component of gca variance estimates was observed to be predominant. They further reported the influence of environment (years) on the expression of these variances for various quantitative traits (Venkateswarlu and Singh, 1983) and suggested the use of diallel selective mating system by selective crossing among good general combiners to release greater genetic variability.

On the basis of general combining ability Singh *et al*. (1985a) identified potentially good general combiners for height (KLMR 9, 6113, Rachna and T163), pods plant^{-1} (P209, T163, BHU397) and seed yield (T163, 6113 and P209). Significance of both gca and sca effects was reported for seed yield, seeds plant^{-1} and test weight (Singh 1985b) whereas, gca and sca variances were also advocated to be significant though sca variance was predominant (Singh 1985c) thereby suggesting a multiple mating programme among suitable hybrids for improvement of seed yield in pea.

In a diallel analysis in pea crop, Csizmadia, (1985) reported that gca variance was higher than sca variance for most of the characters studied. The parents with high gca for important traits showed above average phenotypic performance but sca effects were generally non-proportional to F_1 performance. Gupta and Lodhi (1985) in a similar study over environments reported the significant influence of environments on the gca and sca effects. It was further suggested that 2-3 generations of intercrossing to isolate good

recombinants from crosses involving varieties with good gca followed by pedigree selection could be a suitable strategy for seed yield improvement in pea.

Singh *et al*. (1987) reported higher significant gca and sca variances for all the characters studied in a 10 parent diallel cross of pea. However, the magnitude of gca variance was considerably higher that of corresponding sca variance. In another study, however, Tewatia *et al*. (1988) observed that gca variances and differences among genotypes were highly significant for pod number plant^{-1} node at which the first flower appears, harvest index and protein content. Moitra *et al*. (1988) reported the significant influence of sca variance on the expression of days to maturity in comparison to all the other economic traits studied in pea,

Rannali *et al*. (1989) reported that both gca and sca variances were significant for all traits studied but former was 4-13 times greater than. *Per se* performance of parents was suggested to be a good indicator of gca effects by Singh and Singh (1990a). It was suggested that studies on combining ability be carried across a wide range of environments to get unbiased estimates. Similarly, Pant and Bajpai (1993) reported significant gca variance estimates for seed yield, days to maturity and 100-seed weight. Promising parents and crosses based on estimates of gca and sca, respectively were also tested.

Singh *et al*. (1999) carried out Line x Tester analysis in pea and reported sca variance to be higher than gca variance for all eight traits studied. Studies of Srivastava *et al*. (2000) revealed significant gca variances for days to maturity whileas, sca variance was significant for pods plant^{-1}, seeds pod^{-1}, seed yield plant^{-1} and harvest index. Sachan *et al*. (2001) conducted a half

diallel analysis using 10 diverse genotypes of field pea and evaluation of F_1 and F_2 generations revealed that both gca and sca variances were significant for both seed yield and 100-seed weight but estimates of gca variances was relatively more than sca variance estimate for 100-seed weight. Dixit (2003) using Line x Tester analysis evaluated genotypes for maturity and yield traits and found that variances due to sca were predominant for all the characters. Pedigree method of breeding was advocated using hybrid combinations with high sca effects. Singh and Singh (2003) studied combining ability for yield traits and protein content in 10 x 10 diallel in field pea and reported that both gca and sca variances were highly significant for all traits. However, sca variances were relatively higher in magnitude of for days to flowering, days to maturity and protein content. Studies of Singh and Singh (2004) on combining ability, heritability and genetic advance using a 10 parent diallel cross revealed that both gca and sca variances, contributed significantly in the inheritance of all eleven traits studied.

2.2 Gene action

In any successful breeding programme for improvement of a crop *spp*., the knowledge of nature and extent of gene action involved in the inheritance of yield, maturity and quality traits assume considerable significance. For appropriate management of available genetic variability and realizing a sizeable improvement in performance, it is essential for breeders to be in know of forces acting on the expression of the traits. As a consequence methodologies applied to crop plants are, to a great extent, defined by the additive, dominance and epistatic components operative in the inheritance of traits for which the improvement is sought. Pea has been a model crop for

earlier Geneticists working for quantitative and qualitative characters (including G.J. Mendel) to get an insight into basic principles of inheritance which are of great practical value to the science of plant breeding. It is widely recognized that plant breeding is dictated by action, interaction and linkage relationships of genes conditioning continous variation of quantitative traits. The literature pertaining to nature and extent of gene action is briefly reviewed in the present chapter.

Sizeable amount of information has been generated on nature and extent of gene action for various traits in pea including yield, maturity and quality. Kumar (1976) using diallel analysis technique (in F_1 and F_2 generations), observed that plant height in pea was conditioned by both additive and non-additive gene effects. According to Sharma *et al*. (1977), there was partial dominance for days to flowering and over-dominance for yield and pods plant^{-1}. Studies of Singh and Singh (1979) revealed that dominance and epistatic gene effects were more important than additive effects for seed yield plant^{-1}. Similarly, Asfandiyaro (1980) reported that complimentary epistasis was important for number of pods plant^{-1}. According to Singh (1980), there was significant additive x additive gene effect for days to flowering, primary branches, pods plant^{-1}, and seed yield, whileas additive x dominance gene effects were preponderant for pod length, seeds pod^{-1} and seed weight.

Gadd and El-Sawah (1985) reported significant additive and dominance gene effects for various morphological traits. In their studies on inheritance of yield and quality traits in pea, Gupta *et al*. (1986) observed that both additive and non-additive gene effects were significant for seed yield, 100-seed weight and protein content. Gupta and Lodhi (1988) studied maturity traits in a diallel

set of crosses and observed that additive and non-additive genetic variance was significant for both the traits. There was complete dominance for days to pod formation and over-dominance for days to maturity. Csizmadia (1990) reported predominance of additive gene effects in the inheritance of seeds pod^{-1}, pod length and seed weight. Similarly, Singh and Singh (1991) observed the preponderance of additive gene effect for seed number and seed weight. However, Sirohi and Gupta (1993) found dominance gene action to be predominant for the expression of seed pod^{-1}.

Pandey (1995) used line x tester analysis technique with fourteen lines and three testers to study gene action for quality traits in field pea. He reported the importance of both additive and dominance gene action for most of the quantitative traits. Studies of Rajnarayan *et al*. (1998) revealed that dominance component was more important than additive and component for the various traits studied with epistasis of all three types also observed for some traits. Dixit (1999) studied various quantitative traits in field pea and found that both additive & non-additive gene action was important for plant height with duplicate type of interaction. According to Srivastava *et al*. (2000), there was significant contribution of additive gene action for days to flowering, days to maturity, plant height and seed yield but non-additive gene action was predominant for pods plant^{-1}, seeds pod^{-1}, biological yield and harvest index. Studies of Singh and Sharma (2001) on three crosses of pea revealed significant additive and non-additive gene effects with later being more predominant for number of seeds pod^{-1}, pod length, plant height, pods plant^{-1} and pod yield plant^{-1}. They further reported that only duplicate type of gene interaction was significant, thereby confirming prevalence of dominance

gene effects. Sachan *et al*. (2001) conducted genetic analysis of yield and component analysis of yield and component traits in field pea and reported that there was prevalence of additive gene effects for 100-seed weight, whileas for seed yield, additive x dominance gene effects were significant.

Studies of Singh and Singh (2003) in F_1 and F_2 generations of a 10 x 10 diallel cross of field pea revealed that both additive and non-additive gene action was significant for yield and its component traits. However, the magnitude of non-additive genetic variances was predominant and contributed more in the inheritance of various traits except days to flowering, days to maturity and protein content. Similarly, Dixit (2003) using a Line x Tester analysis design with five lines and three testers in field pea, observed that both additive and non-additive genetic variances were significant for all the traits with preponderance of non-additive gene action . Singh and Singh (2004) studied the relative efficiency of various selection parameters for seed yield in field pea and reported that both additive and non-additive gene action was significant for seeds pod^{-1} and 100 seed weight. They further advocated that biparental matings followed by pedigree selection would be an appropriate strategy for improvement of these traits.

Chapter-3

MATERIAL AND METHODS

The present investigation entitled “Genetic analysis for yield, maturity and protein content in field pea (*Pisum sativum* var. *arvense*)"”was conducted during *rabi*, 2004-05 at Experimental Research Farm of Division of Plant Breeding & Genetics, SKUAST-K Shalimar Campus, Srinagar.

3.1 Experimental Materials

The basic material for study comprised of six diverse genotypes of field pea (*Pisum sativum* var *arvense*) namely $FP_2$80, $FP_2$60, $FP_2$82, P-1-37, VL-1 and Rachna selected out of germplasm (source of parents used- Annexure-I) collection maintained at Pulse Research Sub-station, Habak of SKUAST-K, Srinagar.

Fifteen F_1-crosses (excluding reciprocals) were generated through a 6x6 diallel mating design during *rabi*, 2003-04 at Pulse Research Sub-station SKUAST-K, Habak, Srinagar.

3.2 Experimental Design

The experiment was laid out in Randomized complete Block Design with three replications. Both the parents and crosses were evaluated together. Each experimental plot comprised of two rows of 3 m length with inter-and intra-row spacing of 30 and 10 cm, respectively. Recommended cultural practices were followed to raise a good crop.

