

**COMBINING ABILITY AND
HETEROSIS STUDIES IN CGMS
BASED HYBRIDS OF PIGEONPEA
(*Cajanus cajan* (L.) Millsp)**

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B.Sc. (Ag.)

**MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)**



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PIGEONPEA (*Cajanus cajan* (L.) Millsp)**

**BY
PULINDALA SYAMALA
B.Sc. (Ag.)**

**THESIS SUBMITTED TO THE
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2017

DECLARATION

I, **Miss. P. SYAMALA**, hereby declare that the thesis entitled **“COMBINING ABILITY AND HETEROSIS STUDIES IN CGMS BASED HYBRIDS OF PIGEONPEA (*Cajanus cajan* (L.) Millsp)”** submitted to the **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.

Place: TIRUPATI

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TAM/2015-030

Date:

CERTIFICATE

This is to certify that **Miss. P. SYAMALA** has satisfactorily prosecuted the course of research and that thesis entitled “**COMBINING ABILITY AND HETEROSIS STUDIES IN CGMS BASED HYBRIDS OF 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.

Date:

(Dr. N.V. NAIDU)
Chairperson

CERTIFICATE

This is to certify that the thesis entitled “**COMBINING ABILITY AND HETEROSIS STUDIES IN CGMS BASED HYBRIDS OF PIGEONPEA (*Cajanus cajan* (L.) Millsp).**” submitted in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the Acharya N.G. Ranga Agricultural University, Guntur is a record of the bonafide original research work carried out by **Miss. P. SYAMALA** under our guidance and supervision.

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

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LIST OF SYMBOLS AND ABBREVIATIONS

\bar{X}	: Grand Mean
%	: Per cent
μg	: Microgram
ANOVA	: Analysis of Variances
CD	: Critical Differences
cm	: Centimetre
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 percent of Mean
<i>gca</i>	: General combining ability
GCV	: Genotypic Co-efficient of variation
H	: Heritability in broad sense
h^2	: Heritability in broad sense
ha	: Hectare
HI	: Harvest Index
HS	: Half-sibs
<i>i.e.</i>	: That is
Kg	: Kilogram
Kg ha^{-1}	: Kilogram per hectares
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	: revolution per minute
mg	: Milligram
S.No.	: Serial Number
<i>sca</i>	: Specific combining ability
SEm	: Standard Error of Mean
<i>viz.,</i>	: Namely
σ^2	: Variance

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ABSTRACT

The present investigation comprising of nine parents of pigeonpea (*Cajanus cajan* (L.) Millsp.) and 20 cross combinations developed through Line X Tester (5 X 4) crossing programme were evaluated for genetic parameters, heterosis, combining ability, character association and path coefficient analysis during *kharif*, 2016. The experiment was laid out in Randomized Block Design with three replications at the International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Hyderabad and observations were recorded on 11 characters.

Analysis of variance indicated the existence of significant differences among the genotypes for all the characters. Among the parents, the lines ICPB-2047 and ICPB-2048, the testers ICPL-87119 and ICPL-20123 and among the crosses, ICPA-2092 x ICPL-20108, ICPA-2092 X ICPL-87119 and ICPA-2047 X ICPL-20108 showed high mean performance for secondary branches per plant, pods per plant, harvest index and seed yield per plant in parents and crosses indicating that simple selection may be practiced for improving these characters.

The magnitude of standard heterosis was high for secondary branches per plant, pods per plant, harvest index and seed yield per plant, whereas for seeds per pod and days to 75% maturity it was very low. Out of 20 crosses, the crosses *viz.*, ICPA-2092 x ICPL-20108, ICPA-2047 x ICPL-20108, ICPA-2047

