

**HETEROSIS AND COMBINING
ABILITY ANALYSIS IN PIGEONPEA**
(Cajanus cajan (L.) Millsp.)

S. RAMA DEVI
B.Sc. (Ag.)

MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)



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ABILITY ANALYSIS IN PIGEONPEA
(*Cajanus cajan* (L.) Millsp.)**

BY
S. RAMA DEVI
B.Sc. (Ag.)

**THESIS SUBMITTED TO THE
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2011

DECLARATION

I, **Miss. S. RAMA DEVI**, hereby declare that the thesis entitled **“HETEROSIS AND COMBINING ABILITY ANALYSIS IN PIGEONPEA (*Cajanus cajan* (L.) Millsp.)”** submitted to **Acharya N.G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in this thesis has been published earlier in any manner.

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CERTIFICATE

This is to certify that the thesis entitled “**HETEROSIS AND COMBINING ABILITY ANALYSIS IN PIGEONPEA (*Cajanus cajan* (L.) Millsp.)**” submitted in partial fulfilment of the requirements for the award of degree of ‘**Master of Science in Agriculture**’ of the Acharya N.G. Ranga Agricultural University is a record of the bonafide research work carried out by **Miss. S. RAMA DEVI** under our guidance and supervision.

No part of the thesis has been submitted by the student for the award of any other degree or diploma. The published part and all assistance received during the course of the investigation have been duly acknowledged by the author of the thesis.

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Miss. S. RAMA DEVI has satisfactorily prosecuted the course of research and that the thesis entitled “**HETEROSIS AND COMBINING ABILITY ANALYSIS IN PIGEONPEA (*Cajanus cajan* (L.) Millsp.)**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any university.

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LIST OF SYMBOLS AND ABBREVIATIONS

$\bar{X}$	: Grand Mean
%	: Per cent
μg	: Microgram
ANOVA	: Analysis of Variance
CD	: Critical Difference
cm	: Centimeter
Cov.	: Covariance
CV	: Co-efficient of Variation
DAS	: Days After Sowing
df	: Degree of Freedom
<i>et al.</i>	: And others
F_1	: First Filial Generation
Fig.	: Figure
FS	: Full-sibs
G	: Genotypic
g	: Gram
GA	: Genetic Advance
GAM	: Genetic Advance as per cent of Mean
<i>gca</i>	: General combining ability
GCV	: Genotypic Co-efficient of Variation
H	: Heritability in Broadsense
$h^2_{(b)}$	: Heritability in Broad sense
HS	: Half-sibs

kg ha ⁻¹	: Kilogram per hectare
L x T	: Line x Tester
M ha	: Million hectares
ml	: Milliliter
MSL	: Mean Sea Level
Mt	: Million tonnes
nm	: Nanometer
No.	: Number
OD	: Optical Density
P	: Phenotypic
PCV	: Phenotypic Co-efficient of Variation
<i>Per se</i>	: As such with mean
r	: Correlation Co-efficient
RBD	: Randomized Block Design
r _g	: Genotypic correlation co-efficient
r _p	: Phenotypic correlation co-efficient
rpm	: revolutions per minute
mg	: Milligram
S.No.	: Serial Number
<i>sca</i>	: Specific combining ability
SEm	: Standard Error of Mean
SPAD	: Soil Plant Analytical Development
<i>viz.</i> ,	: Namely
σ ²	: Variance

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ABSTRACT

The present investigation comprising of eight parents of pigeonpea (*Cajanus cajan* (L.) Millsp.) and 15 cross combinations developed through a Line X Tester (5 X 3) crossing programme were evaluated for genetic parameters, heterosis, combining ability, character association and path coefficient analysis during *kharif*, 2010. The experiment was laid out in Randomized Block Design with three replications at the Regional Agricultural Research Station, Tirupati and observations were recorded on 14 characters.

Analysis of variance indicated the existence of significant differences among the genotypes for all the characters. Among the parents, the lines ICPL-15225 and LRG-41, the testers ICPL-8863 and ICPL-87119 and among the crosses, ICPL-15225 X ICPL-8863, ICPL- 15225 X ICPL-87119 and LRG-41 X PRG-158 showed high mean performance for seed yield. Analysis of genetic parameters revealed higher phenotypic and genotypic coefficient of variation, heritability, genetic advance as per cent of mean for pods per plant, 100-seed weight, harvest index, phenol content, seed yield per plant, primary and secondary branches per plant in parents and for pods

per plant and seed yield per plant in crosses indicating that simple selection could be practiced for improving these characters.

The expression of heterosis was most evident for pods per plant, seed yield per plant, phenol content, days to flowering, days to maturity, harvest index, seed protein and SCMR at vegetative phase. Significant heterosis, heterobeltosis, standard heterosis were recorded in the crosses viz., ICPL-15225 X ICPL-8863, LRG-41 X PRG-158, LRG-41 X ICPL-8863, LRG-41 X ICPL-87119 and ICPL-15225 X ICPL-87119 for most of the characters.

The analysis of variance for combining ability indicated the predominance of non-additive gene action for all the traits due to higher *sca* variance than *gca* variance. Among the parents LRG-41 and ICPL-15225 were found to be good general combiners for harvest index, pods per plant and seed yield per plant, ICPL-2376 and ICPL-8863 for seed protein, phenol content and earliness, ICPL-7035 for seeds per pod, pod length, 100-seed weight and SCMR at vegetative phase, LRG-41 for plant height and branches per plant. Based on *sca* effects, *per se* performance, heterosis, ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119 and LRG-41 X PRG-158 were identified as the best specific cross combinations for hybrid breeding programme, while the crosses ICPL-15225 X PRG-158 and LRG-41 X ICPL-8863 were identified for advancing through recombination breeding programme.

Character association studies indicated that the character pods per plant had significant positive correlation with seed yield per plant and also inter-correlations were observed among seeds per pod, pod length and 100-seed weight. Path coefficient analysis revealed the high positive direct influence of pods per plant on seed yield and it also had positive indirect effects on seed yield via all the characters except 100-seed weight and SCMR at vegetative phase in both parents and crosses. Hence, selection for pods per plant is suggested for the improvement of seed yield per plant in pigeonpea.

Chapter ~ I

Introduction

Chapter I

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp] (2n=22), popularly known as arhar or tur or redgram is an often cross pollinated crop belonging to Fabaceae family. It is a protein rich staple food and is consumed in the form of split pulse as dal. The seeds contain 14-29% protein with excellent quality being high in lysine. Therefore, it is an important complement to cereals, root crops and some horticultural crops which are major constituents of the diet of people. It is also used for fodder and fuel purposes. It plays an important role in sustaining soil productivity by fixing atmospheric nitrogen. The fallen leaves of pigeonpea enrich the soil with organic matter. Because of deep root system, it will also helps to bring the nutrients from deeper layers, hence it can be grown as intercrop with ground nut, sorghum, maize, pearl millet, mung bean, soy bean, cotton, castor etc.

Pigeonpea is the second largest grain legume in India, accounting about 20% of total pulse production. India occupies first place in the world with an area of 3.50 mha with a production of 2.47 mt and productivity of 705.7 kg/ha (FAO, 2009). It is grown throughout the country, but major concentration lies in Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Utter Pradesh, Gujarat, and Orissa. In Andhra Pradesh, it is cultivated in an area of 4.63 lakh ha with a production of 2.03 lakh tons and productivity of 438 kg/ha (Plant Doctors Dairy, 2011).

The yield potential of present day pigeonpea cultivars is not being realized owing to several biotic and abiotic constraints. The average yield of the crop is very low (700 kg/ha) due to the lack of high yielding varieties with resistance to pests and diseases. In view of the importance of the crop and low average yields, there is a need for evolving high yielding varieties

with biotic and abiotic stress resistance, by following proper breeding procedures.

Seed yield is a complex quantitative character, which is subjected to the environmental fluctuations and largely dependent on various components. Hence, for improving the yield, the knowledge on genotypic and phenotypic correlations among yield components and their relationship with yield will be useful in selecting superior genotypes. Path analysis helps in determining the relative contribution of the component characters towards yield.

The common approach of selecting parents based on their *per se* performance may not always lead to fruitful results (Allard, 1960). Hence, parents selected from combining ability studies would throw up more desirable segregants and understanding the magnitude of gene action involved in the inheritance of quantitative traits of economic importance. So, studies on general combining ability of parents and specific combining ability of hybrids, heterosis effects, gene action, direct and indirect effects on yield will provide information for selecting suitable parents and hybrids respectively for an efficient breeding programme.

Line x Tester mating design as suggested by Kempthorne (1957) is a modified form of the top cross which is an appropriate method to identify superior parents and hybrids based on *gca* and *sca* respectively and to study nature of gene action. This design provides information on more number of parents with limited number of single crosses. Hence in the present study, an attempt has been made to understand the genetic nature of yield and yield components through studies involving five lines and three testers in Line x Tester mating design.

Realizing the importance for such a comprehensive study in pigeonpea, the present investigation was undertaken with the following objectives:

1. To estimate the variability parameters for yield and yield contributing characters and to study the nature and magnitude of heterosis.
2. To identify the superior parents and crosses by combining ability analysis using L X T mating design.
3. To estimate the relationship among the yield contributing characters and with yield through correlation studies.
4. To identify the character(s), which are directly or indirectly influence the seed yield based on path coefficient analysis.

Chapter ~ II

Review of literature

Chapter II

REVIEW OF LITERATURE

An attempt has been made to critically review the literature of past research work done in relevance to the objectives of present study in pigeonpea (*Cajanus cajan* (L.) Millsp.) under the following heads:

2.1 VARIABILITY AND GENETIC PARAMETERS

2.2 HETEROSIS

2.3 COMBINING ABILITY

2.4 CHARACTER ASSOCIATION

2.5 PATH COEFFICIENT ANALYSIS

2.1 VARIABILITY AND GENETIC PARAMETERS

(Genetic Variability, Heritability and Genetic Advance).

The success of any breeding programme depends on the amount of variability present for different characters in a population and its efficient management. The genetic coefficient of variation is a useful measure of the magnitude of genetic variance present in the population.

Estimation of genetic variability alone cannot indicate the possible improvement achieved through selection, but it should be used in conjunction with heritability and genetic advance.

The degree of success depends on the magnitude of heritability as it measures the relative amount of the heritable portion of variability. Genetic advance (GA) under selection gives an idea about how much of genetic gain could be obtained due to selection. Hence, the estimates of genetic

variability, heritability and genetic advance had an immense value in identifying the superior genotypes.

A brief review of literature on genetic parameters is furnished hereunder:

Bainiwal and Jatasra (1981) studied the nature of genetic variability using twenty nine genotypes of pigeonpea and noticed that maximum variability was observed for secondary branches followed by primary branches and seed yield. The expected genetic advance was also observed to be high for seed yield, secondary branches, plant height and primary branches.

Jagshoran (1983) evaluated one hundred genotypes of pigeonpea and reported that the magnitude of range for phenotypic variability was high for all the characters except seeds per pod and high estimates of genotypic coefficient of variation and heritability were observed to be accompanied by moderate to high genetic advance for pods per plant, days to maturity, plant height and days to flower across the varying environments.

Balyan and Sudhakar (1985), in their study of genetic variability noticed that primary branches, secondary branches, pods per plant, 100-seed weight and seed yield per plant exhibited high estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance as percent of mean suggesting predominance of additive gene effects.

Jagshoran (1985) noticed that the characters days to 50 percent flowering, days to maturity, plant height, number of primary branches per plant, pods per plant, 100-seed weight and seed yield per plant had high amount of genotypic and phenotypic coefficients of variation, while it was low for pod length and seeds per pod.

Sidhu *et al.* (1985) observed that genetic variability was highest for number of pods per plant while it was lowest for number of seeds per pod.

Bhongale and Raut (1987) screened eighty genotypes of pigeonpea to study the extent of genetic variability for yield and yield contributing characters and highest genotypic coefficient of variation for yield per plant followed by pod number was observed. Days to 50 percent flowering, days to maturity and 100-seed weight had high heritability coupled with high genetic advance.

Konwar and Hazarika (1988) studied sixteen pigeonpea genotypes for genetic variability and reported high heritability with high genetic advance for days to maturity, days to flowering and plant height.

Patil *et al.* (1989) observed the high amount of genotypic coefficient of variation for number of branches per plant followed by number of pods per plant, plant height, seed yield per plant and number of seeds per pod, while low estimates were observed for days to 50 percent flowering and days to maturity and high heritability and genetic advance was observed for plant height and 100-seed weight.

Natarajan *et al.* (1990) noticed the highest genotypic coefficient of variation for number of pods followed by number of clusters per plant and seed yield, while it was lowest for seeds per pod. High heritability coupled with high genetic advance was observed for plant height and seed yield per plant, while low heritability with low genetic advance for seeds per pod.

Holker *et al.* (1991) reported high heritability and high genetic advance for days to 50 percent flowering, days to maturity and number of pods per plant.

Khapre and Nerker (1992) observed high amount of genotypic and phenotypic coefficients of variation for plant height, primary branches per

plant, pods per plant and seed yield per plant, while low estimates were observed for days to 50 percent flowering and days to maturity. High heritability and high genetic advance was observed for days to 50 percent flowering, number of pods per plant and seed yield per plant and high heritability and low genetic advance was reported for days to maturity.

Khapre *et al.* (1993) noticed that traits like plant height, pods per plant, seeds per pod, seed yield per plant and harvest index had high genotypic and phenotypic coefficients of variation estimates, while low estimates of genotypic coefficient of variation were recorded for shelling percent and seeds per pod.

Ghodke *et al.* (1994) evaluated ten genotypes under three cropping systems for deciding the selection criteria and noticed that high heritability for pods per plant, days to 50 percent flowering and days to maturity and high genetic advance as percent of mean for secondary branches and number of pods.

Aher *et al.* (1996) reported that the estimates of genotypic and phenotypic coefficients of variation were highest for plant height, number of primary branches per plant, secondary branches per plant and pods per plant, while low estimates were observed for days to 50 percent flowering, days to maturity, seeds per pod and 100-seed weight. High heritability and low genetic advance was reported for days to 50 percent flowering, days to maturity, plant height, number of primary branches per plant, seeds per pod and protein content.

Dahat *et al.* (1997) noticed that high amount of genotypic and phenotypic coefficients of variation for number of primary and secondary branches per plant, plant height, number of pods per plant and seed yield per plant both in sole as well as intercrop situations. High heritability accompanied with high genetic advance was also observed for number of

secondary branches per plant, plant height, number of pods per plant, seed yield per plant under both the conditions.

Aher *et al.* (1998) reported high magnitude of variability for number of secondary branches per plant followed by seed yield per plant, days to 50 percent flowering and plant height, while low estimates of variability were observed for pods per plant. High heritability accompanied with high genetic advance was observed for number of primary and secondary branches per plant, followed by seed yield per plant, days to 50 percent flowering and plant height.

Pansuriya *et al.* (1998) studied 20 early maturing pigeonpea genotypes and reported that dry matter per plant, plant height and pods per plant showed wide range of phenotypic variation. The genotypic and phenotypic coefficients of variation were highest for dry matter per plant, harvest index, pods per plant and seed yield per plant, high heritability estimates for all the characters and high genetic advance for dry matter per plant followed by pods per plant and plant height.

Patel and Patel (1998) observed high genotypic and phenotypic coefficients of variation for number of clusters per plant, number of pods per plant, plant height, number of primary branches per plant and seed yield in all crosses.

Takalkar *et al.* (1998) observed maximum variability for number of pods per plant followed by straw yield per plant. The high heritability estimates were observed for all the characters under study except straw yield per plant. The expected genetic advance was high for number of pods per plant, plant height, straw yield per plant and number of days to maturity and low genetic advance was observed for number of branches per plant, number of seeds per pod, 100-seed weight and harvest index.

Basavarajaiah *et al.* (1999) noticed high amount of phenotypic and genotypic coefficient of variation for days to 50 flowering, straw weight, pods per plant, seed yield per plant and length of pod bearing branches. High heritability and high genetic advance were observed for 100-seed weight and seed yield per plant.

Kingshlin and Subbaraman (1999) reported high heritability and high genetic advance for pod length, seeds per pod and low genetic advance for days to 50 percent flowering.

Srinivas *et al.* (1999) carried out studies in a line x tester set with two male sterile lines and eleven pollen parents. They noticed that genetic variability was highest for number of pods per plant and lowest for number of seeds per pod, high heritability for all the traits except seeds per pod and maximum genetic advance for pods per plant.

Deshmukh *et al.* (2000) noticed highest genetic variability for secondary branches per plant under inter crop. Heritability estimates were high for 100-seed weight, primary and secondary branches per plant under sole as well as inter cropping and for plant height and seed yield per plant under sole crop and plant spread under inter crop. High heritability accompanied with high genetic advance was recorded by the traits plant height, pods per plant and plant spread.

Venkateswarlu (2001) observed the maximum variability for number of pods per plant followed by straw yield per plant and plant height. The high heritability coupled with high genetic advance was observed for seed yield per plant, days to maturity and straw yield per plant.

Magar (2003) reported that genotypic and phenotypic coefficients of variation were highest for number of pods per plant, plant spread, seed yield per plant and number of primary branches per plant and high heritability and

genetic advance was observed for number of pods per plant and seeds per pod.

Gohil (2006) evaluated that protein content showed low estimates of genotypic and phenotypic coefficients of variation.

Firoz Mahamad *et al.* (2006) noticed from a study of forty-nine genotypes of vegetable pigeonpea that high PCV and GCV for the number of branches per plant, number of pods per plant, green pod yield and green seed yield per plant. High heritability coupled with high genetic advance was observed for plant height, number of branches per plant, number of pods per plant and 100-seed weight.

Kalaimagal *et al.* (2008) reported high amount of genotypic and phenotypic coefficients of variation and genetic advance for plant height, number of clusters and pods per plant and low variability, moderate heritability and genetic advance were observed for seed yield per plant.

Anantharaju and Muthiah (2008) revealed that low amount of genotypic and phenotypic coefficient of variations for days to 50 percent flowering, days to maturity and pod length; high heritability coupled with high genetic advance as percent of mean were observed for seed yield per plant, number of seeds per pod and 100-seed weight.

Jogendra Singh *et al.* (2008) studied seven genotypes and ten interspecific crosses and reported high phenotypic coefficient of variation and genotypic coefficient of variation for all the characters except for days to 50 percent flowering and days to maturity. High heritability accompanied with high genetic advance was observed for primary branches per plant, pod length, 100-seed weight and seed yield per plant, whereas days to 50 percent flowering showed high heritability and low genetic advance as percent of mean.

Dodake *et al.* (2009) carried out studies on twenty one genotypes and observed that the variability in plant spread, 100- seed weight, days to 50 percent flowering, days to maturity and seed yield per plant were heritable and additive type of gene action was operative for these characters.

Bhadru (2010) analyzed twenty seven accessions and moderate to high phenotypic and genotypic coefficient of variation were recorded for number of pods, seed yield per plant, plant height and plant spread. High heritability accompanied with high genetic advance as percent of mean was observed for number of pods, primary and secondary branches per plant, test weight, plant height and plant spread.

2.2 HETEROSIS

Heterosis is a complex biological phenomenon manifested in the superiority of hybrids over the parental forms. The term ‘heterosis’ was first coined by Shull (1914) to refer to the phenomenon in which the F_1 obtained by crossing two genetically dissimilar individuals showed an increase or decrease in vigour over the mid-parent value (Muntzing, 1945). The term ‘heterobeltiosis’ was proposed later (Bitzer *et al.*, 1968; Fonesca and Patterson, 1968) to denote the expression of heterosis over better parent helps the breeder in eliminating the less productive crosses at F_1 itself. The potency of heterosis breeding is enormous in terms of increasing the productivity of crops and could be used as indicative of crosses which are likely to generate productive transgressive segregants (Singh and Jain, 1970).

Heterosis manifestation for seed yield is expressed in the form of increased seed yield, which inturn is dependent on the contribution of its components. Therefore, all the component characters of yield need to be studied together with regard to heterosis manifestation in order to assess the worth of a cross (Grafius, 1956).

The discovery of heterosis in chickpea (Pal, 1945) opened the way for heterosis breeding in pulses. Varying degrees of heterosis with respect to yield and yield components have been observed in several pulse crops. Considerable extent of heterosis for yield and other traits has been reported in many legumes (Singh, 1974), including pigeonpea.

Solomon *et al.* (1957) were the first to report hybrid vigour for seed yield in pigeonpea. A wide range of heterosis is also present for almost all characters in pigeonpea.

Chaudhary *et al.* (1980) reported that the heterosis and heterobeltiosis were highly significant for days to flowering, days to maturity, plant height, primary branches, pods per plant, seeds per pod, pod length, 100 seed weight and seed yield per plant.

Singh *et al.* (1983) studied twenty four hybrids derived from line x tester design and reported the heterosis response upto 221 percent for seed yield.

Gupta *et al.* (1983) evaluated early maturing pigeonpea hybrids based on genetic male sterility and reported 42 percent higher yield over the check, UPAS-120. Mohammad Sheriff and Subramanian (1983) while studying the mode of inheritance of seven quantitative characters in pigeonpea observed dominance and over dominance gene effects responsible for the high degree of heterosis for yield and its components.

Patel (1985) evaluated 28 crosses derived from eight parental diallel. High heterosis was observed for the traits pods per plant (-8.13 to 126.7%) and seed yield (-14.8 to 107.9%) while, relatively low heterosis was observed for days to maturity (-5.5 to 1.6%), seeds per pod (-13.0 to 15 %) and 100- seed weight (-24.8 to 22.3%).

Patel (1988) evaluated sixty hybrids from three genetic male sterile lines and reported considerable degree of heterosis over mid and better parents for days to maturity, plant height, pods per plant, seed yield per plant and harvest index and low heterosis was observed in respect of pod length, seeds per pod and 100 seed weight.

Rao (1989) reported considerable degree of heterosis for seed yield and component characters among a set of 63 hybrids derived through line x tester mating between three genetic male sterile lines and 21 short duration pollen parents.

Rana (1990) studied 45 hybrids derived through line x tester mating design using three genetic male sterile lines and 15 pollinators and reported desirable heterosis for seed yield and its component characters like number of pods per plant, branches per plant and per day production.

Mehetre *et al.* (1993) studied the hybrids of 18 pigeonpea varieties and the results showed highly significant heterosis values over better parent for seed yield (-27.5 to 193.8%). For other traits, such as plant height, plant spread, branches per plant and pods per plant heterosis over mid parent was noted, whereas days to flowering and days to maturity over both mid and better parents.

Narladkar and Khapre (1994) observed significant heterosis over better parent (39.99) and standard hybrid ICPH8 (147.37) for seed yield from the study of three male sterile lines and eight diverse testers, and their 24 hybrids.

Sinha *et al.* (1994) reported the desirable relative heterosis for seed yield in 38 hybrids out of sixty cross combinations. Heterosis was also noticed for pods per plant and 100-seed weight, while poor or negative heterosis was recorded for seeds per pod.

Narladkar and Khapre (1996) reported that the crosses involving MS Hy9 showed marked heterosis for height at first effective branch, number of primary branches, pods per plant and seed yield per plant from the study involving eleven parents and 24 hybrids through line x tester mating design.

Manivel *et al.* (1999) in a study of forty hybrids from a line x tester analysis reported that significant negative heterobeltiosis for days to 50 percent flowering (-16.7%) and positive significant heterobeltiosis for plant height (37.6%), 100 seed weight (25.7%) and seed yield per plant (146.4%).

Hooda *et al.* (1999) reported high heterosis for plant height, primary branches per plant, pods per plant, seed yield per plant and significant negative heterosis for days to maturity from a study of 40 hybrids of short duration pigeonpea.

Khorgade *et al.* (2000a) noticed significant heterotic effect over mid parent and standard check for seed yield per plant in 24 pigeonpea hybrids derived from three genetic male sterile lines and eight diverse testers. An appreciable amount of heterosis was also reported for days to 50 percent flowering, plant height, primary branches per plant, pods per plant, 100 seed weight and protein content.

Pandey and Singh (2002) reported that standard heterosis was ranged from 8.75 to 144.32 percent for seed yield. Out of 36 combinations, 12 registered highly significant positive heterosis for seed yield per plant, number of primary and secondary branches per plant, clusters per plant and number of pods per plant by evaluating three genetic male sterile lines and 12 diverse genotypes

Chandirakala and Raveendran (2002) reported that heterosis on seed yield per plant was positively associated with heterosis for number of branches per plant, number of pods per plant, and 100 seed weight by

assessing three genetic male sterile lines, ten testers and their hybrids in line x tester cross.

Sekhar *et al.* (2004) noticed heterosis values of 51.3 and 171.6 percent for seed yield per plant over standard control Sel 90308 and a better parent, respectively from the study of 36 hybrids involving three male sterile lines and 12 pollinator lines.

Raju and Muthiah (2007) carried out an experiment involving four lines and three testers along with their hybrids and observed that the hybrid CO5 X ICPL-87119 was considered as the best with maximum heterosis for seed weight and CO6 X ICPL-87119 for seed yield and other yield contributing characters.

Patel and Tikka (2008) studied 45 hybrids from three lines and 15 testers and observed that, for number of pods per plant 10 and 20 hybrids recorded significant positive heterosis over better parent and control respectively. For seed yield, 18 and 29 hybrids exhibited positive heterosis over the better parent and control respectively.

Sarode *et al.* (2009) estimated heterosis using five lines and three testers in line x tester mating design. The maximum heterosis was recorded for number of pods per plant (52.11%) followed by 100 seed weight, number of seeds per pod, pods per plant and number of primary and secondary branches.

Shoba and Balan (2010) studied twenty seven early maturing hybrids resulting from L x T analysis and reported significant standard heterosis for plant height, number of branches per plant, number of pods per plant, number of seeds per pod and single plant yield (varied from -25.0 percent to 325 percent).

2.3 COMBINING ABILITY

Sprague and Tatum (1942) defined the terms general combining ability (*gca*) and specific combining ability (*sca*). The *gca* refers to average performance of a parent in a series of hybrid combinations and is attributable to additive (fixable) gene action. While *sca* refers to the deviation in the performance of crosses in certain specific combinations (worse or better) that would be expected on the basis of average performance of the lines involved in it and is attributed primarily to dominant and epistatic gene effects (non-additive and non-fixable). Combining ability analysis helps the breeder in selecting the parents to be used in the hybridization programmes and to select an appropriate breeding method by providing necessary information on the nature of gene action governing a character.

Several research workers have studied combining ability and nature of gene action in pigeonpea which are briefly reviewed here under:

Mehetre *et al.* (1988) reported that both additive as well as non-additive gene effects were important for all the traits studied except number of seeds per pod from the study involving 36 crosses along with their nine diverse parents.

Dhameliya *et al.* (1994) reported good *gca* effect for seed yield per plant, earliness, dwarfness, pods per plant, pod length, seeds per pod, seed weight and protein content. The magnitude of additive genetic variance was higher than non-additive variance for all the characters except seed yield per plant from the information on combining ability derived from ten pigeonpea genotypes.

Achamma Oommen *et al.* (1996) reported that number of primary branches was determined by both additive and non-additive genes, whereas number of secondary branches, plant height, days to flowering, days to

maturity, clusters per plant, length of pod bearing branches, pods per plant, seeds per pod, 100-seed weight and seed yield were determined by additive genes.

Srinivas *et al.* (1998) studied six medium to late duration pigeonpea lines, three testers and the resulting 18 hybrids and revealed that the predominance of non-additive gene action for all the traits.

Pandey (1999) observed genetic variation due to over-dominance and non-additive type of gene action for days to flowering, plant height, number of primary and secondary branches per plant, clusters per plant, pods per plant and seed yield per plant and partial dominance of additive gene action for days to maturity.

Jayamala and Rathnaswamy (2000) reported non-additive gene action for the expression of days to first flowering, number of branches per plant, plant height, number of pods per plant, days to maturity, number of seeds per pod and additive gene action for seed yield.

Khorgade *et al.* (2000b) carried out an experiment involving three genetic male sterile lines and eight testers of pigeonpea and indicated the predominance of additive gene effects for seed yield per plant and almost all the traits except plant height.

Ajay Kumar *et al.* (2001) studied three genetic male sterile lines and nine testers in L x T design and revealed that non-additive genetic variance was controlled the expression of yield per plant, primary branches per plant, pods per plant, seeds per pod and 100-seed weight, whereas additive genetic variance governed the expression of days to flowering and plant height.

Pandey and Singh (2002) studied three lines, 12 testers and resulting 36 crosses in L x T design and the estimates of σ^2_{gca} and σ^2_{sca} suggested partial dominance of additive gene action for number of pods per plant and

non-additive genetic variance for days to flowering, days to maturity, plant height, number of primary branches per plant, percent pod setting, harvest index and seed yield per plant were observed. Out of the 36 cross combinations, ten showed higher magnitude of *sca* effects involving high x high and low x high combining ability effects of lines and testers, respectively, for seed yield per plant, number of secondary branches per plant, clusters per plant, number of pods per plant and percent pod setting.

Jahagirdar (2003) analyzed the combining ability of 24 hybrids of pigeonpea obtained from crosses between three lines and 8 testers along with their parents and revealed the significant non-additive gene action for all the traits, as variance due to *sca* were higher than *gca* variances.

Lohithaswa and Dharmaraj (2003) reported non-additive gene action for shoot vigour index, days to maturity, plant height, number of seeds per pod and seed yield per plant, while additive gene action was noticed for days to 50 percent flowering, 100-seed weight and protein content.

Sunilkumar *et al.* (2003) studied combining ability of ten genotypes in diallel fashion revealed non-additive gene action for all the traits except days to 50 percent flowering, 100-seed weight and protein content, for which additive gene action was predominant. Majority of the crosses showing high *sca* effects for seed yield involving low x low or low x average general combiners.

Pandey (2004) reported that in lines, good *gca* effects were observed for seed yield per plant, secondary branches per plant, clusters per plant and number of pods per plant, while in testers, good *gca* effects were observed for primary branches per plant and percent pod setting from a study involving three genetic male sterile lines and 12 testers in L x T design. Out of 36 crosses, 10 crosses showed significant *sca* effects for seed yield per

plant, number of secondary branches per plant, clusters per plant, number of pods per plant and percent pod setting.

Sekhar *et al.* (2004) revealed the predominance of non-additive gene action for days to 50 percent flowering, days to maturity, plant height, plant spread, clusters per plant, pods per cluster, pods per plant, seeds per pod, 100-seed weight, seed yield per plant, biomass and harvest index by using three lines and 12 testers and resulting 36 hybrids.

Banu *et al.* (2006) studied *gca* and *sca* effects in 45 pigeonpea hybrids along with their parents and revealed the pre-dominance of non-additive gene action for days to 50 percent flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight and single plant yield.

Raju and Muthiah (2007) studied 12 crosses along with their parents *viz.*, four lines and three testers, of the line x tester mating design and noticed significant role of non-additive gene action for all the characters except number of primary branches per plant and phenol content.

Phad *et al.* (2007) reported significant *gca* and *sca* effects for seed yield per plant, plant spread, number of primary branches per plant, number of secondary branches per plant and number of pods per plant from the study of five lines, twelve testers and their hybrids in L x T design.

Yadav *et al.* (2008) carried out an experiment involving ten diverse parents in diallel fashion and the results revealed that the mean squares due to *gca* and *sca* effects were significant for all the traits except seeds per pod. The ratio of *gca* and *sca* genetic variances indicated preponderance of non-additive gene effects for all the traits except days to 50 percent flowering, days to maturity and pod length.

Phad *et al.* (2009) evaluated 60 crosses involving five lines and 12 testers in L x T fashion, some crosses showed high significant *sca* effects for number of primary branches per plant, number of pods per plant and seed yield per plant.

Vaghela *et al.* (2009) studied 28 hybrids along with their eight parents of pigeonpea and revealed higher magnitude of *sca* variance over *gca* variance for all the traits which indicated preponderance of non-additive gene action.

Patel *et al.* (2010) studied 45 hybrids resulting from three genetic male sterile lines and 15 testers and indicated that non-additive variances observed for plant height, branches per plant, seed yield per plant and protein content, whereas days to flowering, days to maturity, pods per plant, seeds per pod, pod length and reproductive period were governed by additive genetic variances.

2.4 CHARACTER ASSOCIATION

Genetic improvement of yield is the primary concern to plant breeder as yield is a complex, quantitatively inherited character and is highly influenced by the environment. On the contrary, the yield component traits are not only less complex and relatively simply inherited and are influenced much less due to environmental deviations. Thus effective improvement in yield may be brought about through selections in yield components (Grafius, 1956 and Srivastava *et al.*, 1972).