3.2.1 Recording of Experimental Data

Observations on different quantitative traits were recorded on ten competitive plants selected at random from each of the non-segregating

generations i.e, parents and F_1's except for days to 50% flowering and maturity for which data was recorded on whole plot basis and 100-seed weight that was recorded by weighing three random samples of 100 sun-dried seeds in each experimental plot. The procedure used for recording the data for various observations is as follows :

i. Days to 50% flowering

The number of days taken from the date of sowing to opening of first flower in 50% plants was recorded.

ii. Days to maturity

The number of days taken since the date of sowing to the 80% yellowing of pods.

iii. Plant height (cm)

The plant height was measured from the base of the plant to its apex in cm.

iv. Primary branches plant^{-1}

After the completion of flowering the number of primary branches arising directly from the main stem were counted.

v. Number of pods plant^{-1}

The total number of pods plant^{-1} were counted when the flowering was complete.

vi. Pod length

Average length of all pods from selected plants was calculated in cm.

vii. Number of seeds pod^{-1}

The number of seeds were counted from randomly selected pods in each tagged plant and average was calculated.

viii. 100- seed weight

100-seed of three randomly drawn samples from each experimental plot were weighed and averaged to obtain 100-seed weight in g.

ix. Seed yield plant^{-1}

The yield of seed obtained from selected plants from each experimental plot was weighed and was averaged to single plant basis in g.

x. Biological yield plant^{-1}

Total weight of seeds and vegetative mass, on dry basis, of the selected plants from each experimental plot was weighed in g and averaged to single plant basis.

xi. Harvest Index

It was calculated by dividing the seed yield plant^{-1} with the biological yield of the same plant and was expressed in per cent as :

$$\text{Harvest index} = \frac{\text{Seed yield plant}^{-1}}{\text{Biological yield of the same plant}} \times 100$$

xii. Protein content

Firstly Nitrogen content (per cent) was estimated by modified Kjeldhal's method of Piper (1966) and the protein content was estimated by multiplying the N-content (per cent) by a constant factor of 6.25 (AOAC, 1984).

3.3 Statistical procedure

Replication-wise mean values of experimental plot were compiled for each treatment and subjected to following statistical and biometrical analysis.

3.3.1 Analysis of variance :

The statistical model for an observation on the ith genotype in the jth replication was based on :

$$Y_{ii} = m + g_i + b_j + e_{ij}$$

Where,

m = general mean

g_i = effect of the ith genotype

b_j = effect of jth replication, and

e_{ii} = experimental error associated with ij^{th} observation assumed to be normally and independently distributed with mean zero and variance σ^2.

Anova

Source of variation	d.f	M.S	Expected mean squares
Replications	r-1	MSR	$\sigma^2 + g\,\sigma^2 r$
Genotypes	g-1	MSG	$\sigma^2 + r\,\sigma^2 g$
Error	(r-1) (g-1)	ME	σ^2

where g and r stands for genotypes and replications, respectively.

3.3.2 Combining ability analysis

The analysis was carried out for general combining ability (gca), specific combining ability (sca) and variance components. The estimates of variance for gca and sca and their effects were computed according to model-1 (fixed effect model) and method II (Parents and crosses, excluding reciprocals) as given by Griffing (1956).

The analysis of variance for combining ability was based on the following model :

$$Y_{ijk} = \mu + g_i + g_j + S_{ij} + b_k + e_{ijk}$$

Where,

Y_{ijk} = phenotype from cross of ith and j^{th} parents in k^{th} block,

μ = population mean

g_i = gca of ith parent

g_j = gca of jth parent,

S_{ij} = sca effect of ith cross,

b_k = effect of kth block

e_{ijk} = error associated with the observation

ANOVA for combining ability

Source of variation	d.f	Sum of squares	Mean sum of squares	Expected mean square
gca	P-1	Sg	Mg	$\sigma^2 + (P+2)\frac{1}{(P-1)} \sum_i g^2_I$
Sca	$\frac{P(P-1)}{2}$	Ss	Ms	$\sigma^2 + \frac{2}{P(P-1)} \sum_{1 \leq j} S^2_{ij}$
Error	m	Se	Me	P^2

where,

$$Sg \text{ (SS due to gca)} = \frac{1}{(P+2)} - \left(\sum (X_i + X_{ij})^2 - \frac{4}{P} \quad 2\, X^2_{..} \right)$$

$$1 \qquad 2X^2_{..}$$

$$Ss \text{ (SS due to Sca)} = \sum X^2_{ij} - \frac{}{P+2} (X_i + X_{ij})^2 + \frac{}{(P+1)\ (P+2)}$$

r = number of blocks

m = error d.f.

P = number of parents

The error mean square (Me) was obtained after dividing the error mean square (Me) from RBD Anova by the number of replications.

The significance of mean square due to gca (Mg) and sca (Ms) was tested against error mean square (Me) by F-tesrt at p = 0.05 and p = 0.01

3.3.3 Estimates of combining ability effects and their standard errors :

The gca effect of parent (I) was calculated as under

$$gi = \frac{1}{(P+2)} (X_{i.} + X_{ii}) - \frac{2X..}{P}$$

The sca effect of a cross (i x j) was calculated as under :

$$S_{ij} = X_{ij} - \frac{1}{(P+2)} (X_{i.} + X_{.j} + X_{jj}) + - \frac{2X..}{(P+1)\ (P+2)}$$

where,

Xi. = total of array involving i^{th} parent

$X_{.j}$ = total of array involving j^{th} parent,

X_{ii} = parental value of ith parent,

X_{jj} = parental value of jth parent, and

X.. = total of all P (P +1) items of diallel table

The standard errors for test of significance of gca and sca effects were worked out as follows :

$$S.E\ (g_i) = \left(\frac{P-1}{P\ (P+2)} Me \right)^{0.5}$$

$$S.E\ (S_{ij}) = \left(\frac{P^2 + P + 2}{(P+1)\ \ (P+2)} Me \right)^{0.5}$$

$$S.E\ (g_i - g_j) = \left(\frac{2\ Me'}{(P+2)} \right)^{0.5}$$

3.3.4 Estimates of combining ability variances and their standard errors :

Variance of effects were computed by following formulae :

$$Var\ (g_i) = \frac{(P-1)\ Me}{P\ (P+2)\ a}$$

$$Var\ (S_{ij}) = \frac{(P^2+P\ +2)\ Me}{(P+1)\ (P+2)\ a}$$

The standard errors to test different effects were obtained by square root of the above estimates.

3.3.5 Component analysis

Using Hayman's (1954a) least square estimates, the following genetic components of variations in F_1 were calculated :

i) D= $4\ \Sigma uvd^2$ = components of variation due to additive effect of genes arising from differences between a pair of corresponding homozygotes.

If u = v=0.5 then D = d^2

Where

u = proportion of positive genes in the parents,

v = proportion of negative genes in the parents,

d = additive effect, and

u + v=1

ii) H_1 = Σuvh^2 = component of variation due to dominance effect of genes arising from the departure of heterozygotes from the mean of the corresponding pair of homozygotes.

iii) $H_2 = H_1\ [1 - (u-v)^2] = 16\ \Sigma\ u^2\ v^2\ h^2$

= proportion of dominance variance due to positive (u) and negative (v) effects of genes.

iv) h^2 = net dominance effect (algebric sum over all loci in heterozygous phase in all crosses)

v) Fr = Proportion of dominant and recessive alleles of genes in j^{th} parent

vi) F = relative frequency of dominant and recessive alleles in parents

Group of equations based on the following parameters derived from diallel table were constructed to obtain the above components of variance.

V_0L_0 = VP = variance of parental array

Vr = variance of rth array

V_1L_1 = Vr = mean of array variances

Wr = covariance between parents and their off-springs in r^{th} array

W_0L_{01} = Wr = mean covariance between the parents and off-springs of all the array

V_0L_1 = Vm = variances of means of arrays

$ML_1 - ML_0$ = the difference between the means of parents and means of their P^2 -progenies

E = expected environmental components of variation (observed from analysis of variance of the design).

Following equations were constructed using above parameters

i) $V_0L_0 = Vp = D + E$

ii) $V_1L_1 = \bar{V}r = \frac{1}{4} D + \frac{1}{4} H_1 \frac{1}{4} F + \frac{P + 2E}{2p}$

iii) $W_0L_{01} = Wr = \frac{1}{2} D - \frac{1}{4} F + \frac{1}{P} E$, and

iv) $V_0L_1 = \frac{1}{1} D + \frac{1}{1} H_1 \frac{1}{1} H_2 \frac{1}{1} F + \frac{1}{1} E$

4 4 4 4 2P

where

$$E = Me = \frac{\textbf{\textit{Error variance}}}{\text{Number of replications x number of environments}}$$

The components of genetic variance were estimated as follows :

$$D = V_0L_0 - E$$

$$H_1 = V_0L_0 - C_1W_0L_{01} + 4V_1L_1 - (3P-2)\left(\frac{E}{P^2}\right)$$

$$H_2 = 4V_1L_1 - 4V_0L_1 - 2E$$

$$h^2 = 4\,(ML1 - ML_0)^2 - 4\,(P-1)\left(\frac{E}{P^2}\right)$$

$$F = 2V_0L_0 - 4\,W_0L_{01} - 2\,(P-2)\left(\frac{E}{P}\right)$$

Where

P = number of parents

3.3.6 Standard error of genetic components

To test the significance of various components of variance, their standard errors were calculated using the equation ½ var (Wr – Vr) = S^2 and the terms of main diagonal of covariance matrix given by Hayman (1954a) as corresponding multipliers.

The standard error of each component of variance were thus computed as follows

$$\text{S.E of } D = \left(\frac{S^2\,(P^5 + P^4)}{P^5}\right)^{0.5}$$

$$\text{S.E of } H_1 = \left(\frac{S^2 (P^5 + 4L P^4 - 12 P^3 + 4 P^2)}{P^5} \right)^{0.5}$$

$$\text{S.E of } H_2 = \left(\frac{S^2 (36 P^4)}{P^5} \right)^{0.5}$$

$$\text{S.E of } h^2 = \left(\frac{S^2 (16 P^4 + 16 P^2 - 32P + 16)}{P^5} \right)^{0.5}$$

$$\text{S.E. of } F = \left(\frac{S^2 (4 P^5 + 20P^4 - 16 P^3 + 16P^2)}{P^5} \right)^{0.5}$$

$$\text{S.E of } E = \left(\frac{S^2 (P^4)}{P^5} \right)^{0.5}$$

Where,

P = number of parents

3.3.7 Test of significance of genetic components

t-test at P-2 degrees of freedom was used to test the significance of genetic components as follows

$$t = \frac{\text{Parameter}}{\text{S.E. of parameter}}$$

3.3.8 Proportions of genetic components

Following proportions of various genetic components were calculated

3.3.8.1 Degree of dominance

The average degree of dominance was calculated as positive square root of ratio between component of variation due to dominance effects of the genes to component of variation due to additive effects of genes i.e

Degrees of dominance = $(H_1/D)^{0.5}$

Its value when less than one indicated that genetic control of the character is largely due to additive gene action though some degree of dominance also exists, whereas, more than one indicates over-dominance. If this ratio equaled zero, no dominance was indicated.