x ICPL-20116 and ICPA-2047 x ICPL-20123 had recorded significant and maximum heterosis 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, ICPB-2078 and ICPB-2043 were the best general combiners for days to 50% flowering and days to 75% maturity, while ICPB-2047 for plant height, primary branches per plant, secondary branches per plant, seeds per pod, harvest index and seed yield per plant. ICPB-2092, ICPB-2078 and ICPB-20123 were the promising parents for pods per plant, 100-seed weight and seed protein. Based on *sca* effects, *per se* performance and heterosis, the crosses *viz.*, ICPA-2092 x ICPL-87119 and ICPA-2092 x ICPL-20116 were identified as the best specific crosses for hybrid breeding programme while the crosses ICPA-2092 x ICPL-20123, ICPA-2048 x ICPL-20116, ICPA-2078 x ICPL-20108, ICPA-2043 x ICPL-87119, ICPA-2048 x ICPL-20108, ICPA-2092 x ICPL-20116, ICPA-2092 x ICPL-87119, ICPA-2078 x ICPL-87119, ICPA-2047 x ICPL-87119, ICPA-2043 x ICPL-20108 and ICPA-2047 x ICPL-20123 were identified for advancing through recombination breeding programme.

Character association studies revealed that selection based on all the characters except secondary branches per plant, seed protein, 100-seed weight in parents and seed protein, 100-seed weight in crosses will be effective for selection in improvement of seed yield as they had significant and positive correlation with seed yield per plant. Path analysis revealed high positive direct influence of pods per plant on seed yield and it also had positive indirect effects on seed yield *via* most of the characters in both parents and crosses. Hence, selection for pods per plant alone can be 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 groundnut, sorghum, maize, pearl millet, mungbean, soybean, cotton, castor etc.

Pigeonpea is the second most important pulse crops in India after Chickpea. India accounts for 91% of the world's Pigeonpea production and has the privilege of occupying the first place both in area and production globally among *kharif* grown legumes. India occupies first place in the world with an area of 3.82 M ha with a production of 2.78 Mt and productivity of 727 kg/ha (FAO, 2014-15). It is grown extensively in states like Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Utter Pradesh, Gujarat, and Orissa. In Andhra Pradesh, it is cultivated in an area of 3.71 M ha with a production of 1.65 Mt and with productivity of 445 kg/ha (FAO STAT).

Pigeonpea varietal improvement program started in India in 1931 with selection from landraces for traits such as seed size, *fusarium* wilt, plant type and yield (Ramanujam and Singh, 1981). During this period over 100 pigeonpea cultivars have been released in India (Singh *et. al.*, 2006), but the crop productivity remained stagnant. This is a matter of concern in view of increasing population and reducing per capita availability of protein that led to

malnutrition among growing children and women, in particular. Considering the above mentioned constraints, new scientific approaches and tools are needed to raise the productivity of this important pulse crop. In this context, CMS-based hybrid technology was developed and the world's first pigeonpea commercial hybrid namely ICPH 2671 was released, with 46% yield advantage in farmer's field (Saxena *et. al.*, 2013). This is considered a milestone in the history of pulse breeding so far. In order to popularize hybrids, it is necessary that new high yielding hybrids are bred for different climatic conditions.

Selecting parents based on their *per se* performance may not always lead to fruitful results (Allard, 1960). Hence, parents selected based on combining ability studies would throw up more desirable segregants and understanding the magnitude of gene action involved in the inheritance of quantitative characters of economic importance. 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 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 was made to understand the genetic nature of yield and yield components through studies involving five lines and four testers in Line x Tester mating design.

Seed yield is a complex quantitative character, which is subjected to the environmental fluctuations and largely dependent on various components. Knowledge on genotypic and phenotypic correlations among yield components and their relationship with yield will be useful in selecting superior genotypes. Path coefficient analysis permits separation of correlation coefficient into components of direct and indirect effects (Dewey and 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.

Keeping in view the above perspectives, the present research workon was formulated with the following objectives:

1. To estimate the variability parameters for seed yield and yield contributing characters among the parental genotypes.
2. To identify the superior parents and crosses by combining ability analysis using L x T mating design.
3. To study the nature of gene action and magnitude of heterosis for seed yield and yield attributing characters.
4. To estimate the relationship among the yield contributing characters and with seed yield in hybrids.
5. To identify the character(s), which are directly or indirectly influence seed yield in hybrids.

Chapter – II

Review of Literature

Chapter - II

REVIEW OF LITERATURE

An attempt was made to critically review the literature of past research work documented 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. 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, viability, heritability and genetic advance had an immense value in identifying the superior genotypes.