Yield component characters show associations among themselves and with yield. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, study of associations of component characters with yield enables a plant breeder to know how improvement of one character will bring about simultaneous improvement

in other characters and also aid in planning of an effective selection programme. Hence a brief review of literature is presented here under.

Asawa *et al.* (1981) noted that yield was positively correlated with secondary branches, pods per plant, seeds per plant and days to maturity and weak correlation among seeds per plant and pods per plant due to variation in number of seeds per pod among varieties.

Balyan and Sudhakar (1985) reported seed yield per plant had positive and significant association with plant height, days to maturity, primary branches, and secondary branches, pods per plant, seeds per pod and 100-seed weight.

Bhongale and Raut (1987) found that plant height, branches per plant, pod number, pod weight and seeds per pod were positively correlated with each other and also with seed yield.

Angadi *et al.* (1988) noted that pod yield was significantly correlated with seed yield, pods per plant, days to flowering and plant height.

Balakrishnan and Natarajaratnam (1989) revealed that seed yield had a positive correlation with number of pods per plant and pod setting percentage. Among the yield components, 100-seed weight was positively correlated with number of pods per plant.

Natarajan *et al.* (1990) observed pod number, cluster number and plant height were positively and significantly correlated with yield. They also reported that plant height, branch number, cluster number, seed number and 100-seed weight were highly correlated with one another.

Paul and Upadhaya (1991) observed positive correlation of yield per hectare with total number of branches per plant, number of pods per plant, number of pods per cluster and yield per plant. The correlation between the number of pods per plant and yield per plant was found to be positively

significant and the length of pod was significant but negatively correlated with yield per plant as well as with the number of pods per plant.

Dhameliya and Pathak (1994) reported significant and positive association of seed yield with plant height and pods per plant, whereas significant and negative association of seed yield with pod length and seeds per pod. They also reported that days to 50 percent flowering, days to maturity, plant height, primary branches per plant, pod length, seeds per pod and 100-seed weight were highly correlated with one another.

Salunke *et al.* (1995) observed in a study of 54 diverse genotypes of pigeonpea that seed yield was significantly and positively associated with pods per plant, primary and secondary branches, plant spread, plant height and 100-seed weight. It had a strong negative association with seeds per pod. The yield components like days to 50 percent flowering, days to maturity, plant height, plant spread, number of primary and secondary branches and 100-seed weight were positively associated with each other.

Gumber *et al.* (1996) studied twenty eight genotypes and noted that the days to flowering and days to maturity showed significant positive association among themselves and with seed yield.

Chandirakala and Raveendran (1998) indicated that seed yield was significantly and positively correlated with number of branches per plant, pods per plant, clusters per plant, seeds per pod, 100-seed weight.

Srinivas *et al.* (1999) reported that seed yield per plant had significant and positive association with plant height, number of primary branches, secondary branches and pods per plant.

Basavarajaiah *et al.* (1999) studied eighty-one genotypes of pigeonpea and their association studies indicated significant positive

correlation of seed yield observed with pods per plant and branches per plant.

Deshmukh *et al.* (2000) noticed that seed yield was positively and significantly associated with all traits under different cropping systems. Pods per plant exhibited highly significant correlation with seed yield which was also significantly associated with majority of the characters under sole crop. Whereas, secondary branches per plant was significantly associated with majority of the characters under inter crop.

Bharadwaj and Gupta (2004) studied 55 diverse genotypes of pigeonpea and reported that the protein content was positively correlated with days to flowering, harvest index and days to maturity, but exhibited negative correlation with plant height, number of primary and secondary branches, number of pods per plant, seeds per pod, 100-seed weight and seed yield per plant.

Chattopadhyay and Dhiman (2005) studied 100 accessions of pigeonpea and the reported that plant height, number of seeds per pod contributed positively and directly, whereas 100-seed weight was negatively correlated with seed yield.

Gangwar and Bajpai (2006) observed negative correlations for protein content with primary branches, pod length, 100-seed weight and seed yield.

Baskaran and Muthiah (2007) assessed twenty seven genotypes and their correlation studies indicated that seed yield per plant had significant positive relationship with number of pods per plant, number of clusters per plant, 100-seed weight and plant height.

Mahajan *et al.* (2007) evaluated nine pigeonpea genotypes to understand the contribution of various characters to the yield and reported

that pods per plant, pod length, plant height and days to maturity had significant positive association with yield.

Jogendra Singh *et al.* (2008) studied 29 genotypes of pigeonpea and reported that seed yield per plant exhibited positive and significant correlation with pods per plant and harvest index, indicating the higher values for these characters contribute towards higher yield potential.

Dodake *et al.* (2009) noticed that the seed yield was positively and significantly correlated with days to 50 percent flowering, plant spread and number of pods per plant.

Sawant *et al.* (2009) studied forty six genotypes and revealed that the genotypic correlation coefficients were higher than corresponding phenotypic correlations. Seed yield showed significant positive correlation with plant spread, number of secondary branches per plant, pods per plant and days to maturity.

Sodavadiya *et al.* (2009) observed that genotypic correlation coefficients were higher than phenotypic correlation coefficients. The seed yield per plant had significant and positive association with days to 50 percent flowering, days to maturity, number of branches per plant, pods per plant and 100-seed weight at both genotypic and phenotypic levels.

Bhadru (2010) reported that seed yield was significantly and positively associated with days to 50 percent flowering, plant height, primary and secondary branches per plant, pods per plant and raceme length.

2.5 PATH COEFFICIENT ANALYSIS

Knowledge on the association of quantitative characters, especially yield and its attributes will be of immense practical value in crop improvement breeding. Correlation, which is the primary tool of a plant breeding programme only provides the degree of association of the

characters, while path coefficient analysis which is a standard partial regression coefficient, measures the direct influence of one variable upon another and permits the separation of correlation coefficient into components of direct and indirect effects (Dewey & Lu, 1959). Direct selection for yield is not a reliable approach since it is highly influenced by the environment. Therefore, it is essential to identify the component characters through which yield can be improved. Thus, correlation in conjunction with path analysis would give better insight into the cause and effect relationship between different character pairs. The available literature on path coefficient analysis is furnished here under.

Dumbre *et al.* (1985) revealed that days to flowering had highest positive direct effect on seed yield followed by number of pods per plant, 100-seed weight and plant height. The indirect effects via these traits were also positive for all traits except seeds per pod which had negative indirect effect via 100-seed weight.

Marekar and Nerkar (1987) observed biomass and harvest index had largest positive direct effect on seed yield and days to first flowering, days to maturity, plant height, height at first effective branch, number of primary branches, secondary branches, number of clusters and 100-seed weight had indirect positive effects on seed yield.

Angadi *et al.* (1988) noticed that pod yield was the only character with a direct effect on seed yield. Characters like pods per plant, plant height, branches per plant and days to flower influenced seed yield through pod yield which alone had direct influence on seed yield.

Balakrishnan and Natarajaratnam (1989) observed that pods per plant had the highest positive direct effect on seed yield followed by harvest index and dry matter efficiency.

Natarajan *et al.* (1990) reported that cluster number followed by pod number showed high positive direct effect on seed yield.

Satpute (1994) revealed that number of seeds per pod exhibited highest magnitude of positive direct effect on seed yield, followed by dry matter production.

Salunke *et al.* (1995) noticed that pods per plant, seeds per pod, and 100-seed weight had direct positive effects on seed yield. The pods per plant and 100-seed weight also exhibited high positive indirect effects on seed yield through most of the other characters. It is suggested that pods per plant, seeds per pod and 100-seed weight could prove useful as selection criteria for early pigeonpea.

Paul *et al.* (1996) revealed that six independent characters having positive direct effect on seed yield, maximum contribution was of number of pods per plant, followed by dry matter at maturity and 100-seed weight.

Kingshlin and Subbaraman (1997) assessed that pod length, seeds per pod and 100-seed weight made the greatest contribution towards seed yield, both directly and indirectly.

Musaana and Nahdy (1998) indicated that pod clusters per plant, pods per plant, seeds per pod and seed weight were the main yield components having maximum direct effects on yield.

Chandirakala and Raveendran (1998) revealed from their studies on 13 pigeonpea genotypes that 100-seed weight had the highest positive direct effect on seed yield followed by number of pods per plant and number of clusters per plant. Number of branches per plant, number of pods per plant, number of clusters per plant, number of seeds per pod and 100-seed weight showed high positive indirect effect on seed yield.

Srinivas *et al.* (1999) observed high and positive direct effect of pods per plant, plant height and secondary branches on seed yield.

Basavarajaiah *et al.* (1999) evaluated eight-one pigeonpea genotypes and reported that plant height, branches per plant and pods per plant showed maximum direct effects on seed yield.

Bharadwaj and Gupta (2004) reported that protein content showed positive direct effect and negative correlation with yield.

Chattopadhyay and Dhiman (2005) observed that plant height and number of seeds per pod contributed positive and direct effect on seed yield.

Mittal *et al.* (2006) reported from a study of 21 diverse progenies of pigeonpea that seeds per pod, followed by pods per plant and plant height had high positive direct effect on seed yield.

Baskaran and Muthiah (2007) revealed pods per plant, 100-seed weight and plant height to be the major contributors for seed yield and the selection based on these attributes will be most advantageous in pigeonpea from path analysis studies of 27 genotypes.

Mahajan *et al.* (2007) evaluated nine genotypes, the maximum direct positive and negative contribution to yield was observed from pods per plant and days to flower initiation, respectively.

Anuradha *et al.* (2007) studied thirty genotypes of pigeonpea and revealed that the harvest index had a high positive direct effect on seed yield followed by seeds per pod, primary branches per plant.

Jogendra Singh *et al.* (2008) noticed from their path coefficient studies of 29 genotypes that pods per plant, 100-seed weight and harvest index are main components of seed yield. Hence, more emphasis should be given on these characters in selection programme.

Sawant *et al.* (2009) revealed that pods per plant had the highest positive direct effect on seed yield, followed by plant spread and 100-seed weight.

Sodavadiya *et al.* (2009) reported that 100-seed weight, days to maturity and pod length exerted high direct effects on seed yield. 100-seed weight, days to maturity also contributed indirectly towards seed yield per plant through most of the characters.

Bhadru (2010) noticed that days to 50 percent flowering, plant spread, primary and secondary branches per plant, number of pods and raceme length had moderate to low direct effect on seed yield.

Chapter ~ III

Material and Methods

Chapter III

MATERIAL AND METHODS

The present study was undertaken with a view to evaluate heterosis and combining ability by adopting L x T analysis in certain pigeonpea varieties during *Kharif*, 2010 at Dry Land Farm of Regional Agricultural Research Station, Tirupati. The experimental site is situated at an altitude of 189.2 m above MSL, 13°N latitude and 79°E longitude geographically. The materials used and methods followed in the present investigation are described below.

3.1 MATERIALS

The experimental material comprised of eight parental genotypes viz., five females (Lines) namely, ICPL-6974, ICPL-15225, ICPL-7035, ICPL-2376 and LRG-41, three males with resistance to *Fusarium* wilt (Testers) namely, ICPL-87119, ICPL-8863 and PRG-158 and 15 cross combinations which were obtained through Line x Tester mating design. The standard check included in the experiment was LRG-30. The details of the parents and their source are furnished in the Table 3.1.

3.2 METHODS

3.2.1 Field Layout

The crosses made during *kharif*, 2009 at Regional Agricultural Research Station (RARS), Tirupati were evaluated during *kharif*, 2010 at RARS, Tirupati. The parents (5 lines and 3 testers) and 15 cross combinations along with standard check were sown on 13th July, 2010 in a Randomized Block Design with three replications. Each entry was grown in three rows of 4 m length in each plot. The spacing adopted between row to row was

Table 3.1. Salient features of parental lines of pigeonpea

Sl. No.	Genotype	Source	Characters
1.	ICPL-6974 (Pant A3)	ICRISAT, Hyderabad	Early duration, medium plant, erect in growth habit, flower is yellow in colour, pod is green with brown streaks, medium bold seeds with light brown colour, susceptible to wilt and resistant to sterility mosaic disease.
2.	ICPL-15225 (T401-1)	ICRISAT, Hyderabad	Medium duration, semi spreading in growth habit, flower is yellow with purple streaks, pod is greenish brown in colour, seeds are white and medium in size, resistant to sterility mosaic disease.
3.	ICPL-7035	ICRISAT, Hyderabad	Early duration, medium plant, erect in growth habit, deep red flower, purple pods with 5 to 6 seeds are very bold with deep brown colour.
4	ICPL-2376	ICRISAT, Hyderabad	Early duration, medium plant, spreading and bushy type in growth habit, flower is yellowish with purple streaks, pod is shiny, light green colour, small white seed, susceptible to wilt.
5.	LRG-41	RARS, Lam Farm, Guntur, A.P.	Medium to late duration, tall plant, semi spreading and droopy growth habit, flower is yellow in colour, pod is purple red in colour and seed is bold and brownish red in colour, susceptible to wilt and sterility mosaic disease.
6.	Asha (ICPL-87119)	ICRISAT, Hyderabad	Medium duration, tall plant, erect in growth habit, flower is light yellow in colour, pod is green with brown coloured streaks and medium bold seed with brown colour resistant to fusarium wilt.
7.	Maruti (ICPL-8863)	ICRISAT, Hyderabad	Early duration, tall plant, semi spreading in growth habit, flower is yellow in colour, pod is green with streaks and medium bold seed with brown colour, resistant to fusarium wilt.
8.	PRG-158	RARS, Palem, A.P.	Early to medium duration, tall erect plant, profuse branching, flower is yellowish, pods are green with brown streaks, seeds are small with light brown colour, wilt resistant but susceptible to sterility mosaic disease.
9.	Palnadu (LRG-30)	RARS, Lam Farm, Guntur, A.P.	Medium to late duration, medium plant, semi spreading in growth habit, flower is yellow in colour, pod is green with honey coloured streaks and seed is medium bold with brown colour, susceptible to wilt and sterility mosaic disease.

150 cm and 30 cm between plant to plant within a row. In parents and crosses, 15 plants were tagged randomly for recording the data. The overall view of experimental field layout was shown in Plate 1.

3.2.2 Crop Husbandry

The field was ploughed and harrowed to a fine tilth. The crop was raised during *kharif* 2010. A fertilizer dose of 20:50:0 NPK kg/ha was applied to the crop as a basal application. Weeding was carried out two times *i.e.* 30 DAS and 60 DAS. Other recommended cultural practices and plant protection measures were taken to raise a good crop.

3.2.3 Data Recorded

Fifteen plants in each plot in each replication were selected at random and single plant observations were recorded and their means were used for statistical analysis.

The details of the characters for study are presented here under.

3.2.3.1 Number of days to flowering: The number of days taken from date of sowing to the day when 50% of flowering of the plants in each genotype in each replication.

3.2.3.2 Number of days to maturity: The number of days recorded from the date of sowing to the day when 75% of the pods in the genotype had turned brown and matured.

3.2.3.3 Plant height (cm): The plant height was measured in centimeters of a stretched plant from ground level to the tip of the main stem at maturity.

3.2.3.4 Number of primary branches per plant: Number of branches arising from the main stem was recorded at harvest.

3.2.3.5 Number of secondary branches per plant: Total number of branches arising from primary branches was recorded at harvest.



Plate 1. Overall view of the experimental field layout

3.2.3.6 Number of pods per plant: Number of well filled matured pods was counted at the time of harvest.

3.2.3.7 Number of seeds per pod: The average of seeds on ten fully developed, mature and undamaged pods taken at random from each selected plant.

3.2.3.8 Pod length (cm): Ten randomly selected pods from each sample plant were taken and length of each pod was measured in centimeters from the base of the pod to the tip and averaged to obtain the pod length.

3.2.3.9 100 - seed weight (g): From each sample plant at random, one hundred dry seeds were counted and weighed in grams.

3.2.3.10 Seed yield per plant (g): The seeds from each sample plant were dried and weighed in grams.

3.2.3.11 SCMR at vegetative phase: SPAD Chlorophyll Meter Reading (SCMR) was recorded on five leaflets of third and fourth leaf on each plant and its average was taken.

3.2.3.12 Harvest index (%): The ratio of single plant seed yield to the total plant dry weight was taken and expressed in per cent.

$$\text{Harvest index} = \frac{\text{Single plant seed yield (g)}}{\text{Total plant dry weight(g)}} \times 100$$

3.2.3.13 Seed protein (%): Protein content in this study refers to the total protein content in the seed. The method of Lowry *et al.* (1951) was adopted for estimating protein content with folin-ciocalteu reagent. The seed sample of 500 mg was homogenized with 10 ml of cold 10% TCA (Trichloro Acetic Acid). Seed sample in TCA was collected in a test tube and kept in ice for 15 minutes. The contents were centrifuged at 3500 rpm for 15 minutes. The pellet was washed thrice with 5 ml of TCA, 3 ml of hexane and 1 ml of

acetone. It was suspended in 4 ml of 2 N sodium hydroxide, thoroughly mixed and incubated at room temperature overnight. The contents were centrifuged at 3500 rpm for 15 minutes. Two ml of the supernatant was collected and the volume was made upto 10 ml with distilled water. Then 0.1 ml of the sample extract was used to estimate the protein content by adding 5 ml of alkaline copper sulphate solution. After 10 minutes 0.5 ml of freshly prepared folin-ciocalteu reagent was added, thoroughly mixed and allowed to stand for 30 minutes for colour development. The optical density was measured at 660 nm in a spectrophotometer against a reagent blank. 0.1 ml of distilled water was used in place of the sample in preparation of blank. A standard curve was prepared with a range of 0 to 300 $\mu\text{g ml}^{-1}$ of bovine serum albumin and it was linear within range ($R^2 = 0.997$). The protein content of the sample was calculated substituting sample OD values in the formula derived from the graph ($Y = 1.838X$), where Y = OD Value of the sample and X = concentration of the protein ($\mu\text{g ml}^{-1}$). Then the concentration of protein in $\mu\text{g ml}^{-1}$ was converted in per cent for different entries.

3.2.3.14 Phenol content (%): Phenol content in the seed was estimated by adopting the method suggested by Sadasivam and Manickam (1961). 500 mg of seed sample was ground in 10 times volume of 80% ethanol with a pestle and mortar. Then the homogenate was centrifuged at 10000 rpm for 20 minutes, supernatant was saved. Then the residue was extracted with 5 times volume of 80% ethanol and centrifuged. Then the supernatants were pooled and evaporated to dryness. The residue was dissolved in 5 ml of distilled water. 0.2 ml of the sample extract was used to estimate the phenol content by adding 0.5 ml of folin-ciocalteu reagent. After 3 minutes, 2 ml of 20% sodium carbonate was added and kept in boiling water bath for one minute, cooled and the absorbance was measured against a reagent blank at 650 nm. A standard curve was prepared by using catechol and it was linear within the range ($R^2=0.927$). The phenol content of the sample was calculated by

substituting the sample OD values in the formula derived from the graph ($Y=2.990X$), where Y =OD value of the sample and X =concentration ($\mu\text{g ml}^{-1}$) of the phenol. Then the concentration of phenols in $\mu\text{g ml}^{-1}$ was converted to concentration of phenols in per cent for different entries.

3.3 STATISTICAL ANALYSIS

The mean values were computed for the observations recorded in respect of 14 characters in each of the genotypes and were subjected to statistical analysis.

3.3.1 General analysis of variance (ANOVA)

The mean values of data recorded for 14 characters in each entry of three replications were first subjected to ANOVA as given below.

Table 3.2. Analysis of variance of RBD

Source of variation	DF	Sum of squares	Mean sum of squares		F test
Replications	$r - 1$	RSS	RMS	M_r	M_r/M_e
Genotypes	$g - 1$	GSS	GMS	M_g	M_g/M_e
Error	$(r - 1)(g - 1)$	ESS	EMS	M_e	
Total	$(rg - 1)$	TSS			

where,

r = Number of replications

g = Number of genotypes

The significance of F- value for genotypes indicate significant differences among the genotypes studied and the statistical analysis may be continued further.

3.3.2 Estimation of variability, heritability, genetic advance as per cent of mean

3.3.2.1 Phenotypic and genotypic variance: The phenotypic and genotypic variances were estimated according the method of Lush (1940).

Genotypic variance(σ^2_g)=

$$\frac{\text{Meansquares due to treatments} - \text{Meansquares due to error}}{\text{Number of replications}}$$

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

$$(\sigma^2_e) = \text{Error variance}$$

3.3.2.2 Phenotypic and genotypic co-efficient of variation (PCV and GCV):

These were computed according to Burton (1952).

Phenotypic coefficient of variation (%) =

$$\frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

Genotypic coefficient of variation (%) =

$$\frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

Categorization of the range of variation was effected as proposed by Siva Subramanian and Menon (1973).

Low	-	Less than 10%
Moderate	-	10 - 20%
High	-	More than 20%

3.3.2.3 Heritability in broad sense [$h^2_{(b)}$]: Heritability in broad sense was estimated using the formula of Allard (1960).

$$\text{Heritability } [h^2_{(b)}] = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

As suggested by Johnson *et al.* (1955), heritability estimates were categorized as

Low	-	0 - 30 %
Medium	-	30 - 60 %
High	-	61 % and above

3.3.2.4 Genetic advance (GA): This was estimated as per the formula proposed by Lush (1949) and Johnson *et al.* (1955).

$$GA = K \cdot \sigma_p \cdot H$$

where,

K = Selection differential at 5% selection intensity, which accounts to a constant value 2.06 (Lush, 1949).

H = Heritability coefficient

σ_p = Phenotypic standard deviation

Genetic advance as percent of mean (GAM) =

$$\frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

Low	-	Less than 10%
Medium	-	10 - 20%
High	-	More than 20%

3.3.3 Estimation of Heterosis

Heterosis can be classified into three types on the basis of estimation.

3.3.3.1 Relative heterosis: Heterosis was expressed as per cent increase or decrease of F_1 over the mid-parental value.

$$\text{Relative heterosis} = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

where,

$$\bar{F}_1 = \text{Mean of } F_1$$

$$\overline{MP} = \text{Mean of mid parent}$$

3.3.3.2 Heterobeltiosis. Heterobeltiosis was expressed as per cent increase or decrease of F_1 over the better parental value.

$$\text{Heterobeltiosis} = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

where,

$$\overline{BP} = \text{Mean of better parent}$$

3.3.3.3 Standard heterosis. Standard heterosis was expressed as per cent increase or decrease observed by F_1 over the standard check variety.

$$\text{Standard heterosis} = \frac{\bar{F}_1 - \overline{SC}}{\overline{SC}} \times 100$$

where,

$\overline{SC}$ = Mean of standard check

Test for significance of heterosis was conducted following the formula given by Arunachalam (1976).

$$\text{Relative heterosis} = \frac{\overline{F_1} - \overline{MP}}{\sqrt{1.5 \text{EMS}/r}}$$

$$\text{Heterobeltiosis} = \frac{\overline{F_1} - \overline{BP}}{\sqrt{2 \text{EMS}/r}}$$

$$\text{Standard heterosis} = \frac{\overline{F_1} - \overline{SC}}{\sqrt{2 \text{EMS}/r}}$$

where,

EMS = Error mean squares

r = Number of replications

The calculated 't' value was compared with table 't' values at respective error degrees of freedom.

3.3.4 Combining Ability Analysis

Analysis of variance for combining ability in randomized block design, including parents and crosses was carried out as per the model given by Singh and Chaudhary (1977).

Table 3.3. ANOVA structure for combining ability

Source of variation	Degrees of freedom	Mean sum of squares
Replications	$(r-1)$	M_g
Genotypes	$(a - 1)$	
Parents	$(P - 1)$	
Parents vs. Crosses	1	
Crosses	$c-1$	M_l
Lines	$(l-1)$	
Testers	$(t - 1)$	
Line x Tester	$(l-1) (t - 1)$	
Error	$(r-1) (a - 1)$	M_e

where, r , a , P , c , l and t are number of replications, genotypes, parents, crosses, lines and testers respectively. M_l , M_t , M_{lt} and M_e are the mean sum of squares of lines, testers, lines x testers and error respectively.

The mathematical model for combining ability analysis was given below

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

where,

Y_{ijk} = Any measurable character of the cross $i \times j$

μ = Population mean effect

g_i = *gca* effect of the female parent

g_j = *gca* effect of the male parent

S_{ij} = *sca* effect of the cross ij

r_k = K^{th} replication effect

e_{ijk} = Environmental effect particular to $(ijk)^{\text{th}}$ individual

3.3.4.1 *gca* and *sca* effects: The individual effects are estimated as follows

$$gca \text{ effect of lines } (g_i) = \frac{X_{i..}}{rt} - \frac{X_{...}}{rlt}$$

$$gca \text{ effect of testers } (g_j) = \frac{X_{.j.}}{rl} - \frac{X_{...}}{rlt}$$

$$sca \text{ effect of crosses} = \frac{X_{ij.}}{r} - \frac{X_{i..}}{rt} - \frac{X_{.j.}}{rl} + \frac{X_{...}}{rlt}$$

where,

$X_{i..}$ = Total of i^{th} line over 't' testers and 'r' replications

$X_{.j.}$ = Total of j^{th} tester over 'l' lines and 'r' replications

$X_{...}$ = Total of all cross combinations over all replications

$X_{ij.}$ = Total of the hybrid between i^{th} line and j^{th} tester over 'r' replications.

t = Number of testers

l = Number of lines

r = Number of replications

3.3.4.2 Estimation of standard errors for combining ability effects: The standard error pertaining to *gca* effect of lines and testers and *sca* effects of different cross combinations were calculated as shown below.

$$\text{SE for } gca \text{ effects of lines } (g_i) = \sqrt{\frac{EMS}{rt}}$$

$$\text{SE for } gca \text{ effects of testers } (g_j) = \sqrt{\frac{EMS}{rl}}$$

$$\text{SE for } sca \text{ effects of hybrids } (S_{ij}) = \sqrt{\frac{EMS}{r}}$$

$$SE (g_i - g_j) \text{ lines} = \sqrt{\frac{2EMS}{rt}}$$

$$SE (g_i - g_j) \text{ testers} = \sqrt{\frac{2EMS}{rl}}$$

$$SE (S_{ij} - S_{ik}) = \sqrt{\frac{2EMS}{r}}$$

$$\text{Cov. HS (line)} = \frac{M_1 - M_3}{rt}$$

$$\text{Cov. HS (tester)} = \frac{M_1 - M_3}{rl}$$

$$\text{Cov. HS (average)} = \frac{1}{r(2lt - l - t)} \left[\frac{(l-1)(M_1) + (t-1)(M_2)}{l+t-2} - M_3 \right]$$

$$\text{Cov. FS} = \frac{(M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4)}{3r} + \frac{6r\text{CovHS} - r(l+t)\text{CovHS}}{3r}$$

$$\sigma^2_{gca} = \text{Cov HS} = \frac{(M_1 - M_3) + (M_2 - M_3)}{r(1+t)} \text{ or } \left[\frac{1+F}{4} \right]^2 \sigma^2_A$$

$$\sigma^2_{sca} = \frac{M_3 - M_4}{r} \text{ or } \left[\frac{1+F}{2} \right]^2 \sigma^2_D$$

$$\sigma^2_{gca} : \sigma^2_{sca} = \frac{\sigma^2_{gca}}{\sigma^2_{sca}}$$

3.3.5 Character Association Analysis

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955).

3.3.5.1 Phenotypic correlation coefficient (r_p)

$$r_p (x_i x_j) = \frac{Cov_p (x_i x_j)}{\sqrt{V_p (x_i) \cdot V_p (x_j)}}$$

where,

$r_p (x_i x_j)$ = Phenotypic correlation coefficient between ' i^{th} ' and ' j^{th} ' characters.

$V_p(x_i)$ = Phenotypic variance of ' i^{th} ' character

$V_p(x_j)$ = Phenotypic variance of ' j^{th} ' character

$CoV_p (x_i x_j)$ = Phenotypic covariance between ' i^{th} ' and ' j^{th} ' characters.

3.3.5.2 Genotypic correlation coefficient (r_g)

$$r_g (x_i x_j) = \frac{Cov_g (x_i x_j)}{\sqrt{V_g (x_i) V_g (x_j)}}$$

where,

$r_g (x_i x_j)$ = Genotypic correlation coefficient between ' i^{th} ' and ' j^{th} ' characters

$V_g (x_i)$ = Genotypic variance of ' i^{th} ' character

$V_g (x_j)$ = Genotypic variance of ' j^{th} ' character

$Cov_g (x_i x_j)$ = Genotypic covariance between ' i^{th} ' and ' j^{th} ' characters.

Significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1967)] at (n-2) degree of freedom at 5% and 1% level where, 'n' denotes the number of observations worked out.

3.3.6 Path Coefficient Analysis

The direct and indirect contributions of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

The following set of simultaneous equations were formed and solved for estimating direct and indirect effects.

$$\begin{array}{rcl}
 r_{1y} & = & P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1i} P_{iy} \\
 r_{2y} & = & r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2i} P_{iy} \\
 \cdot & & \cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot \\
 \cdot & & \cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot \\
 \cdot & & \cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot \\
 r_{iy} & = & r_{i1} P_{1y} + r_{i2} P_{2y} + r_{i3} P_{3y} + \dots + P_{iy}
 \end{array}$$

where,

r_{1y} to r_{iy} = Coefficient of correlation among causal factors

P_{1y} to P_{iy} = Direct effects of characters 1 to i on character y.

The above equations were written in the matrix form as under.

$$\begin{array}{ccc}
 \text{A} & \text{C} & \text{B} \\
 \begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ \cdot \\ \cdot \\ r_{iy} \end{pmatrix} & \begin{pmatrix} 1 & r_{12} & r_{13} & \dots & r_{1i} \\ r_{21} & 1 & r_{23} & \dots & r_{2i} \\ r_{31} & r_{32} & 1 & \dots & r_{3i} \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ r_{i1} & r_{i2} & r_{i3} & \dots & 1 \end{pmatrix} & \begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{3y} \\ \cdot \\ \cdot \\ P_{iy} \end{pmatrix}
 \end{array}$$

Then $B = [C]^{-1} A$

where,

$$[C] = \begin{pmatrix} C_{11} & C_{12} & C_{13} \dots \dots \dots C_{1i} \\ C_{21} & C_{22} & C_{23} \dots \dots \dots C_{2i} \\ C_{i1} & C_{i2} & C_{i3} \dots \dots \dots C_{ii} \end{pmatrix}$$

Then, direct effects were calculated as follows:

$$P_{1y} = \sum_{i=1}^I C_{1i} r_{1y}$$

$$P_{2y} = \sum_{i=2}^I C_{2i} r_{2y}$$

$$P_{iy} = \sum_{i=i}^I C_{ii} r_{iy}$$

Besides the direct and indirect effects, the residual effect, which measures the contribution of the characters not considered in the causal scheme was obtained as residual effect.

$$\text{Residual effect } (P_{Ry}) = \sqrt{1 - (P_{1y}r_{1y} + P_{2y}r_{2y} + \dots \dots \dots + P_{iy}r_{iy})^2}$$

where,

P_{Ry} = Residual effect

P_{iy} = Direct effect of 'x_i' on 'y'

r_{iy} = Correlation coefficient of 'x_i' on 'y'

The direct and indirect effects were classified based on the scale given by Lenka and Mishra (1973).

Very high	-	More than 1.0
High	-	0.3 to 0.99
Moderate	-	0.2 to 0.29
Low	-	0.1 to 0.19
Negligible	-	0.00 to 0.09

Chapter ~ IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

The present study on genetic analysis of yield and yield components along with seed protein and phenol content in pigeonpea was conducted using line x tester mating design utilizing five lines viz., ICPL-6974, ICPL-15225, ICPL-7035, ICPL-2376 and LRG-41, three testers viz., ICPL-87119, ICPL-8863 and PRG-158 and their 15 crosses. The results obtained on mean performance, genetic parameters, heterosis, combining ability and character association for 14 characters viz., days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, harvest index, SCMR at vegetative phase, seed protein, phenol content and seed yield per plant were discussed here under.

4.1 ANALYSIS OF VARIANCE

The analysis of variance for Randomized Block Design with respect to 14 characters is presented in Table 4.1. The mean sum of squares for treatments were found to be significant for all the traits, indicating the existence of sufficient genetic variation among the genotypes studied, while the mean sum of squares for replications were found to be non-significant for all the traits except pods per plant, 100-seed weight, seed protein and seed yield per plant.