3.3.8.2 Proportions of genes with positive and negative effects in parents

The proportion of positive and negative alleles at loci exhibiting dominance was calculated by formulae :

$UV = H_2/4H_1$.

The ratio has maximum value of 0.25 signifying thereby that there is symetrical distribution of positive and negative alleles. The value less than 0.25 indicates that positive and negative alleles are not in equal proportion in parents.

Since U+V = 1and U-V = (1-4 Ur)½

The value of U and V could be found out

3.3.8.3 Ratio of dominant and recessive genes in parents

The prevalence of dominant and recessive genes was calculated by ratio :

$$\frac{(4\ DH_1)^{½} + F}{(4\ DH_1)^{½} - F}$$

where positive and negative sign of F indicated dominant and recessive genes respectively. If the ratio was 1 dominant and recessive genes in parents were indicated to be in equal proportion. If it was less than 1, it indicated an excess of recessive genes and if it was more than 1, it indicated an excess of dominant genes.

Chapter-4

EXPERIMENTAL FINDINGS

The results of present investigation with respect to various genetic parameters are presented under the following heads :

4.1 Analysis of variance

4.2 Analysis of variance for combining ability

4.3 Analysis of mean performance and estimates of combining ability effects

4.4 Analysis of genetic components of variance

4.1 Analysis of variance

The analysis of variance of the experimental design for 11 quantitative traits viz. days to 50% flowering, days to maturity, plant height, primary branches plant^{-1}, number of pods plant^{-1}, pod length, number of seeds pod^{-1}, 100-seed weight, seed yield plant^{-1}, harvest index and protein content are presented in Table 1. The analysis revealed that the treatments differed significantly from each other indicating considerable variability among parental lines used in the study. The hybrids however, showed significant differences for all traits except pod length and number of seeds pod^{-1}.

4.2 Analysis of variance for combining ability

The analysis of variance for combining ability for various traits is presented in Table 2. The results showed highly significant mean squares due to general combining ability for all the traits except number of pods plant^{-1} and seeds pod^{-1}. The mean squares due to specific combining ability were highly significant for all traits. When estimates of variance due to general combining ability (σ^2_S) and specific combining ability (σ^2_S) were compared using appropriate expected mean squares, the magnitude of sca variances was observed to be considerably higher than that of corresponding estimate of gca variance for all the quantitative traits except plant height and pod length.

4.3 Analysis of mean performance & estimates of combining ability effects.

The Annexure-II presents the mean performance of 6 parents viz., FP-2-80, FP-2-60, FP-2-82, P-1-37, VL-1 and Rachna and their all possible cross combinations. Similarly, the analysis of general and specific combining ability effects are presented in Table-3 and Table-4 respectively. The character-wise results are discussed below:

4.3.1 Days to 50% flowering

Among parents Rachna and FP-2-60 were earlier and rest were late in flowering. FP-2-60 and Rachna exhibited high desirable significant gca where as FP-2-80 was significantly undesirable (late maturing) in terms of gca effects.

Among cross combinations FP-2-60 x FP-2-82, FP-2-82 x P-1-37 and FP-2-60 x FP-2-80 were earliest to flower. The cross combinations FP-2-60 x VL-

1, FP-2-60 x Rachna and P-1-37 x VL-1 exhibited significant desirable sca effects for days to flowering

4.3.2 Days to maturity

The parents P-1-37 and FP-2-82 were early in maturity whereas rest were late/intermediate in maturity expression. FP-2-60 and Rachna had significant desirable gca effects for maturity, whereas, FP-2-82 was found to be undesirable based on gca effects.

Among crosses, FP-2-60 x FP-2-82, FP-2-60 x P-1-37 and FP-2-82 x VL-1 were early to mature and the crosses showing significant desirable sca effects for early maturity included FP-2-60 x VL-1, P-1-37 x VL-1 and P-1-37 x Rachna. The cross combination FP-2-80 x P-1-37 exhibited significant sca effects for lateness.

4.3.3 Plant height (cm)

The parents Rachna, FP-2-82 and Vl-1 were tall and P-1-37 and FP-2-80 were dwarf. Among parents Rachna, P-1, FP-2-80 and VL-1 had highly significant and desirable gca effects for this trait whereas, FP-2-60 had significant but undesirable gca effects for height.

Out of 16 cross combinations, FP-2-82 x VL-1, FP-2-82 x Rachna and FP-2-60 x Vl-1 were tall and FP-2-80 x P-1-37 and Fp-2-80x FP-2-60 were dwarf. The F_1 hybrids exhibiting high significant sca effects for height were marked out in FP-2-80 x P-1-37, FP-2-80 x Rachna, VL-1 x Rachna, FP-2-82

x VL-12, FP-2-82 x P-1-37, FP-2-60 x P-1-37 and FP-2-82 x Rachna. The cross P-1-37 x VBl-1 exhibited significant sca effect for dwarfness.

4.3.4 Primary branches plant^{-1}

Among parents VL-1 had the highest number of primary branches plant^{-1}, followed by Rachna, FP-2-82 and FP-2-60. The parents P-1-37, Rachna and VL-1 had highly significant gca effects for this trait.

The crosses showing higher number of primary branches plant^{-1} included VL-1 x Rachna, FP-2-60 x VL-1 and FP-60 x Rachna. The hybrid combinations FP-2-60 x FP-2-82, FP-2-80 x P-1-37 and FP-2-80 x FP-2-82 showed highly significant sca effects for primary branches whileas for remaining crosses, it was largely non-significant and negative in some cases as well.

4.3.5 No. of pods plant^{-1}

The parental lines FP-2-80 and FP-2-82 had highest number of pods plant^{-1} followed by P-1-37, VL-1 and Rachna whereas, FP-2-60 had lowest number of pods plant^{-1}. In the present study none of the parents showed significant desirable gca effects for this trait. On the other hand the parent line FP-2-60 exhibited significant negative gca for number of pods plant^{-1}.

Among the cross combinations FP-2-80 x FP-2-60 and FP-2-80 x VL-1 possessed highest number of pods plant^{-1} followed by FP-2-80 x FP-2-82. In order of merit only two crosses viz. FP-2-80 x Rachna and FP-2-80 x FP-2-82 exhibited significant and desirable sca effects for pods plant^{-1}. Again a few crosses exhibited significant negative sca effects for this trait whileas rest were non-significant.

4.3.6 Pod length

Among parents the highest pod length was shown by FP-2-80 followed by FP-2-82 and P-1-37 whileas, FP-2-60 exhibited shortest pod length. The parents FP-2-60 and FP-2-82 exhibited highly significant and desirable gca effects for this trait whileas P-1-37 had negative significant and undesirable gca effects.

The highest pod length, among cross combinations, was demonstrated by FP-2-80 x FP-2-60, FP-2-80 x VL-1, FP-2-80 x FP-2-82 followed by FP-2-80 x Rachna. However, only two crosses viz. FP-2-80 x P-1-37 and FP-2-80 x FP-2-82 exhibited significant desirable sca effects for pod length whileas for rest of crosses, it was, by and large, non-significant

4.3.7 No. of seeds pod^{-1}

Out of 6 parents Rachna possessed highest number of seeds pod^{-1} followed by VL-1, FP-2-80 and FP-2-60. Not a single parent showed significant desirable gca effect, but the parent FP-2-60 exhibited significant negative gca for number of seeds pod^{-1}.

Among the crosses VL-1 x Rachna possessed highest number of seeds pod^{-1} followed by FP-2-82 x VL-1, FP-2-80 x FP-2-82 and FP-2-80 x FP-2-60.The crosses exhibiting highly significant gca effects for this trait were FP-2-80 x P-1-37, FP-2-80 x FP-2-82 and FP-2-60 x Rachna.

4.3.8 100-seed weight

For 100-seed weight, the highest mean performance was shown by VL-1 followed by FP-2-80 and Rachna. The parents FP-2-80 and P-1-37 exhibited highly significant gca effect while as Rachna had significant negative gca effects for 100 seed weight.

High mean performance for 100-seed weight was shown by P-1-37 x VL-1, FP-2-80 x P-1-37ans P-1-37 x Rachna. The crosses FP-2-80 x Rachna, P-1-37 x Rachna & FP-2-80 x VL-1 exhibited highly significant and desirable sca effects for 100-seed weight.

4.3.9 Seed yield plant^{-1}

Among parental lines, VL-1, Rachna and FP-2-80 showed higher mean performance for seed yield plant^{-1}, whileas, FP-2-82 was lowest seed yielder. The parents FP-2-80 and P-1-37 exhibited highly significant gca effects for seed yield plant^{-1} whereas, Rachna had significant negative gca effect for this trait.

The highest overall seed yield plant^{-1}, among crosses, was showed by VL-1 x Rachna followed by FP-2-80 x P-1-37, FP-2-80 x VL-1 and FP-2-82 x VL-1. The F_1 hybrid combinations exhibiting highly significant and desirable sca effects for seed yield included FP-2-80 x VL-1, FP-2-80 x Rachna and FP-2-60 x FP-2-82.

4.3.10 Harvest index

Highest harvest index was recorded in VL-1 followed by P-1-37, Rachna and FP-2-60, whileas, FP-2-82 recorded lowest harvest index. Among parents only FP-2-80 exhibited significant desirable gca effect for harvest index while as for other parents, gca effects were largely non-significant.