A brief review of literature on genetic parameters is furnished here under:

Bainiwal and Jatasra (1981) studied the nature of genetic variability using 29 genotypes of pigeonpea and noticed that maximum variability 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 100 genotypes of pigeonpea and reported that the range for phenotypic variability was high for all the characters except seeds per pod. 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 environments.

Balyan and Sudhakar (1985), in their study on 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 per cent of mean suggesting predominance of additive gene effects for the characters.

Jagshoran (1985) observed that the characters days to 50% flowering, days to maturity, plant height, 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 pods per plant while it was lowest for seeds per pod.

Bhongale and Raut (1987) screened 80 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% flowering, days to maturity and 100-seed weight had high heritability coupled with high genetic advance.

Konwar and Hozarika (1988) studied 16 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 high amount of genotypic coefficient of variation for branches per plant followed by pods per plant, plant height, seed yield per plant and seeds per pod, while low estimates were observed for days to 50% flowering and days to maturity and high heritability and genetic advance for plant height and 100-seed weight.

Natarajan *et al.* (1990) noticed the highest genotypic coefficient of variation for pods followed by 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% flowering, days to maturity and 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% flowering and days to maturity. High heritability and high genetic advance was observed for days to 50% flowering, 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 plant height, pods per plant, seeds per pod, seed yield per plant and harvest index had high genotypic and phenotypic coefficients of variation, while low estimates of genotypic coefficient of variation were recorded for shelling per cent and seeds per pod.

Ghodke *et al.* (1994) evaluated 10 genotypes under three cropping systems for deciding the selection criteria and noticed that high heritability for pods per plant, days to 50% flowering and days to maturity and high genetic advance as per cent of mean for secondary branches and pods.

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

Aher *et al.* (1998) reported high magnitude of variability for secondary branches per plant followed by seed yield per plant, days to 50% 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 primary and secondary branches per plant, followed by seed yield per plant, days to 50% 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 clusters per plant, pods per plant, plant height, primary branches per plant and seed yield in all hybrids.

Takalkar *et al.* (1998) observed maximum variability for 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 pods per plant, plant height, straw yield per plant and days to maturity and low genetic advance was observed for branches per plant, 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, 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% flowering.

Srinivas *et al.* (1999) carried out studies in a line x tester set with two male sterile lines and 11 pollen parents. They noticed that genetic variability was highest for pods per plant and lowest for seeds per pod, high heritability for all the characters 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 for characters plant height, pods per plant and plant spread.

Venkateswarlu (2001) observed the maximum variability for pods per plant followed by 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 yield per plant.

Magar (2003) reported that genotypic and phenotypic coefficients of variation were highest for pods per plant, plant spread, seed yield per plant and primary branches per plant and high heritability and genetic advance was observed for pods per plant and seeds per pod.

Gohil (2006) studied 39 genotypes of pigeonpea for 13 characters related to yield and yield contributing characters and noticed high phenotypic coefficients of variation were observed for grain yield per plant, plant height, branches per plant, clusters per plant, pods per plant, pods per cluster and harvest index. Grain yield per plant, days to 50% flowering, days to maturity, clusters per plant, pods per plant, pods per cluster and harvest index showed high heritability. Considering high genetic advance, percentage of mean was found for grain yield per plant, clusters per plant, pods per plant and harvest index.

Firoz Mahamad *et al.* (2006) studied 49 genotypes of vegetable pigeonpea that high amount of PCV and GCV for branches for per plant, pods per plant, green pod yield and green seed yield per plant. High heritability coupled with high genetic advance was observed for plant height, branches per plant, pods per plant and 100-seed weight.

Anantharaju and Muthiah (2008) reported low amount of PCV and GCV for days to 50% 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, seeds per pod and 100-seed weight.

Kalaimagal *et al.* (2008) reported high genotypic and phenotypic coefficients of variation and genetic advance for plant height, clusters and pods

per plant and low variability, moderate heritability and genetic advance were observed for seed yield per plant.

Singh *et al.* (2008) studied seven genotypes and 10 interspecific crosses and reported high PCV and GCV for all the characters except for days to 50% 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% flowering showed high heritability and low genetic advance as per cent of mean.