4.2 MEAN PERFORMANCE

The mean performance of the parents, standard check (LRG-30) and crosses were presented in Tables 4.2 and 4.3, respectively. The results and discussions were furnished character wise hereunder. Pods and seeds of eight parents in present study was shown in Plate 2.

Table 4.1. Analysis of variance for yield and yield components in pigeonpea

S. No.	Characters	Mean sum of squares		
		Replications (df=2)	Treatments (df= 22)	Error (df=44)
1	Days to flowering	2.17	246.37*	3.64
2	Days to maturity	24.28	385.53**	7.7
3	Plant height	913.23	2052.90**	449.2
4	Primary branches per plant	3.88	53.13**	10.55
5	Secondary branches per plant	127.17	297.99**	50.36
6	Pods per plant	38551.04*	368227.71**	11859.1
7	Seeds per pod	0.02	0.66**	0.07
8	Pod length (cm)	0.26	1.59**	0.11
9	100-seed weight (g)	6.78**	17.27**	0.99
10	Harvest index (%)	0.44	45.87**	4.45
11	SCMR at vegetative phase	0.29	15.79**	1.23
12	Seed protein (%)	0.08*	3.02**	0.02
13	Phenol content (%)	0.06	4.63**	0.04
14	Seed yield per plant (g)	3498.80*	23150.45**	983.07

** Significant at 0.01; * Significant at 0.05

Table 4.2. Mean performance of 5 lines, 3 testers and one standard check for seed yield and yield components in pigeonpea.

Parents	Days to flowering	Days to maturity	Plant height (cm)	Primary branches plant	Secondary branches plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
LINES														
ICPL-6974	97.00	140.00	205.00	16.00	13.33	295.67	3.73	4.85	10.67	17.00	42.60	26.33	6.62	53.33
ICPL-15225	116.67	172.33	182.00	14.67	10.67	411.33	4.73	6.04	13.00	32.10	37.70	23.83	5.65	101.00
ICPL-7035	121.33	168.33	174.33	7.67	4.00	107.00	5.40	7.24	20.67	22.13	39.27	24.33	3.23	50.00
ICPL-2376	99.00	151.00	216.67	17.00	32.00	329.00	3.40	4.33	10.00	14.86	45.20	22.23	5.61	82.33
LRG-41	123.67	181.33	223.33	19.00	35.67	472.00	3.90	5.90	11.33	18.22	42.23	24.69	7.55	114.33
TESTERS														
ICPL-87119	121.67	169.67	241.67	22.67	32.67	606.67	3.60	5.00	11.67	25.31	39.80	24.50	6.11	165.33
ICPL-8863	103.00	161.67	263.67	16.67	30.67	593.00	3.50	4.85	11.67	20.21	40.77	24.62	4.51	150.00
PRG-158	120.33	172.33	176.00	16.33	18.00	460.67	3.60	4.98	10.67	15.47	40.23	24.81	6.41	95.67
Mean of parents	112.83	164.58	210.33	16.25	22.13	409.42	3.98	5.40	12.46	20.66	40.98	24.42	5.71	101.50
Range (min)	97.00	140.00	174.33	7.67	4.00	107.00	3.40	4.33	10.00	14.86	37.70	22.23	3.23	50.00
Range (max)	123.67	181.33	263.67	22.67	35.67	606.67	5.40	7.24	20.67	32.10	45.20	26.33	7.55	165.33
Standard check (LRG-30)	123.67	186	224.67	12	17	253.33	3.53	5.06	8.33	15.77	43.14	24.2	6.25	77.67
S E	1.37	1.68	13.94	1.62	4.98	37.33	0.20	0.19	0.58	0.92	0.84	0.08	0.16	14.13
C.D.(0.05)	4.16	5.08	42.28	4.91	15.10	113.24	0.62	0.58	1.75	2.79	2.55	0.24	0.49	42.87
C.V.(%)	2.11	1.76	11.48	17.26	38.96	15.79	8.89	6.13	8.00	7.72	3.56	0.57	4.87	24.12

Table 4.3. Mean performance of 15 F₁ crosses for seed yield and yield components in pigeonpea

Parents	Days to flowering	Days to maturity	Plant height (cm)	Primary branches plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
ICPL-6974 X ICPL-87119	112.67	142.33	222.33	21.00	22.33	708.33	3.60	4.73	10.33	19.50	42.93	25.21	8.35	163.67
ICPL-6974 X ICPL-8863	100.67	146.67	233.00	16.67	17.33	516.00	3.60	4.91	10.00	20.02	39.63	26.35	6.70	110.67
ICPL-6974 X PRG-158	104.00	142.67	221.33	14.33	20.67	604.33	3.87	5.25	12.00	22.45	40.53	25.66	6.33	141.67
ICPL-15225 X ICPL-87119	120.67	173.67	245.00	22.33	28.00	1411.33	4.33	5.21	12.00	26.03	40.80	26.11	7.52	369.33
ICPL-15225 X ICPL- 8863	115.33	158.00	244.33	17.67	33.33	1563.33	4.53	6.35	13.00	25.89	40.97	26.69	7.60	390.00
ICPL--15225 X PRG-158	115.00	162.67	210.33	16.33	20.67	485.33	3.73	4.95	11.33	24.08	43.10	24.94	6.13	106.33
ICPL-7035 X ICPL-87119	115.00	165.67	183.67	16.00	23.33	336.67	4.33	5.95	16.33	21.53	44.37	25.72	6.68	93.00
ICPL-7035 X ICPL-8863	105.00	156.33	188.67	9.67	13.67	363.67	4.27	6.89	14.67	21.84	48.07	25.73	7.89	94.33
ICPL-7035 X PRG-158	123.00	162.67	195.33	10.33	15.67	260.67	4.33	5.79	12.67	21.02	43.87	24.46	6.02	67.00
ICPL-2376 X ICPL-87119	104.33	153.33	234.33	21.00	31.00	406.33	3.63	5.31	10.33	18.60	44.20	26.07	6.78	95.33
ICPL-2376 X ICPL-8863	99.33	150.67	185.33	16.33	16.00	369.67	3.67	5.02	10.67	17.30	41.27	25.40	8.36	84.67
ICPL-2376 X PRG-158	111.00	155.00	199.33	15.00	21.00	383.33	3.93	4.91	10.33	17.78	43.63	26.11	8.41	89.33
LRG-41 X ICPL-87119	120.00	170.00	239.00	20.33	35.33	894.33	4.00	5.88	11.67	21.21	42.17	24.95	7.73	192.67
LRG-41 X ICPL-8863	108.33	162.67	243.33	25.67	42.00	512.33	4.07	6.02	11.67	22.91	43.97	26.11	6.93	146.33
LRG-41 X PRG-158	124.67	171.00	235.33	18.00	38.67	989.67	4.07	5.89	11.33	22.87	41.93	25.16	7.30	231.00
Mean of crosses	111.93	158.22	218.71	17.38	25.27	653.69	4.00	5.54	11.89	21.54	42.76	25.64	7.25	158.36
Range (min)	99.33	142.33	183.67	9.67	13.67	260.67	3.60	4.73	10.00	17.30	39.63	24.46	6.02	67.00
Range (max)	124.67	173.67	245.00	25.67	42.00	1563.33	4.53	6.89	16.33	26.03	48.07	26.69	8.41	390.00
S E	0.979	1.444	11.266	2.004	3.517	69.342	0.130	0.192	0.589	1.367	0.531	0.082	0.088	19.487
C.D.(0.05)	2.836	4.183	32.629	5.805	10.186	200.836	0.375	0.557	1.706	3.960	1.539	0.236	0.253	56.439
C.V. (%)	1.515	1.581	8.922	19.976	24.108	18.373	5.616	6.019	8.583	10.995	2.152	0.551	2.091	21.314

4.2.1 Yield attributes

4.2.1.1 Days to flowering (No.): In parents, among the lines ICPL-6974 (97.0 days) and LRG-41 (123.67), among testers ICPL-8863 (103.0 days) and ICPL-87119 (121.67) were early and late flowering, respectively with a mean of 112.83 days for parents. In crosses early flowering was observed in the cross ICPL-2376 x ICPL-8863 (99.33 days) while the crosses LRG-41 x PRG-158 (124.67 days) and ICPL-7035 x PRG-158 (123.0 days) were very late with a mean of 111.93 days which was surpassed by eight crosses.

4.2.1.2 Days to maturity (No.): The genotypes, ICPL-6974 (140.0 days) among lines and ICPL-8863 (161.67 days) among testers were early to mature, whereas the line LRG-41(181.33) and the tester PRG-158 (172.33) were late to mature with a mean of 164.5 days for parents. In crosses it ranged from 142.33 days (ICPL-6974 x ICPL-87119) to 173.67 days (ICPL-15225 x ICPL-87119) with a mean of 158.22 days which surpassed by seven crosses.

4.2.1.3 Plant height (cm): The mean plant height for parents was 210.33 cm. The line LRG-41 (223.33 cm) and the tester ICPL-8863 (263.67 cm) were the tallest, while the line ICPL-7035 (174.33 cm) and the tester PRG-158 (176.0) were the shortest parents. Among the crosses ICPL-15225 x ICPL-87119 (245 cm) was the tallest, whereas ICPL-7035 x ICPL-87119 (183.67 cm) was the shortest with a mean plant height of 218.71 cm. Out of 15 crosses, nine crosses were observed to have higher plant height than the hybrid mean.

4.2.1.4 Primary branches per plant (No.): The line LRG-41 (19.0) and the tester ICPL-87119 (22.67) recorded higher number of primary branches with a mean of 16.25. The line ICPL-7035 (7.67) and the tester PRG-158 (16.33) had lowest number of primary branches per plant among the parents. Among the crosses, LRG-41 x ICPL-8863 (25.67) and ICPL-7035 x ICPL-8863

(9.67) showed more and less number of primary branches per plant, respectively, with a hybrid mean of 17.38. Seven crosses surpassed the mean of F_1 crosses.

4.2.1.5 Secondary branches per plant (No.): The mean of the parents was 22.13. Among the parents, the line LRG-41 (35.67) and the tester ICPL-87119 (32.67) showed highest number of secondary branches per plant whereas the line ICPL-7035 (4.0) and the tester PRG-158 (18.0) had lowest number of secondary branches per plant. Among the crosses, LRG-41 x ICPL-8863 (42.0) and ICPL-7035 x ICPL-8863 (13.67) showed highest and lowest values for this trait with a hybrid mean of 25.27, which surpassed by five crosses out of 15 crosses.

4.2.1.6 Pods per plant (No.): The genotype LRG- 41 (472.0) among lines and ICPL-87119 (606.67) among testers recorded more number of pods per plant, whereas the line ICPL-7035 (107.0) and the tester PRG-158 (460.67) recorded less pod number per plant. All lines except LRG-41 and ICPL-15225 were recorded below the parental mean (409.42) and all the testers were above the parental mean. In F_1 's it ranged from ICPL-7035 x PRG-158 (260.67) showed less number of pods and ICPL-15225 x ICPL-8863 (1563.33) and ICPL-15225 x ICPL-87119 (1411.33) showed more number of pods with a hybrid mean of 653.69. Five crosses recorded highest value than the F_1 mean.

4.2.1.7 Seeds per pod (No.): Among the parents, the lines ICPL-7035 (5.4) and ICPL-2376 (3.4) showed maximum and minimum number of seeds per pod, respectively with the parental mean of 3.98. All testers had less number of seeds per pod than the mean value. Among the hybrids, ICPL-15225 x ICPL-8863 (4.53) showed highest, whereas ICPL-6974 x ICPL-87119 (3.6) and ICPL-6974 x ICPL-8863 (3.6) showed lowest values for this trait. Seven crosses were showed higher values than hybrid mean (4.0).

4.2.1.8 Pod length (cm): Among the parents, ICPL-7035 (7.24) had lengthy pods and ICPL-2376 (4.33) had shortest pod length. The parental mean of pod length was 5.40. All testers had lowest pod length than the mean. In crosses, it was ranged from 4.73 (ICPL- 6974 x ICPL-87119) to 6.89 (ICPL- 7035 x ICPL-8863) with F_1 mean of 5.54, which surpassed by seven crosses.

4.2.1.9 100-seed weight (g): Among all the parents, ICPL-7035 (20.67 g) recorded maximum seed weight with a parental mean of 12.46. The line ICPL-2376 (10.0) recorded lowest seed weight among the parents. The three testers showed lower seed weight than the mean. In crosses it was ranged from 10.0 (ICPL-6974 x ICPL-8863) to 16.33 (ICPL-7035 x ICPL-87119). Six crosses exceeded the mean seed weight (11.89).

4.2.1.10 Harvest index (%): Among the parents, the line ICPL-15225 (32.1) and the tester ICPL-87119 (25.31) recorded highest harvest index whereas the line ICPL-2376 (14.86) and the tester PRG-158 (15.47) had lowest harvest index with a mean of 20.66. In crosses, it ranged from 17.3 (ICPL-2376 x ICPL-8863) to 26.03 (ICPL-15225 x ICPL-87119) with a mean of 21.54. Seven crosses showed high harvest index than hybrid mean.

4.2.1.11 SCMR at vegetative phase: Among the parents, the lines ICPL-2376 (45.2) and ICPL-15225 (37.7) and the testers ICPL-8863 (40.77) and ICPL-87119 (39.8) showed highest and lowest SCMR contents, respectively, with a mean of 40.98. All the three testers had low SCMR content than mean. Among the 15 crosses, it ranged from 39.63 (ICPL-6974 x ICPL-8863) to 48.07 (ICPL-7035 x ICPL-8863) and eight crosses exceeded the hybrid mean (42.76) value.

4.2.1.12 Seed yield per plant (g): The genotype LRG-41 (114.33) among the lines and ICPL-87119 (165.33) among the testers showed highest seed yield per plant. The line ICPL-7035 (50.0) and the tester PRG-158 (95.67) had lowest seed yield among the parents with a mean of 101.50. In crosses,

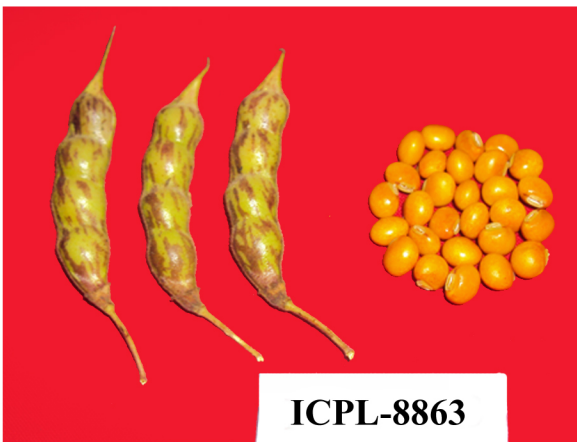


Plate 2. Plate showing pods and seeds of eight parents of pigeonpea

it ranged from 67 (ICPL-7035 x PRG-158) to 390 (ICPL-15225 x ICPL-8863) with a mean of 158.36. Five crosses recorded highest seed yield per plant over the F₁ mean.

4.2.2 Quality attributes

4.2.2.1 Seed protein (%): In parents, the line ICPL-6974 (26.33) and the tester PRG-158 (24.81) recorded superior protein percentage with a mean of 24.42. The line ICPL-2376 (22.23) and the tester ICPL-87119 (24.5) had low seed protein among the parents. The seed protein in F₁'s ranged from 24.46 (ICPL- 7035 x PRG-158) to 26.69 (ICPL-15225 x ICPL-8863) with a mean of 25.64, which surpassed by nine crosses.

4.2.2.2 Phenol content (%): The genotype LRG-41 (7.55) among the lines and PRG-158 (6.41) among the testers had high phenol content with a mean of 5.71 in parents. The line ICPL-7035 (3.23) and the tester ICPL-8863 (4.51) showed lowest phenol content in parents. In crosses, it was ranged from 6.02 (ICPL-7035 x PRG-158) to 8.41 (ICPL-2376 x PRG-158) with a mean of 7.25, which exceeded by eight crosses.

Among the parents, the line LRG-41 and the tester ICPL-87119 were promising for seed yield. Among the lines ICPL-6974 and ICPL-2376 for earliness, ICPL-7035 for more number of seeds per pod, pod length and 100-seed weight, whereas for the rest of the characters LRG-41 followed by ICPL-15225 recorded high *per se* performance. In testers, ICPL-8863 was most desirable for earliness and other yield contributing characters.

The crosses ICPL-15225 x ICPL-8863, ICPL-15225 x ICPL-87119 and LRG-41 x PRG-158 recorded high *per se* performance for yield and most of the yield components. The lines ICPL-6974 and ICPL-2376 involving cross combinations recorded high performance for earliness. Hence, these genotypes were compared for combining ability, heterosis

along with phenotypic *per se* performance to identify the superior genotypes for further breeding programmes to improve the yield.

4.3 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Improvement in any crop species depends upon the amount of variation present in a given breeding material and its mode of utilization in the breeding programmes. The measure of transmission of a character from parent to offspring is termed as heritability and the consistency of performance of selected material in succeeding generations depends upon the magnitude of heritable variation present in relation to the observed variation. The estimates of genotypic variation alone could not provide the necessary heritable variance that could be required for selection. Hence, information on heritability is a prerequisite for planning a sound-breeding programme for selection. The genetic advance is commonly predicted, as a product of heritability, phenotypic standard deviation and selection differential. High estimates of heritability accompanied by high expectation of genetic advance indicates that additive gene effects governing the characters. High heritability accompanied by a low genetic advance indicates the presence of non-additive (epistasis and dominance) component. Therefore, the estimate of heritability and genetic gain is important to have an idea about effectiveness of selection.

In the present study, variability estimates as phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV), estimates of heritability (broad sense) and genetic advance as per cent of mean for 14 characters in eight parents and 15 crosses were furnished in the Table 4.4. The estimates of PCV and GCV for parents and crosses were also presented in Fig. 4.1 and 4.2, respectively, whereas heritability and genetic advance as per cent of mean for parents and crosses showed in Fig. 4.3 and 4.4,

Table 4.4. Range, mean, coefficient of variability, heritability and genetic advance for yield and yield components in parents and F₁ crosses of pigeonpea

Characters	Range		Mean		GCV		PCV		Heritability (%)		Genetic advance		Genetic advance as % of mean	
	Parents	F ₁ 's	Parents	F ₁ 's	Parents	F ₁ 's	Parents	F ₁ 's	Parents	F ₁ 's	Parents	F ₁ 's	Parents	F ₁ 's
Days to flowering	97.00 - 123.67	99.33 - 124.67	112.83	111.93	9.85	7.21	10.07	7.37	95.63	95.77	22.38	16.27	19.84	14.53
Days to maturity	140.00 - 181.33	142.33 - 173.67	164.58	158.22	8.02	6.20	8.21	6.40	95.38	93.90	26.54	19.59	16.13	12.38
Plant height (cm)	174.33 - 263.67	183.67 - 245.00	210.33	218.71	13.90	9.12	18.02	12.76	59.45	51.10	46.43	29.37	22.07	13.43
Primary branches per plant	7.67 - 22.67	9.67 - 25.67	16.25	17.38	24.10	21.81	29.64	29.57	66.11	54.38	6.56	5.76	40.37	33.13
Secondary branches per plant	4.00 - 35.67	13.67 - 42.00	22.13	25.27	49.68	32.46	63.13	40.43	61.92	64.45	17.82	13.56	80.54	53.68
Pods per plant	107.00 - 606.67	260.67 - 1563.33	409.42	653.69	39.20	59.69	42.26	62.46	86.03	91.35	306.62	768.26	74.89	117.53
Seeds per pod	3.40 - 5.40	3.60 - 4.53	3.98	4.00	17.01	7.08	19.20	9.04	78.53	61.37	1.24	0.46	31.05	11.42
Pod length (cm)	4.33 - 7.24	4.73 - 6.89	5.40	5.54	16.96	10.77	18.03	12.33	88.45	76.19	1.77	1.07	32.85	19.36
100-seed weight (g)	10.00 - 20.67	10.00 - 16.33	12.46	11.89	27.19	13.77	28.35	16.22	92.03	72.01	6.69	2.86	53.74	24.07
Harvest index (%)	14.86 - 32.10	17.30 - 26.03	20.66	21.54	27.66	10.50	28.72	15.20	92.77	47.69	11.34	3.22	54.89	14.94
SCMR at vegetative phase	37.70 - 45.20	39.63 - 48.07	40.98	42.76	5.28	4.74	6.37	5.21	68.72	82.91	3.69	3.80	9.01	8.89
Seed protein (%)	22.23 - 26.33	24.46 - 26.69	24.42	25.64	4.65	2.38	4.68	2.44	98.52	94.92	2.32	1.23	9.51	4.78
Phenol content (%)	3.23 - 7.55	6.02 - 8.41	5.71	7.25	23.17	11.13	23.68	11.33	95.77	96.60	2.67	1.63	46.71	22.54
Seed yield per plant (g)	50.00 - 165.33	67.00 - 390.00	101.50	158.36	38.28	62.15	45.24	65.71	71.59	89.48	67.72	191.79	66.72	121.11

Fig. 4.1. Phenotypic co-efficient of variation for 14 characters in parents and crosses of pigeonpea

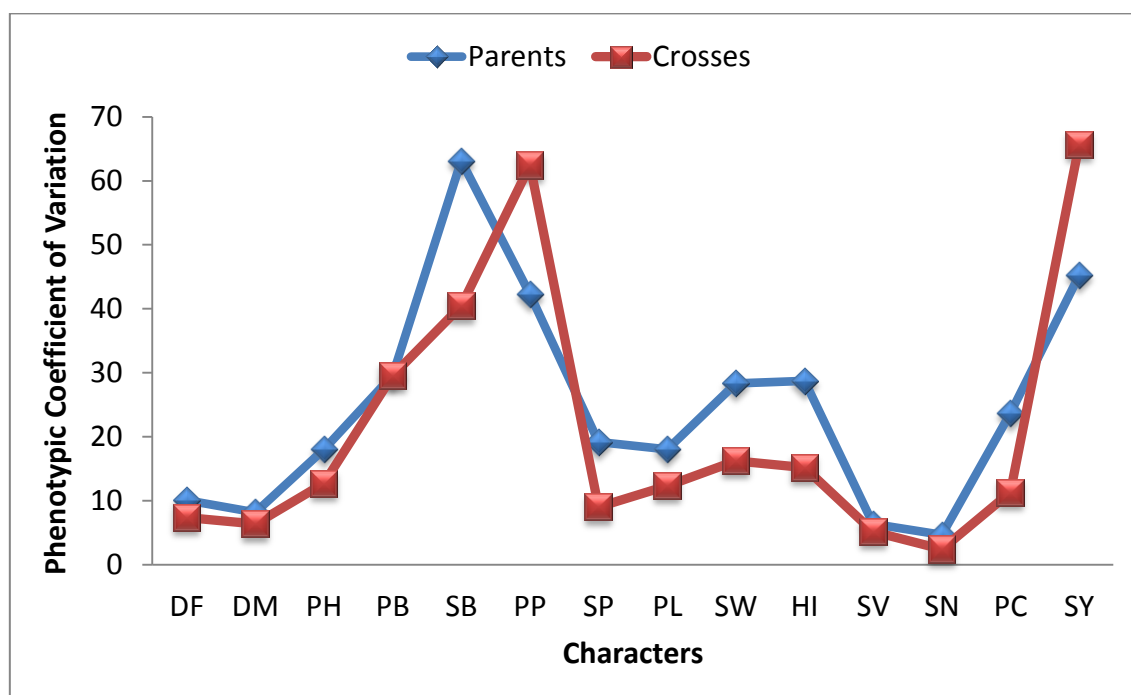
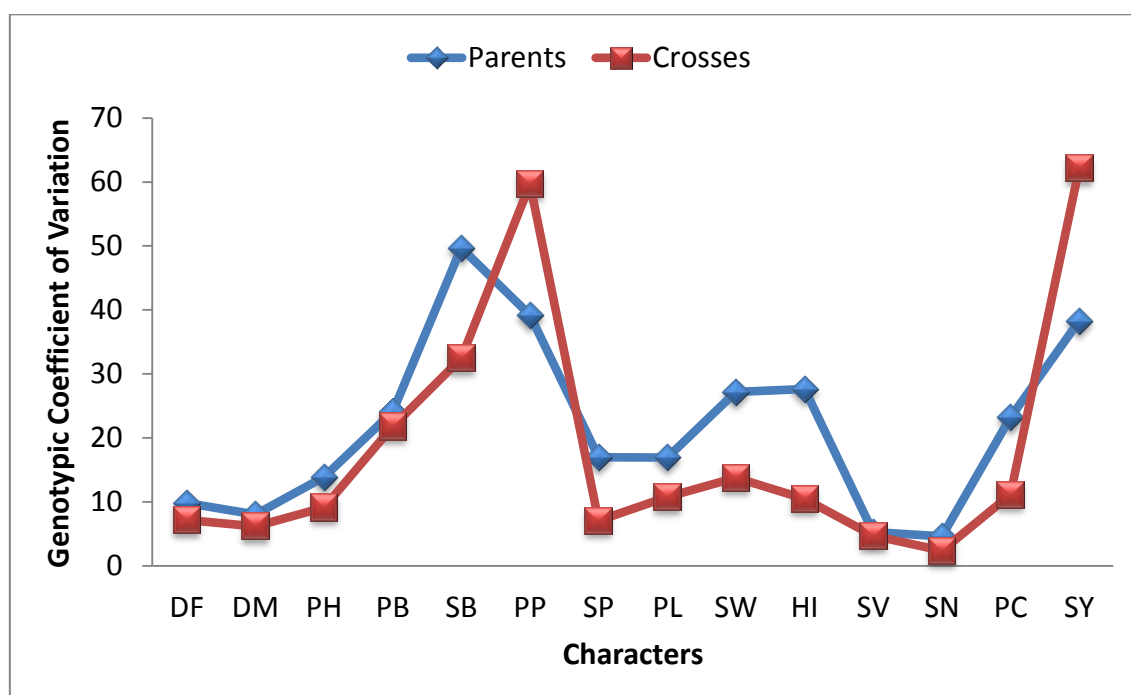


Fig. 4.2. Genotypic co-efficient of variation for 14 characters in parents and crosses of pigeonpea



DF= Days to flowering	PP= Pods per plant	SV= SCMR at vegetative phase
DM= Days to maturity	SP= Seeds per pod	SN= Seed protein
PH=Plant height	PL=Pod length	PC= Phenol content
PB= Primary branches per plant	SW= 100-seed weight	SY= Seed yield per plant
SB= Secondary branches per plant	HI= Harvest index	

Fig 4.3. Heritability and genetic advance as per cent of mean for 14 characters in parents of pigeonpea

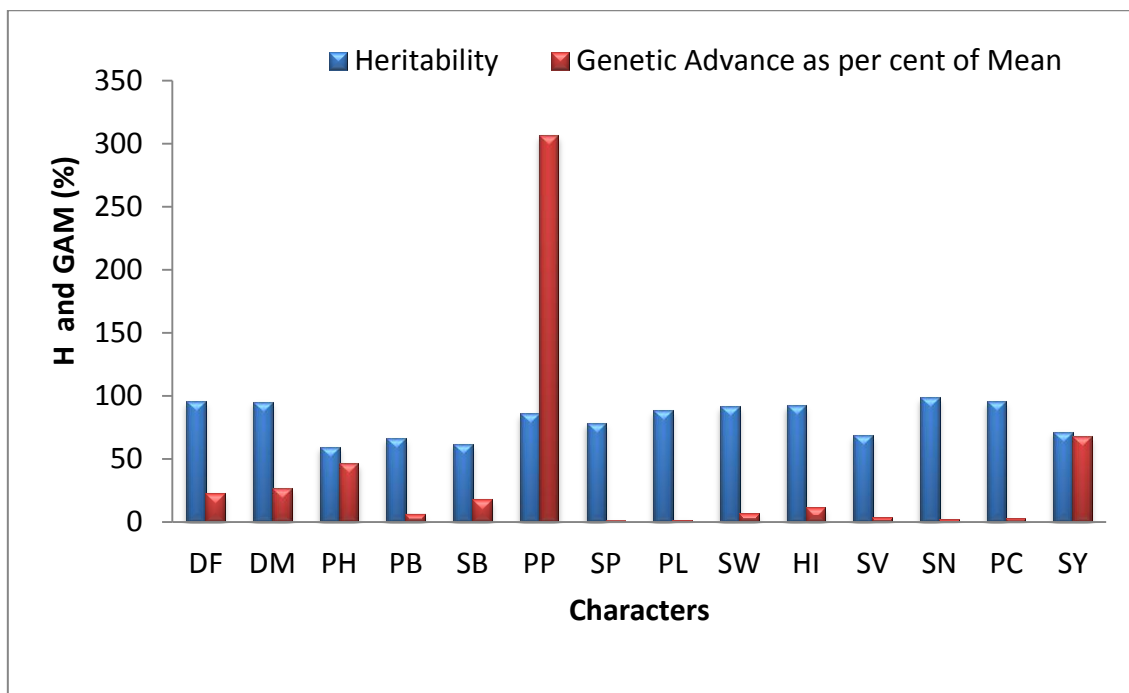
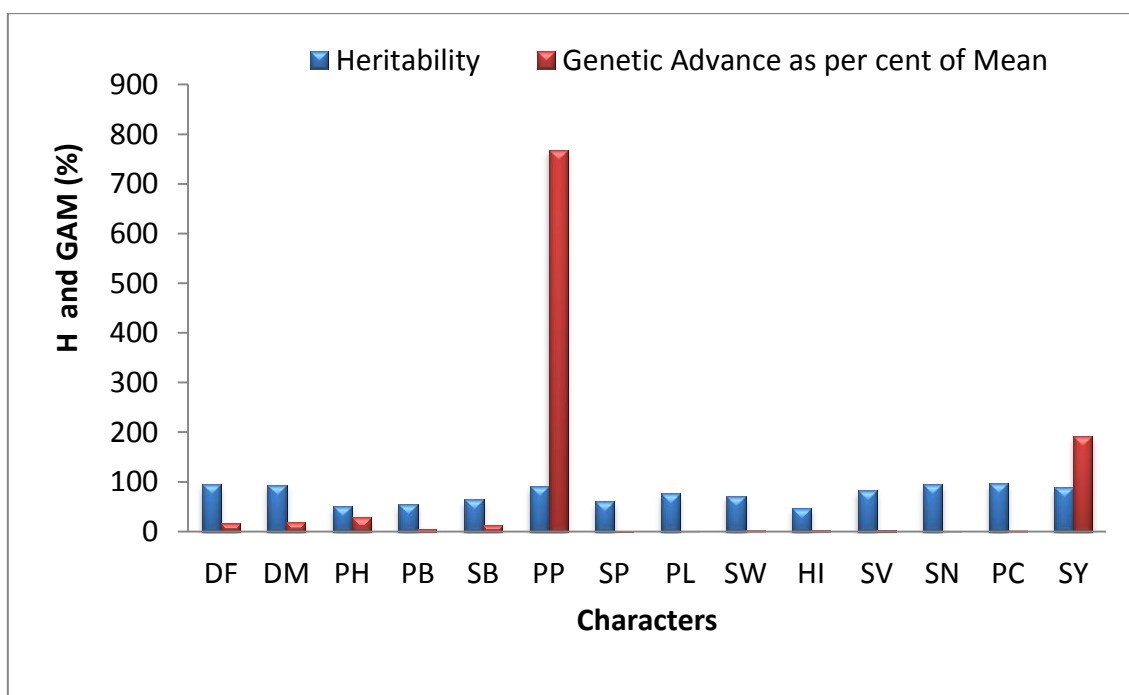


Fig. 4.4. Heritability and genetic advance as per cent of mean for 14 characters in crosses of pigeonpea



DF= Days to flowering	PP= Pods per plant	SV= SCMR at vegetative phase
DM= Days to maturity	SP= Seeds per pod	SN= Seed protein
PH=Plant height	PL=Pod length	PC= Phenol content
PB= Primary branches per plant	SW= 100-seed weight	SY= Seed yield per plant
SB= Secondary branches per plant	HI= Harvest index	

respectively. The results and discussion were described character wise hereunder.

4.3.1 Yield attributes

4.3.1.1 Days to flowering: Days to flowering in parents showed low genotypic co-efficient of variation (9.85) and moderate phenotypic co-efficient of variation (10.07). The heritability estimate for this trait was high (95.63) with moderate genetic advance (22.38) and genetic advance as per cent of mean was 19.84.

In crosses, the low GCV and PCV estimates observed for this trait were 7.21 and 7.37 respectively. The heritability estimate for this trait was high (95.77) with a moderate genetic advance (16.27) and genetic advance as per cent of mean (14.53).