Among crosses, the combinations FP-2-80 x FP-2-82, FP-2-80 x FP-2-60 and FP-2-80 x P-1-37 exhibited high harvest harvest index. The cross combination FP-2-60 x Rachna and FP-2-60 x FP-2-82 showed highly significant and desirable sca effects for harvest index whileas for rest of crosses, sca effects were largely non-significant.

4.3.11 Protein content

Among parental lines, the highest and lowest protein content were revealed by FP-2-82 and VL-1 respectively. Only FP-2-60 recorded significant desirable gca effect for protein content and for rest of parental lines, it was either non-significant or significantly negative.

Among F_1 hybrids, the highest protein content in order of merit was recorded for FP-2-60 x FP-2-82, FP-2-60 x P-1-37, FP-2-82 x P-1-37 and FP-2-82 x Rachna. The cross combinations viz. FP-2-60 x VL-1, P-1-37 x VL-1 and FP-2-60 x Rachna exhibited highly significant and desirable sca effects for protein content, whileas for rest of crosses, sca effects were largely non-significant

4.4 Analysis of genetic components of variance

The estimates of various genetic components of variance viz., D (additive) H_1 and H_2 (dominance), h^2 (dominance effects), F (Mean of Fr over array) and E (environmental effect) are presented in Table 5. Various proportions of genetic components viz. mean degree of dominance (H_1/D), proportion of positive and negative genes ($H_2/4H_1$), proportion of dominant and recessive genes in parents (KD/KR), number of effective factors controlling a trait (h^2/H_2) and heritability (n.s) are presented in Table 6. Character-wise results are described below.

4.4.1 Days to flowering

The dominance component was only significant for this trait whileas additive component (D) was non-significant. F value was positive but non-significant and environmental variance (E) was also non-significant

The analysis of ratio of genetic components revealed that mean degree of dominance was in the range of overdominance. The value of $H_2/4H_1$ (0.18) was less than the theoretical value of 0.25 indicating asymmetrical distribution of

positive and negative alleles in parents. The ratio KD/KR was greater than unity indicating prevalence of dominant alleles. Heritability estimate was moderate (33 per cent).

4.4.2 Days to maturity

Dominance component only was significant for this trait whereas D was non-significant. Both F and E components were non-significant but positive.

Mean degree of dominance was in the range of over-dominance (3.63). The estimate of $H_2/4H_1$ was less than theoretical value (0.17) and indicated assymetrical distribution of positive and negative alleles. The ratio KD/KR (7.56) indicated predominance of dominant alleles. The heritability estimates was moderate (38 per cent).

4.4.3 Plant height

Both additive (D) and dominant (H_1 & H_2) components were significant but later was relatively higher in magnitude indicating preponderance of non-additive gene action. The F value was positive and significant whileas environmental variance was non-significant.

The analysis of proportion of genetic components revealed partial dominance ($(H_1/D)^{½}$ = 0.92). The proportion $H_2/4H_1$ was less than the theoretical value. The ratio KD/KR was greater than unity and the heritability estimates were moderate (48 per cent)

4.4.4 Primary branches plant^{-1}

Both additive and dominance components were significant but latter was greater in magnitude indicating its greater importance in the inheritance of the trait. F value was positive and significant whereas E value was non-significant. The value of h^2 was significant.

The mean degree of dominance (H1/D)½ = 1.05) revealed almost complete dominance for this trait. The proportion of positive and negative alleles in parents was less than its theoretical value ($H_2/4H_1$ = 0.17). The ratio KD/KR was greater than unity. Heritability estimates were low at 26 per cent.

4.4.5 No. of pods plant $^{-1}$

Only dominance components were significant whileas additive component was non-significant indicating preponderance of non-additive gene action. Values of h^2, F & E values were positive but non-significant.

The mean degree of dominance was in the range of overdominance. The ratio $H_2/4H_1$ was less than its theoretical estimate of 0.25. The proportion KD/KR was greater than unity indicating prevalence of dominant alleles in parents. Heritability estimates for the trait was low (15 per cent).

4.4.6 Pod length

Additive component (D) was non-significant and dominance components (H_1 & H_2) were significant . F & h^2 values were positive and significant. The estimates of environmental variance (E) was significant indicating greater interaction of this trait with the environment.

Mean degree of dominance (3.23) revealed over-dominance. The value of proportion $H_2/4H_1$ (0.20) was less than the theoretical value. The ratio KD/Kr was greater than unity. Heritability estimate was moderate (41 per cent)

4.4.7 No. of seeds pod^{-1}

Both D and H_1 were non-significant for seeds pod^{-1} and only H_2 was significant. The h^2 values was negative and non-significant. The estimates of both F and E were positive and significant.

Analysis of proportion of genetic components revealed overdominance (H_1/D)½ = 2.24). The ratio $H_2/4H_1$ was less than its theoretical value of 0.25.

The estimate of KD/KR was less than unity (23.25) indicating prevalence of recessive alleles in the parents for this trait. Heritability for the trait was low (28. per cent).

4.4.8 100- seed weight

Both additive and dominance components were significant but the magnitude of latter component was relatively greater than former indicating prevalence of non-additive gene action. The value of h^2 and E were positive and significant. However, F value was positive but non-significant

Mean degree of dominance revealed over-dominance. The proportion $H_2/4H_1$ which shows distribution of positive and negative alleles in the parents was less than its theoretical value of 0.25. The ratio KD/KR was greater than unity. Heritability estimate was moderate (32 per cent).

4.4.9 Seed yield plant^{-1}

Only dominance components (H_1 & H_2) were significant whileas, additive component (D) was non-significant. The value of h^2, F and E were positive but non-significant.

The estimates of (H_1/D)½ was greater than unity indicating over-dominance. The value of $H_2/4H_1$ was less than its theoretical value whileas the ratio KD/KR was greater than unity indicating prevalence of dominant alleles in parents. The estimate of heritability for seed yield was observed to be moderate (31 per cent).

4.4.10 Harvest index

Both additive and dominance components were significant but latter were more pronounced as indicated by relatively greater magnitude of H_1 and H_2. The

values of h^2 and E were non-significant though both were positive. F value was positive and significant.

The analysis of various proportions of genetic components revealed over-dominance as $(H_1/D)^{1/2}$ value exceeded unity. The ratio $H_2/4H_1$ was less than its theoretical value of 0.25. KD/KR value was greater than unity and heritability (n.s) was estimated to be low (27 per cent).

4.4.11 Protein content

Dominance component (H_1) was significant whereas, additive component (D) was non-significant indicating preponderance of non-additive gene effects. The values of h^2, F and E were non-significant though positive.

Mean degree of dominance indicated overdominance. The ratio $H_2/4H_1$ (0.20) was less than the theoretical value of 0.25 indicating asymmetrical distribution of positive and negative alleles in parental lines. The estimate of KD/KR was greater than unity and heritability estimates was low (27. per cent).

Chapter-5

DISCUSSION

Towards increasing sustainable agricultural growth and enhancing agricultural productivity food legumes deserve special attention. Despite the fact that grain legumes possess the outstanding features such as high protein and mineral content, and serve as important source of nitrogen for the soil, the production of these crops has been stagnating world over. In India, which accounts for nearly one-third of the world's pulses area and one fourth of the world's pulses production, the production during the last several years has not improved resulting in significant decline in the per capita availability of pulses the, highly valued nutrient resource for its poor people. Therefore, important task is to devise the strategies in order to promote the production of leguminous crops so that these are affordable to all. The situation is all the more dismal in J&K state where productivity levels of grain legumes, including field pea are low. The productivity of pea in the region is just 4.55 q ha^{-1} (Anonymous 2003) as compared to national average of 8.56 q ha^{-1} (Anonymous, 2002). Any focused strategy in production improvement would need to take into account the realities of this scenario notwithstanding the fact that nearly all the pea production materializes in rainfed areas characterized by small farm character.

Present yield levels of pea cultivars are much less than the HYV's of cereals, putting a pressing responsibility on plant breeders to restructure breeding programmes. Besides, the breeding system of a crop has a bearing on the amenability of various breeding strategies. Field pea is a strictly autogamous crop and therefore, suffers from the same bottle necks as selfers do,

particularly a restriction on free exchange of genes. Despite extensive studies carried out in pea crop, the progress in developing a large spectrum of cultivars with high yield potential as well as resilience to withstand biotic and abiotic stresses has been limited. Physically more efficient plant types can bring about tremendous gain in yield and efforts are needed to redesign the plant type of varieties with appropriate growth habit and source-sink kinetics. The problems associated with limited productivity can be effectively addressed by modern genetic techniques.

In the case of self pollinated crops possibilities to recover potential high yielding lines primarily depends upon the availability of potential putative parents in a hybridization programme. Selection of such promising parents must not only depend on the *per se* performance of the genotypes but also on the nature of genetic value they exhibit once tested in an appropriate genetic evaluation programme. It has to be recognized that the ability of parents to "nick" well in a hybridization programme is the consequence of complex gene interactions and in the case of characters governed by polygenes (like yield), the knowledge of genetic parameters which elucidate this basic information is essential for the formulation of a systematic breeding programme.

Techniques of biometrical genetics have been extensively used in plant breeding programmes to elucidate the information concerning the genetics of polygenic traits. Combining ability of the parents and and crosses have been estimated to determine their nicking ability and obtain unbiased estimates of genetic components of variance that ultimately contribute to the efficiency of selection. Multiple mating programmes involving crossing of the parental

genotypes in an appropriate genetic design have been extensively used in agricultural crops to generate information on important genetic parameters.

Jinks and Hayman (1953) proposed a diallel mating design that was subsequently used to estimate the components of genetic variance. Similarly, Griffing (1956) put forth the numerical approach of diallel analysis that also enabled the determination of combining ability of parents and their crosses. The information generated through these designs being limited in its applicability to the material in question and in a particular set of environmental conditions, the approach was used in estimate the important genetic parameters with respect to promising field pea genotypes primarily with the objective to obtain the estimates of general and specific combining ability effects of parents and their crosses and to identify superior general (gca) and specific (sca) combiners for future breeding programmes together with the objective to estimate the nature and magnitude of gene action and in planning future breeding programme. It was ensured that the assumptions underlying the use of the technique are, by and large, accounted for in the material used.