Dodake *et al.* (2009) studied 21 genotypes and observed that the variability in plant spread, 100-seed weight, days to 50% flowering, days to maturity and seed yield per plant were heritable and additive type of gene action was operative for the characters.

Bhadru (2010) analyzed 27 accessions and recorded moderate to high phenotypic and genotypic coefficient of variation for pods, seed yield per plant, plant height and plant spread. High heritability accompanied with high genetic advance as per cent of mean was observed for pods per plant, primary and secondary branches per plant, test weight, plant height and plant spread.

Patel and Acharya (2011) reported high GCV and PCV for yield per plant, pods per plant and branches per plant. High heritability coupled with moderate to high genetic advance for grain yield per plant, plant height, pods per plant, days to 50% flowering and days to maturity.

Sreelakshmi *et al.* (2011) studied 36 hybrids and three checks of pigeonpea and noted higher value of PCV over GCV for yield and yield related characters. High heritability coupled with high genetic advance as per cent of mean were observed for seed yield, primary branches per plant and secondary branches per plant.

Jaggal *et al.* (2012) evaluated 135 pigeonpea [*Cajanus cajan* (L.) Millsp.] accessions of mini core collection for 14 characters related to yield and noticed high genotypic and phenotypic coefficient of variation, genetic

advance mean and heritability was recorded for harvest index and seed yield. High heritability and genetic advance mean also found in plant height, days to 50% flowering, days to maturity and seed protein.

Nagy *et al.* (2013) studied 45 genotypes of pigeonpea and reported pod clusters per plant had the highest magnitude of GCV and PCV followed by seed yield per plant and pods per plant. High heritability coupled with high genetic advance was recorded for pods per plant, pod clusters per plant, seed yield per plant and 100-seed weight.

Rangare *et al.* (2013) evaluated 27 genotypes of pigeonpea for 13 characters related to yield and noticed high heritability coupled with high genetic advance for days to maturity, days to 50% flowering, plant height, pods per plant, biological yield per plant, seed yield per plant and harvest index.

Prasad *et al.* (2013) studied 11 parents and their 28 hybrids of pigeonpea and reported high magnitude of PCV and GCV was observed for primary and secondary branches per plant, leaf area, pods per plant, harvest index, pollen viability and grain yield. All the characters exhibited low heritability in narrow sense except leaf area and 100-seed weight and low to high genetic advance as per cent of mean.

Saroj *et al.* (2013) evaluated 70 pigeonpea genotypes. Highest GCV was recorded for secondary branches per plant followed by pods per plant. Heritability in broad sense ranged from 61.33 (seeds per pod) to 98.26 (days to 50% flowering). High genetic advance were observed for primary branches per plant, secondary branches per plant, 100-seed weight, grain yield per plant, pods per plant, plant height and days to 50% flowering.

Kumar *et al.* (2014) evaluated 38 genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp] for yield and yield contributing characters. Moderate to high PCV and GCV were recorded for 50% flowering, pods per plant, seed, grain yield and straw yield. High heritability and genetic advance was observed for pods, plant height, test weight, days to maturity and primary and secondary

branches per plants, whereas the characters like days to 50% flowering, test weight, pod length and primary branches showed high heritability along with moderate or low genetic advance.

Ajay *et al.* (2014) evaluated F₂ and F₃ generations from three crosses of pigeonpea namely BRG-1×ICP-8863, TTB-7×ICP-8863 and TTB-7×ICPL87119 for yield and yield contributing characters. High variance, heritability and genetic advance were recorded for secondary branches per plant, pods per plant and seed yield in F₂ and F₃ generations.

Vanisree and Sreedhar (2014) evaluated 482 genotypes of pigeonpea and reported that the characters seed yield per plant, pods per plant, plant height, primary branches and days to 50% flowering showed higher genotypic and phenotypic coefficient of variation. High heritability, high genetic variance and high genetic advance as per cent of mean was recorded for seed yield per plant, pods per plant, plant height, days to 50% flowering and days to maturity.