The genotypic coefficient of variation for this trait was low in parents and crosses and phenotypic co-efficient of variation was moderate in parents and low in crosses. This is in confirmity with Patil *et al.* (1989), Kapre and Nerker (1992), Aher *et al.* (1996) and Srinivas (1996), indicating that there is a limited scope of selection for this character. High heritability in parents and crosses coupled with moderate genetic advance as per cent of mean, this trait can be improved by simple selection methods. Similar results were reported by Kingshlin and Subbaraman (1999), Anantharaju and Muthaiah (2008) and Jogendra Sindra *et al.* (2008).

4.3.1.2 Days to maturity: In parents, low GCV and PCV estimates of 8.02 and 8.21 were observed for this trait, respectively. Heritability estimates for this trait was high 95.38 with high genetic advance (26.54) and moderate genetic advance as per cent of mean (16.13).

In crosses, the GCV (6.2) and PCV (6.4) estimates were low. High heritability (93.9) estimates were recorded for this trait with a moderate genetic advance (19.59) and genetic advance as per cent of mean (12.38).

This trait exhibited low GCV and PCV both in parents and crosses indicating that the selection can be done in later generations. This is in agreement with the results of Patil *et al.* (1989), Khapre and Nerker (1992) and Srinivas (1996). High heritability in parents and crosses indicates least influence of environment on this trait. High heritability coupled with moderate genetic advance as per cent of mean indicates the importance of both additive and non-additive gene effects for this trait. Similar results were also reported by Aher *et al.* (1996) and Anantharaju and Muthaiah (2008).

4.3.1.3 Plant height: In parents, plant height was recorded moderate GCV (13.9) and PCV (18.02). Moderate heritability (59.45), high genetic advance (46.43) and genetic advance as per cent of mean (22.07) were observed for this trait.

Low GCV (9.12) and moderate PCV (12.76) were observed in crosses, while heritability estimates were moderate (51.1) with high genetic advance (29.37) and moderate genetic advance as per cent of mean (13.43).

Plant height exhibited low GCV and PCV in parents, while low GCV and moderate PCV in crosses indicates the selection may be effective in later generations for this trait. Moderate to high heritability with genetic advance as per cent of mean was observed, which indicates additive effects for this trait and is confirmed with the results of Konwar and Hazarika (1988), Natarajan *et al.* (1990), Takalkar *et al.* (1998) and Firoz Mahamad *et al.* (2006).

4.3.1.4 Primary branches per plant: In parents this trait was recorded high GCV (24.1) and PCV (29.64). The heritability estimate was high (66.11)

with low genetic advance (6.56) and high genetic advance as per cent of mean (40.37).

In crosses, high variation was observed for this trait with GCV (21.81) and PCV (29.57). The heritability estimate (54.38) was moderate with a low genetic advance (5.76) and high genetic advance as per cent of mean (33.13).

This trait exhibited high variability in parents and crosses indicating its amenability for selection in early generation. This is in confirmity with the results of Bainiwal and Jatasra (1981), Balyan and Sudhakar (1985), Jagshoran (1985), Dahat *et al.* (1997), Patel and Patel (1998) and Deshmukh *et al.* (2000). Moderate to high heritability coupled with high genetic advance as per cent of mean reported in parents and crosses, confirmed with the results of Jogendra Singh *et al.* (2008) and Bhadru (2010).

4.3.1.5 Secondary branches per plant: In parents high variation was noticed with GCV (49.68) and PCV (63.13). High heritability estimate (61.92) was observed with moderate genetic advance (17.82) and high genetic advance as per cent of mean (80.54).

In case of crosses high variation was observed with GCV (32.46) and PCV (40.43). High heritability (64.45) with moderate genetic advance (13.56) and high genetic advance as per cent of mean (53.68) was reported.

This exhibited high GCV and PCV both in parents and crosses indicating existence of high variability of this character which is required for selection. This is in agreement with the results of Bainiwal and Jatasra (1981), Aher *et al.* (1996), Deshmukh *et al.* (2000) and Firoz mahamad *et al.* (2006). High heritability with high genetic advance as per cent of mean was observed in parents and crosses indicating that the selection is effective because of additive gene action on this trait. These results are in

confirmity with Balyan and Sudhakar (1985), Dahat *et al.* (1997) and Bhadru (2010).

4.3.1.6 Pods per plant: In parents high variation recorded with GCV (39.2) and PCV (42.26). High heritability (86.03) estimates recorded with a high genetic advance (306.62) and genetic advance as per cent of mean (74.89).

F₁ crosses recorded high variation recorded with 59.69 GCV and 62.46 PCV. High heritability (91.35) recorded with high genetic advance (768.26) and genetic advance as per cent of mean (117.53).

This trait showed very high variability both in parents and crosses, hence this trait can be utilized in early generations. This is in agreement with the results of Jagshoran (1985), Sidhu *et al.* (1985), Bhongale and Raut (1987), Patil *et al.* (1989), Khapre *et al.* (1993), Pansuriya *et al.* (1998), Takalkar *et al.* (1998) and Kalaimagal *et al.* (2008). High heritability coupled with very high genetic advance as per cent of mean was noticed in parents and crosses, the same reported by Balyan and Sudhakar (1985), Holker *et al.* (1991), Khapre and Nerker (1992), Dahat *et al.* (1997), Srinivas *et al.* (1999) and Magar (2003) and Bhadru (2010).

4.3.1.7 Seeds per pod: In parents, moderate GCV (17.01) and PCV (19.2) and high heritability (78.53) estimates were recorded with a low genetic advance (1.24) and genetic advance as per cent of mean (31.05).

In crosses variation was low with GCV (7.08) and PCV (9.04). The heritability (61.37) was high with a very low genetic advance (0.46) and moderate genetic advance as per cent of mean (11.42).

Moderate variability was observed in parents and low variability was observed in crosses, indicates selection can be done in later generations. Low variability for this trait was also reported by Jagshoran (1985), Sidhu *et al.* (1985), Natarajan *et al.* (1990), Kapre *et al.* (1993) and Aher *et al.*

(1996). High heritability with moderate to high genetic advance as per cent of mean indicated this trait can be improved by simple selection methods in early generations. The results were supported by Kingshlin and Subbaraman (1999), Magar (2003) and Anantharaju and Muthaiah (2008).

4.3.1.8 Pod length: In parents, moderate variation was recorded with GCV (16.96) and PCV (18.03). High heritability estimate (88.45) with low genetic advance (1.77) and genetic advance as per cent of mean (32.85) was observed.

In crosses, GCV (10.77) and PCV (12.33) estimates were moderate. High heritability (76.19) with low genetic advance (1.07) and moderate genetic advance as per cent of mean (19.36) reported.

The variability estimates for this trait were moderate in both parents and crosses indicating selection can be exercised in early generations. Narrow variability for pod length was observed by Jagshoran (1985) whereas high variability was observed by Hiramath and Talawar (1971) in pigeonpea. High heritability and moderate to high genetic advance as per cent of mean were recorded for this trait. Similar results were also reported by Kingshlin and Subbaraman (1999) and Jogendra Singh *et al.* (2008).

4.3.1.9 100-seed weight: In parents, high variation was observed with GCV (27.19) and PCV (28.35). Heritability was high (92.03) with low genetic advance (6.69) and high genetic advance as per cent of mean (53.74).

In crosses moderate variation recorded with 13.77 GCV and 16.22 PCV. High heritability (72.01) with low genetic advance (2.86) and high genetic advance as per cent of mean (24.07).

100-seed weight exhibited high variability in parents and moderate variability in crosses, which indicates selection for this trait is suitable for selection. This is in accordance with the results of Balyan and Sudhakar

(1985), Jagshoran (1985), Jogendra Singh *et al.* (2008) and Dodake *et al.* (2009) reported high variability for this character. High heritability coupled with high genetic advance as per cent of mean was noticed, indicating that this trait is governed by additive gene action. This is in confirmity with the results of Bhongale and Raut (1987), Patil *et al.* (1989), Basavarajaiah *et al.* (1999), Anantharaju and Muthaiah (2008) and Bhadru (2010).

4.3.1.10 Harvest index: The parents were recorded high GCV (27.66) and PCV (28.72) for this trait. High heritability (92.77), moderate genetic advance (11.34) and genetic advance as per cent of mean (54.89) were recorded.

In F_1 's moderate GCV (10.5) and PCV (15.2) values were noticed. Moderate heritability (47.69) was observed with low genetic advance (3.22) and moderate genetic advance as per cent of mean (14.94).

Harvest index exhibited high variability in parents indicating the usefulness of selection of this trait in early generations, while moderate variability in crosses. The high variability for harvest index was also reported earlier by Khapre *et al.* (1993) and Pansuriya *et al.* (1998). High heritability and high genetic advance as per cent of mean was observed in parents, indicating this trait is controlled by additive gene action, whereas moderate heritability and moderate genetic advance as per cent of mean in crosses indicating the presence of both additive and non-additive gene action on this trait. High heritability coupled with low genetic advance as per cent of mean for this trait was reported by Takalkar *et al.* (1998).

4.3.1.11 SCMR at vegetative phase: In parents the variation observed was very low with GCV of (5.28) and PCV of (6.37). Heritability was high (68.72) with low genetic advance (3.69) and genetic advance as per cent of mean (9.01).

In crosses, the variation was low with 4.74 GCV and 5.21 PCV. High heritability (82.91) with low genetic advance (3.8) and genetic advance as per cent of mean (8.89) were observed.

SCMR content at vegetative phase exhibited low variability in parents and crosses, indicating there is a limited scope of selection for this trait. High heritability coupled with low genetic advance indicates it is controlled by non-additive gene action. This is in accordance with the results of Krishna Chaithanya (2010).

4.3.1.12 Seed yield per plant: In parents, high variation was recorded with 38.28 GCV and 45.24 PCV. High estimates of heritability of 71.58, genetic advance of 67.72 and genetic advance as per cent of mean of 66.72 were observed.

In case of crosses high estimate of 62.15 GCV and 65.71 PCV was observed. High estimate of heritability (89.48) was noticed with high genetic advance (191.79) and genetic advance as per cent of mean (121.11).

Seed yield exhibited high variability in parents and crosses, indicating selection is required in early generations to improve this trait. These results are supported by Baniwal and Jatasra (1981), Balyan and Sudhakar (1985), Jagshoran (1985), Bhongale and Raut (1987), Patil *et al.* (1989), Khapre and Nerker (1992), Aher *et al.* (1998), Pansuriya *et al.* (1998) and Patel and Patel (1998). High heritability coupled with high genetic advance as per cent of mean was noticed, indicating that it is controlled by additive gene action and selection is effective. These results are supported by Balyan and Sudhakar (1985), Natarajan *et al.* (1990), Dahat *et al.* (1997), Aher *et al.* (1998), Basavarajaiah *et al.* (1999), Anantharaju and Muthaiah (2008), Jogendra Singh *et al.* (2008) and Bhadru (2010).

4.3.2 Quality attributes

4.3.2.1 Seed protein: In parents low variation of 4.65 GCV and 4.68 PCV values were observed. High heritability (98.52) with low genetic advance (2.32) and genetic advance as per cent of mean (9.51) were observed.

In case of crosses a very low GCV (2.38) and PCV (2.44) values were observed. High heritability (94.92) with low genetic advance (1.23) and genetic advance as per cent of mean (4.78) were observed.

Seed protein exhibited very low variability in parents and crosses, indicating a limited scope of selection for this character. This was in confirmity with the findings of Gohil (2006). High heritability coupled with low genetic advance as per cent of mean indicating that it is controlled by non-additive gene action in parents and crosses. This is supported by the findings of Aher *et al.* (1996).

4.3.2.2 Phenol content: In parents, this trait recorded higher values of 23.17 GCV and 23.68 PCV were recorded. This character also registered high heritability (95.77) value with low genetic advance (2.67) and high genetic advance as per cent of mean (46.71).

In crosses moderate variation recorded with 11.13 GCV and 11.33 PCV. Heritability estimate (96.6) was high with low genetic advance (1.63) and high genetic advance as per cent of mean (22.54).

Phenol content exhibited high variability in parents and moderate variability in crosses, indicating that the selection can be done in early generations. High heritability coupled with high genetic advance as per cent of mean was observed in parents and crosses, indicates it is controlled by additive gene effects and selection for this trait is effective. These results are in accordance with Rekha (2009).

From the foregoing discussion, it can be concluded that high estimates of variability, heritability and genetic advance as per cent of mean were observed for primary and secondary branches per plant, pods per plant, 100-seed weight, harvest index, phenol content and seed yield per plant in parents, whereas secondary branches per plant, pods per plant and seed yield per plant in crosses, indicating that these characters were under the control of additive gene effects, hence, simple selection may be effective to improve these characters. Hence, for commercial exploitation, high standard heterosis coupled with high *per se* performance was considered in the present study.

4.4 HETEROSIS

Estimation of the extent of heterosis in diverse cross combinations would always be useful in choosing the best performing crosses for commercial exploitation. In general, the extent of heterosis has often been estimated over mid or better parent with the objective of studying the nature of gene action involved in the parental combinations. However, the heterosis recorded over mid or better parent has little utility if parents have relatively poor *per se* performance. For commercial exploitation, the magnitude of heterosis should be at least 20 to 30 per cent higher in yield than the standard variety under study. Hence, the heterosis over the standard parent (LRG-30) was estimated and termed as standard heterosis.

In present investigation, the estimates of heterosis in 15 crosses over mid parent, better parent and standard check was presented in Table 4.5 and the relative merit of superior crosses is discussed here under.

4.4.1 Yield attributes

4.4.1.1 Days to flowering: The cross ICPL-7035 x ICPL-8863 recorded maximum negative significant heterosis over mid parent (-6.39 %) and ICPL-7035 x ICPL-87119 for better parent (-5.22 %) while the cross ICPL-2376 x

Table 4.5. Heterosis over mid parent (MP), better parent (BP) and standard check (SC) for yield and yield components of pigeonpea

Cross	Days to flowering			Days to maturity			Plant height (cm)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPL-6974 x ICPL-87119	3.05*	16.15**	-8.89**	-8.07**	-16.11**	-23.48**	-0.45	-8.00	-1.04
ICPL-6974 x ICPL-8863	0.67	3.78*	-18.60**	-2.76	-9.28**	-21.15**	-0.57	-11.63	3.71
ICPL-6974 x PRG-158	-4.29**	7.22**	-15.90**	-8.64**	-17.21**	-23.30**	16.19	7.97	-1.48
ICPL-15225 x ICPL-87119	1.26	3.43*	-2.43	1.56	0.77	-6.63**	15.66	1.38	9.05
ICPL-15225 x ICPL-8863	5.01**	11.97**	-6.74**	-5.39**	-8.32**	-15.05**	9.65	-7.33	8.75
ICPL-15225 x PRG-158	-2.95*	-1.43	-7.01**	-5.61**	-5.61**	-12.54**	17.50	15.57	-6.38
ICPL-7035 x ICPL-87119	-5.35**	-5.22**	-7.01**	-1.97	-2.36	-10.93**	-11.70	-24.00**	-18.25*
ICPL-7035 x ICPL-8863	-6.39**	1.94	-15.09**	-5.25**	-7.13**	-15.95**	-13.85	-28.45**	-16.02*
ICPL-7035 x PRG-158	1.79	2.22	-0.54	-4.50**	-5.61**	-12.54**	11.51	10.98	-13.06
ICPL-2376 x ICPL-87119	-5.44**	5.39**	-15.63**	-4.37**	-9.63**	-17.56**	2.25	-3.03	4.30
ICPL-2376 x ICPL-8863	-1.65	0.34	-19.68**	-3.62*	-6.80**	-19.00**	-22.83**	-29.71**	-17.51*
ICPL-2376 x PRG-158	1.22	12.12**	-10.24**	-4.12**	-10.06**	-16.67**	1.53	-8.00	-11.28
LRG-41 x ICPL-87119	-2.17	-1.37	-2.96*	-3.13*	-6.25**	-8.60**	2.80	-1.10	6.38
LRG-41 x ICPL-8863	-4.41**	5.18**	-12.40**	-5.15**	-10.29**	-12.54**	-0.07	-7.71	8.31
LRG-41 x PRG-158	2.19	3.60**	0.81	-3.30*	-5.70**	-8.06**	17.86*	5.37	4.75

Cross	Primary branches per plant			Secondary branches per plant			Pods per plant		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPL-6974 x ICPL-87119	8.62	-7.35	75.00**	-2.90	-31.63	28.85	57.00**	16.76	179.61**
ICPL-6974 x ICPL-8863	2.04	0.00	38.89	-21.21	-43.48*	0.00	16.13	-12.98	103.68**
ICPL-6974 x PRG-158	-11.34	-12.24	19.44	31.91	14.81	19.23	59.81*	31.19	138.55**
ICPL-15225 x ICPL-87119	19.64	-1.47	86.11**	29.23	-14.29	61.54	177.28**	132.64**	457.11**
ICPL-15225 x ICPL-8863	12.77	6.00	47.22*	61.29*	8.70	92.31**	211.32**	163.63**	517.11**
ICPL-15225 x PRG-158	5.38	0.00	36.11	44.19	14.81	19.23	11.31	5.35	91.58*
ICPL-7035 x ICPL-87119	5.49	-29.41*	33.33	27.27	-28.57	34.62	-5.65	-44.51**	32.89
ICPL-7035 x ICPL-8863	-20.55	-42.00*	-19.44	-21.15	-55.43**	-21.15	3.90	-38.67*	43.55
ICPL-7035 x PRG-158	-13.89	-36.73*	-13.89	42.42	-12.96	-9.62	-8.16	-43.42*	2.89
ICPL-2376 x ICPL-87119	5.88	-7.35	75.00**	-4.12	-5.10	78.85*	-13.15	-33.02*	60.39
ICPL-2376 x ICPL-8863	-2.97	-3.92	36.11	-48.94*	-50.00**	-7.69	-19.81	-37.66*	45.92
ICPL-2376 x PRG-158	-10.00	-11.76	25.00	-16.00	-34.38	21.15	-2.91	-16.79	51.32
LRG-41 x ICPL-87119	-2.40	-10.29	69.44**	3.41	-0.93	103.85**	65.82**	47.42**	253.03**
LRG-41 x ICPL-8863	43.93**	35.09*	113.89**	26.63	17.76	142.31**	-3.79	-13.60	102.24**
LRG-41 x PRG-158	1.89	-5.26	50.00*	44.10*	8.41	123.08**	112.22**	109.68**	290.66**

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Cross	Seeds per pod			Pod length (cm)			100- seed weight (g)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPL-6974 x ICPL-87119	-1.82	-3.57	2.08	-3.99	-5.47	-6.65	-7.46	-11.43	24.00*
ICPL-6974 x ICPL-8863	-0.46	-3.57	2.08	1.17	1.10	-3.09	-10.45	-14.29*	20.00*
ICPL-6974 x PRG-158	5.45	3.57	9.64	6.92	5.49	3.75	12.50	12.50	44.00**
ICPL-15225 x ICPL-87119	4.00	-8.45	22.87**	-5.56	-13.69**	2.96	-2.70	-7.69	44.00**
ICPL-15225 x ICPL-8863	10.12	-4.23	28.54**	16.52**	5.08	25.35**	5.41	0.00	56.00**
ICPL-15225 x PRG-158	-10.40	-21.13**	5.86	-10.10*	-17.99**	-2.17	-4.23	-12.82*	36.00**
ICPL-7035 x ICPL-87119	-3.70	-19.75**	22.87**	-2.72	-17.77**	17.58**	1.03	-20.97**	96.00**
ICPL-7035 x ICPL-8863	-4.12	-20.99**	20.98**	14.00**	-4.79	36.14**	-9.28	-29.03**	76.00**
ICPL-7035 x PRG-158	-3.70	-19.75**	22.87**	-5.29	-20.07**	14.29**	-19.15**	-38.71**	52.00**
ICPL-2376 x ICPL-87119	3.81	0.93	3.02	13.79*	6.20	4.87	-4.62	-11.43	24.00*
ICPL-2376 x ICPL-8863	6.28	4.76	3.97	9.29	3.43	-0.86	-1.54	-8.57	28.00**
ICPL-2376 x PRG-158	12.38	9.26	11.53	5.51	-1.34	-2.96	0.00	-3.13	24.00*
LRG-41 x ICPL-87119	6.67	2.56	13.42*	7.92	-0.28	16.13**	1.45	0.00	40.00**
LRG-41 x ICPL-8863	9.91	4.27	15.31*	12.06*	2.15	18.96**	1.45	0.00	40.00**
LRG-41 x PRG-158	8.44	4.27	15.31*	8.24	-0.17	16.26**	3.03	0.00	36.00**

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Cross	Harvest index (%)			SCMR at vegetative phase			Seed protein (%)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPL-6974 x ICPL-87119	-7.81	-22.94**	23.70*	4.21	0.78	-0.47	-0.82	-4.25**	4.16**
ICPL-6974 x ICPL-8863	7.58	-0.96	26.96*	-4.92*	-6.96**	-8.12**	3.43**	0.09	8.88**
ICPL-6974 x PRG-158	38.25**	32.03**	42.39**	-2.13	-4.85*	-6.04**	0.35	-2.53**	6.03**
ICPL-15225 x ICPL-87119	-9.32	-18.91**	65.10**	5.29*	2.51	-5.42*	8.06**	6.57**	7.91**
ICPL-15225 x ICPL-8863	-1.01	-19.35**	64.21**	4.42	0.49	-5.03*	10.17**	8.39**	10.29**
ICPL-15225 x PRG-158	1.25	-24.97**	52.75**	10.61**	7.13**	-0.09	2.53**	0.50	3.04**
ICPL-7035 x ICPL-87119	-9.23	-14.92*	36.58**	12.23**	11.47**	2.85	5.35**	4.97**	6.28**
ICPL-7035 x ICPL-8863	3.17	-1.31	38.54**	20.12**	17.91**	11.43**	5.11**	4.48**	6.31**
ICPL-7035 x PRG-158	11.81	-5.02	33.34**	10.36**	9.03**	1.69	-0.43	-1.41**	1.09*
ICPL-2376 x ICPL-87119	-7.40	-26.51**	17.97	4.00	-2.21	2.47	11.57**	6.39**	7.73**
ICPL-2376 x ICPL-8863	-1.37	-14.42	9.70	-3.99	-8.70**	-4.34*	8.41**	3.14**	4.94**
ICPL-2376 x PRG-158	17.24	14.93	12.79	2.15	-3.47	1.15	11.00**	5.23**	7.89**
LRG-41 x ICPL-87119	-2.56	-16.20*	34.52**	2.80	-0.16	-2.25	1.42**	1.03*	3.09**
LRG-41 x ICPL-8863	19.22*	13.36	45.31**	5.94**	4.10	1.92	5.89**	5.74**	7.89**
LRG-41 x PRG-158	35.76**	25.52**	45.07**	1.70	-0.71	-2.79	1.64**	1.40**	3.97**

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Cross	Phenol content (%)			Seed yield per plant (g)		
	MP	BP	SC	MP	BP	SC
ICPL-6974 x ICPL-87119	31.27**	26.18**	33.65**	49.70*	-1.01	110.73**
ICPL-6974 x ICPL-8863	20.36**	1.21	7.20*	8.85	-26.22	42.49
ICPL-6974 x PRG-158	-2.87	-4.43	1.23	90.16*	48.08	82.40*
ICPL-15225 x ICPL-87119	27.93**	23.14**	20.32**	177.35**	123.39**	375.54**
ICPL-15225 x ICPL-8863	49.56**	34.51**	21.60**	210.76**	160.00**	402.15**
ICPL-15225 x PRG-158	1.63	-4.37	-1.97	8.14	5.28	36.91
ICPL-7035 x ICPL-87119	43.04**	9.39**	6.88*	-13.62	-43.75**	19.74
ICPL-7035 x ICPL-8863	103.61**	74.74**	26.19**	-5.67	-37.11*	21.46
ICPL-7035 x PRG-158	24.83**	-6.09*	-3.73	-8.01	-29.97	-13.73
ICPL-2376 x ICPL-87119	15.71**	10.97**	8.43**	-23.01	-42.34**	22.75
ICPL-2376 x ICPL-8863	65.28**	49.17**	33.81**	-27.12	-43.56*	9.01
ICPL-2376 x PRG-158	40.01**	31.27**	34.56**	0.37	-6.62	15.02
LRG-41 x ICPL-87119	13.20**	2.38	23.68**	37.78*	16.53	148.07**
LRG-41 x ICPL-8863	14.89**	-8.21**	10.88**	10.72	-2.44	88.41*
LRG-41 x PRG-158	4.56	-3.36	16.75**	120.00**	102.04**	197.42**

* Significant at 5% level

** Significant at 1% level

ICPL-8863 recorded negative significant standard heterosis (-19.68 %). Heterosis for this trait ranged from -6.39 per cent to 5.01 per cent (ICPL-15225 x ICPL-8863) and -5.22 per cent to 16.15 per cent (ICPL-6974 x ICPL-87119) over mid parent and better parent, respectively, while for standard heterosis it ranged from -19.68 per cent (ICPL-2376 x ICPL-8863) to 0.81 per cent (LRG-41 x PRG-158).

Heterosis for mid parent was negative and highly significant in six crosses, heterobeltiosis in one cross (ICPL-7035 x ICPL-87119) and standard heterosis in twelve crosses out of 15 hybrids indicating early flowering of hybrids over their parents. The crosses ICPL-2376 x ICPL-8863 (L X L) and ICPL-6974 x ICPL-8863 (L X L) were exhibited highest desirable standard heterosis for earliness, indicated that the *per se* performance and heterosis were in same direction. These reports are supported by Pankaja Reddy *et al.* (1979), Venkateswarlu *et al.* (1981), Patel *et al.* (1992) and Pandey and Singh (2002) for desirable heterosis for earliness. Negative heterobeltiosis and standard heterosis reported by Manivel *et al.* (1999), Sekhar *et al.* (2004) and Aher *et al.* (2006).

4.4.1.2 Days to maturity: The cross ICPL-6974 x PRG-158 recorded maximum negative significant relative heterosis (-8.64 %) and heterobeltiosis (-17.21 %), while the cross ICPL-6974 x ICPL-87119 recorded maximum negative significant standard heterosis (-23.48 %). Heterosis over mid parent ranged from -8.64 per cent (ICPL-6974 x PRG-158) to 1.56 per cent (ICPL-15225 x ICPL-87119), whereas over better parent, it ranged from -17.21 per cent (ICPL-6974 x PRG-158) to 0.77 per cent (ICPL-15225 x ICPL-87119) and standard heterosis from -23.48 per cent (ICPL-6974 x ICPL-87119) to -6.63 per cent (ICPL-15225 x ICPL-87119).

Heterosis over mid parent was negative and significant in twelve crosses, heterobeltiosis in thirteen crosses and standard heterosis in fifteen crosses. The crosses viz., ICPL-6974 x ICPL-87119 (L X H), ICPL-6974 x

ICPL-8863 (L X L) and ICPL-6974 x PRG-158 (L X H) were showed high desirable standard heterosis along with desirable *per se* performance. The significance of negative heterosis for this trait is advantageous in getting early maturing hybrids. These results were also supported by Pankaja Reddy *et al.* (1979), Sinha *et al.* (1986), Patel *et al.* (1992), Hooda *et al.* (1999), Aher *et al.* (2006) and heterobeltiosis and standard heterosis reported by Sekhar *et al.* (2004).

4.4.1.3 Plant height: The cross LRG-41 x PRG-158 recorded high percentage of heterosis over mid parent (17.86 %), ICPL-15225 x PRG-158 (15.57 %) over better parent and standard heterosis was high in the cross ICPL-15225 x ICPL-87119 (9.05 %). Relative heterosis ranged from -22.83 per cent (ICPL-2376 x ICPL-8863) to 17.86 per cent (LRG-41 x PRG-158), heterobeltiosis ranged from -29.71 per cent (ICPL-2376 x ICPL-8863) to 15.57 per cent (ICPL-15225 x PRG-158) and standard heterosis ranged from -18.25 per cent (ICPL-7035 x ICPL-87119) to 9.05 per cent (ICPL-15225 x ICPL-87119).

Relative heterosis was positive and significant in the cross LRG-41 x PRG-158 (L X H) with high *per se* performance and it can be utilized in breeding programme to obtain tall plants. Positive non-significant heterobeltiosis was observed in five crosses out of 15 crosses and standard heterosis in seven crosses. Negative significant heterosis was observed in ICPL-2376 x ICPL-8863 (H X H) cross combination over mid, better and standard parent, indicating its utilization for breeding programme to obtain dwarf plants. In present study, tall plants recorded high yield hence, positive heterosis is desirable. High heterosis for tallness over better parent was also reported by Mehetre *et al.* (1993), Verulkar and Singh (1997), Hooda *et al.* (1999), Pandey (1999) and Khorgade *et al.* (2000a) over mid parent, whereas Shoba abd Balan (2010) reported significant standard heterosis for plant height.

4.4.1.4 Primary branches per plant: The only cross LRG-41 x ICPL-8863 recorded maximum values for relative heterosis (43.93 %), heterobeltiosis (35.09 %) and standard heterosis (113.89 %) for this trait. Heterosis over mid parent ranged from -20.55 per cent (ICPL-7035 x ICPL-8863) to 43.93 per cent, heterobeltiosis from -42.0 per cent (ICPL-7035 x ICPL-8863) to 35.09 per cent and standard heterosis from -19.44 per cent (ICPL-7035 x ICPL-8863) to 113.89 per cent.

Heterosis was positive and significant in only one cross LRG-41 x ICPL-8863 over mid-parent and better parent, whereas standard heterosis was observed positive significant in seven crosses. The crosses viz., LRG-41 x ICPL-8863 (H X H), ICPL-15225 x ICPL-87119 (L X H), ICPL-6974 x ICPL-87119 (L X H) and ICPL-2376 x ICPL-87119 (H X H) were exhibited high standard heterosis in desirable direction along with high *per se* performance. The similar reports were observed by Chaudhary *et al.* (1980), Narladkar and Khapre (1996), Hooda *et al.* (1999), Khorgade *et al.* (2000a), Pandey and Singh (2002) and Sarode *et al.* (2009) for significant positive heterosis and heterobeltiosis. Pandey (1999) and Shoba and Balan (2010) reported significant positive standard heterosis for this trait.

4.4.1.5 Secondary branches per plant: The cross ICPL-15225 x ICPL-8863 recorded high percentage of heterosis over mid parent (61.29 %), heterobeltiosis recorded for ICPL-6974 x PRG-158 and ICPL-15225 x PRG-158 (14.81 %), while maximum standard heterosis for LRG-41 x ICPL-8863 (142.31 %). Relative heterosis ranged from -48.94 per cent (ICPL-2376 x ICPL-8863) to 61.29 per cent, heterobeltiosis ranged from -55.43 per cent (ICPL-7035 x ICPL-8863) to 14.81 per cent, whereas standard heterosis ranged from -21.15 per cent (ICPL-7035 x ICPL-8863) to 142.31 per cent.

Relative heterosis was positive and significant for the cross ICPL-15225 x ICPL-8863 and five crosses over standard parent, while positive non-

significant heterosis over better parent was observed for five crosses. The three crosses involving LRG-41 showed highest desirable standard heterosis along with high performance for this trait may be due to high *per se* performance of LRG-41. Similar results for significant positive heterosis over mid parent and better parent were also reported by Pandey and Singh (2002) and Sarode *et al.* (2009).

4.4.1.6 Pods per plant: The cross ICPL-15225 x ICPL-8863 recorded maximum relative heterosis (211.32 %), heterobeltiosis (163.63 %) and standard heterosis (517.11 %). Heterosis over mid parent was ranged from -19.81 per cent (ICPL-2376 x ICPL-8863) to 211.32 per cent, heterobeltiosis from -44.51 per cent (ICPL-7035 x ICPL-8863) to 163.63 per cent and standard heterosis from 2.89 per cent (ICPL-7035 x PRG-158) to 517.11 per cent.

Heterosis in positive direction is desirable for this trait as more number of pods can accommodate high seed yield per plant. Out of 15 crosses, six crosses showed positive significant relative heterosis, four crosses showed heterobeltiosis and nine crosses showed positive significant standard heterosis. The crosses involving ICPL-15225, LRG-41 and ICPL-6974 exhibited high heterosis values and also showed high *per se* performance for this trait, indicated that the heterosis and *per se* performance were in same direction. These results are in agreement with the earlier findings of Chaudhary *et al.* (1980), Patel (1988), Rana (1990), Mehetre *et al.* (1993), Hooda *et al.* (1999), Khorgade *et al.* (2000a), Pandey and Singh (2002) and Sarode *et al.* (2009) for positive heterosis over mid parent, Patel and Tikka (2008), Sekhar *et al.* (2004) and Aher *et al.* (2006) over better parent, whereas Pandey (1999), Sekhar *et al.* (2004), Patel and Tikka (2008) and Shoba and Balan (2010) over standard check.