The analysis of variance for experimental design for eleven quantitative traits, viz days to 50% flowering, days to maturity, plant height, primary branches plant^{-1}, number of pods plant^{-1}, pod length, number of seeds pod^{-1}, 100-seed weight, seed yield plant^{-1}, harvest index and protein content revealed highly significant differences for all the traits indicating thereby, that parental lines were having considerable variability. Based on the mean *per se* performance, three crosses were earlier than the earliest parents for maturity traits whereas, for plant height, three crosses surpassed the tallest parent (Rachna) and none of

the crosses was shorter than the parent. For most of the other traits particularly number of primary branches plant^{-1}, number of seeds pod^{-1}, 100-seed weight, seed yield plant^{-1} and harvest index, none of the crosses surpassed the best parent even though the performance with respect to these traits was at par. For number of pods plant^{-1}, only a single cross exceeded the best parent, whereas, for pod length and protein content six crosses each surpassed the best parent. However, for most of the traits a sizeable number of crosses surpassed the better parent performance. There was significant correspondence between gca and sca relationship of parents and crosses, respectively as was evident from the fact that good combining parents with better *per se* performance were also involved in superior cross combinations. Observations with regard to availability of considerable variation in terms of *per se* performance in field pea has been reported by several workers (Sharma, 1975).

The analysis for estimation of combining ability variances revealed that mean squares due to gca and sca were highly significant for all the traits except number of pods plant^{-1} and number of seeds pod^{-1} for which mean squares due to gca were non-significant. The significance of both gca and sca mean squares for the traits implied the importance of both additive and non-additive gene action in the inheritance of these traits. The fact that the estimates of relative magnitude of gca and sca could not be unambiguous (Arunchalam 1976), the relative importance of genetic components was measured on the basis of variances due to gca (σ^2g) and sca (σ^2_S). The analysis of gca and sca variances revealed that estimates of σ^2_S were higher in magnitude than their corresponding σ^2g estimates for all the traits except plant height and pod length, indicating greater

contribution of non-additive gene effects in the expression of these traits. When translated into genetic components of variance (σ^2_A and σ^2_D) the inference with regard to nature of gene action did not change. Analysis further revealed that average degree of dominance was greater than unity for all characters, except plant height and primary branches plant^{-1} indicating overdominance. For plant height (0.92) and primary branches plant^{-1} (1.05) the average degree of dominance revealed partial and complete dominance for these traits respectively. These results are in full agreement with the findings of Kalia and Sharma (1998), Singh *et al*. (1999), Srivastava *et al*. (2000) and Singh and Singh (2003).

The basic premise of any study involving combining ability effects is to get a first hand information about the worth of parents in terms of their nicking ability in cross combinations as well identify the superior crosses that can be starting materials for any systematic breeding programme. Based on planned hybridization, such crosses can also give desirable segregants in advanced generations containing superior gene combinations.

The general combining ability effects of the six parents used in the study revealed that none of the parents was a good general combiner for all the eleven traits (Table 7). The parent P-1-37 was a good general combiner for most of the traits including seed yield plant^{-1}, which implies that it contains favourable alleles for these traits. FP-2-80 was a good combiner for yield traits but was a poor combiner for maturity and harvest index. FP-2-60 was a poor combiner for most of the traits as was evident from the negative value of its gca effects. Rachna was good general combiner for days to flowering, days to maturity, plant height and primary branches plant^{-1} but did not combine well for yield traits as

shown by its negative gca effects for 100-seed weight and seed yield plant^{-1}. Similarly poor general combining ability of VL-1 was the result of its poor combining ability effects for number of pods plant^{-1}, pod length, number of seeds pod^{-1} and 100-seed weight. Panday and Gritton (1975) and Singh ands Joshi

Table 7 : Identification of elite parents on the basis of general combining ability in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Characters	Parents with high gca value
Days to 50%flowering	i) FP_2-60 (-0-45**)
	ii) FP_2-82 (-0.09**)
	iii) VL_1 (-0.07**)
Days to maturity	i) FP_2-60 (-0.66**)
	ii) P_1-37 (0.02**)
	iii) VL_1 (0.08**)
Plant height (cm)	i) Rachna (7.16**)
	ii) P_1-37 (7.08**)
	iii) FP_2-82 (1.76**)
Primary branches plant^{-1}	i) P1-37 (1.17**)
	ii) Rachna (0.48**)
	iii) VL1 (0.14**)
No. of pods plant^{-1}	i) Rachna (0.118**)
	ii) FP_2-80 (0.07**)
	iii) P_1-37 (0.06**)
	iv) VL_1 (0.03**)
Pod length (cm)	i) FP_2 -80 (0.16**)
	ii) FP_2-82 (0.10**)

Continued……

Table 7: (Contd.)

No. of seed pod^{-1}	i) VL_1 (0.04**)
	ii) Rachna x FP_2-82 (0.03**)
100 seed weight (g)	i) FP_2-80 (0.52**)
	ii) P_1-37 (0.36**)
	iii) VL_1 (0.02**)
Seed yield plant^{-1}	i) $FP_2$80 (0.31**)
	ii) P_1-37 (0.27**)
	iii) FP_2-82 (0.07**)
	iv) VL_1-(0.02**)
Harvest index	i) FP_2-80 (0.85**)
	ii) P_1-37 (0.08**)
	iii) VL_1 (0.03**)
Protein content	i) FP_2-60 (0.61**)
	ii) VL_1 (0.32**)
	iii) FP_2-82 (0.12**)

(1982) emphasized the importance of these traits for improvement of yield in field pea.

The comparison of mean performance *per se* and gca effects of parents revealed that parents with high mean performance were also good and desirable general combiners particularly for number of pods plant^{-1}, 100-seed weight and

seed yield plant^{-1}, although such a correspondence could not be generalized for all the traits. The results support the earlier observations of Shiv Kumar *et al.* (2001) and Sofi (2003). Non correspondence of mean performance and gca effects for traits such as days to flowering and days to maturity have also been reported by Katiyar *et al.* (1987).

Present investigation revealed that none of the crosses exhibited significant sca effects for all the traits. For yield, the cross FP-2-80 x VL-1 had highest sca effects closely followed by FP-2-80 x Rachna and FP-2-60 x FP-2-82 (Table 8). The cross FP-2-80 x FP-2-82 even though a good specific combiner for yield attributing traits particularly number of pods plant^{-1}, number of seed pod^{-1} and 100-seed weight was strikingly a poor combiner for seed yield. In contrast the good sca effects of the cross FP-2-80 x Rachna was consequential of its high sca effects for yield component traits. For maturity traits (days to 50% flowering and days to maturity), the crosses FP-2-60 x

Table 8 : Identification of elite cross combinations on the basis of specific combining ability in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Characters	Cross combinations	
Days to 50%flowering	i)	FP_2-60 x Rachna (-1.48)
	ii)	FP_2-60 x VL_1 (-1.42)
	iii)	P1 37 x VL_1 (-1.08)
Days to maturity	i)	FP_2-60 x VL_1 (-2.85)
	ii)	P_1-37 x Rachna (-2.11)
	iii)	P_1-37 x VL_1 (-1.39)
Plant height (cm)	i)	FP_2-80 x P_1-37 (10.69)
	ii)	FP_2-80 x Rachna (10.54)

	iii)	FP_2-80 x FP_2-82 (4.92)
	iv)	VL_1 x Rachna (4.83)
	v)	FP_2-82 x VL_1 (4.21)
Primary branches plant^{-1}	i)	FP_2-60 x FP_2-82 (1.12)
	ii)	FP_2-80 x P_1-37 (1.00)
	iii)	FP_2-80 x FP_2-82 (0.80)
No. of pods plant^{-1}	i)	FP_2-80 x Rachna (2.13)
	ii)	FP_2-80 x FP_2-82 (0.62)
	iii)	FP_2-60 x FP_2-82 (0.54)

Continued……

Table 8 : (Contd.)

Pod length (cm)	i)	FP_2-80 x P_1-37 (0.42)
	ii)	FP_2 x FP_2-82 (0.31)
No. of seed pod^{-1}	i)	FP_2-80 x P_1-37 (0.45)
	ii)	FP_2-80 x FP_2-82 (0.31)
	iii)	FP_2-60 x Rachna (0.28)
100 seed weight (g)	i)	FP_2-80 x Rachna (1.25)
	ii)	P_1-37 x Rachna (1.12)
	iii)	FP_2-80 x VL_1 (0.92)
Seed yield plant^{-1}	i)	FP_2-80 x VL_1 (1.10)
	ii)	FP_2-80 x Rachna (0.89)
	iii)	FP_2-60 x FP_2-82 (0.59)
Harvest index	i)	FP_2-60 x Rachna (1.91)
	ii)	FP_2-60 x FP_2-82 (1.80)

Protein content	i)	FP_2-60 x VL_1(3.05)
	ii)	P_1-37 x VL_1 (1.61)
	iii)	FP_2-60 x Rachna (1.44)

VL-1, FP-2-60 x VL-1 and P-1-37 x VL-1 exhibited significant desirable sca effects . A comparison of gca and sca effects revealed that parent FP-2-60 even though a poor general combiner for most of the traits was involved in a sizeable number of superior combinations. Such an observation indicated that yield and other traits are complex in inheritance and that specific performances of crosses were more important for these traits than gca effects, possibly due to preponderance of non-additive gene effects for most of the quantitative traits as was already demonstrated by estimated combining ability variances

For seed yield plant^{-1} the promising cross combinations involved either good x good or good x poor general combiners, while as for other traits even poor x poor combinations were superior. The superiority of crosses due to good x good general combiners can be attributed to concentration of favourable alleles whereas, the superiority of the crosses as a result of good x poor or poor x poor general combiners could be due to favourable interaction between alleles with positive and negative effects (overdominance or complementary epistasis). Since only a small number of crosses exhibited significant sca effects for yield, heterosis breeding within the current level of feasibility of large scale seed production can not be a viable option. However, since both additive and non-additive gene effects were observed to be predominant, breeding strategies that

generate transgressive segregants would be advantageous for effecting fruitful improvement in the present set of materials.