Lakhote *et al.* (2015) evaluated 24 vegetable type genotypes of pigeonpea and reported high GCV and PCV for plant height, 100 green pod weight, 100 green seed weight, shelling percentage, TSS (per cent), days to 50% flowering, pod length, as well as for primary branches. High heritability and genetic advance was reported for 100 green pod weight and days to 50% flowering.

Pandey *et al.* (2015) reported secondary branches per plant showed highest phenotypic as well as genotypic coefficient of variation followed by seed yield per plant and biological yield. High heritability coupled with high genetic advance as per cent of mean was observed by 100-seed weight, pods per plant, seed yield per plant, biological yield per plant and secondary branches per plant suggesting preponderance of additive gene action in the expression of these characters, while plant height, primary branches per plant, pods per plant, seeds per pod and harvest index showed high heritability with moderate genetic advance as per cent of mean suggesting greater role of non additive gene action.

Ram *et al.* (2016) reported that phenotypic and genotypic variances, heritability and genetic advances were estimated for yield and yield characters in 30 pigeonpea genotypes. The highest GCV was recorded for secondary branches per plant followed by pods per plant. Heritability in broad sense ranged from 60.31 (seeds per pod) to 96.28 (days to 50% flowering). High genetic advance were observed for primary branches per plant indicating the prevalence of additive gene action for inheritance.

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 characters 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 24 hybrids derived from line x tester design and reported the heterosis response upto 221% for seed yield.

Gupta *et al.* (1983) evaluated early maturing pigeonpea hybrids based on genetic male sterility and reported 42% 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 characters 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 60 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 pods per plant, branches per plant and per day productivity.

Mehetre *et al.* (1993) studied the hybrids of 18 pigeonpea varieties and the results showed significant heterosis values over better parent for seed yield (-27.5 to 193.8%). For other characters, 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 60 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, primary branches, pods per plant and seed yield per plant from the study involving 11 parents and 24 hybrids through line x tester mating design.

Manivel *et al.* (1999) in a study of 40 hybrids from a line x tester analysis reported that significant negative heterobeltiosis for days to 50% 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% 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% for seed yield. Out of 36 combinations, 12 registered significant positive heterosis for seed yield per plant, primary and secondary branches per plant, clusters per plant and 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 branches per plant, 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% 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 C05 X ICPL-87119 was considered as the best with maximum heterosis for seed weight and C06 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 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. Maximum heterosis was recorded for pods per plant (52.11%) followed by 100-seed weight, seeds per pod, pods per plant and primary and secondary branches.

Shoba and Balan (2010) studied 27 early maturing hybrids resulting from line x tester analysis and reported significant standard heterosis for plant height, branches per plant, pods per plant, seeds per pod and single plant yield (varied from -25.0% to 325%).

Chandirakala *et al.* (2010) studied the heterosis, heterobeltiosis and standard heterosis in 30 GMS based pigeonpea hybrids. Among these, 13 hybrids exhibited significant and positive heterosis over all the three bases of estimation. The 2 hybrids showed highly significant and positive heterosis over mid parent, better parent and standard check. The proportion of hybrids exhibiting significant heterotic effect for yield with genetic male sterile line MS Prabhat DT was greater as compared to lines, MS Prabhat NDT and MS CO5.

Pandey *et al.* (2013) evaluated 60 hybrids along with their parents and standard check variety (NDA 2) and reported that heterobeltiosis for seed yield per plant was significantly superior of 14 hybrids and 15 hybrids over standard variety. Among all the crosses, NDACMS1-64 x NDA98-6, NDACMS1-6 x NDA5-14, NDACMS1-4 x IPA208, NDACMS1-6 x ICP870 recorded more than 20% standard heterosis for seed yield.

Gite and Madrap (2014) studies revealed that highest values for mid parent heterosis and heterobeltiosis for plant height, primary and secondary branches per plant, pods per plant and 100-seed weight.

Patel and Tikka (2014) reported high heterosis was recorded for grain yield per plant, pods per plant and harvest index, while, medium heterosis for plant height, branches per plant, 100-seed weight, protein content, biological yield and reproductive period. Days to flowering, days to maturity, seeds per pod and pod length recorded low magnitude of heterosis.