4.4.1.7 Seeds per pod: The cross ICPL-2376 x PRG-158 was recorded highest positive heterosis over mid parent (12.38 %) and better parent (9.26 %),

whereas ICPL-15225 x ICPL-8863 was showed maximum positive significant standard heterosis (28.54 %). Relative heterosis ranged from -10.4 per cent (ICPL-15225 x PRG-158) to 12.38 per cent, heterobeltiosis from -21.13 per cent (ICPL-15225 x PRG-158) to 9.26 per cent and standard heterosis ranged from 2.08 per cent (ICPL-6974 x ICPL-87119) to 28.54 per cent.

Positive significant standard heterosis values were observed for eight crosses but for heterobeltiosis and relative heterosis, positive non-significant values were observed for nine and seven crosses, respectively. The crosses ICPL-15225 x ICPL-8863, ICPL-15225 x ICPL-87119, ICPL-7035 x ICPL-87119 and ICPL-7035 x PRG-158, which were involved high x low parental combinations showed high desirable standard heterosis with high mean performance for this trait. High heterosis was also reported earlier by Shoba and Balan (2010) over standard check for number of seeds per pod.

4.4.1.8 Pod length: The cross ICPL-15225 x ICPL-8863 recorded maximum relative heterosis (16.52 %), while ICPL-2376 x ICPL-87119 (6.2 %) recorded higher heterobeltiosis and ICPL-7035 x ICPL-8863 was noticed for standard heterosis (36.14 %). Heterosis over mid parent ranged from -10.1 per cent (ICPL-15225 x PRG-158) to 16.52 per cent, heterobeltiosis from -20.07 per cent (ICPL-7035 x PRG-158) to 6.2 per cent and standard heterosis from -6.65 per cent (ICPL-6974 x ICPL-87119) to 36.14 per cent.

Positive and significant values were observed for four crosses and seven crosses for relative heterosis and standard heterosis, respectively. Positive non-significant heterobeltiosis was observed for six crosses out of 15 crosses, which is highly desirable, as more pod length, more will be the number of seeds can accommodate. The crosses ICPL-7035 x ICPL-8863 and ICPL-15225 x ICPL-8863 with high x low parental combinations showed high desirable standard heterosis with high *per se* performance. As

insight into the previous work Chaudhary *et al.* (1980) reported significant relative heterosis and heterobeltiosis for pod length.

4.4.1.9 100-seed weight: Out of all fifteen crosses, ICPL-6974 x PRG-158 recorded maximum heterosis (12.5 %) and heterobeltiosis (12.5 %) for this trait while, ICPL-7035 x ICPL-87119 was recorded highest standard heterosis (96.0 %). Relative heterosis ranged from -19.15 per cent (ICPL-7035 x PRG-158) to 12.5 per cent, heterobeltiosis from -38.71 per cent (ICPL-7035 x PRG-158) to 12.5 per cent and standard heterosis from 20.0 per cent (ICPL-6974 x ICPL-87119) to 96.0 per cent.

Positive significant values were noticed in all the crosses over standard check only. The crosses involving LRG-41 line performed as better as the better parent for this trait, hence the heterobeltiosis was zero for these crosses. Positive but non-significant values were observed for relative heterosis in six crosses and in one cross, ICPL-6974 x PRG-158 for heterobeltiosis. One and five crosses showed significant negative relative heterosis and heterobeltiosis respectively. The crosses, ICPL-7035 x ICPL-87119, ICPL-7035 x ICPL-8863 and ICPL-15225 x ICPL-8863 with high x low parental combinations recorded high desirable standard heterosis along with high *per se* performance, may be due to involvement of ICPL-7035 with high *per se* for this trait. Desirable relative heterosis for this trait was also reported by Patel *et al.* (1992), Khorgade *et al.* (2000a), Sarode *et al.* (2009), whereas Chaudary *et al.* (1980) and Manivel *et al.* (1999) reported significant positive heterobeltiosis.

4.4.1.10 Harvest index: The cross, ICPL-6974 x PRG-158 recorded maximum heterosis over mid parent (38.25 %) and better parent (32.03 %) while, ICPL-15225 x ICPL-87119 was showed maximum heterosis over standard parent (65.1 %). Relative heterosis ranged from -9.32 per cent (ICPL-15225 x ICPL-87119) to 38.25 per cent, heterobeltiosis from -26.51

per cent (ICPL-2376 x ICPL-87119) to 32.03 per cent and standard heterosis ranged from 9.7 per cent (ICPL-2376 x ICPL-8863) to 65.1 per cent.

Positive significant values were observed in three, two and twelve crosses for heterosis over mid parent, better parent and standard check, respectively. Positive heterosis is desirable as high harvest index will result in high economic yield. The crosses involved ICPL-15225 with high x low parental combinations reported high heterosis over standard parent along with high *per se* performance, may be due to high performing parent ICPL-15225. The significant positive heterosis was also reported by Singh *et al.* (1983), Omanga (1984), Patel (1988) and Aghav *et al.* (1997).

4.4.1.11 SCMR at vegetative phase: The cross ICPL-7035 x ICPL-8863 recorded maximum relative heterosis (20.12 %), heterobeltiosis (17.91 %) and standard heterosis (11.43 %). Heterosis over mid parent ranged from -4.92 per cent (ICPL-6974 x ICPL-8863) to 20.12 per cent, heterobeltiosis from -8.7 per cent (ICPL-2376 x ICPL-8863) to 17.91 per cent and standard heterosis from -8.12 per cent (ICPL-6974 x ICPL-8863) to 11.43 per cent.

Six crosses showed significant positive heterosis values over mid parent, four crosses over better parent and one cross (ICPL-7035 x ICPL-8863) over standard check out of 15 crosses. The cross, ICPL-7035 x ICPL-8863 showed highest heterosis over mid, better and standard parents in desirable direction along with high *per se* performance for this trait, which involved low x low cross combination, indicated its efficient utilization for further breeding programme to obtain maximum SCMR at vegetative phase.

4.4.1.12 Seed yield per plant: Seed yield per plant decides the economic worth of hybrids. Out of 15 crosses, the cross ICPL-15225 x ICPL-8863 recorded maximum heterosis over mid parent (210.76 %), better parent (160.0 %) and standard check (402.15 %), which had high *per se* performance also, indicates its superiority over all crosses. Relative heterosis

for seed yield ranged from -27.12 per cent (ICPL-2376 x ICPL-8863) to 210.76 per cent, heterobeltiosis from -43.75 per cent (ICPL-7035 x ICPL-87119) to 160.0 per cent and standard heterosis from -13.73 per cent (ICPL-7035 x PRG-158) to 402.15 per cent.

Six crosses showed positive significant heterosis over their mid parent, three crosses over better parent indicated the crosses involving ICPL-15225 and LRG-41 lines exhibited highest heterosis values and eight crosses exhibited superiority more than 40 per cent over standard check (LRG-30), among these three top crosses viz., ICPL-15225 x ICPL-87119 (L X H), ICPL-15225 x ICPL-8863 (L X H) and LRG-41 x PRG-158 (H X L) may throw superior segregants for grain yield in the succeeding generations for selection and isolation of superior genotypes as they also had significant positive heterobeltiosis. These crosses also exhibited significant and useful heterosis for most of characters. These results are in confirmity with the findings of Narladker and Kapre (1996), Verulkar and Singh (1997), Manivel *et al.* (1999), Khorgade *et al.* (2000a), Pandey and Singh (2002), Sekhar *et al.* (2004), Aher (2006), Patel and Tikka (2008) and Shoba and Balan (2010).

4.4.2 Quality attributes

4.4.2.1 Seed protein: The cross ICPL-2376 x ICPL-87119 recorded maximum relative heterosis (11.57 %), ICPL-15225 x ICPL-8863 for heterobeltiosis (8.39 %) and ICPL-6974 x ICPL-87119 for standard heterosis (8.88 %). Heterosis over mid parent ranged from -0.82 per cent (ICPL-6974 x ICPL-87119) to 11.57 per cent, heterobeltiosis from -4.25 per cent (ICPL-6974 x ICPL-87119) to 8.39 per cent and standard heterosis from 1.09 per cent (ICPL-7035 x PRG-158) to 8.88 per cent.

Twelve crosses recorded positive significant heterosis over mid parent, ten crosses over better parent, whereas all the 15 crosses showed

positive significant heterosis over the standard check. The crosses, ICPL-15225 x ICPL-8863 (L X H), ICPL-6974 x ICPL-8863 (H X H) and ICPL-15225 x ICPL-87119 (L X H) were showed highest desirable standard heterosis along with high *per se* performance. Hence, the heterosis and *per se* performance were in same direction. Significant positive heterosis was observed earlier by Khorgade *et al.* (2000a), while negative heterosis was noticed by Pankaja Reddy *et al.* (1979) for seed protein.

4.4.2.2 Phenol content: Maximum heterosis was observed in ICPL-7035 x ICPL-8863 over mid parent (103.61 %) and better parent (74.74 %), whereas ICPL-2376 x PRG-158 was recorded maximum significant standard heterosis values (34.56 %). Relative heterosis ranged from -2.87 per cent (ICPL-6974 x PRG-158) to 103.61 per cent, heterobeltiosis from -8.21 per cent (LRG-41 x ICPL-8863) to 74.74 per cent and standard heterosis from -3.73 per cent (ICPL-7035 x PRG-158) to 34.56 per cent.

Positive significant heterosis was observed in twelve crosses for relative heterosis, in eight crosses for heterobeltiosis and in twelve crosses for standard heterosis, indicating that this is the one of the important trait that contributes to the heterosis of seed yield. The crosses, ICPL-2376 x PRG-158 (L X H), ICPL-2376 x ICPL-8863 (L X L) and ICPL-6974 x ICPL-87119 (H X H) were showed highest desirable standard heterosis along with high performance for this trait. Hence, the heterosis is directly related to the *per se* performance for phenol content.

In present investigation, the crosses, ICPL-15225 x ICPL-8863, LRG-41 x PRG-158, LRG-41 x ICPL-8863, LRG-41 x ICPL-87119 and ICPL-7035 x ICPL-8863 showed positive significant heterosis in desirable direction for most of the traits along with seed yield. The differences in magnitudes of positive and negative heterosis of different characters in F_1 over the parental means indicated overall dominance or positively acting genes. Wide range

of heterosis for different characters can be exploited due to non-allelic interaction which can either increase or decrease the expression of heterosis.

In most of the cross combinations the significant positive heterosis observed for seed yield per plant was mainly due to the manifestation of heterosis for its component characters viz., days to maturity, pods per plant, seeds per pod, pod length, 100-seed weight, harvest index, seed protein and phenol content. This would clearly indicate that heterosis for seed yield was through heterosis for individual component characters.

4.5 COMBINING ABILITY

Combining ability studies helps the breeder in selecting the parents and breeding methods to be employed to improve a particular trait, as it provides the information on the genetic nature of the traits. General combining ability (*gca*) is attributed to additive (fixable) gene action, while specific combining ability (*sca*) is attributed primarily due to dominance, over dominance and epistatic effects of genes (non-additive). The non-additive gene action is mostly non-fixable, but often brings about in phenotypes that are not attainable under normal additive gene action. The ratio of *gca* to *sca* variance provides an estimate of the predominance of additive gene effects or the non-additive gene effects.

The analysis of variance for combining ability was carried out for 14 characters and mean sum of squares are presented in Table 4.6. It revealed that treatments registered highly significant differences for all the characters. The parents and crosses exhibited significant differences for all the characters, while parents vs. crosses showed significant differences for days to maturity, pods per plant, 100-seed weight, SCMR at vegetative phase, seed protein, phenol content and seed yield per plant.

The effect of crosses was partitioned into lines, testers and their interactions. The lines were found to be significant for all the characters

Table 4.6. Analysis of variance for combining ability in Line x Tester experiment for 14 characters in pigeonpea

Source of variation	Df	Days to flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	seed yield per plant (g)
Replications	2	2.17	24.28	913.23	3.88	127.17	38551.04*	0.02	0.26	6.78**	0.44	0.29	0.08*	0.06	3498.80*
Treatments	22	246.37*	385.53**	2052.90**	53.13**	297.99**	368227.71**	0.66**	1.59**	17.27**	45.87**	15.79**	3.02**	4.63**	23150.45**
Parents	7	376.00**	530.55**	3146.29**	53.88**	436.76**	81436.74**	1.50**	2.63**	35.43**	100.58**	16.15**	3.89**	5.33**	5128.09**
Parents vs crosses	1	12.68	633.39**	1098.67	19.91	154.49	933948.50**	0.0031	0.30	5.076*	11.91	49.96**	3.52**	36.97**	50596.44**
crosses	14	198.25**	295.32**	1574.38**	55.14**	238.87**	471214.66**	0.29**	1.18**	9.08**	20.94**	13.17**	1.14**	1.98**	30201.21**
Lines	4	341.59*	855.55**	3827.09*	104.70*	622.42**	1024174.69	0.68*	2.58*	23.83*	65.49**	25.88	0.68	1.26	64029.73
Testers	2	436.21*	144.81	589.56	107.02*	88.87	161709.33	0.01	1.03	1.49	0.30	0.29	2.35	1.94	12175.26
Line x Tester	8	67.09**	52.83**	694.22	17.38	84.59	272111.00**	0.17*	0.51**	3.60**	3.83	10.04**	1.07**	2.35**	17793.44**
Error	44	3.64	7.70	449.20	10.55	50.36	11859.10	0.07	0.11	0.99	4.45	1.23	0.02	0.04	983.07

* Significant at 5% level, ** Significant at 1% level

except pods per plant, SCMR at vegetative phase, seed protein, phenol content and seed yield per plant. Among testers, the differences were non-significant for all the characters except days to flowering and primary branches per plant. The interaction effects (lines x testers) were found to be significant for all the characters except plant height, primary branches per plant, secondary branches per plant and harvest index.

Estimates of the relative contribution of *gca* and *sca* within the genetic variability present in a population are of interest to plant breeders, as breeding methods most appropriate for specific objectives may differ appreciably upon the type of gene action assumed. The estimates of components of variance and their ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) indicated the preponderance of non-additive gene action for all the traits under study (Table 4.7 and Fig. 4.5). From the estimates of additive and dominance variance, it was observed that dominance variance was predominant for all the characters except days to maturity and primary branches per plant indicated the major role of non-additive gene action and was highest for pods per plant followed by seed yield per plant and plant height.

In the present investigation, the combining ability analysis was carried out based on mean value of fifteen plants for eight parents and fifteen crosses derived from 5 lines x 3 testers programme. General combining ability effects of the parents and specific combining ability effects of crosses are presented in the Table 4.8 and Table 4.9 for parents and crosses, respectively, and the results and discussion are presented character wise hereunder.

4.5.1 Yield attributes

4.5.1.1 Days to flowering: Among the lines ICPL-2376 (-7.04) and ICPL-6974 (-6.16) and in the testers, ICPL-8863 (-6.2) had highly significant negative *gca* effect, which were desirable for earliness, whereas the lines LRG-41

Table 4.7. Magnitude of genetic variance due to general and specific combining ability for 14 characters of pigeonpea

S. No.	Characters	σ^2 gca	σ^2 sca	σ^2 gca/ σ^2 sca	σ^2 A	σ^2 D	σ^2 A/ σ^2 D
1	Days to flowering	4.64	21.15	0.22	9.28	21.15	0.44
2	Days to maturity	8.57	15.04	0.57	17.14	15.04	1.14
3	Plant height	31.12	81.67	0.38	62.24	81.67	0.76
4	Primary branches per plant	1.33	2.28	0.59	2.66	2.28	1.17
5	Secondary branches per plant	5.45	11.41	0.48	10.9	11.41	0.96
6	Pods per plant	7039.02	86750.63	0.08	14078.04	86750.63	0.16
7	Seeds per pod	0.00	0.03	0.13	0.001	0.03	0.03
8	Pod length (cm)	0.02	0.14	0.17	0.04	0.14	0.29
9	100-seed weight (g)	0.19	0.87	0.22	0.38	0.87	0.44
10	Harvest index (%)	0.61	-0.21	-2.90	1.22	-0.21	-5.81
11	SCMR at vegetative phase	0.11	2.94	0.04	0.22	2.94	0.07
12	Seed protein (%)	0.00	0.35	0.00	0	0.35	0.00
13	Phenol content (%)	-0.01	0.77	-0.01	-0.02	0.77	-0.03
14	Seed yield per plant (g)	438.66	5603.46	0.08	877.32	5603.46	0.16

Table 4.8. Estimates of general combining ability (gca) effects in parents for seed yield and yield components of pigeonpea

Parents	Days to flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod Length	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
LINES														
ICPL-6974	-6.16**	-14.33**	6.84	-0.04	-5.16*	-44.13	-0.31**	-0.58**	-1.11**	-0.88	-1.73**	0.09	-0.12	-19.69
ICPL-15225	5.07**	6.56**	14.51*	1.4	2.07	499.64**	0.20*	-0.03	0.22	3.80**	-1.14**	0.27**	-0.17*	130.20**
ICPL-7035	2.40**	3.33**	-29.49**	-5.38**	-7.71**	-333.36**	0.31**	0.67**	2.67**	-0.07	2.67**	-0.34**	-0.39**	-73.58**
ICPL-2376	-7.04**	-5.22**	-12.38	0.07	-2.6	-267.24**	-0.25**	-0.46**	-1.44**	-3.64**	0.27	0.21**	0.60**	-68.58**
LRG-41	5.73**	9.67**	20.51**	3.96**	13.40**	145.09**	0.05	0.39**	-0.33	0.79	-0.07	-0.24**	0.07	31.64**
SE	0.64	0.92	7.06	1.08	2.37	36.30	0.09	0.11	0.33	0.70	0.37	0.05	0.07	10.45
(gi-gj)	0.90	1.31	9.99	1.53	3.35	51.34	0.13	0.15	0.47	0.99	0.52	0.07	0.10	14.78
TESTERS														
ICPL-87119	2.60**	2.78**	6.16	2.76**	2.73	97.71**	-0.02	-0.12	0.24	-0.16	0.13	-0.03	0.16**	24.44**
ICPL-8863	-6.20**	-3.36**	0.22	-0.18	-0.8	11.31	0.03	0.30**	0.11	0.05	0.02	0.41**	0.25**	6.84
PRG-158	3.60**	0.58	-6.38	-2.58**	-1.93	-109.02**	-0.01	-0.18*	-0.36	0.11	-0.15	-0.38**	-0.41**	-31.29**
SE	0.49	0.72	5.47	0.84	1.83	28.12	0.07	0.08	0.26	0.54	0.29	0.04	0.05	8.10
(gi-gj)	0.70	1.01	7.74	1.19	2.59	39.76	0.10	0.12	0.36	0.77	0.40	0.05	0.08	11.45

* Significant at 5% level; ** Significant at 1% level

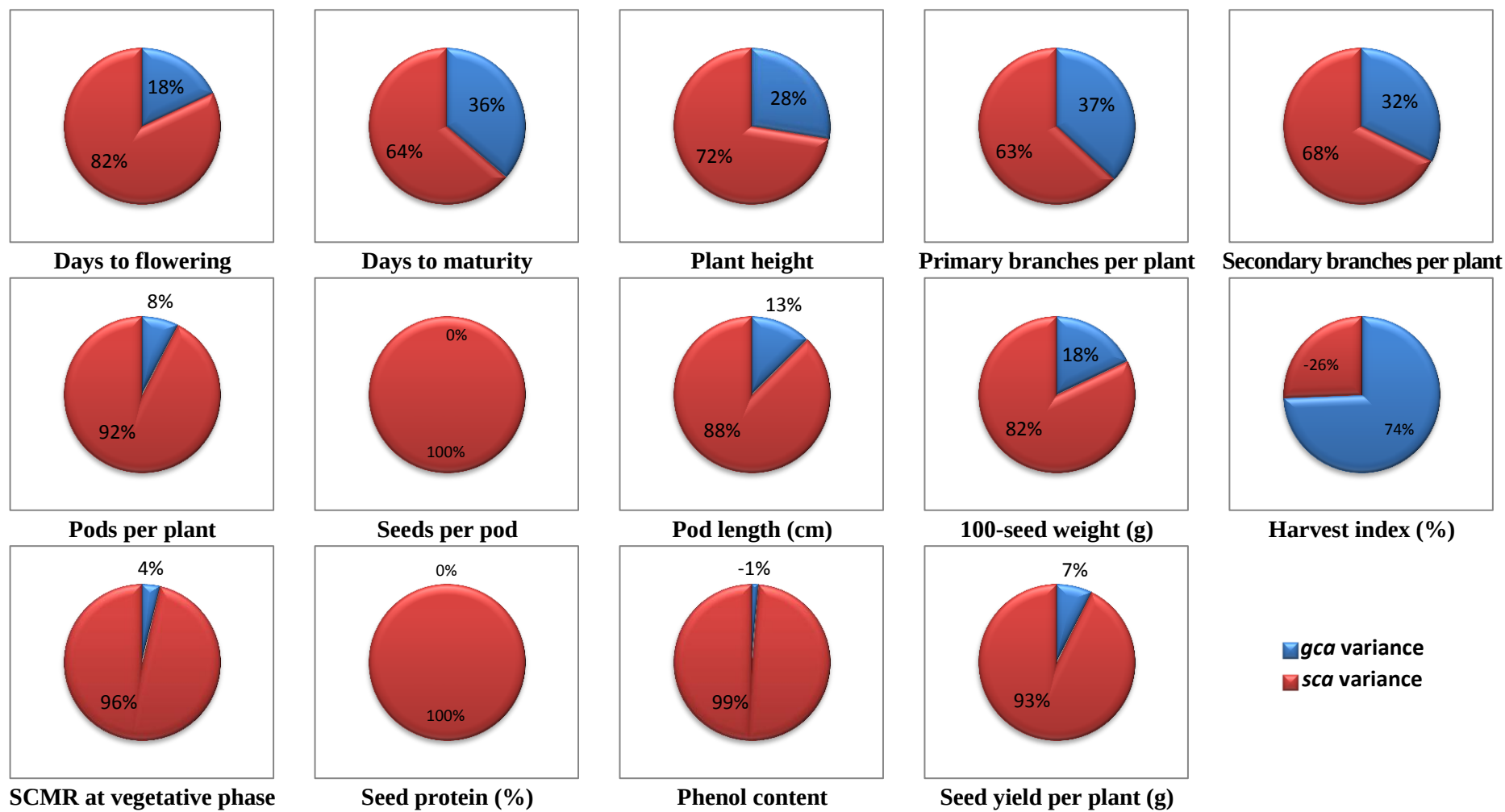
Table 4.9. Estimates of specific combining ability (sca) effects in crosses for seed yield and yield components of pigeonpea

Crosses	Days to flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
ICPL-6974 x ICPL-87119	4.29**	-4.33**	-9.38	0.91	-0.51	1.07	-0.07	-0.11	-0.69	-0.99	1.77**	-0.50**	1.06**	0.56
ICPL-6974 x ICPL-8863	1.09	-3.13*	7.22	-0.49	-1.98	-104.87	-0.12	-0.36	-0.89	-0.69	-1.42*	0.20*	-0.67**	-34.84
ICPL-6974 x PRG-158	-5.38**	-1.8	2.16	-0.42	2.49	103.8	0.19	0.47*	1.58**	1.69	-0.35	0.30**	-0.39**	34.29
ICPL-15225 x ICPL-87119	1.07	6.11**	5.62	0.8	-2.07	160.29*	0.15	-0.17	-0.36	0.86	-0.95	0.23**	0.27*	56.33**
ICPL-15225 x ICPL-8863	4.53**	-3.42*	10.89	-0.93	6.8	398.69**	0.3	0.54**	0.78	0.5	-0.67	0.37**	0.27*	94.60**
ICPL-15225 x PRG-158	-5.60**	-2.69	-16.51	0.13	-4.73	-558.98**	-0.46**	-0.37	-0.42	-1.36	1.63*	-0.60**	-0.54**	-150.93**
ICPL-7035 x ICPL-87119	-1.93	1.33	-11.71	1.24	3.04	-81.38	0.04	-0.14	1.53*	0.23	-1.2	0.45**	-0.35**	-16.22
ICPL-7035 x ICPL-8863	-3.13**	-1.87	-0.78	-2.16	-3.09	32.02	-0.07	0.38*	0	0.32	2.62**	0.01	0.78**	2.71
ICPL-7035 x PRG-158	5.07**	0.53	12.49	0.91	0.04	49.36	0.03	-0.25	-1.53*	-0.55	-1.42*	-0.46**	-0.43**	13.51
ICPL-2376 x ICPL-87119	-3.16**	-2.44	21.84	0.8	5.6	-77.82	-0.09	0.35	-0.36	0.87	1.04	0.24**	-1.24**	-18.89
ICPL-2376 x ICPL-8863	0.64	1.02	-21.22	-0.93	-5.87	-28.09	-0.11	-0.36	0.11	-0.65	-1.78**	-0.87**	0.27*	-11.96
ICPL-2376 x PRG-158	2.51*	1.42	-0.62	0.13	0.27	105.91	0.2	0.01	0.24	-0.22	0.75	0.63**	0.97**	30.84
LRG-41 x ICPL-87119	-0.27	-0.67	-6.38	-3.76	-6.07	-2.16	-0.03	0.07	-0.13	-0.96	-0.65	-0.43**	0.25*	-21.78
LRG-41 x ICPL-8863	-3.13**	-1.87	3.89	4.51*	4.13	-297.76**	-0.01	-0.21	0	0.52	1.26	0.29**	-0.64**	-50.51**
LRG-41 x PRG-158	3.40**	2.53	2.49	-0.76	1.93	299.91**	0.03	0.14	0.13	0.44	-0.61	0.13	0.39**	72.29**
SE	1.10	1.60	12.24	1.88	4.10	62.87	0.16	0.19	0.58	1.22	0.64	0.08	0.12	18.10
Sij-Sjk	1.56	2.27	17.31	2.65	5.79	88.92	0.22	0.27	0.81	1.72	0.91	0.12	0.17	25.60

* Significant at 5% level

** Significant at 1% level

Fig. 4.5. Pie chart of *gca* and *sca* variances for 14 characters in pigeonpea



(5.73), ICPL-15225 (5.07) and ICPL-7035 (2.4) and the testers ICPL-87119 (2.6) and PRG-158 (3.6) had positive significant *gca* effects, which were related to late flowering.

Five crosses viz., ICPL-15225 x PRG-158 (-5.6), ICPL-6974 x PRG-158 (-5.38), ICPL-2376 x ICPL-87119 (-3.16), ICPL-7035 x ICPL-8863 (-3.13) and LRG-41 x ICPL-8863 (-3.13) recorded negative and highly significant *sca* effects indicating the possibility of improvement of early flowering. On contrary, the crosses viz., ICPL-7035 x PRG-158 (5.07), ICPL-15225 x ICPL-8863 (4.53), ICPL-6974 x ICPL-87119 (4.29), LRG-41 x PRG-158 (3.4) and ICPL-2376 x PRG-158 (2.51) registered positive and highly significant *sca* effects, indicating these crosses were late to flower.

The importance of non-additive gene action for days to flowering in the present investigation was in conformity with the results reported by Srinivas *et al.* (1998), Pandey (1999), Jayamala and Rathnaswamy (2000), Pandey and Singh (2002), Jahagirdar (2003), Sekhar *et al.* (2004), Banu *et al.*, (2006), Raju and Muthiah (2007) and Vaghela *et al.* (2009).

The lines viz., ICPL-6974 and ICPL-2376 and the tester ICPL-8863 were found to be good combiners for earliness by recording significant desirable (negative) *gca* effects and may be used in crop improvement programmes in development of genotypes with earliness. Five crosses recorded significant negative *sca* effects viz., ICPL-15225 x PRG-158 (L X L), ICPL-6974 x PRG-158 (H X L), ICPL-2376 x ICPL-87119 (H X L), ICPL-7035 x ICPL-8863 (L X H) and LRG-41 x ICPL-8863 (L X H). All these crosses involved atleast one parent as low general combiner indicating the influence of non-additive gene action for earliness. This trait can be improved by diallel selective mating or intermating in segregating populations in the above combinations.

4.5.1.2 Days to maturity: The lines ICPL-6974 (-14.33) and ICPL-2376 (-5.22) and the tester ICPL-8863 (-3.36) showed significant negative *gca* effect indicating their use as general combiner in getting early maturing types. The lines LRG-41 (9.67), ICPL-15225 (6.56) and ICPL-7035 (3.33) recorded positive significant *gca* effects.

In crosses, ICPL-6974 x ICPL-87119 (-4.33), ICPL-76974 x ICPL-8863 (-3.13) and ICPL-15225 x ICPL-8863 (-3.42) showed significant and negative *sca* effects indicating that the possibility to get early maturing hybrids whereas, ICPL-15225 x ICPL-87119 (6.11) recorded positive and highly significant *sca* effect indicating late maturity.

High magnitude of *sca* variance than *gca* variance reported non-additive gene action for this trait. The predominance of non-additive gene action in the inheritance of days to maturity was earlier reported by Srinivas *et al.* (1998), Jayamala and Rathnaswamy (2000), Pandey and Singh (2002), Lohithaswa and Dharmaraj (2003), Sunilkumar *et al.* (2003), Sekhar *et al.* (2004), Banu *et al.* (2006), Raju and Muthiah (2007) and Vaghela *et al.* (2009).

In respect of days to maturity, the lines ICPL-6974 and ICPL-2376 and the tester ICPL-8863 displayed negative significant *gca* effects. Hence, they could be utilized as good donor sources in breeding for earliness and the resulting cross combinations between them also showed significant negative *sca* effects for early maturity. Out of 15 crosses, two crosses *viz.*, ICPL-6974 x ICPL-87119 (H X L) and ICPL-15225 x ICPL-8863 (L X H) with high *per se* performance, involving one parent with significant *gca* effect and the other with poor negative *gca* effects may throw the desirable transgressive segregants if additive genetic system present in good combiners and the epistatic effects present in cross act in a complementary fashion to maximize desirable plant attributes which could be exploited for further breeding purposes. So for these combinations, diallel mating or

intermating in segregating populations followed by cyclic selections can be practiced for improving this character.

4.5.1.3 Plant height: In parents, the lines LRG-41 (20.51) and ICPL-15225 (14.51) recorded highly significant positive effect for tallness, whereas the line ICPL-7035 (-29.49) showed highly significant negative *gca* effect indicating the possibility of obtaining dwarf plants in its crosses.

Eight out of fifteen crosses recorded positive non-significant *sca* effects and seven crosses showed negative non-significant *sca* effects for plant height. None of the crosses were positive and significant for this trait.

In respect of plant height, the lines LRG-41 and ICPL-15225 and none of the testers were found to be the best general combiners with high *per se* performance indicated a limited scope for improving this trait. The cross ICPL-2376 x ICPL-87119 (L X M) recorded non-significant but positive *sca* effect for plant height indicating the operation of both additive and non-additive gene actions. None of the crosses showed significant *sca* effects for plant height. The high *sca* effect than *gca* effect indicated the importance of non-additive gene action for plant height. These results are in confirmity with the findings of Srinivas *et al.* (1998), Pandey (1999), Pandey and Singh (2002), Lohithaswa and Dharmaraj (2003), Sunilkumar *et al.*, (2003), Sekhar *et al.* (2004), Yadav *et al.* (2008), Vaghela *et al.* (2009) and Patel *et al.* (2010).

4.5.1.4 Primary branches per plant: Positive significant *gca* effects were observed in the line LRG-41 (3.96) and the tester ICPL-87119 (2.76) with high *per se* performance. But their combination did not show significant *sca* effect. On contrary, the line ICPL-7035 (-5.38) and the tester PRG-158 (-2.58) recorded negative significant *gca* effects.

Only one cross LRG-41 x ICPL-8863 (H X L) recorded significant *sca* effect, indicating the possibility of interaction between positive alleles

from good combiners and negative alleles from poor combiners in high x low combiner crosses and suggested for the exploitation of heterosis in F₁ generation as their high yield potential would be unfixable in succeeding generations. High *sca* than *gca* indicated non-additive gene action for this trait. It was also reported by Srinivas *et al.* (1998), Pandey (1999), Ajay Kumar *et al.* (2001), Pandey and Singh (2002), Jahagirdar (2003), Sunilkumar *et al.* (2003), Banu *et al.* (2006), Yadav *et al.* (2008) and Phad *et al.* (2009) in the inheritance of primary branches per plant.