For any successful breeding programme, it is essential to get ample insight into the architecture of yield and its component traits. It has been established that various aspects of genetic architecture dictate the usefulness of breeding programmes with equal applicability to inbreeders and outbreeders, even though they may significantly differ in their genetic systems. The method of estimation of genetic component of variance (Hayman, 1954) has proved to be a useful tool for breeders for operational dissection of traits at genic level and its expression in the phenotype. The procedure, however, has to proceed within the same set of basic limitations and is never assumption free, especially for the genetic mechanisms such as epistasis, multiple allelism and linkage which one can hardly exclude while dealing with polygenic traits. However, Hayman (1960) insisted that despite partial non-fulfillment of assumption, dominance is not greatly affected. Same has also been put forth by Verhallen & Murray (1967). The genetic component of variance estimated in the present investigation are therefore discussed with the limitations imposed by the model. Both additive (D) and dominance (H_1 & H_2) components were significant for important traits viz Plant height, primary branches plant^{-1}, 100-seed weight, harvest index and protein content indicating importance of both the components in the expression of these traits. However, the magnitude of dominance component was greater than its corresponding additive component indicating greater contribution of former. Similar results in pea have been reported for primary branches plant^{-1} (Singh and Singh, 1990 ; Singh and Sharma, 2001) , 100-seed weight (Kumar and Dar, 1974), plant height (Srivastava *et al.*, 2000 ; Singh and Sharma, 2001) and harvest index (Singh and Sharma, 2001). For days to 50% flowering, days

to maturity, number of pods plant^{-1}, pod length, number of seeds pod^{-1}, seed yield plant^{-1}, and harvest index only dominance components (H_1 & H_2) were significant while as additive component (D) was non-significant indicating preponderance of non-additive components. Similar results have been reported by Singh *et al*. (1986), Srivastra *et al*. (2000), Rajnarayan *et al*. (1998) and Sofi (2003).

Them estimates of H_2 were non-significant for all traits except primary branches plant^{-1}, pod length and 100-seed weight indicating ambidirectional nature of dominance. F values were significant for plant height, primary branches plant^{-1}, pod length, number of seeds pod^{-1} and harvest index indicating unequal frequency of dominant and recessive alleles in parents. For remaining traits it was non-significant. Such non-significant F values have also been observed in pea by Singh *et al*. (1986) and Singh and Singh (1989) and Sofi (2003). The environmental component (E) was non-significant for most of traits except pod length, number of seeds pod^{-1} and 100-seed weight indicating restricted influence of environment on the expression of these traits. Similar findings have been reported by Singh and Singh (1989) and Sofi (2003).

The proportion of various genetic components of variance revealed that mean degree of dominance was in the range of over-dominance (H_1/D >1) for all the traits except plant height for which it indicated partial dominance. These results are in full agreement with earlier reports of Gupta *et al*. (1983) and Sofi (2003). The estimate of H_1 = /4H which provides information on proportion of positive and negative genes in parents were less than theoretical value of 0.25 indicating asymmetrical distribution of positive and negative alleles in parents. Effective factors were not detected for any trait. Similar results in pea have been reported by Singh *et al*. (1986) and Sofi (2003). The proportion of dominant and

recessive alleles in parents as exhibited by the ratio of KD/KR revealed that for most of the traits there was prevalence of dominant alleles in parents (KD/KR > 1). Only in case of number of seeds pod^{-1}, KD/KR was less than unity indicating prevalence of recessive alleles in parents.

The estimate of narrow sense heritability, which defines efficiency of selection, was low for primary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, harvest index and protein content whileas, it was moderate for all the other traits studied. The low to moderate estimates of heritability indicates that expected genetic gain under selection is likely to get affected by various non-genetic factors including environment. Low to medium estimates of heritability have also been observed in pea by Srivastava *et al*. (1986), Sirohi and Gupta (1993) and Dixit (2003). Indirect selection for the traits showing low heritability would be feasible in selection breeding programmes.

Gene Action

The results of present study revealed that both additive and non-additive types of gene action were involved in the inheritance of plant height, primary branches plant-1, 100-seed weight and harvest index with greater magnitude of non-additive component. For most of the yield component traits maturity traits and protein content only non-additive types of gene effects were predominant. Given that, heterosis breeding would have been an ideal breeding approach to capitalize on the use of non-additive gene action, for the very fact that the system of fertilization imposes restriction on large-scale hybrid seed production. Recurrent selection has been advocated by several pea breeders for such situations (Ram, 1980 ; Seth, 1982). However, recurrent selection also involves cyclical intermating of the selects and as such would be feasible only if suitable male sterility systems are identified in pea. Though Gupta *et al*. (1981) and

Myers & Gritton (1980) did identify few sterility genes in pea but there are still no reports of large scale utilization of such systems. Besides, the heritability estimates for most of the traits were low to moderate Singh and Singh (2004) observed same results in field pea and advocated that major thrust in pea breeding should be biparental mating followed by pedigree selection for isolating desirable transgressive segregants and good recombinants .

Some breeders (Webel & Lonquist, 1967 ; Jenson, 1970) have also advocated multiple crosses to generate a wide genetic base population followed by few cycles of recombination to break tight linkages and make the potential variability available for selection. The component breeding could be an excellent option, eventually improving yield. Some workers have also advocated mass selection with random mating in pea (Reddin & Jensen, 1974).

Chapter-6

SUMMARY AND CONCLUSSION

The present investigation entitled "Genetic analysis for yield, maturity and protein content in field pea *Pisum sativum* var arvense" was carried out during rabi,2004-05 at the Experimental Research Farm of the Division of Plant Breeding & Genetics SKUAST-K, Shalimar. Six diverse pure-lines namely $FP_2$80), $FP_2$60, $FP_2$82, $P_1$37, VL-1 and Rachna were crossed in half diallel fashion to generate 15 crosses. The crosses were generated at the Pulse Research Sub-station Habak, SKUAST-K during *rabi*, 2003-04. Both the parents and crosses (21 entries in all) were evaluated at Shalimar campus in Randomized Complete Block Design with three replications.

Each genotype was represented by 2 rows of 3 meter length with inter- and inter-row spacing of 30 and 10 cm, respectively. Recommended package of practices were followed to raise a good crop. Data was collected on 10 competitive plants for various yield, maturity and quality traits, whereas median values were used for recording maturity traits.

The analysis of variance of the Experimental Design revealed significant mean squares due to treatments indicating considerable variability in the parental lines. The analysis of variance for combining ability revealed significant mean squares due to gca and sca for all traits except of pods plant^{-1} and seeds pod^{-1} for which mean square due to gca were non-significant. Comparatively, variances due to sca were greater than the estimates of their corresponding greater role of non-additive gene effects.

None of the parents was a good general combiner for all traits. However, $FP_2$80 and $P_1$37 were good general combiners for yield and its attributes. For maturity traits only FP260 and Rachna exhibited significant desirable gca effects. Rachna $P_1$37, $FP_2$82 and VL_1 were good general combiners in the order of merit. For protein content only $FP_2$60 possessed significant gca but was a poor combiner for yield and its attributing traits. A number of crosses showed desirable significant sca effects for the traits studied. $FP_2$80 x VL_1, $FP_2$80 x Rachna and $FP_2$80 x $FP_2$82 exhibited significant sca effects for yield, 100-seed weight, seeds pod^{-1}, pod length and number of pods plant^{-1}. for maturity traits $FP_2$60 x VL1 and $P_1$37 x VL_1 had significant desirable sca effects. The crosses $FP_2$60 x VL_1, $P_1$37 x VL_1 and $FP_2$60 x Rachna exhibited good specific combining ability effects for protein content.

The estimates of genetic components of variance revealed significance of both additive and non-additive components for plant height, primary branches plant^{-1}, 100-seed weight and harvest index whileas only non-additive components were significant for rest of the traits. Overall, the relative values of non-additive variances were greater than their corresponding additive variance estimates. There was asymmetrical distribution of dominant and recessive alleles in parents for plant height, primary branches plant^{-1}, pod length, seeds pod^{-1} and harvest index, whereas, for the remaining traits it was symmetrical. The environmental component was non-significant for most of the traits except pod length, number of seed pod^{-1} and 100-seed weight. The analysis of proportions of various components revealed that average degree of dominance was in the range of overdominance, except plant height where it was almost complete dominance.

There was asymmetrical distribution of positive and negative alleles in the parents for all traits, besides excess of dominant genes in parents. The heritability estimates were generally moderate except for pods plant^{-1}, where it was low.

Field pea is a strictly self pollinated crop which precludes the chances of recombination under normal mating system therefore, it is imperative to generate adequate genetic variability through plant hybridization. For this endeavor to be successful it is essential to have basic knowledge about the breeding values of parental lines and the genetic architecture of the quantitative traits. In the present study various lines and crosses were found to exhibit significant desirable gca and sca effects, respectively for various traits of economic importance. Thus these parents and crosses could be used to derive transgressive segregants in the subsequent generations. This assumption is further encouraged by preponderance of non-additive gene action and overdominance, essential ingredients in hybrid breeding. But since no sound male sterility system has been practically utilized, even though a number of them stand identified, heterosis breeding has obvious limitations due to large seed requirements for commercial purposes. Under present situations most of the workers have advocated bi--parental matings followed by pedigree selection as a strategy in pea breeding, whereas some breeders have proposed multiple crosses followed by recurrent selection which will help break tight linkages and thus make potential variability available for selection.

From the results of present investigation it is concluded that :

1. The parents and the crosses exhibiting superior performance for yield and its component traits should be used to isolate transgressive segregants with desirable allelic equilibrium of economic traits.
2. The performance of superior crosses may be tested for its stability across locations.
3. the parental lines may be involved in hybridization programmes using exotic germplasm to widen their genetic base for further improvement and identification of superior varieties of pea suitable for Kashmir region.