Patil *et al.* (2014) recorded highly significant positive heterosis over better parent for seed yield and its component with protein content. The best three hybrids on the basis of heterobeltiosis were GT 102 x ICPL 87119 (33.80%), ICPL 87119 x AGT 2 (25.23%) and BSMR 853 x ICPL 87119 (25.35%).

Ajay *et al.* (2015) observed maximum positive heterosis over mid parent was observed for seed yield per plant (132.88%) and pods per plant (114.53%). In addition to it, maximum heterosis over better parent was observed for pods per plant (96.97%) followed by seed yield per plant (96.11%), and concluded that significant heterosis was observed for branches per plant and pods per plant have resulted in increased yield of hybrids.

Kumar *et al.* (2015) reported that majority of hybrids showed standard heterosis in desirable direction for yield and yield attributing characters over the standard checks (Asha and Maruti).

Mhasal *et al.* (2015) studied 11 genotypes of pigeonpea and found that the cross ICPA-2047A x AKPR-324 depicted high mean performance (33.67) and high magnitude of useful heterosis (17.72% over check PKV-TARA and 23.17% over check Asha). Another cross ICPA-2047A x AKPR-372 also revealed high mean performance (33.00g) and high magnitude of useful heterosis (15.38% over check PKV-TARA and 20.73% over Asha).

Reddy *et al.* (2015) reported that 24 pigeonpea hybrids showed maximum heterosis over mid parent, better parent and standard check were observed for seed yield per plant, followed by secondary branches and pods per plant. High heterosis, more than 100%, over the check, 'Asha' more than 50% over mid parent and more than 30% over better parent, was noticed in the hybrids, 'ICPH 3762' and 'ICPH 3474'.

Singh and Singh (2016) concluded the cross, MAL-17 × NDA 49-6 (266.32%) showed maximum estimates of yield heterosis, also exhibited significant heterosis for days to 50% flowering, primary and secondary branches, pods per plant, pod length and harvest index.

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 characters studied except 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 10 pigeonpea genotypes.

Achamma Oommen *et al.* (1996) reported that primary branches was determined by both additive and non-additive genes, whereas 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 characters.

Pandey (1999) observed genetic variation due to over-dominance and non-additive type of gene action for days to flowering, plant height, 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, branches per plant, plant height, pods per plant, days to maturity, 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 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 pods per plant and non-additive genetic variance for days to flowering, days to maturity, plant height, primary branches per plant, percent pod setting, harvest index and seed yield per plant. Out of the 36 cross combinations, 10 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, secondary branches per plant, clusters per plant, 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 characters, 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, seeds per pod and seed yield per plant, while additive gene action was noticed for days to 50% flowering, 100-seed weight and protein content.

Sunil kumar *et al.* (2003) studied combining ability of 10 genotypes in diallele fashion revealed non-additive gene action for all the characters except days to 50% 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 pods per plant while in testers, good *gca* effects were observed for primary branches per plant and% pod setting from a study involving three genetic male sterile

lines and 12 testers in line x tester design. Out of 36 crosses, 10 crosses showed significant *sca* effects for seed yield per plant, secondary branches per plant, clusters per plant, pods per plant and per cent pod setting.

Sekhar *et al.* (2004) revealed the predominance of non-additive gene action for days to 50% 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.

Banu *et al.* (2007) 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% 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 and noticed significant role of non-additive gene action for all the character except primary branches per plant and phenol content.

Phad *et al.* (2007) reported significant *gca* and *sca* effects for seed yield per plant, plant spread, primary branches per plant, secondary branches per plant and pods per plant from the study of five lines, 12 testers and their hybrids in L x T design.

Yadav *et al.* (2008) carried out an experiment involving 10 diverse parents in diallel fashion and the results revealed that the mean squares due to *gca* and *sca* effects were significant for all characters except seeds per pod. The ratio of *gca* and *sca* genetic variances indicated preponderance of non-additive gene effects for all the characters except days to 50% 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 primary branches per plant, 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 characters 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.