4.5.1.5 Secondary branches per plant: In parents, the line LRG-41 (13.4) recorded highly significant positive *gca* effect, whereas the lines ICPL-7035 (-7.71) and ICPL-6974 (-5.16) showed significant negative *gca* effects but none of the tester recorded significant *gca*, indicated there is a limited scope for improvement of this character.

Out of 15 crosses, eight crosses recorded positive non-significant and seven crosses recorded negative non-significant *sca* effects. None of the crosses was positive significant for this trait. It was controlled by non-additive gene action by high *sca* effect than *gca* effect. This was also reported by Srinivas *et al.* (1998), Jahagirdar (2003), Sunilkumar *et al.* (2003), Pandey (2004), Raju and Muthiah (2007) and Vaghela *et al.* (2009).

4.5.1.6 Pods per plant: The lines ICPL-15225 (499.64) and LRG-41 (145.09) and the tester ICPL-87119 (606.67) recorded highly significant positive *gca* effect for this trait indicating their use as good general combiners to get maximum number of pods per plant. On contrary, the genotypes, ICPL-7035 (-333.36), ICPL-2376 (-267.24), ICPL-6974 (-44.13) and PRG-158 (-109.02) recorded negative significant *gca* effects.

Three crosses *viz.*, ICPL-15225 x ICPL-8863 (398.69), LRG-41 x PRG-158 (299.91) and ICPL-15225 x ICPL-87119 (160.29) recorded positive significant *sca* effects for this trait while, ICPL-15225 x PRG-158

(-558.98) and LRG-41 x ICPL-8863 (-297.76) recorded negative significant *sca* effects.

In respect of pods per plant, non-additive gene action was predominant in the present study and is in agreement with earlier reports of Srinivas *et al.* (1998), Pandey (1999), Jayamala and Rathnaswamy (2000), Ajay Kumar *et al.* (2001), Sunilkumar *et al.* (2003), Sekhar *et al.* (2004), Banu *et al.* (2006), Raju and Muthiah (2007), Yadav *et al.* (2008), Vaghela *et al.* (2009) and Phad *et al.* (2009).

Among the lines, ICPL-15225 and LRG-41 and the tester ICPL-87119 were found to be best general combiners. The cross combinations, ICPL-15225 x ICPL-87119 (H X M), LRG-41 x PRG-158 (H X L) and ICPL-15225 x ICPL-8863 (H X H) recorded significant *sca* effects. These results clearly indicated that the crosses showing H X H combination may be exploited through the simple pedigree method while H X L and L X L combinations through diallel selective mating or intermating in segregating populations followed by cyclic selections for improvement of this character.

4.5.1.7 Seeds per pod: In parents, the lines ICPL-7035 (0.31) and ICPL-15225 (0.2) showed positive significant *gca* effect to improve this character in their crosses but none of the tester recorded significant *gca* effects for this trait, indicating there is a limited scope for improving this character. The lines ICPL-6974 (-0.31) and ICPL-2376 (-0.25) showed negative significant *gca* effects.

Among crosses, ICPL-15225 x PRG-158 (-0.46) was showed significant negative *sca* effect, while seven crosses were reported positive non-significant *sca* effects. Non-additive gene action was involving in controlling this character, which is in agreement with the results of Patel *et al.* (1992), Srinivas *et al.* (1998), Ajay Kumar *et al.* (2001), Lohithaswa and

Dharmaraj (2003), Sekhar *et al.* (2004), Banu *et al.* (2006), Raju and Muthiah (2007) and Yadav *et al.* (2008).

4.5.1.8 Pod length: The line ICPL-7035 (0.67) and the tester ICPL-8863 (0.3) recorded positive significant *gca* effects indicated the possibility of improving this character through their crosses. The lines viz., ICPL-6974 (-0.58), ICPL-2376 (-0.46) and the tester PRG-158 (-0.18) recorded negative significant *gca* effects.

The crosses, ICPL-6974 x PRG-158 (0.47), ICPL-15225 x ICPL-8863 (0.54) and ICPL-7035 x ICPL-8863 (0.38) recorded positive significant *sca* effects for this trait. In governing the pod length non-additive gene action was found to be important because of high *sca* than *gca* effects. This is in argument with earlier reports of Rana (1990), Omanga *et al.* (1992), Vanniarajan *et al.* (1999), Jahagirdar (2003), Sunilkumar *et al.* (2003) and Vaghela *et al.* (2009).

The line ICPL-7035 and the tester ICPL-8863 were found to be good general combiners. The crosses, ICPL-6974 x PRG-158 (L X L), ICPL-15225 x ICPL-8863 (L X H) and ICPL-7035 x ICPL-8863 (H X H) were good specific combiners for this character, indicating the operation of additive gene action for H X H cross combination and can be exploited through pedigree method, and the cross combinations of H X L and L X L may be studied through bi-parental or recurrent selection method in early generations followed by single plant selections so as to exploit both additive and non-additive gene effects.

4.5.1.9 100-seed weight: The line ICPL-7035 (2.67) showed positive and significant *gca* effect and it can be utilized as good general combiner in breeding programmes for improving this trait, but none of the tester was found to be the good combiner, while the lines ICPL-2376 (-1.44) and ICPL-6974 (1.11) showed negative significant *gca* effects.

In crosses, ICPL-6974 x PRG-158 (1.58) and ICPL-7035 x PRG-158 (1.53) recorded desirable positive and significant *sca* effects for this trait. ICPL-7035 x PRG-158 (-1.53) had negative significant *sca* effect. In the crosses, ICPL-6974 x PRG-158 (L X L) and ICPL-7035 x PRG-158 (H X M) were good specific combiners indicating that both additive and non-additive components were important for this trait. The importance of non-additive gene action for 100-seed weight is in agreement with the findings of Singh *et al.* (1983), Srinivas *et al.* (1998), Ajay Kumar *et al.* (2001), Jahagirdar (2003), Sekhar *et al.* (2004), Raju and Muthiah (2007), Yadav *et al.* (2008) and Vaghela *et al.* (2009).

4.5.1.10 Harvest index: The line ICPL-15225 (3.8) and ICPL-2376 (-3.64) recorded positive significant and negative significant *gca* effects for this character, respectively. But none of the tester was found to be good general combiner.

None of the crosses was positive significant for *sca* effects. Out of the 15 crosses, eight crosses recorded positive non-significant *sca* effects while seven were negative non-significant for *sca* effects.

Harvest index recorded non-additive gene action because of high *sca* variance than *gca* variance. These results are supported by Patel *et al.* (1992) and Sekhar *et al.* (2004).

In respect of harvest index, line ICPL-15225 was found to be good general combiner, but there is a limited scope to improve this trait because no tester was found to be good combiner for this trait. The crosses, ICPL-6974 x PRG-158 (L X M), ICPL-15225 x ICPL-87119 (H X L) and ICPL-2376 x ICPL-87119 (L X L) exhibited positive non-significant *sca* effects besides high *per se* performance. The superiority of crosses with low x low and high x low general combiners may be due to complementary gene actions. Population improvement through mass selection or bi-parental mating and

recurrent selection may be employed to release the variability or alternatively heterosis breeding can also be exploited in view of high *sca* variances.

4.5.1.11 SCMR at vegetative phase: In parents, the line ICPL-7035 recorded positive significant *gca* effect and it can be used as good general combiner, while ICPL-6974 (-1.73) and ICPL-15225 (-1.14) recorded negative significant *gca* effects. The tester ICPL-87119 showed moderate *gca* for this trait.

Three crosses *viz.*, ICPL-7035 x ICPL-8863 (2.62), ICPL-15225 x PRG-158 (1.63) and ICPL-6974 x ICPL-87119 (1.77) recorded positive significant *sca* effects, while ICPL-6974 x ICPL-8863 (-1.42) and ICPL-2376 x ICPL-8863 (1.42) recorded negative significant *sca* effects for this trait. High *sca* variance than *gca* variance indicated the presence of non-additive gene action.

The crosses, ICPL-7035 x ICPL-8863 (H X M), ICPL-15225 x PRG-158 (L X L) and ICPL-6974 x ICPL-87119 (L X M) recorded highly significant positive *sca* effects for this trait, indicating the presence of both additive and non-additive type of gene action. This can be improved by bi-parental or recurrent selection methods.

4.5.1.12 Seed yield per plant: The lines ICPL-15225 (130.2) and LRG-41 (31.64) and the tester ICPL-87119 (24.44) reported highly significant positive *gca* effects. On contrary, the lines ICPL-7035 (-73.58) and ICPL-2376 (-68.58) and the tester PRG-158 (-31.29) reported highly significant negative *gca* effects.

The three *viz.*, ICPL-15225 x ICPL-8863 (94.60), LRG-41 x PRG-158 (72.29) and ICPL-15225 x ICPL-87119 (56.33) recorded positive significant *sca* effects and can be utilized for hybrid breeding programmes, whereas ICPL-15225 x PRG-158 (-150.93) and LRG-41 x ICPL-8863 (-50.51)

recorded negative significant *sca* effects for this trait, which can be advanced through recombination breeding programmes.

The relative importance of non-additive gene action for seed yield per plant in the present study is in agreement with the results of Srinivas *et al.* (1998), Pandey (1999), Ajay Kumar *et al.* (2001), Lohithaswa and Dharmaraj (2003), Sunilkumar *et al.* (2003), Jahagirdar (2003), Pandey (2004), Sekhar *et al.* (2004), Yadav *et al.* (2008), Vaghela *et al.* (2009), Phad *et al.* (2009) and Patel *et al.* (2010).

For seed yield per plant, the lines ICPL-15225 and LRG-41 and the tester ICPL-87119 were found to be good general combiners for their utility in breeding programmes for the improvement of seed yield. The crosses ICPL-15225 x ICPL-8863 (H X M), LRG-41 x PRG-158 (H X L) and ICPL-15225 x ICPL-87119 (H X H) recorded significant *sca* effects. These crosses involved one good combiner in their combinations. These results clearly indicated that the crosses showing H X H combination may be exploited through the simple pedigree method while the other combinations through diallel selective mating or intermating in segregating populations followed by cyclic selections for improvement of this character.

4.5.2 Quality attributes

4.5.2.1 Seed protein: In parents, the lines ICPL-15225 (0.27) and ICPL-2376 (0.21) and the tester ICPL-8863 (0.41) recorded positive significant *gca* effects. Whereas the lines ICPL-7035 (-0.34) and LRG-41 (-0.24) and the tester PRG-158 (-0.38) recorded negative significant *gca* effects.

Eight out of the fifteen crosses recorded positive significant *sca* effects, namely, ICPL-2376 x PRG-158 (0.63), ICPL-7035 x ICPL-87119 (0.45), ICPL-15225 x ICPL-8863 (0.37), ICPL- 6974 x PRG-158 (0.3), LRG-41 x ICPL-8863 (0.29), ICPL-2376 x ICPL-87119 (0.24), ICPL-15225 x

ICPL-87119 (0.23) and ICPL-6974 x ICPL-8863 (0.2), while five crosses recorded negative significant *sca* effects for this character.

Due to low *gca* /*sca* variance ratio, we can conclude that seed protein was controlled by non-additive gene action, which was also reported by Patel *et al.* (2010).

In parents, the lines ICPL-15225 and ICPL-2376 and the tester ICPL-8863 were found to be good general combiners. These can be used as good donors for improving this trait. The crosses, ICPL-2376 x PRG-158 (H X L), ICPL-7035 x ICPL-87119 (H X L), ICPL-15225 x ICPL-8863 (H X H), ICPL- 6974 x PRG-158 (L X L), LRG-41 x ICPL-8863 (L X H), ICPL-2376 x ICPL-87119 (H X L), ICPL-15225 x ICPL-87119 (H X L) and ICPL-6974 x ICPL-8863 (L X H) recorded significant *sca* effects. The crosses showing H X H combinations may be exploited through the simple pedigree method, while H X L, L X H and L X L combinations through diallel selective mating or intermating in segregating populations followed by cyclic selections for improvement of this character.

4.5.2.2 Phenol content: In parents, the line ICPL-2376 (0.6) and the testers ICPL-8863 (0.25) and ICPL-87119 (0.16) were found to be good combiners because of positive significant *gca* effects, whereas PRG-158 (-0.41), ICPL-7035 (-0.39) and ICPL-15225 (-0.17) recorded negative significant *gca* effects for this character.

The crosses viz., ICPL-6974 x ICPL-87119 (1.06), ICPL-2376 x PRG-158 (0.97), ICPL-7035 x ICPL-8863 (0.78), LRG-41 x PRG-158 (0.39), ICPL-15225 x ICPL-87119 (0.27), ICPL-15225 x ICPL-8863 (0.27), ICPL-2376 x ICPL-8863 (0.27) and LRG-41 x ICPL-87119 (0.25) were noticed as the best specific combiners for this trait, while other seven crosses recorded negative significant *sca* effects. Non-additive gene action reported for phenol content in present study.

For phenol content, the line ICPL-2376 and the testers ICPL-8863 and ICPL-87119 were found to be good general combiners and can be utilized in further breeding programmes for improving this trait. The best specific crosses with high *sca* effects were ICPL-6974 x ICPL-87119 (L X H), ICPL-2376 x PRG-158 (H X L), ICPL-7035 x ICPL-8863 (L X H), LRG-41 x PRG-158 (M X L), ICPL-15225 x ICPL-87119 (L X H), ICPL-15225 x ICPL-8863 (L X H), ICPL-2376 x ICPL-8863 (H X H) and LRG-41 x ICPL-87119 (M X H), in which atleast one parent with high *gca* effect was involved. The cross combination ICPL-2376 x ICPL-8863 had high x high *gca* parents which indicated that this trait is under the strong influence of additive type of gene action, which is highly fixable. Hence, selection of single plants can be effectively practiced in segregating generations to achieve pure lines with high phenol content.

Based on the overall *gca* effects, the crosses were classified as HH (both the parents of the cross with high overall *gca* status), HL (female parent with high and male parent with low overall *gca* status), LH (female parent with low and the male parent with high overall *gca* status). The results clearly indicated that both the parents with low overall *gca* status (L X L) also produced hybrids with high (H) overall *sca* status and the hybrids with H X H *gca* combination of parents expressed high (H) as well as low (L) overall *sca* status. On contrary, the hybrids involving high (H) x low (L) or low (L) x high (H) *gca* status expressed high (H) overall *sca* status in higher frequency in most of the crosses indicating major role of non-additive gene action. So these hybrid combinations are suitable for heterosis breeding. Whereas, the other combinations of H X H or L X L can be utilized to get useful transgressive segregants in the subsequent segregating generations.

From the foregoing discussion, it was concluded that based on *per se* performance and *gca* effects of the parents, ICPL-6974, ICPL-2376 and

ICPL-8863 were the best general combiners for days to flowering and days to maturity, while LRG-41 for plant height, primary branches per plant, secondary branches per plant, pods per plant and seed yield per plant. For 100-seed weight, pod length, seeds per pod and harvest index ICPL-7035 and ICPL-15225 were the best general combiners while, ICPL-2376 and ICPL-8863 were the best for seed protein and phenol contents.

Critical evaluation of *per se* performance, standard heterosis and *sca* effects of crosses, indicated ICPL-6974 x ICPL-87119, ICPL-6974 x ICPL-87119, ICPL-2376 x ICPL-8863 and ICPL-2376 x ICPL-87119 were the promising crosses for days to flowering, days to maturity, primary branches per plant and phenol content, while LRG-41 x ICPL-8863 and ICPL-15225 x ICPL-87119 for plant height, primary branches per plant and pod length. Whereas ICPL-7035 x ICPL-8863 and ICPL-15225 x ICPL-8863 for pod length, seeds per pod, 100-seed weight and SCMR at vegetative phase. Similarly, the crosses *viz.*, ICPL-15225 x ICPL-8863, ICPL-15225 x ICPL-87119, LRG-41 x PRG-158 were found to be most rewarding for the traits, pods per plant, harvest index, seed protein and seed yield (Table 4.10). The details of the crosses which showed highly significant standard heterosis along with their genetic parameter estimates were presented in Table 4.11.

The proportional contribution of lines, testers and line x tester interaction towards total variation in hybrids (per cent) was presented in Table 4.12. The contribution of lines towards total variation was maximum in respect of all the characters except seed protein and phenol content, which were contributed highly by the line x tester interaction. The top two high yielding hybrids were shown in Plate 3.

4.6 CHARACTER ASSOCIATION

The aim of correlation studies is primarily to know the various characters for indirect selection, because selection on any particular trait may induce desirable or undesirable changes in other associated characters.



ICPL-15225 X ICPL-8863



LRG-41 X PRG-158

Plate 3. Plate showing top two high yielding hybrids of present study in pigeonpea

Table 4.10: Best parents, general combiners and hybrids with high *sca* effect for different characters in pigeonpea

S. No	Character	Best performing parents	Good general combiners	Best performing crosses	Crosses with high <i>sca</i> effect	Crosses with high standard heterosis
1	Days to flowering	ICPL-6974, ICPL-2376, ICPL-8863	ICPL-2376, ICPL-6974, ICPL-8863	ICPL-2376 X ICPL-6974, ICPL-6974 X ICPL-8863, ICPL-6974 X PRG-158	ICPL-15225 X PRG-158, ICPL-6974 X PRG-158, ICPL-2376 X ICPL-87119	ICPL-2376 X ICPL-8863, ICPL-6974 X ICPL-8863,
2	Days to maturity	ICPL-6974, ICPL-2376, ICPL-8863	ICPL-6974, ICPL-2376, ICPL-8863	ICPL-6974 X ICPL-87119, ICPL-6974 X ICPL-8863, ICPL-6974 X PRG-158	ICPL-6974 X ICPL-87119, ICPL-15225 X ICPL-8863, ICPL-15225 X PRG-158	ICPL-6974 X ICPL-87119, ICPL-6974 X ICPL-8863, ICPL-6974 X PRG-158
3	Plant height (cm)	ICPL-8863, ICPL-87119, ICPL-2376	LRG-41, ICPL-15225, ICPL-87119	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X ICPL-8863	ICPL-2376 X ICPL-87119, ICPL-7035 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X ICPL-8863
4	Primary branches per plant	ICPL-87119, LRG-41, ICPL-2376	LRG-41, ICPL-87119	LRG-41 X ICPL-8863, ICPL-15225 X ICPL-87119, ICPL-6974 X ICPL-87119	LRG-41 X ICPL-87119	LRG-41 X ICPL-8863, ICPL-15225 X ICPL-87119, ICPL-6974 X ICPL-87119
5	Secondary branches per plant	LRG-41, ICPL-87119, ICPL-2376	LRG-41, ICPL-87119	LRG-41 X ICPL-8863, LRG-41 X ICPL-87119, LRG-41 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-2376 X ICPL-87119	LRG-41 X ICPL-8863, LRG-41 X PRG-158, LRG-41 X ICPL-87119
6	Pods per plant	ICPL-87119, ICPL-8863, LRG-41, ICPL-15225	ICPL-15225, LRG-41, ICPL-87119	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X PRG-158
7	Seeds per pod	ICPL-7035, ICPL-15225, ICPL-87119, LRG-41	ICPL-7035, ICPL-15225, ICPL-8863	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, ICPL-7035 X ICPL-87119	ICPL-2376 X PRG-158, ICPL-6974 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, ICPL-7035 X ICPL-87119

Cont...

S. No.	Character	Best performing parents	Good general combiners	Best performing crosses	Crosses with high sca effect	Crosses with high standard heterosis
8	Pod length (cm)	ICPL-7035, ICPL-15225, ICPL-87119	ICPL-7035, LRG-41, ICPL-8863	ICPL-7035 X ICPL8863, ICPL-15225 X ICPL-8863, LRG-41 X ICPL-8863	ICPL-15225 X ICPL-8863, ICPL-6974 X ICPL-8863, ICPLL7035 X ICPL-8863	ICPL-7035 X ICPL-8863, ICPL-15225 X ICPL-8863, LRG-41 X ICPL-8863
9	100-seed weight (g)	ICPL-7035, ICPL-15225, ICPL-87119	ICPL-7035, ICPL-87119	ICPL-7035 X ICPL-87119, ICPL-7035 X ICPL-8863, ICPL-7035X X PRG-158	ICPL-6974 X PRG-158, ICPL-7035 X ICPL-87119	ICPL-7035 X ICPL-87119, ICPL-7035 X ICPL-8863, ICPL-15225 X ICPL-8863
10	Harvest index (%)	ICPL-15225, ICPL-87119, ICPL-7035, ICPL-8863	ICPL-15225, ICPL-8863	ICPL-15225 X ICPL-87119, ICPL-15225 X ICPL-8863, ICPL-15225 X PRG-158	ICPL-6974 X PRG-158, ICPL-2376 X ICPL-87119, ICPL-15225 X ICPL-87119	ICPL-15225 X ICPL-87119, ICPL-15225 X ICPL-8863, ICPL-15225 X PRG-158
11	SCMR at vegetative phase	ICPL-2376, ICPL-6974, LRG-41, ICPL-8863	ICPL-7035, ICPL-87119	ICPL-7035 X ICPL-8863, ICPL-7035 X ICPL-87119, ICPL-2376 X ICPL-87119	ICPL-7035 X ICPL-8863, ICPL-6974 X ICPL-87119, ICPL-15225 X PRG-158	ICPL-7035 X ICPL-8863
12	Seed protein (%)	ICPL-6974, PRG-158, LRG-41	ICPL-2376, ICPL-15225, ICPL-8863	ICPL-15225 X ICPL-8863, ICPL-6974 X ICPL-8863, ICPL-6974 X ICPL-87119	ICPL-2376 X PRG-158, ICPL-7035 X ICPL-87119, ICPL-15225 X ICPL-8863	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, ICPL-6974 X ICPL-8863
13	Phenol content (%)	LRG-41, ICPL-6974, ICPL-87119, PRG-158	ICPL-2376, ICPL-87119, ICPL-8863	ICPL-6974 X ICPL-87119, ICPL-2376 X ICPL-8863, ICPL-2376 X PRG-158	ICPL-6974 X ICPL-87119, ICPL-2376 X PRG-158, ICPL-7035 X ICPL-8863	ICPL-2376 X PRG-158, ICPL-2376 X ICPL-8863, ICPL-6974 X ICPL-87119
14	Seed yield plant (g)	ICPL-87119, ICPL-8863, LRG-41, ICPL-15225	ICPL-15225, LRG-41, ICPL-87119	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X PRG-158	ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119, LRG-41 X PRG-158, LRG-41 X ICPL-87119

Table 4.11. High yielding hybrids over standard check (LRG-30) and estimates of their genetic parameters in pigeonpea

S. No.	Hybrids	Mean seed yield (g)	Heterosis		<i>gca</i> effect		<i>sca</i> effect	Useful significant heterosis for component trait in desired direction
			BP	SC	Line	Tester		
1	ICPL-15225 X ICPL-8863	390.00	160.00**	402.15**	130.2**	6.84	94.60**	DF, DM, PB, SB, PP, SP, PL, SW, HI, PC, PH, SY
2	ICPL-15225 X ICPL-87119	369.33	123.39**	375.54**	130.2**	24.44**	56.33**	DM, PB, PP, SP, SW, HI, PC, PH, SY
3	LRG-41 X PRG-158	231.00	102.04**	197.42**	31.64**	-31.29**	72.29**	DM, PB, SB, PP, SP, PL, SW, HI, PC, PH, SY
4	LRG-41 X ICPL-87119	192.67	16.53	148.07**	31.64**	24.44**	-21.78	DF, DM, PB, SB, PP, SP, PL, SW, HI, PC, PH, SY
5	ICPL-6974 X ICPL-87119	163.67	-1.01	110.73**	-19.69	24.44**	0.56	DF, DM, PB, PP, SW, HI, PC, PH
6	LRG-41 X ICPL-8863	146.33	-2.44	88.41*	31.64**	6.84	-50.51**	DF, DM, PB, SB, PP, SP, PL, SW, HI, PC, PH, SY
7	ICPL-6974 X PRG-158	141.67	48.08	82.40*	-19.69	-31.29**	34.29	DF, DM, PP, SW, HI, PC, SY

Table 4.12. Proportionate contribution of lines, testers and line x tester interaction towards total variance in hybrids (in per cent) in pigeonpea

S. No.	Characters	Lines	Testers	Line x Tester interaction
1	Days to flowering	49.23	31.43	19.34
2	Days to maturity	82.77	7.01	10.22
3	Plant height	69.45	5.35	25.20
4	Primary branches per plant	54.26	27.73	18.02
5	Secondary branches per plant	74.45	5.31	20.24
6	Pods per plant	62.10	4.90	33.00
7	Seeds per pod	66.53	0.47	33.00
8	Pod length (cm)	62.68	12.46	24.86
9	100-seed weight (g)	75.00	2.34	22.66
10	Harvest index (%)	89.35	0.21	10.44
11	SCMR at vegetative phase	56.14	0.32	43.54
12	Seed protein (%)	16.99	29.44	53.57
13	Phenol content (%)	18.19	14.02	67.79
14	Seed yield per plant (g)	60.57	5.76	33.67

Generally, direct selection for yield is not aimed at, as it is a complex and quantitatively inherited character and is highly influenced by environment. As such, high genotypic and environmental interactions are likely to restrict the improvement, if selection is based on yield as a simple trait. Therefore, correlation between yield and yield components are of considerable importance in selection programmes.

In present study, the results revealed that the genotypic correlation coefficients were generally higher than phenotypic correlation coefficients and in the same direction. The phenotypic correlations are discussed here under, as the significant phenotypic correlations will be useful criteria when coupled with significant genotypic correlations. Here, phenotypic and genotypic correlation coefficients were computed separately for parents and crosses to assess the direction and magnitude of association existing between seed yield and other component characters and are presented in Tables 4.13 and 4.14 respectively. The phenotypic and genotypic correlation coefficients were also given in Fig. 4.6 and 4.7, respectively.

In parents, seed yield per plant was recorded significant and positive association with pods per plant (0.9163*). Further, days to flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, harvest index and phenol content recorded positive correlations with seed yield per plant. Seeds per pod, pod length, 100-seed weight, SCMR at vegetative phase and seed protein were associated negatively with seed yield. In crosses, seed yield per plant was associated significantly and positively with plant height (0.5357*), pods per plant (0.9811**) and harvest index (0.6309*). Whereas, rest of the characters were associated positively except SCMR at vegetative phase, which was negatively correlated with seed yield.

Seed yield had positive significant association with pods per plant in parents, while plant height, pods per plant and harvest index in crosses and it

Table 4.13. Correlation coefficients for yield and yield components in parents of pigeonpea

Character		Days to flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
Days to flowering	P	1.0000	0.9024*	-0.2554	-0.0259	-0.0806	0.0671	0.3874	0.5797	0.3860	0.3624	-0.5030	0.0122	0.0605	0.1706
	G	1.0000	0.9191	-0.3467	0.0042	-0.0713	0.1252	0.4748	0.6473	0.4170	0.3969	-0.6843	0.0227	0.0583	0.2792
Days to maturity	P		1.0000	-0.0457	0.0786	0.1245	0.2684	0.2610	0.4692	0.2325	0.3702	-0.4834	-0.1426	0.0831	0.3528
	G		1.0000	-0.1664	0.0733	0.1388	0.3258	0.3356	0.5356	0.2498	0.3907	-0.5966	-0.1351	0.0917	0.4555
Plant height(cm)	P			1.0000	0.5812	0.6326	0.5983	-0.5771	-0.5109	-0.3620	-0.0506	0.2507	-0.0017	0.0793	0.6373
	G			1.0000	0.6896	0.9393	0.7674	-0.6631	-0.5205	-0.4845	-0.1279	0.3676	-0.0018	0.1356	0.8242
Primary branches per plant	P				1.0000	0.6316	0.7227*	-0.6196	-0.5908	-0.6306	-0.0350	0.2379	0.0203	0.6383	0.6314
	G				1.0000	0.9570	0.9117	-0.9140	-0.7452	-0.9098	-0.0894	0.2887	0.0366	0.7655	0.8156
Secondary branches per plant	P					1.0000	0.6583	-0.6448	-0.5001	-0.4786	-0.2161	0.3958	-0.2376	0.3664	0.6379
	G					1.0000	0.7576	-0.8482	-0.6584	-0.7560	-0.3667	0.6150	-0.2814	0.5365	0.7545
Pods per plant	P						1.0000	-0.6106	-0.5156	-0.5882	0.1482	-0.0872	0.0630	0.4062	0.9163*
	G						1.0000	-0.6944	-0.5450	-0.6720	0.1214	-0.0937	0.0568	0.4454	0.9488
Seeds/pod(no.)	P							1.0000	0.9282*	0.8139*	0.4988	-0.5617	-0.0177	-0.5036	-0.4052
	G							1.0000	0.9578	0.9574	0.5703	-0.6439	-0.0116	-0.5975	-0.5182
Pod length (cm)	P								1.0000	0.8384*	0.4447	-0.5492	0.0616	-0.4203	-0.3136
	G								1.0000	0.9178	0.4750	-0.6356	0.0820	-0.4567	-0.3525
100-seed weight (g)	P									1.0000	0.3482	-0.3909	-0.0229	-0.7366*	-0.3429
	G									1.0000	0.3405	-0.5758	-0.0078	-0.7752	-0.4115
Harvest index (%)	P										1.0000	-0.6846	-0.0856	-0.2278	0.2809
	G										1.0000	-0.8716	-0.0733	-0.2412	0.2904
SCMR at vegetative phase	P											1.0000	-0.2151	0.2777	-0.1927
	G											1.0000	-0.2315	0.3570	-0.2051
Seed protein (%)	P												1.0000	0.2612	-0.0730
	G												1.0000	0.2643	-0.0943
Phenol content (%)	P													1.0000	0.1679
	G													1.0000	0.2010
Seed yield per plant (g)	P														1.0000
	G														1.0000

Table 4.14. Correlation coefficients for yield and yield components in crosses of pigeonpea

Character		Days to flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
Days to flowering	P	1.0000	0.7348**	0.1943	0.0629	0.3439	0.4358	0.5249*	0.2091	0.2013	0.4179	-0.0105	-0.4075	-0.1256	0.4340
	G	1.0000	0.7648	0.2343	0.0858	0.4254	0.4579	0.5817	0.2299	0.2510	0.5782	-0.0032	-0.4463	-0.1201	0.4527
Days to maturity	P		1.0000	0.1307	0.1461	0.3841	0.3393	0.5280*	0.3681	0.3226	0.4379	0.1329	-0.1857	-0.1157	0.3635
	G		1.0000	0.2288	0.2442	0.5711	0.3597	0.6562	0.4440	0.3791	0.5918	0.1172	-0.1961	-0.1238	0.3891
Plant height (cm)	P			1.0000	0.4564	0.5837*	0.5597*	-0.0338	-0.0600	-0.3879	0.2938	-0.4248	0.2696	-0.0764	0.5357*
	G			1.0000	0.9816	0.8946	0.8237	0.0131	-0.0078	-0.4228	0.6582	-0.5549	0.4331	-0.0489	0.8035
Primary branches per plant	P				1.0000	0.6376*	0.3607	-0.0939	-0.1770	-0.3013	0.1537	-0.2432	0.2429	0.1423	0.4017
	G				1.0000	0.8639	0.4594	-0.2949	-0.2756	-0.4450	0.1870	-0.3693	0.3405	0.1658	0.4468
Secondary branches per plant	P					1.0000	0.4862	0.2109	0.2107	-0.0651	0.2959	-0.1234	0.1706	0.0236	0.4933
	G					1.0000	0.5543	0.1898	0.2990	-0.1261	0.4667	-0.1775	0.2302	0.0139	0.5518
Pods per plant	P						1.0000	0.3558	0.1292	-0.0371	0.5907*	-0.4758	0.3280	0.2206	0.9811**
	G						1.0000	0.4655	0.1646	-0.0138	0.7942	-0.5214	0.3469	0.2358	0.9966
Seed per pod	P							1.0000	0.6692**	0.6143*	0.5165*	0.1848	0.1356	-0.0578	0.4231
	G							1.0000	0.7998	0.8451	0.7401	0.2504	0.1229	-0.0780	0.5374
Pod length (cm)	P								1.0000	0.6882**	0.2888	0.4622	0.0841	-0.0514	0.1634
	G								1.0000	0.7427	0.5107	0.5589	0.0742	-0.0328	0.2115
100-seed weight(g)	P									1.0000	0.2398	0.4506	0.0236	-0.1735	0.0163
	G									1.0000	0.5223	0.4926	-0.0315	-0.2165	0.0567
Harvest index (%)	P										1.0000	-0.1676	0.1027	-0.2468	0.6309*
	G										1.0000	-0.1650	0.2027	-0.3914	0.8286
SCMR at vegetative phase	P											1.0000	-0.1599	0.0593	-0.4347
	G											1.0000	-0.1988	0.0642	-0.4680
Seed protein (%)	P												1.0000	0.2001	0.3643
	G												1.0000	0.2054	0.3979
Phenol content (%)	P													1.0000	0.1981
	G													1.0000	0.2234
Seed yield per plant (g)	P														1.0000
	G														1.0000