Table 1 : Analysis of variance for different characters in a 6 x 6 diallel cross of field pea (*Pisum sativum*)

Source of Variation	d.f	MEAN SQUARES										
		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
Replicates	2	1.23	0.08	3.66	0.83	0.28	0.42	0.28	0.49	0.56	0.26	3.30*
Treatments	20	3.34**	6.31**	524.99**	7.66**	2.23**	0.22**	6.17**	4.41**	3.67**	6.61**	5.59**
Parents	5	1.22	3.38	874.94	17.13	1.86	0.13	0.22	4.13	1.62	8.56	2.21*
Hybrids	14	4.19**	7.56**	443.62**	3.97**	2.46**	0.20	0.17	4.27**	4.19**	4.73**	6.53**
Parents x Hybrids	1	2.05	3.40	64.40	11.96	0.91	0.95	0.007	7.80	6.67**	1.84	9.27
Error	40	0.76	1.47	1.30	0.16	0.29	0.07	0.04	0.29	0.15	1.39	0.88

*,** significant at 5% and 1% level, respectively

Table 2: Analysis of variance for combining ability for different characters of a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Source of Variation	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
gca	5	1.01**	2.00**	535.31**	5.80**	0.18	0.100**	0.02	1.47**	0.74**	2.31**	1.72**
sca	15	1.14**	2.13**	54.89**	1.47**	0.93**	0.06**	0.06**	1.47**	1.38**	1.72**	1.91**
Error	40	0.25	0.49	0.43	0.05	0.09	0.02	0.01	0.09	0.05	0.46	0.29
$\sigma^2 g$	--	0.09	0.18	66.85	0.71	0.01	0.09	0.01	0.17	0.08	0.23	0.17
$\sigma^2 s$	--	0.89	1.64	54.45	1.41	0.83	0.04	0.05	1.37	1.33	1.26	1.61
σ^2_A	--	0.19	0.37	133.71	1.43	0.02	0.01	0.00	0.34	0.17	0.16	0.35
σ^2_D	--	0.89	1.64	54.45	1.41	0.83	0.04	0.05	1.37	1.33	1.26	1.61
$2\sigma^2 g / 2\sigma^2 g + \sigma^2_S$	--	0.09	0.09	0.55	0.33	0.01	0.69	0.01	0.11	0.05	0.15	0.95
$\left(\frac{\sigma^2_D}{\sigma^2_A}\right)^{0.5}$	--	2.16	2.10	0.63	0.99	6.28	2.02	4.08	2.00	2.79	2.80	2.14

Table 3: General combining ability effects for different characters of a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Source of Variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
FP_2-80	0.64**	0.39	-15.06**	-1.24**	0.07	0.16**	0.003	0.52**	0.31**	0.85**	-0.57**
FP_2 – 60	-0.45**	-0.66**	-1.60**	-0.64**	-0.29**	-0.06	-0.110**	-0.04	-0.51**	-0.83**	0.61**
FP_2 – 82	-0.09	0.64**	1.76**	0.08	0.04	0.10*	6.030	-0.18	0.07	-0.10	0.12
P_1 – 37	-0.003	0.02	7.05**	1.17**	0.06	-0.12*	-0.001	0.36**	0.27**	0.08	-0.50**
VL_1	-0.07	0.08	0.64**	0.14**	0.03	-0.03	0.040	0.02	0.02	0.03	0.32
Rachna	-0.028	-0.49*	7.16**	0.48**	0.10	-0.06	0.030	-0.68**	-0.16*	-0.031	0.01
S.E (g) $\pm$	0.16	0.22	0.21	0.07	0.10	0.05	0.030	0.10	0.07	0.21	0.17
C.D (50%)	0.32	0.45	0.43	0.15	0.20	0.10	0.080	0.20	0.14	0.44	0.35

*,** significant at 5% and 1% level, respectively

Table 4: Specific combining ability effects for different characters in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
FP_2 80 x $FP_2$60	0.58	1.40**	-3.63	-0.03	-0.51	-0.10	-0.05	-0.33	0.35	-1.05	-6.64**
$FP_2$80 x $FP_2$82	-0.16	0.56	4.92**	0.80**	0.62**	0.31**	0.31*	-0.23	-0.43**	0.36	0.88
Fp_2 80 x P_1 37	0.96**	-0.38	10.69**	1.00**	0.15	0.42**	0.45*	0.46	0.35	0.66	0.40
FP_2 80 x VL_1	0.72	1.82**	-14.84	-1.24**	-0.56*	0.16	-0.04	0.92**	1.10*	0.67	-1.75**
$FP_2$80 x Rachna	0.63	0.33	10.54**	0.10	2.13**	0.23	0.01	1.25**	0.89**	0.73	-0.74
$FP_2$60 x $FP_2$82	1.06**	0.00	0.81	1.12**	0.54	0.13	-0.08	0.10	0.59**	1.80**	-1.26**
$FP_2$60 x $P_1$37	0.40	1.15**	3.12**	-1.77**	0.44	-0.22	-0.08	-2.35**	0.04	0.43	-0.50
$FP_2$60 x VL_1	-1.42**	-2.85**	1.12	-0.47**	-0.026	-0.10	-0.34**	-0.62**	-2.13**	-1.05	3.05**
$FP_2$60 x Rachna	-1.48**	-0.83	-9.50**	-0.74**	-0.59**	0.19	0.28**	-0.45	-1.44**	1.91**	1.44**
$FP_2$82 x $P_1$37	-0.57	0.23	2.73**	0.14	0.27	-0.02	-0.05	0.35	0.31	-0.89	-0.13
$FP_2$82 x VL_1	-0.05	0.13	4.21**	0.00	0.31	-0.08	0.05	-1.44**	0.39	-1.09	-0.31
$FP_2$82 x Rachna	1.84**	0.02	1.70**	-1.113**	-1.28**	-0.03	-0.29*	-1.39**	-0.85**	-0.83	0.58

Continued…..

Table 4 (Contd.)

Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
$P_1$37 x VL_1	-1.08**	-1.39**	-6.28**	-1.57**	-0.78**	-0.01	-0.25*	-0.52	-2.03**	-2.01**	1.61**
$P_1$37 x Rachna	-0.35	-2.11**	-0.85	-0.49**	-0.58**	-0.21	0.19	1.12**	-0.02	-0.88	0.30
VL_1 x Rachna	0.62	-0.30	4.83**	-0.740	-0.29	0.08	-0.13	-0.19	-0.21	-0.39	0.71
S.E (S_{ij}) $\pm$	0.44	0.52	0.58	0.20	0.27	0.14	0.10	0.27	0.20	0.60	0.48
S.E (S_{ij} x S_{jk}) $\pm$	0.50	0.70	0.66	0.23	0.31	0.15	0.12	0.31	0.22	0.68	0.54
SE (S_{ij} x S_{ik}) $\pm$	0.66	0.92	0.87	0.31	0.41	0.21	0.16	0.41	0.30	0.90	0.71
SE (S_{ij} x S_{kj}) $\pm$	0.61	0.85	0.80	0.28	0.38	0.19	0.15	0.38	0.28	0.83	0.66
CD at 5%	0.90	1.25	1.17	0.42	0.55	0.23	0.18	0.58	0.41	1.22	0.97
(S_{ij} –S_{ik})	1.34	1.93	1.63	0.58	0.77	0.39	0.30	0.77	0.56	1.68	1.34

Table 5: Estimation of components of genetic variance for different characters in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Components	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
D	0.14	0.65	281.17*	5.65*	0.52	0.19	0.05	1.27**	0.48	2.41**	0.40
	± 0.46	±1.17	±35.06	±0.53	±0.61	± 0.02	± 0.02	± 0.51	± 0.88	± 0.67	±1.40
H_1	17.79*	34.76*	956.79*	25.23*	15.43**	0.81*	1.11	25.18**	23.78**	27.45**	28.85**
	±4.76	±11.89	±356.08	±5.47	±6.20	±0.26	± 0.21	± 5.18	± 9.00	± 6.84	±14.24
H_2	13.42	23.89*	771.89*	17.31*	12.36**	0.56**	0.73**	17.70**	17.42**	18.89**	23.31
	±4.25	±10.62	±318.10	±4.89	± 6.54	±0.23	±0.19	± 4.63	± 8.04	± 6.11	± 12.72
h^2	1.19	1.89	54.61	10.21*	0.57	0.77*	-0.03	6.52**	5.63	0.60	7.27
	±2.86	±7.15	± 214.10	±3.29	±3.73	±0.15	± 0.12	± 3.11	± 5.41	±4.11	± 8.56
F	0.93	3.67	105.85*	10.37*	2.40	0.36**	0.27**	4.34	2.73	6.99**	1.19
	±2.29	±5.72	± 17.33	±2.63	±2.98	± 0.12	± 0.10	± 2.49	± 4.33	± 3.29	± 6.85
E	0.26	0.47	0.47	0.05	0.09	0.02**	0.01**	0.10**	0.05	0.44	0.33
	±0.17	±1.44	±13.25	±0.20	±0.23	± 0.09	± 0.008	± 0.19	± 0.33	± 0.25	± 0.53

Table 6: Proportion of genetic components of variance for different characters in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Proportion	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Harvest index	Protein content
$\left(\frac{H_1}{D}\right)^{0.5}$	5.48	3.63	0.92	1.05	2.71	3.23	2.24	2.21	3.51	1.68	4.22
$\left(\frac{H2}{4H_1}\right)$	0.18	0.17	0.20	0.17	0.20	0.17	0.16	0.17	0.18	0.17	0.20
$\frac{KD}{KR}$	3.70	7.56	1.51	14.18	11.92	1.81	-23.25	7.52	9.40	13.32	2.07
$\frac{h^2}{H_2}$	0.08	0.08	0.07	0.59	0.04	1.35	-0.04	0.36	0.32	0.03	0.31
Heritability (n.s)	0.33	0.38	0.48	0.26	0.15	0.41	0.28	0.32	0.31	0.27	0.27
b	-0.218**	-0.04	0.67**	0.70	0.02	-0.10	0.95**	0.28	-0.23	0.75	-0.10
	±0.08	± 0.18	± 0.17	±0.43	±0.22	±0.20	±0.51	±0.59	± 0.18	±0.54	±0.09
$\frac{b-0}{S.E\ (b)}$	2.64**	0.21	-3.82	-1.63*	-0.12	0.51**	-1.84**	-0.47	1.24	-1.38**	1.12**
$\frac{b-1}{S.E\ (b)}$	14.76**	0.21	1.81**	0.68	4.28**	5.46**	0.09	1.20**	6.63**	0.44	11.52**
t^2	31.43**	5.30**	1.35	0.07	3.05**	4.19**	0.88	0.17	4.74**	0.49	24.48**

Annexure 1 : Mean performance of parents x crosses for 12 quantitative traits in a 6 x 6 diallel of field pea.