Fig. 4.6. Phenotypic correlation of yield components with seed yield of pigeonpea

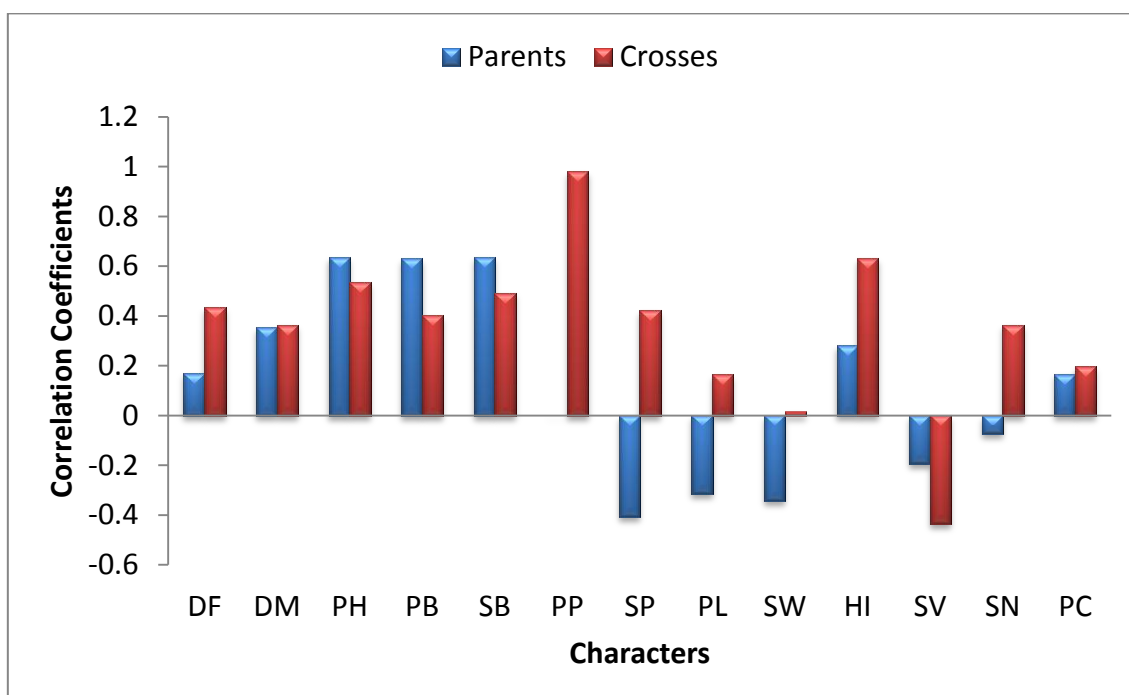
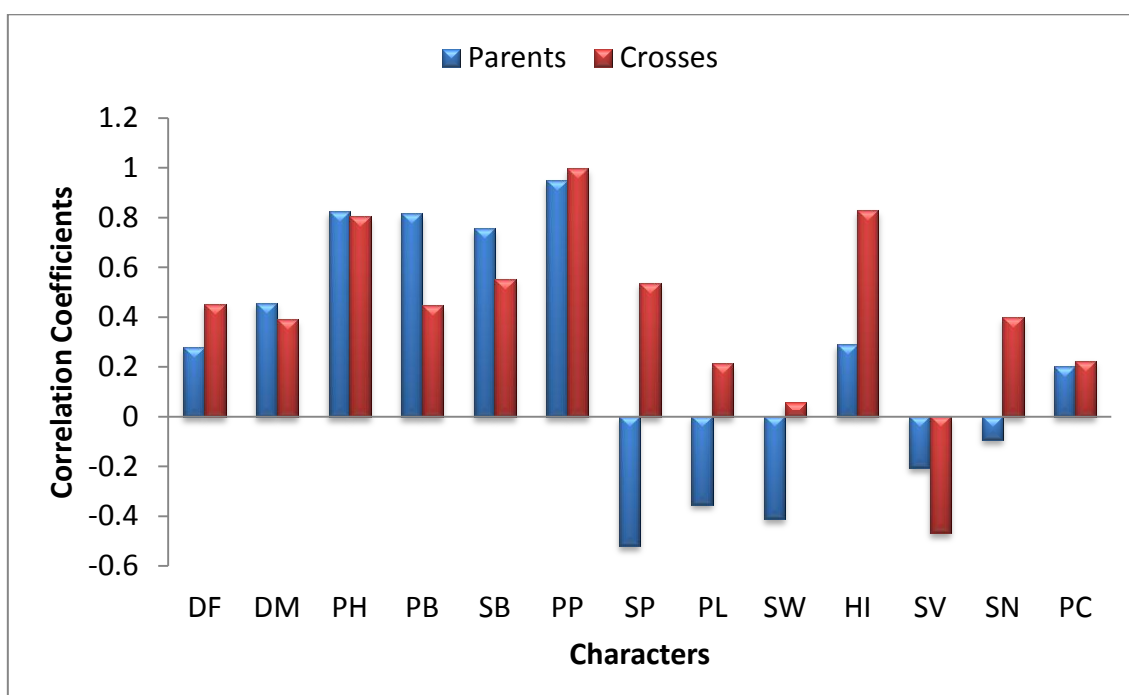


Fig. 4.7. Genotypic correlation of yield components with seed yield of pigeonpea



DF= Days to flowering	SP= Seeds per pod	PC= Phenol content
DM= Days to maturity	PL=Pod length	SY= Seed yield per plant
PH=Plant height	SW= 100-seed weight	PB= Primary branches per plant
HI= Harvest index	SB= Secondary branches per plant	SV= SCMR at vegetative phase
PP= Pods per plant	SN= Seed protein	

was revealed by Asawa *et al.* (1981), Natarajan *et al.* (1990), Paul and Upadhaya (1991), Dhameliya and Pathak (1994), Deshmukh *et al.* (2000), Baskaran and Mutiah (2007), Jogendra Singh *et al.* (2008) and Dodake *et al.* (2009) for pods per plant, while Balyan and Sudhakar (1985), Bhongale and Raut (1987), Salunke *et al.* (1995), Srinivas *et al.* (1999) and Bhadru (2010) for plant height and Jogendra Singh *et al.* (2008) for harvest index. It is indicated that seed yield can be increased whenever there is an increase in pods per plant in parents and crosses, while plant height and harvest index in crosses. Hence, these characters can be considered as criteria for selection of higher yielding genotypes as these were mutually and directly associated with seed yield.

Positive and non-significant correlation with seed yield observed for characters in the present study was also reported earlier by Gumber *et al.* (1996) and Sawant *et al.* (2009) for days to flowering, Srinivas *et al.* (1999), Sodavadiya *et al.* (2009) and Bhadru (2010) for days to maturity, Natarajan *et al.* (1990), Dhameliya and Pathak (1994) and Chattopadyay and Dhiman (2005) for plant height, Rekha (2009) for phenol content, Mahajan *et al.* (2007) for primary branches per plant, Baskaran and Muthiah (2007) for pod length, Marekar and Nerker (1987) for harvest index.

Negative and non-significant association with seed yield recorded in the present study were in confirmity with the reports of Balyan and Sudhakar (1985), Bhongale and Raut (1987) and Paul *et al.* (1996) for seeds per pod, Chattopadyay and Dhiman (2005) for 100-seed weight, Baradwaj and Gupta (2004) and Gangwar and Bajpai (2006) for protein content, Krishna Chaithanya (2010) for SCMR at vegetative phase, while Paul and Upadhaya (1991) and Dhameliya and Pathak (1994) for pod length.

In parents, the yield component pods per plant showed significant and positive association with primary branches per plant (0.7227*), while with secondary branches per plant and plant height, days to maturity and days to

flowering, the association was positive non-significant. It was indicated that increase in primary branches per plant will increase pods per plant, finally the total seed yield. In crosses, pods per plant was associated positively and significantly with plant height (0.5597*), while its association with secondary branches per plant, days to flowering, primary branches per plant and days to maturity was non-significant and positive.. It was indicated that increase in plant height will increase primary branches per plant and thus pods per plant, which was highly correlated with seed yield. This is in confirmity with the results of Veeraswamy *et al.* (1973) and Natarajan *et al.* (1990) for plant height and Bhongale and Raut (1987) and Mahajan *et al.* (2007) for primary branches per plant.

Secondary branches per plant displayed high and non-significant positive association with days to maturity in parents, whereas in crosses, it had significant positive association with plant height (0.5837*) and primary branches per plant (0.6376*), while positive non-significant association with days to flowering and days to maturity. These results indicated that increase in plant height and primary branches per plant will increase pods per plant, finally it could result in improvement of seed yield. This was in confirmity with the results of Paul *et al.* (1996), Deshmukh *et al.* (2000), Gangwar and Bajpai (2006) and Mahajan *et al.* (2007).

Plant height manifested non-significant negative association with days to flowering and days to maturity in parents, while in crosses it had positive non-significant association with these characters. These results were in accordance with the findings of Veeraswamy *et al.* (1973), Dhameliya and Pathak (1994) and Salunke *et al.* (1995).

The yield component trait, primary branches per plant had non-significant and positive association with plant height and days to maturity in parents and crosses. In addition, it had positive non-significant association

with days to flowering in crosses. These results were in accordance with the results of Dhameliya and Pathak (1994) and Salunke *et al.* (1995).

Days to maturity expressed significant and positive association with days to flowering (0.9024*) in parents and (0.7348*) in crosses, indicated that delayed in flowering will increase in crop duration. This was also supported by Mahajan *et al.* (2007).

Harvest index exhibited non-significant and positive association with seeds per pod, pod length, days to maturity, days to flowering, 100-seed weight and pods per plant in parents, while in crosses, it had high and positive significant association with pods per plant (0.5907*) and seeds per pod (0.5165*). This was suggested that increase in pods per plant and seeds per pod will increase the harvest index, which was also reported earlier by Marekar and Nerkar (1987).

Phenol content displayed negative significant association with 100-seed weight (-0.7366*), while it had positive and non-significant correlation with days to flowering, days to maturity, plant height, secondary branches per plant, pods per plant, SCMR at vegetative phase and seed protein in parents. In crosses, phenol content had positive non-significant association with pods per plant, seed protein, primary branches per plant, SCMR at vegetative phase and secondary branches per plant. These results are in confirmity with the findings of Rekha (2009).

Seeds per pod expressed positive non-significant association with days to flowering and days to maturity in parents, while it had positive and significant association with days to flowering (0.5249*) and days to maturity (0.5280*) and positive non-significant association with pods per plant and secondary branches per plant in crosses. This indicated that increase in these characters may increase in seeds per pod. These results

were in coincidence with the reports of Dhameliya and Pathak (1994) and Salunke *et al.* (1995).

The trait, 100-seed weight exhibited highly significant and positive association with pod length (0.8384* and 0.6882**) and seeds per pod (0.8139* and 0.6143*) and it had non-significant positive correlation with days to flowering and days to maturity in parents and crosses suggested that a desirable plant type with lengthy pods and more number of seeds per pod would have higher seed weight to increase the final seed yield. These results were as per the findings of Mahajan *et al.* (2007), Dhameliya and Pathak (1994) and Salunke *et al.* (1995).

Pod length had high positive significant correlation with seeds per pod (0.9282* and 0.6992*) and positive non-significant association was observed with days to flowering and days to maturity in parents and crosses. In addition, secondary branches per plant was also exhibited positive non-significant association with pod length in crosses. It was suggested that lengthy pods will have more number of seeds per pod. These results were in confirmity with the earlier reports of Dhameliya and Pathak (1994), Salunke *et al.* (1995), Baskaran and Muthiah (2007) and Mahajan *et al.* (2007).

SCMR at vegetative phase had positive non-significant association with secondary branches per plant, plant height, primary branches per plant and phenol content in parents, while in crosses it had positive non-significant association with days to maturity, seeds per pod, pod length and 100-seed weight. Similar kind of results were observed by Krishna Chaithanya (2010).

Seed protein had positive non-significant association with pods per plant, pod length, primary branches per plant and days to flowering in parents, while in crosses it had positive non-significant association with plant height, pods per plant, pod length, primary branches per plant,

secondary branches per plant, seeds per pod, 100-seed weight and harvest index. The results are in close agreement with Chandirakala and Raveendran (1998), Bharadwaj and Gupta (2004) and Anuradha *et al.* (2007).

It was evident from the investigation that highly significant positive association of pods per plant and positive association for days to flowering, days to maturity, primary and secondary branches per plant and phenol content and negative association of SCMR at vegetative phase with seed yield in parents as well as in crosses was recorded.

The negative and non-significant association of seeds per pod with seed yield in parents became positive in crosses. Harvest index had non-significant positive association with seed yield in parents and became positive significant in crosses. Whereas pod length, 100-seed weight and protein content were associated negatively with seed yield became positive in crosses maybe due to new re-combinations.

Among the yield components, seeds per pod, pod length and 100-seed weight showed either positive non-significant or negative association with all other characters but they registered significant positive association among themselves in parents.

The non-significant positive association observed among the yield components in parents between the following character pairs became significant in crosses. They were secondary branches per plant with plant height and primary branches per plant; seeds per pod with days to flowering and days to maturity; pods per plant with plant height. The positive significant association in parents between character pairs viz., pods per plant with primary branches per plant became non-significant in crosses.

Negative non-significant association of character pairs in parents became positive non-significant in crosses viz., plant height, primary branches per plant and secondary branches per plant with days to flowering;

plant height and SCMR at vegetative phase with days to maturity; secondary branches per plant and pods per plant with seeds per pod and pod length; plant height, primary and secondary branches per plant with harvest index; seeds per pod, pod length and 100-seed weight with SCMR at vegetative phase; plant height, secondary branches per plant seeds per pod, 100-seed weight and harvest index with seed protein. On contrary, positive non-significant association between character pairs in parents became negative non-significant in crosses. They were plant height, primary and secondary branches per plant with SCMR at vegetative phase, days to flowering with seed protein and phenol content, days to maturity and plant height with phenol content. These changes in correlations between pairs of characters from parents to crosses might have resulted due to the modifications in the linkages as a result of re-combinations in those populations.

In general, the yield component traits which showed significant positive association with seed yield in parents and crosses are of prime importance in determining the seed yield. Hence, such a situation is favourable to a plant breeder as it helps in simultaneous improvement of these characters along with seed yield *per se*. Hence, the emphasis should be given on pods per plant for obtaining higher yield in present study.

4.7 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and a particular yield component is the net result of direct effect of those component and indirect effects through the other yield attributes. The direct effect may be different from the observed correlations. The total correlation between yield and a component trait may sometimes be misleading since it may be the overestimate or under estimate because of its association with other traits. Hence, direct selection by correlated response may sometimes be not fruitful. If the direct effect is equal to correlation co-efficient, then correlation explains the true relationship and direct selection of this will be effective.

Table 4.15. Direct and indirect effects of yield component characters on seed yield in parents of pigeonpea.

Character		Days to flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
Days to flowering	P	0.4416	-0.5175	-0.0781	-0.0001	-0.0014	0.0756	0.0511	0.1843	0.0034	-0.0536	0.0698	-0.0034	-0.0011	0.1706
	G	0.5129	-0.6115	-0.0929	0.0000	-0.0011	0.1508	0.0727	0.1978	0.0179	-0.0606	0.0994	-0.0075	0.0013	0.2792
Days to maturity	P	0.3985	-0.5735	-0.0140	0.0003	0.0021	0.3027	0.0344	0.1492	0.0021	-0.0548	0.0670	0.0402	-0.0015	0.3528
	G	0.4715	-0.6653	-0.0446	-0.0004	0.0021	0.3923	0.0514	0.1637	0.0107	-0.0596	0.0867	0.0450	0.0021	0.4555
Plant height(cm)	P	-0.1128	0.0262	0.3058	0.0026	0.0107	0.6747	-0.0761	-0.1624	-0.0032	0.0075	-0.0348	0.0005	-0.0014	0.6373
	G	-0.1778	0.1107	0.2681	-0.0035	0.0144	0.9241	-0.1015	-0.1591	-0.0208	0.0195	-0.0534	0.0006	0.0031	0.8242
Primary branches per plant	P	-0.0114	-0.0451	0.1777	0.0044	0.0107	0.8150	-0.0817	-0.1878	-0.0056	0.0052	-0.0330	-0.0057	-0.0112	0.6314
	G	0.0022	-0.0488	0.1849	-0.0051	0.0147	1.0978	-0.1400	-0.2277	-0.0391	0.0136	-0.0419	-0.0122	0.0172	0.8156
Secondary branches per plant	P	-0.0356	-0.0714	0.1934	0.0028	0.0169	0.7424	-0.0850	-0.1590	-0.0043	0.0320	-0.0549	0.0669	-0.0064	0.6379
	G	-0.0366	-0.0923	0.2518	-0.0049	0.0153	0.9123	-0.1299	-0.2012	-0.0325	0.0560	-0.0893	0.0937	0.0121	0.7545*
Pods per plant	P	0.0296	-0.1539	0.1829	0.0032	0.0112	1.1277	-0.0805	-0.1639	-0.0052	-0.0219	0.0121	-0.0178	-0.0071	0.9163*
	G	0.0642	-0.2167	0.2057	-0.0047	0.0116	1.2041	-0.1063	-0.1665	-0.0289	-0.0185	0.0136	-0.0189	0.0100	0.9488
Seeds per pod	P	0.1711	-0.1497	-0.1765	-0.0027	-0.0109	-0.6886	0.1319	0.2951	0.0072	-0.0738	0.0779	0.0050	0.0089	-0.4052
	G	0.2435	-0.2233	-0.1778	0.0047	-0.0130	-0.8362	0.1531	0.2927	0.0412	-0.0870	0.0935	0.0038	-0.0135	-0.5182
Pod length (cm)	P	0.2560	-0.2691	-0.1562	-0.0026	-0.0085	-0.5814	0.1224	0.3179	0.0074	-0.0658	0.0762	-0.0173	0.0074	-0.3136
	G	0.3320	-0.3563	-0.1395	0.0038	-0.0101	-0.6563	0.1467	0.3056	0.0395	-0.0725	0.0923	-0.0273	-0.0103	-0.3525
100-seed weight (g)	P	0.1705	-0.1333	-0.1107	-0.0028	-0.0081	-0.6634	0.1073	0.2666	0.0089	-0.0515	0.0542	0.0065	0.0130	-0.3429
	G	0.2139	-0.1662	-0.1299	0.0047	-0.0116	-0.8092	0.1466	0.2805	0.0430	-0.0520	0.0836	0.0026	-0.0175	-0.4115
Harvest index (%)	P	0.1601	-0.2123	-0.0155	-0.0002	-0.0037	0.1672	0.0658	0.1414	0.0031	-0.1480	0.0949	0.0241	0.0040	0.2809
	G	0.2036	-0.2599	-0.0343	0.0005	-0.0056	0.1461	0.0873	0.1451	0.0146	-0.1526	0.1266	0.0244	-0.0054	0.2904
SCMR at vegetative phase	P	-0.2222	0.2772	0.0767	0.0011	0.0067	-0.0984	-0.0741	-0.1746	-0.0035	0.1013	-0.1387	0.0606	-0.0049	-0.1927
	G	-0.3510	0.3969	0.0985	-0.0015	0.0094	-0.1128	-0.0986	-0.1942	-0.0248	0.1330	-0.1452	0.0771	0.0080	-0.2051
Seed protein (%)	P	0.0054	0.0818	-0.0005	0.0001	-0.0040	0.0711	-0.0023	0.0196	-0.0002	0.0127	0.0298	-0.2818	-0.0046	-0.0730
	G	0.0116	0.0899	-0.0005	-0.0002	-0.0043	0.0683	-0.0018	0.0251	-0.0003	0.0112	0.0336	-0.3329	0.0059	-0.0943
Phenol content (%)	P	0.0267	-0.0476	0.0242	0.0028	0.0062	0.4581	-0.0664	-0.1336	-0.0065	0.0337	-0.0385	-0.0736	-0.0176	0.1679
	G	0.0299	-0.0610	0.0364	-0.0039	0.0082	0.5363	-0.0915	-0.1395	-0.0333	0.0368	-0.0518	-0.0880	0.0225	0.2010

Table 4.16. Direct and indirect effects of yield component characters on seed yield in crosses of pigeonpea

Character		Days to flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	Pod length (cm)	100-seed weight (g)	Harvest index (%)	SCMR at vegetative phase	Seed protein (%)	Phenol content (%)	Seed yield per plant (g)
Days to flowering	P	-0.0155	-0.0012	-0.0002	0.0062	-0.0128	0.3992	0.0542	-0.0066	0.0036	0.0181	-0.0002	-0.0116	0.0010	0.4340
	G	0.1112	0.0555	-0.0087	-0.0036	-0.0143	0.4257	-0.1199	0.0076	0.0193	0.0627	0.0000	-0.0780	-0.0047	0.4527
Days to maturity	P	-0.0114	-0.0017	-0.0001	0.0144	-0.0143	0.3108	0.0545	-0.0117	0.0057	0.0189	0.0026	-0.0053	0.0009	0.3635
	G	0.0850	0.0725	-0.0085	-0.0101	-0.0192	0.3344	-0.1352	0.0147	0.0291	0.0642	0.0014	-0.0343	-0.0049	0.3891
Plant height(cm)	P	-0.0030	-0.0002	-0.0010	0.0450	-0.0217	0.5126	-0.0035	0.0019	-0.0069	0.0127	-0.0085	0.0077	0.0006	0.5357*
	G	0.0260	0.0166	-0.0371	-0.0408	-0.0300	0.7657	-0.0027	-0.0003	-0.0324	0.0714	-0.0067	0.0757	-0.0019	0.8035
Primary branches per plant	P	-0.0010	-0.0002	-0.0005	0.0986	-0.0237	0.3304	-0.0097	0.0056	-0.0054	0.0066	-0.0048	0.0069	-0.0012	0.4017
	G	0.0095	0.0177	-0.0364	-0.0415	-0.0290	0.4271	0.0608	-0.0091	-0.0341	0.0203	-0.0044	0.0595	0.0065	0.4468
Secondary branches per plant	P	-0.0053	-0.0006	-0.0006	0.0628	-0.0372	0.4453	0.0218	-0.0067	-0.0012	0.0128	-0.0025	0.0049	-0.0002	0.4933
	G	0.0473	0.0414	-0.0332	-0.0359	-0.0335	0.5153	-0.0391	0.0099	-0.0097	0.0506	-0.0021	0.0402	0.0005	0.5518
Pods per plant	P	-0.0068	-0.0006	-0.0006	0.0356	-0.0181	0.9159	0.0367	-0.0041	-0.0007	0.0255	-0.0095	0.0094	-0.0018	0.9811**
	G	0.0509	0.0261	-0.0306	-0.0191	-0.0186	0.9296	-0.0959	0.0055	-0.0011	0.0861	-0.0063	0.0606	0.0093	0.9966
Seeds per pod	P	-0.0082	-0.0009	0.0000	-0.0093	-0.0078	0.3259	0.1033	-0.0212	0.0109	0.0223	0.0037	0.0039	0.0005	0.4231
	G	0.0647	0.0476	-0.0005	0.0122	-0.0064	0.4328	-0.2060	0.0265	0.0648	0.0802	0.0030	0.0215	-0.0031	0.5374
Pod length (cm)	P	-0.0033	-0.0006	0.0001	-0.0174	-0.0078	0.1183	0.0691	-0.0317	0.0122	0.0125	0.0092	0.0024	0.0004	0.1634
	G	0.0256	0.0322	0.0003	0.0115	-0.0100	0.1530	-0.1648	0.0332	0.0570	0.0554	0.0067	0.0130	-0.0013	0.2115
100-seed weight(g)	P	-0.0031	-0.0005	0.0004	-0.0297	0.0024	-0.0340	0.0634	-0.0218	0.0178	0.0104	0.0090	0.0007	0.0014	0.0163
	G	0.0279	0.0275	0.0157	0.0185	0.0042	-0.0128	-0.1741	0.0246	0.0767	0.0566	0.0059	-0.0055	-0.0085	0.0567
Harvest index (%)	P	-0.0065	-0.0007	-0.0003	0.0151	-0.0110	0.5410	0.0533	-0.0092	0.0043	0.0432	-0.0033	0.0029	0.0020	0.6309*
	G	0.0643	0.0429	-0.0244	-0.0078	-0.0157	0.7383	-0.1525	0.0169	0.0401	0.1084	-0.0020	0.0354	-0.0154	0.8286
SCMR at vegetative phase	P	0.0002	-0.0002	0.0004	-0.0240	0.0046	-0.4358	0.0191	-0.0147	0.0080	-0.0072	0.0199	-0.0046	-0.0005	-0.4347
	G	-0.0004	0.0085	0.0206	0.0153	0.0060	-0.4847	-0.0516	0.0185	0.0378	-0.0179	0.0120	-0.0347	0.0025	-0.4680
Seed protein (%)	P	0.0063	0.0003	-0.0003	0.0239	-0.0063	0.3005	0.0140	-0.0027	0.0004	0.0044	-0.0032	0.0285	-0.0016	0.3643
	G	-0.0496	-0.0142	-0.0161	-0.0141	-0.0077	0.3225	-0.0253	0.0025	-0.0024	0.0220	-0.0024	0.1748	0.0081	0.3979
Phenol content (%)	P	0.0020	0.0002	0.0001	0.0140	-0.0009	0.2021	-0.0060	0.0016	-0.0031	-0.0107	0.0012	0.0057	-0.0082	0.1981
	G	-0.0134	-0.0090	0.0018	-0.0069	-0.0005	0.2192	0.0161	-0.0011	-0.0166	-0.0424	0.0008	0.0359	0.0394	0.2234

If the correlation co-efficient is positive, but the direct effect is negative or negligible the indirect effects seem to be the cause of correlation. In such situations, the other factors have to be considered simultaneously. If correlation is negative, but the direct effect is positive and high, a restricted simultaneous selection model is to be followed i.e., restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

In the present study, path coefficient analysis for 8 parents and 15 crosses was worked out and furnished in Tables 4.14 and 4.15 respectively. Phenotypic path diagrams were situated in Fig. 4.8 and 4.9, while genotypic path diagrams were given in Fig. 4.10 and 4.11 in parents and crosses respectively. The results and discussion were presented hereunder.

4.7.1 Direct and indirect effects of yield attributes

In parents, days to flowering exhibited high positive direct effect on seed yield (0.4416). It had positive indirect effects through pods per plant (0.0756), seeds per pod (0.0522), pod length (0.1843), 100-seed weight (0.0034) and SCMR at vegetative phase (0.0698), which resulted in positive correlation with seed yield (0.1706). In crosses this trait exhibited direct negative effect on seed yield (-0.0155). Its positive indirect effects through primary branches per plant (0.0062), pods per plant (0.3992), seeds per pod (0.0542), 100-seed weight (0.0036), harvest index (0.0181) and phenol content (0.001) suppressed both direct and indirect negative effects and produced positive correlation with seed yield (0.4340). Its positive direct effect on seed yield in parents was in confirmity with the findings of Dumbre *et al.* (1985) and negative direct effect was supported by the results of Paul *et al.* (1996) and Anuradha *et al.* (2007).

Days to maturity had high negative direct effect on seed yield (-0.5735), but its positive indirect effects via days to flowering (0.3985),

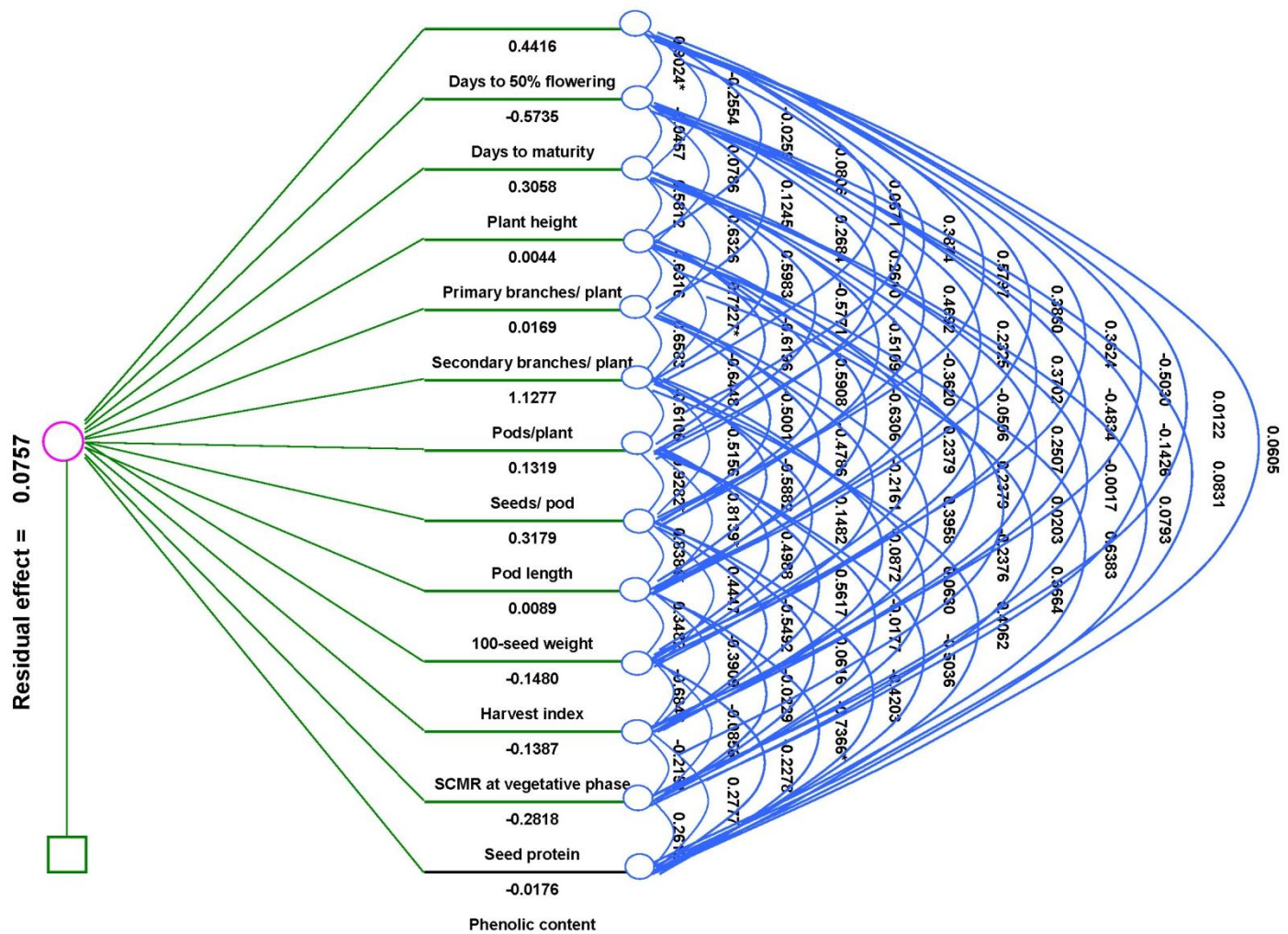


Fig. 4.8: Phenotypic path diagram of seed yield and yield components in parents of pigeonpea

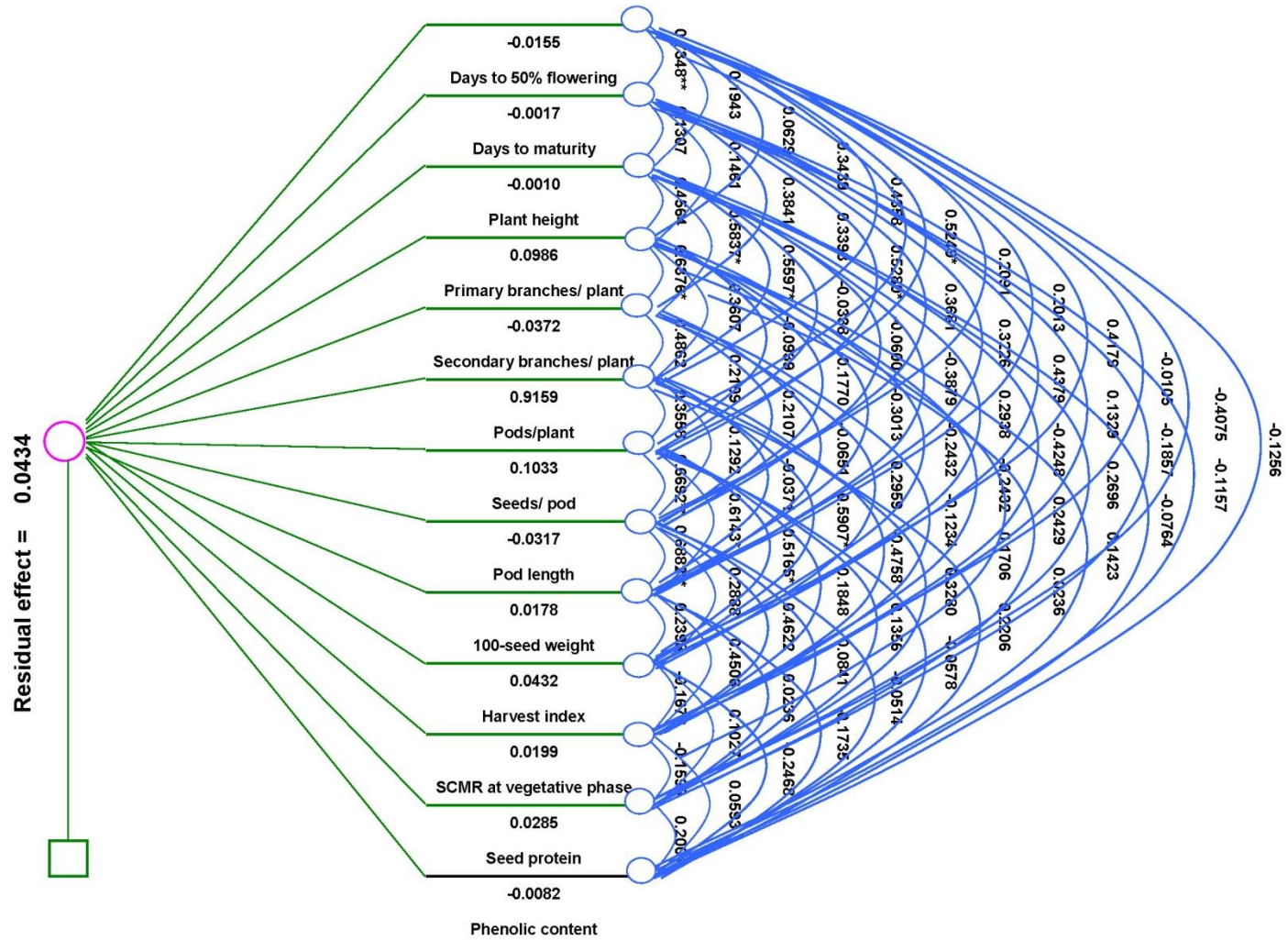


Fig. 4.9: Phenotypic path diagram of seed yield and yield components in crosses of pigeonpea

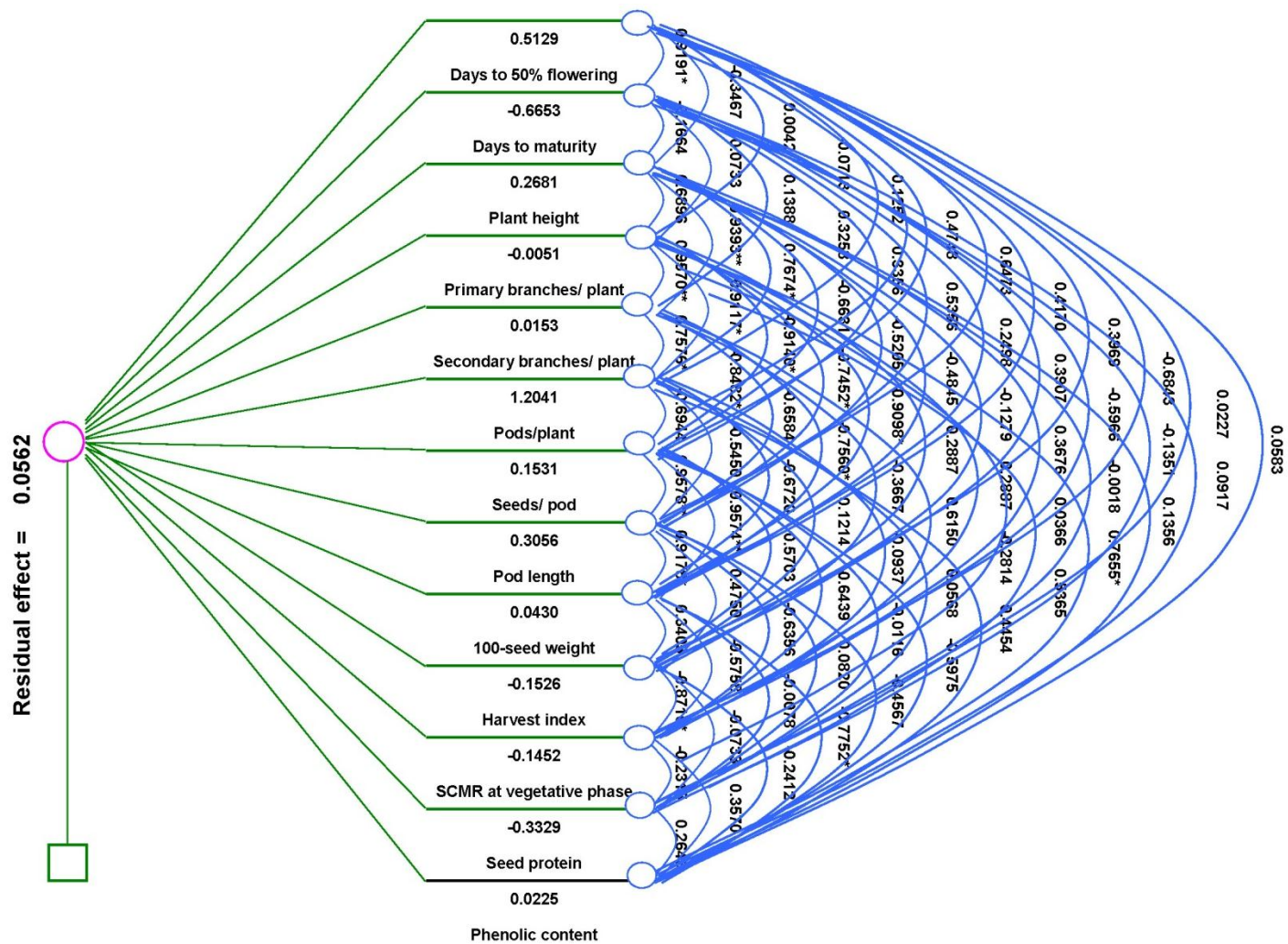


Fig. 4.10: Genotypic path diagram of seed yield and yield components in parents of pigeonpea

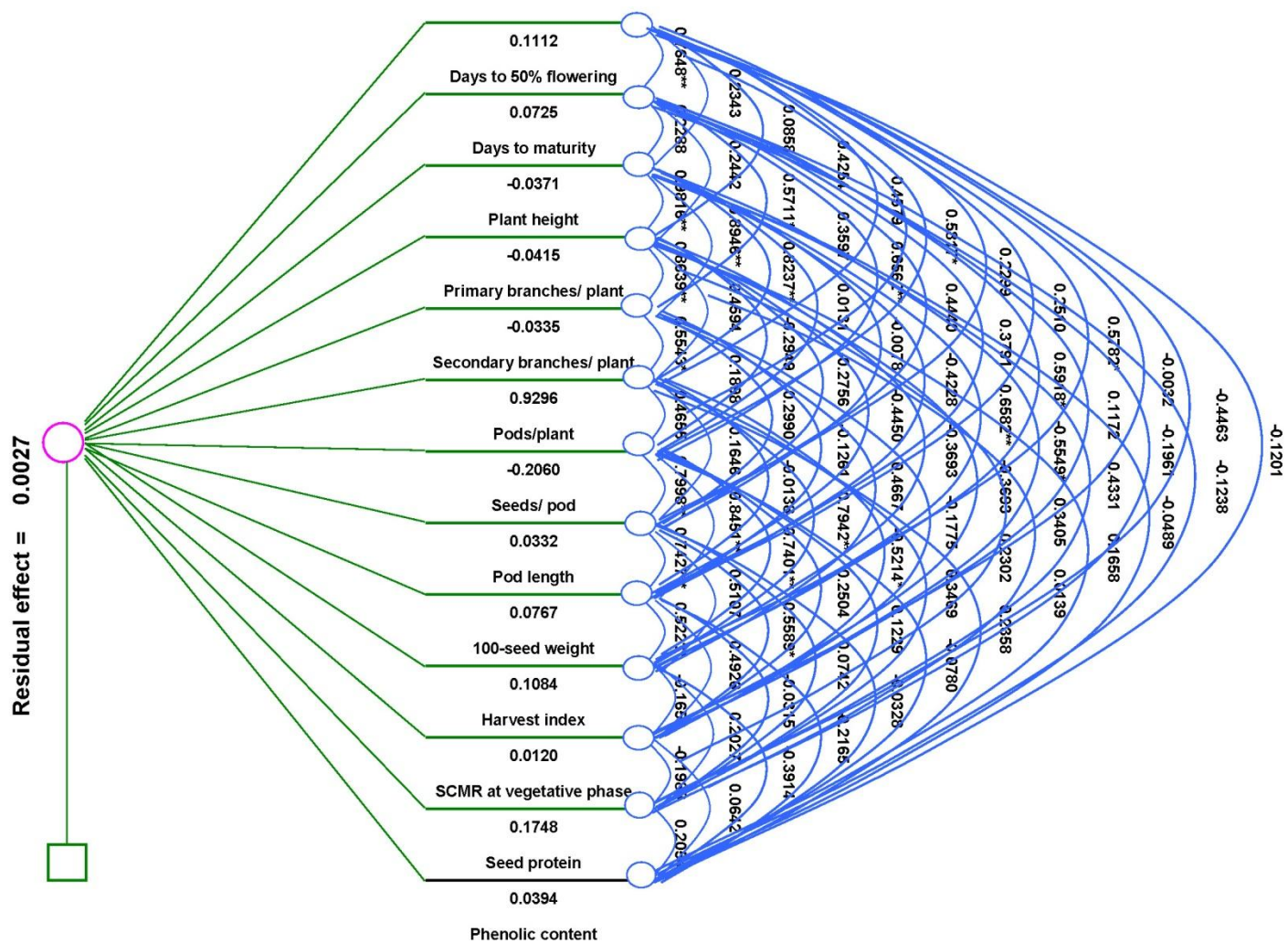


Fig. 4.11: Genotypic path diagram of seed yield and yield components in crosses of pigeonpea

pods per plant (0.3027), seeds per pod (0.0344), pod length (0.1492), 100-seed weight (0.0021), SCMR at vegetative phase (0.067) and seed protein (0.0402) nullified both negative direct and indirect effects and finally resulted in positive association with seed yield (0.3528). In crosses this trait exhibited low negative direct effect on seed yield (-0.0017). But its positive indirect effects via primary branches per plant (0.0144), pods per plant (0.3108), seeds per pod (0.0545), 100-seed weight (0.0057), harvest index (0.0189), SCMR at vegetative phase (0.0026) and phenol content (0.0009) nullified both negative direct effects and indirect effects resulted in positive association with seed yield (0.3635). Negative direct effect of days to maturity on seed yield was supported by Mahajan *et al.* (2007).

Plant height exhibited high direct positive effect on seed yield (0.3058). The low positive indirect effects through days to maturity (0.0262), primary branches per plant (0.0026), secondary branches per plant (0.0107), pods per plant (0.6747), harvest index (0.0075) and seed protein (0.0005) suppressed indirect negative effects and resulted in positive correlation with seed yield (0.6373). In crosses plant height had negligible negative direct effect on seed yield (-0.001). The indirect positive effects via primary branches per plant (0.045), pods per plant (0.5126), pod length (0.0019), harvest index (0.0127), seed protein (0.0077) and phenol content (0.0006) suppressed negative direct and indirect effects and resulted in positive significant association with seed yield (0.5357*). The positive direct effect on seed yield in parents was in conformity with the results of Srinivas *et al.* (1999), Chattopadhyay and Dhiman (2005) and Baskaran and Muthiah (2007) and its negative direct effect on seed yield in crosses was supported by Asawa *et al.* (1981).

In parents, primary branches per plant had low positive direct effect on seed yield (0.0044). The indirect positive effects via plant height (0.1777), secondary branches per plant (0.0107), pods per plant (0.815) and

harvest index (0.0052) suppressed negative indirect effects and resulted in positive correlation with seed yield (0.6373). In crosses, primary branches per plant showed positive direct effect on seed yield (0.0986). Its positive indirect effects via pods per plant (0.3304), pod length (0.0056), harvest index (0.0066) and seed protein (0.0069) nullified negative indirect effects and resulted in high positive correlation with seed yield (0.4017). Its positive direct effect on seed yield was also reported earlier by Bhadru (2010).

In parents, secondary branches per plant had low positive direct effect on seed yield (0.0169). Its positive indirect effects via plant height (0.1934), primary branches per plant (0.0028), pods per plant (0.7424), harvest index (0.032) and seed protein (0.0669) nullified indirect negative effects and resulted high positive correlation with seed yield (0.6379). In crosses, it had negative direct effect on seed yield (-0.0372). Its positive indirect effects via pods per plant (0.4453), primary branches per plant 0.0628), seeds per pod (0.0218), harvest index (0.0128) and seed protein (0.0049) suppressed negative direct and indirect effects and produced high positive correlation with seed yield (0.4933). Its positive direct effect on seed yield in parents was supported by Srinivas *et al.* (1999) and Bhadru (2010) and its negative direct effect in crosses was reported earlier by Paul *et al.* (1996) and Anuradha *et al.* (2007).

In parents, pods per plant had high positive direct effect on seed yield (1.1277). It also exerted positive indirect effects via days to flowering (0.0296), plant height (0.1829), primary branches per plant (0.0032), secondary branches per plant (0.0112) and SCMR at vegetative phase (0.0121). These positive direct and indirect effects were high enough to nullify negative indirect effects and resulted in significant positive correlation with seed yield (0.9163). In crosses, the direct effect of this trait on seed yield was high and positive (0.9159). Its positive indirect effects via

primary branches per plant (0.0356), seeds per pod (0.0367), harvest index (0.0255) and seed protein (0.0094) nullified the negative indirect effects and resulted in highly significant positive correlation with seed yield (0.9811*). The high positive direct effect on seed yield in parents and crosses was also reported by Balakrishnan and Natarajaratnam (1989), Natarajan *et al.* (1990), Paul *et al.* (1996), Chandirakala and Raveendran (1998), Mittal *et al.* (2006), Jogendra Singh *et al.* (2008) and Sawant *et al.* (2009).

In parents, seeds per pod exhibited positive direct effect on seed yield (0.1319). However, its negative effects via days to maturity (-0.1497), plant height (-0.1765), primary branches per plant (-0.0027), secondary branches per plant (-0.0109), pods per plant (-0.6886) and harvest index (-0.0738) suppressed positive direct and indirect effects and resulted high negative correlation with seed yield (-0.4052). In crosses, it had positive direct effect on seed yield (0.1033). Its positive indirect effects via pods per plant (0.3259), 100-seed weight (0.0109), harvest index (0.0223), SCMR at vegetative phase (0.0037), seed protein (0.0039) and phenol content (0.0005) nullified negative indirect effects and finally resulted in high positive association with seed yield (0.4231). Its positive direct effect on seed yield in parents and crosses was earlier reported by Satpute (1994), Salunke *et al.* (1995), Kingshlin and Subbaraman (1997), Musaana and Nahdy (1998), Chattopadhyay and Dhiman (2005) and Mittal *et al.* (2006).

In parents, pod length had high positive direct effect on seed yield (0.3179). Its negative indirect effects via days to maturity (-0.2691), plant height (-0.1562), primary branches per plant (-0.0026), secondary branches per plant (-0.0085), pods per plant (-0.5814), harvest index (-0.0658) and seed protein (-0.0173) suppressed the positive direct and indirect effects and resulted high negative correlation with seed yield (-0.3136). In crosses, it showed negative direct effect (-0.0317). However, its positive indirect effects via pods per plant (0.1183), seeds per pod (0.0691), 100-seed weight

(0.0122), harvest index (0.0125), SCMR at vegetative phase (0.0092), seed protein (0.0024), phenol content (0.0004) and plant height (0.0001) suppressed the negative direct and indirect effects and finally resulted positive correlation with seed yield (0.1634). These results were in confirmity with the findings of Kingshlin and Subbaraman (1997), Sodavadiya *et al.* (2009) and Mahajan *et al.* (2007) for its positive direct effect in parents and Anuradha *et al.* (2007) for its negative direct effect on seed yield in crosses.

In parents, direct effect of 100-seed weight on seed yield was very low and positive (0.0089). It had negative indirect effect via days to maturity (-0.1333), plant height (-0.1107), primary branches per plant (-0.0028), secondary branches per plant (-0.0081), pods per plant (-0.6634) and harvest index (-0.0515). In crosses, it exerted positive direct effect on seed yield (0.178). Its positive indirect effects through plant height (0.0004), secondary branches per plant (0.0024), seeds per pod (0.0634), harvest index (0.0104), SCMR at vegetative phase (0.009), seed protein (0.0007) and phenol content (0.0014) suppressed negative indirect effects and resulted in low positive correlation with seed yield (0.0163). Positive direct effect of this trait on seed yield was in confirmity with the results of Dumbre *et al.* (1985), Salunke *et al.* (1995), Paul *et al.* (1996), Kingshlin and Subbaraman (1997), Musaana and Nahdy (1998), Chandirakala and Raveendran (1998), Baskaran and Muthiah (2007), Jogendra Singh *et al.* (2008) and Sodavadiya *et al.* (2009).

In parents, harvest index exerted negative direct effect on seed yield (-0.1480). Its positive indirect effects through days to flowering (0.1601), pods per plant (0.1672), seeds per pod (0.0658), pod length (0.1414), 100-seed weight (0.0031), SCMR at vegetative phase (0.0949), seed protein (0.0241) and phenol content (0.004) suppressed negative direct and indirect effects and finally resulted in positive correlation with seed yield (0.2809).

In crosses, direct effect of this character on seed yield was positive and low (0.0432). It also exerted positive indirect effects through primary branches per plant (0.0151), pods per plant (0.5410), seeds per pod (0.0533), 100-seed weight (0.0043), seed protein (0.0029) and phenol content (0.002). These positive direct and indirect effects were high enough to nullify the negative indirect effects and resulted in significant positive correlation with seed yield (0.6309*). The positive direct effect of harvest index on seed yield in crosses was supported by Marekar and Nerkar (1987), Balakrishnan and Natarajaratnam (1989), Jogendra Singh *et al.* (2008) and Anuradha *et al.* (2007).

In parents, SCMR at vegetative phase exerted negative direct effect on seed yield (-0.1387). Its correlation on yield was negative (-0.1927) indicating the existence of negative indirect effects through days to flowering (-0.2222), pods per plant (-0.0984), seeds per pod (-0.0741), pod length (-0.1746), 100-seed weight (-0.0035) and phenol content (-0.0049). In crosses, it had positive direct effect on seed yield (0.0199). But its negative indirect effects via days to maturity (-0.0002), primary branches per plant (-0.024), pods per plant (-0.4358), pod length (-0.0147), harvest index (-0.0072), seed protein (-0.0046) and phenol content (-0.0005) suppressed positive direct and indirect effects and finally resulted in negative correlation with seed yield (-0.4347). These results were coinciding with the reports of Krishna Chaithanya (2010).

4.7.2 Direct and indirect effects of quality attributes

In parents, direct effect of seed protein on seed yield was negative (-0.2818). Its correlation on seed yield was also negative (-0.0730) indicating the existence of negative indirect effects via plant height (-0.0005), secondary branches per plant (-0.0040), seeds per pod (-0.0023), 100-seed weight (-0.0002) and phenol content (-0.0046). In crosses, it exerted positive direct effect on seed yield (0.0285). Its positive indirect

effects via days to flowering (0.0063), days to maturity (0.0003), primary branches per plant (0.0239), pods per plant (0.3005), seeds per pod (0.0140), 100-seed weight (0.0004) and harvest index (0.0044) suppressed negative indirect effects and resulted in positive correlation with seed yield (0.3643). The negative direct effect of seed protein on seed yield was supported by Bharadwaj and Gupta (2004) and Anuradha *et al.* (2007).

In parents, phenol content showed negative direct effect on seed yield (-0.0176). But its positive indirect effects on seed yield via days to flowering (0.0267), plant height (0.0242), primary branches per plant (0.0028), secondary branches per plant (0.0062), pods per plant (0.4581) and harvest index (0.0337) nullify the negative direct and indirect effects and finally resulted in positive correlation with seed yield (0.1679). In crosses, it had negative direct effect on seed yield (-0.0082). But its positive indirect effects via pods per plant (0.2021), primary branches per plant (0.0140), days to flowering (0.0020), days to maturity (0.0002), pod length (0.0016), SCMR at vegetative phase (0.0012), seed protein (0.0057) and plant height (0.0001) suppressed negative direct and indirect effects and finally produced positive correlation on seed yield (0.1981). These results were coinciding with the findings of Rekha (2009).

From the path analysis, it was suggested that high direct effect of pods per plant was appeared to be the main factor for its strong positive correlation with seed yield in parents and crosses. Hence, a direct selection for pods per plant would be effective. Similarly, days to flowering, pod length and plant height also exerted high direct effects on seed yield followed by seeds per pod, secondary branches per plant, and 100-seed weight in parents in the decreasing order. Though seeds per pod, pod length and 100-seed weight had positive direct effects, they recorded negative correlation with seed yield. This may be attributed to the direct effects of these characters on seed yield were neutralized by their indirect effects

mainly via pods per plant, days to maturity and plant height in parents. Whereas in crosses, seeds per pod, primary branches per plant, harvest index, seed protein, SCMR at vegetative phase and 100-seed weight exhibited positive direct effect and positive association on seed yield except SCMR at vegetative phase, which had negative association with seed yield due to its high negative indirect effect via pods per plant.

In parents, the character days to maturity followed by harvest index and phenol content had negative direct influence on seed yield but they had significant positive association with seed yield. In crosses, similar results were observed for secondary branches per plant, pod length, days to flowering, phenol content, days to maturity and plant height. This may be due to their high positive indirect contribution via pod per plant. Hence, the indirect effects of most of the characters were found positive and high via pods per plant both in parents and crosses.

The genotypic residual effect was 0.0757 in parents and 0.0434 in crosses, while phenotypic residual effects were 0.0562 and 0.0027 in parents and crosses, respectively. Here, the residual effects observed were very low, indicating that the characters not included in the present study exert insignificant effect on seed yield. It is assumed that the causal system visualized in path taken into account factors involved in determining the end product. Since, the determination of such product is very complex, it is not obviously possible to have a complete path diagram. This warrants the inclusion of residual path in the analysis.

Chapter ~ V

Summary and Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled "Heterosis and combining ability analysis in pigeonpea (*Cajanus cajan* (L.) Millsp.)" was undertaken to study the nature and magnitude of gene action, combining ability of parents and hybrids, extent of heterosis, variability, heritability and genetic advance as per cent of mean, correlation between yield and different yield components and direct and indirect effects of yield contributing traits on grain yield. The experiment was carried out in Randomized Block Design with three replications during *Kharif*, 2010 with five lines viz., ICPL-6974, ICPL-15225, ICPL-7035, ICPL-2376 and LRG-41, three testers with resistance to *Fusarium* wilt viz., ICPL-87119, ICPL-8863 and PRG-158 and their fifteen F₁'s of pigeonpea obtained by L x T mating design along with a standard check (LRG-30) at RARS, Tirupati, Andhra Pradesh. Data was collected on 14 characters viz., days to flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, pod length, 100-seed weight, harvest index, SCMR at vegetative phase, seed protein, phenol content and seed yield per plant.

An overall view of mean performance of parents revealed that no single genotype was superior in respect of all the traits studied. However among the lines, ICPL-6974 and ICPL-2376 were the best for earliness, while ICPL-7035 was best for seeds per pod, pod length and 100-seed weight and the line LRG-41 was superior for primary branches per plant, secondary branches per plant, pods per plant, plant height, phenol content and seed yield per plant. Among the testers, ICPL-87119 emerged as the best for primary branches per plant, secondary branches per plant, pods per plant and seed yield per plant, while ICPL-8863 for earliness, plant height, which can be suggested for their utilization in further breeding programmes.

The genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were high for primary branches per plant, secondary branches per plant, pods per plant and seed yield per plant both in parents and crosses. Heritability (broad sense) estimates were high for all the characters except plant height, primary branches per plant and harvest index both in parents and crosses. Genetic advance as per cent of mean was high for primary branches per plant, secondary branches per plant, pods per plant, 100-seed weight and seed yield per plant in both parents and crosses. High GCV and PCV, heritability and genetic advance as per cent mean were observed for the characters secondary branches per plant, pods per plant and seed yield per plant both in parents and crosses, indicating these characters are under the control of additive genetic variance. Hence, simple directional selection could be effective for improving these characters.

The analysis of variance revealed considerable genotypic variation among the parents and hybrids for all the characters. The magnitude of heterosis expressed by the hybrids for 14 characters varied among themselves. The magnitude of standard heterosis was high for days to maturity, days to flowering, 100-seed weight, seed protein, phenol content and harvest index, whereas for plant height and SCMR at vegetative phase it was very low. Out of fifteen crosses, the crosses viz., ICPL-15225 x ICPL-8863, LRG-41 x ICPL-8863, LRG-41 x PRG-158, LRG-41 x ICPL-87119, ICPL-7035 x ICPL-8863 had recorded significant and maximum heterosis for most of the characters.

Heterosis studies suggested that higher significant heterosis was contributed through all the characters except plant height and SCMR at vegetative phase in LRG-41 x ICPL-8863 and LRG-41 x ICPL-87119, through all the traits except plant height, secondary branches per plant and SCMR at vegetative phase in ICPL-15225 x ICPL-8863, through all the traits except days to flowering, plant height and SCMR at vegetative phase

in LRG-41 x PRG-158, through days to flowering, days to maturity, seeds per pod, pod length, 100-seed weight, harvest index, SCMR at vegetative phase, seed protein and phenol content in ICPL-7035 x ICPL-8863. Hence, significant positive heterosis observed for seed yield per plant was mainly due to the manifestation of heterosis for its component characters viz., days to maturity, pods per plant, seeds per pod, pod length, 100-seed weight, harvest index, seed protein and phenol content. This would clearly indicate that heterosis for seed yield was through heterosis for individual component characters.

The analysis of variance for combining ability revealed that presence of considerable variability for majority of characters among the lines than in testers and substantial variability for most of characters among hybrids. High significant variances due to line x tester interaction component indicated differential behaviour of lines with testers across the characters.

Predominance of non-additive gene action for all the characters was noticed from the ratio of *gca* / *sca* variance suggesting good scope for heterotic breeding and the ratio of variance due to additive and dominance components indicated the predominance of dominant gene action in the genetic control of all the characters except plant height and primary branches per plant studied.

The proportional contribution of lines, testers and line x tester interaction towards total variation in hybrids indicated the contribution of lines towards total variation was maximum in respect of all the characters except seed protein and phenol content, which were contributed highly by the line x tester interaction.

Based on *per se* performance and *gca* effects, the parents LRG-41 and ICPL-15225 were found to be good general combiners for seed yield per plant, harvest index and pods per plant; ICPL-2376 and ICPL-8863 for seed

protein, phenol content and earliness; ICPL-7035 for 100-seed weight and SCMR at vegetative phase; LRG-41 for plant height and pod length. Based on *sca* effects, *per se* performance and heterosis, the crosses *viz.*, ICPL-15225 x ICPL-8863, ICPL-15225 x ICPL-87119 and LRG-41 x PRG-158 were identified as the best specific crosses for hybrid breeding programme, while the crosses ICPL-15225 x PRG-158 and LRG-41 x ICPL-8863 were identified for advancing through recombination breeding programme.

Character association studies revealed that selection based on pods per plant in parents, while plant height, pods per plant and harvest index in crosses will be effective for selection in improvement of seed yield as they show significant positive correlation with seed yield per plant. In parents, inter-se association between days to flowering and days to maturity; seeds per pod, pod length and 100-seed weight was significant positive among themselves in both the parents and crosses, whereas the association between character pairs *viz.*, pods per plant with plant height, secondary branches per plant with plant height and primary branches per plant, seeds per pod with days to flowering and days to maturity, harvest index with pods per plant and seeds per pod was positive non-significant in parents become significant positive in crosses and the association of seeds per pod, pod length, 100-seed weight and seed protein with seed yield per plant was negative in parents become positive in crosses may be due to new re-combinations. Thus simultaneous selection for these traits brings about considerable improvement in seed yield.

Path coefficient analysis indicated a direct selection for pods per plant would be effective due to high positive direct effect on seed yield. In parents, though seeds per pod, pod length and 100-seed weight had positive direct effects, they recorded negative correlation with seed yield which may be due to indirect effects mainly via pods per plant, days to maturity and plant height in parents. Whereas in crosses, seeds per pod, primary branches

per plant, harvest index, seed protein, SCMR at vegetative phase and 100-seed weight exhibited positive direct effect and positive association on seed yield except SCMR at vegetative phase, which had negative association with seed yield due to its high negative indirect effect via pods per plant. Hence the direct and indirect effects of pods per plant on seed yield indicated that the selection for pods per plant will be effective in improvement of seed yield.

Based on these studies, it was suggested that inter-mating of superior segregants in future generation followed by recurrent selection or multiple crossing in a judicious approach to harness both additive and non-additive kinds of gene effects in the present set of biological material. The transgressive segregants produced as a result of this will lead to the development of desirable high yielding genotypes of pigeonpea.

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HETEROSIS AND COMBINING ABILITY ANALYSIS IN PIGEONPEA
(*Cajanus cajan* (L.) Millsp.)
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ABSTRACT

The evaluation of combining ability and heterosis in a study involving eight parents and 15 F₁ hybrids of pigeonpea revealed that the lines ICPL-15225 and LRG-41, the testers ICPL-8863 and ICPL-87119 and among the crosses, ICPL-15225 X ICPL-8863, ICPL- 15225 X ICPL-87119 and LRG-41 X PRG-158 showed high mean performance for seed yield. Analysis of genetic parameters revealed higher phenotypic and genotypic coefficient of variation, heritability, genetic advance as per cent of mean for pods per plant, 100-seed weight, harvest index, phenol content, seed yield per plant, primary and secondary branches per plant in parents and for pods per plant and seed yield per plant in crosses indicating that simple selection could be practiced for improving these characters.

The expression of heterosis was most evident for pods per plant, seed yield per plant, phenol content, days to flowering, days to maturity, harvest index, seed protein and SCMR at vegetative phase. Significant heterosis, heterobeltiosis, standard heterosis were recorded in the crosses viz., ICPL-15225 X ICPL-8863, LRG-41 X PRG-158, LRG-41 X ICPL-8863, LRG-41 X ICPL-87119 and ICPL-15225 X ICPL-87119 for most of the characters. The parents LRG-41 and ICPL-15225 were found to be good general combiners for harvest index, pods per plant and seed yield per plant, ICPL-2376 and ICPL-8863 for seed protein, phenol content and earliness, ICPL-7035 for seeds per pod, pod length, 100-seed weight and SCMR at vegetative phase, LRG-41 for plant height and branches per plant. Based on *sca* effects, *per se* performance, heterosis, ICPL-15225 X ICPL-8863, ICPL-15225 X ICPL-87119 and LRG-41 X PRG-158 were identified as the best specific crosses for hybrid breeding programme, while the crosses ICPL-15225 X PRG-158 and LRG-41 X ICPL-8863 were identified for advancing through recombination breeding programme.

Character association studies indicated that the character pods per plant had significant positive correlation with seed yield per plant and also inter-correlations were observed among seeds per pod, pod length and 100-seed weight. Path coefficient analysis revealed the high positive direct influence of pods per plant on seed yield and it also had positive indirect effects on seed yield via all the characters except 100-seed weight and SCMR at vegetative phase in both parents and crosses. Hence, selection for pods per plant is suggested for the improvement of seed yield per plant in pigeonpea.