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Biological yield (g)	Harvest index	Protein content
1	176.43	226.06	56.66	7.73	8.34	6.00	5.08	22.91	11.13	23.57	47.21	19.69
2	175.60	225.43	85.56	8.41	9.29	5.58	5.04	20.73	10.78	22.80	47.93	19.86
3	177.37	225.08	87.61	9.08	7.91	6.01	5.02	20.49	10.03	21.24	47.29	21.02
4	175.24	223.84	43.00	6.83	8.32	5.81	4.92	21.26	10.47	21.25	49.27	20.08
5	175.96	226.23	86.43	13.20	9.95	5.57	5.13	23.97	12.19	23.16	49.76	18.44
6	174.37	225.38	87.94	12.13	10.12	5.52	5.28	21.22	11.46	23.92	47.92	19.19
1 x 2	176.05	226.52	68.59	9.29	9.78	6.58	5.61	22.87	10.93	22.15	49.37	20.74
1 x 3	177.26	224.96	79.75	10.58	9.37	6.46	5.70	24.13	11.92	23.92	49.85	19.62
1 x 4	176.95	227.22	47.70	7.29	8.63	6.29	5.24	24.25	12.42	24.93	49.81	18.30
1 x 5	176.90	225.16	79.61	8.99	11.41	6.34	5.40	23.86	12.02	24.12	49.81	18.99
1 x 6	176.18	224.90	77.94	10.22	9.33	6.17	5.09	22.63	11.13	22.66	49.12	19.77
2 x 3	173.70	221.48	77.13	8.67	8.79	5.80	4.83	22.12	8.36	18.04	46.40	22.62
2 x 4	173.69	222.93	73.02	8.74	8.31	6.07	5.45	21.57	8.85	17.95	49.31	22.37
2 x 5	174.99	225.81	88.54	11.36	9.42	5.95	5.23	23.30	11.63	24.58	47.33	19.78
2 x 6	175.43	225.78	83.42	10.48	9.44	5.98	5.33	21.16	11.47	24.35	47.09	20.43
3 x 4	174.49	223.64	78.41	9.40	8.40	5.82	5.03	22.63	9.24	19.94	46.36	21.73
3 x 5	175.27	222.34	90.36	10.82	11.34	6.02	5.47	23.57	11.06	23.35	47.42	20.11
3 x 6	176.37	224.21	89.62	9.53	8.94	5.99	5.19	21.91	10.63	22.24	47.86	21.35
4 x 5	175.18	224.16	77.79	9.31	8.55	5.93	5.16	24.51	11.25	24.17	46.56	20.47
4 x 6	174.41	225.71	73.30	8.89	10.18	6.06	5.38	23.71	11.11	22.99	48.37	20.66
5 x 6	176.10	226.38	83.73	11.65	10.50	5.90	5.72	23.75	12.47	24.81	50.26	19.29

Annexure-11 : Source of parents used in the study

Parents	Source
FP280	Selection from co-ordinated material
FP260	-do-
FP292	-do-
P1-37	-do-
VL-1	A release variety developed by V.P.K.A.S Almora, Uttranchal
Rachna	A released variety developed by C.S. Azad University, Kanpur

Table 7 : Identification of elite parents on the basis of general combining ability in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Characters	Parents with high gca value
Days to 50%flowering	i) FP_2-60 (-0-45**)
	ii) FP_2-82 (-0.09**)
	iii) VL_1 (-0.07**)
Days to maturity	i) FP_2-60 (-0.66**)
	ii) P_1-37 (0.02**)
	iii) VL_1 (0.08**)
Plant height (cm)	i) Rachna (7.16**)
	ii) P_1-37 (7.08**)
	iii) FP_2-82 (1.76**)
Primary branches plant^{-1}	i) P1-37 (1.17**)
	ii) Rachna (0.48**)

	iii) VL1 (0.14**)
No. of pods plant^{-1}	i) Rachna (0.118**)
	ii) FP_2-80 (0.07**)
	iii) P_1-37 (0.06**)
	iv) VL_1 (0.03**)
Pod length (cm)	i) FP_2 -80 (0.16**)
	ii) FP_2-82 (0.10**)
No. of seed pod^{-1}	i) VL_1 (0.04**)
	ii) Rachna x FP_2-82 (0.03**)

Continued……

Table 7: (Contd.)

100 seed weight (g)	i) FP_2-80 (0.52**)
	ii) P_1-37 (0.36**)
	iii) VL_1 (0.02**)
Seed yield plant^{-1}	i) $FP_2$80 (0.31**)
	ii) P_1-37 (0.27**)
	iii) FP_2-82 (0.07**)
	iv) VL_1-(0.02**)
Harvest index	i) FP_2-80 (0.85**)

	ii) P_1-37 (0.08**)
	iii) VL_1 (0.03**)
Protein content	i) FP_2-60 (0.61**)
	ii) VL_1 (0.32**)
	iii) FP_2-82 (0.12**)

Table 8 : Identification of elite cross combinations on the basis of specific combining ability in a 6 x 6 diallel cross of field pea (*Pisum sativum* var. arvense)

Characters	Cross combinations	
Days to 50%flowering	iii)	FP_2-60 x Rachna (-1.48)
	iv)	FP_2-60 x VL_1 (-1.42)
	iii)	P1 37 x VL_1 (-1.08)
Days to maturity	i)	FP_2-60 x VL_1 (-2.85)
	ii)	P_1-37 x Rachna (-2.11)
	iii)	P_1-37 x VL_1 (-1.39)
Plant height (cm)	vi)	FP_2-80 x P_1-37 (10.69)
	vii)	FP_2-80 x Rachna (10.54)
	viii)	FP_2-80 x FP_2-82 (4.92)
	ix)	VL_1 x Rachna (4.83)

	x)	FP_2-82 x VL_1 (4.21)
Primary branches plant^{-1}	iv)	FP_2-60 x FP_2-82 (1.12)
	v)	FP_2-80 x P_1-37 (1.00)
	vi)	FP_2-80 x FP_2-82 (0.80)
No. of pods plant^{-1}	iv)	FP_2-80 x Rachna (2.13)
	v)	FP_2-80 x FP_2-82 (0.62)
	vi)	FP_2-60 x FP_2-82 (0.54)
Pod length (cm)	iii)	FP_2-80 x P_1-37 (0.42)
	iv)	FP_2 x FP_2-82 (0.31)

Continued……

Table 8 : (Contd.)

No. of seed pod^{-1}	i)	FP_2-80 x P_1-37 (0.45)
	ii)	FP_2-80 x FP_2-82 (0.31)
	iii)	FP_2-60 x Rachna (0.28)
100 seed weight (g)	i)	FP_2-80 x Rachna (1.25)
	ii)	P_1-37 x Rachna (1.12)
	iii)	FP_2-80 x VL_1 (0.92)
Seed yield plant^{-1}	iv)	FP_2-80 x VL_1 (1.10)

	v)	FP_2-80 x Rachna (0.89)
	vi)	FP_2-60 x FP_2-82 (0.59)
Harvest index	iii)	FP_2-60 x Rachna (1.91)
	iv)	FP_2-60 x FP_2-82 (1.80)
Protein content	iv)	FP_2-60 x VL_1(3.05)
	v)	P_1-37 x VL_1 (1.61)
	vi)	FP_2-60 x Rachna (1.44)

STATISTICAL ANALYSIS

Analysis of variance was carried out using conventional procedure. Combining ability analysis was performed using the method II model I as suggested by Griffing (1956), whereas least square estimates (Hayman,1954) were followed for component analysis of genetic variance.

OBSERVATIONS RECORDED

Observations were recorded on 10 randomly selected plants from each parent and cross in respect of the following :

a) Maturity traits

1. Days to 50% flowering
2. Days to maturity

b) Yield and yield attributing traits

1. Plant height (cm)
2. Primary branches plant^{-1}
3. No. of pods planr^{-1}
4. Pod length (cm)
5. No. of seeds pod^{-1}
6. 100-seed weight (g)
7. Seed yield plant^{-1} (g)
8. Harvest index (%)

c) Quality traits

1) Protein content (%)

TECHNICAL PROGRAMME OF WORK

1) Experiment Material

The material for the present investigation comprised of six genotypes of field

pea. These include the following.

1. FP_2-80
2. FP_2-6O
3. FP_2-82
4. P_I-37
5. VL-l
6. Rachna

2) Experimental Design:

i) Fifteen crosses (excluding reciprocals) were generated through 6 x 6 diallel mating design during *rabi* 2003-04 at Pulse Research Sub-station, SKUAST(K), Habak, Srinagar.

v) The experimental material comprising parents and crosses were laid in a Randomized Complete Block Design with 3 replications at SKUAST(K), Shalimar campus Srinagar during *rabi* 2004-2005.

OBJECTIVES

- To estimate the general and specific combining ability effects and identify superior general and specific combiners for future breeding progarmmes.
- To estimate the nature and magnitude of genetic variances for aiding in selection breeding programmes.
- To generate information for genetic component of variance in the control of yield, yield attributes, maturity and protein content.

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