Gupta *et al.* (2011) observed that lines 'CMSGT 33A', 'CMSGT 100A', 'CMSGT 288A', 'CMSGT 301A' and 'CMSGT 311A' among females (A lines); and 'GTR 27' and 'GTR 29' among males (R lines) were good general combiners for seed yield and other one or more characters. 'CMSGT 311A' × 'GTR 29', 'CMSGT 310A' × 'GTR 27', 'CMSGT 288A' × 'GTR 26', 'CMSGT 301A' × 'GTR 27', 'CMSGT 301A' × 'GTR 30' and 'CMSGT 100A' × 'GTR 28' showed desired higher *sca* effects for seed yield per plant, pods per plant, 100-seed weight, water absorption, leaf area index at 100 DAS and rate of photo synthesis at 80 DAS, respectively.

Parmar *et al.* (2012) observed that lines ICPA 2086, ICPA 2089, ICPA 2052, Asha and GT 101 were good general combiners for seed yield and crosses ICPA 2086 x ASHA, ICPA 20 x JKE 114 and GT 33 x JKM 189 showed higher *sca* effect for seed yield per plant.

Meshram *et al.* (2013) noticed predominance of non additive gene action was observed for almost all the characters including seed yield except plant height which was under the influence of additive gene action. None of the parents exhibit significant *gca* effects for all the characters under study.

However, among the lines AKCMS 10A, AKCMS 13A and AKCMS 09A and among the testers AKPR 8, AKPR 359 and AKPR 292 were identified as potential parents as they exhibited significant *gca* effects for most of the important characters.

Yamunura *et al.* (2014) noticed predominance of non-additive gene effects for 10 characters indicating relevance of heterosis breeding for improving yield attributes. The *gca* effects of parents revealed that ICPA-2078, GT-308A, PKV-TATA, ARCCV-2 and GPHR-08-11 were good general combiners for seed yield and its direct components. The estimates of *sca* effects revealed that nine experimental hybrids had significant, desirable and positive *sca* effects for seed yield. The cross combination ICPA-2092 x VIPUL, ICPA-2078 x BSMR-856 and ICPA-2078 x ARCCV-2 were good specific combiners for secondary branches, pods per plant, seed yield per plant.

Patil *et al.* (2015) reported higher magnitude of specific combining ability (*sca*) effect showed that, hybrid yield was under the control of non-additive genes. Among A-lines, ICPA-2204 was the best general combiner. Among testers, ICPL-20116 was the best general combiner. Among hybrids, ICPA-2208 x ICPL-20108 a cross between high general combining ability (*gca*) parents was the best with positive significant *sca* effect and higher mean performance for grain yield, hundred seed mass, seeds per pod and resistance to *fusarium* wilt disease.

Patel and Tikka (2015) observed the specific combining ability (*sca*) variance was found to be more important compared to general combining ability (*gca*) variance for days to flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod, pod length, 100-seed weight, seed yield per plant, protein content, biological yield per plant, harvest index, vegetative period and reproductive period.

Tikle *et al.* (2016) observed the estimates of *gca* effects indicated male parent ICPL-87119 was good general combiner for days to maturity and pollen fertility and among the female parent ICP-2043 was good general combiner.

Cross combinations ICP-2043 x ICP-87119, ICP-2048 x ICP-20108, ICP-2078 x ICP-87119 and ICP-2092 x ICP-20108 were found to be good specific combinations for seed yield plant and other desirable characters.

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 characters 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.

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 pods per plant and pod setting percentage. Among the yield components, 100-seed weight was positively correlated with 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.

Paul and Upadhaya (1991) observed positive correlation of yield per hectare with branches per plant, pods per plant, pods per cluster and yield per plant. The correlation between the 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 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% flowering, days to maturity, plant height, primary branches per plant, pod length, seeds per pod and 100-seed weight were highly correlated.

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% flowering, days to maturity, plant height, plant spread, primary and secondary branches and 100-seed weight were positively associated with each other.

Gumber *et al.* (1996) studied 28 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 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, primary branches, secondary branches and pods per plant.

Basavarajaiah *et al.* (1999) studied 81 genotypes of pigeonpea and 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 characters 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, primary and secondary branches, 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, 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 27 genotypes and their correlation studies indicated that seed yield per plant had significant positive relationship with pods per plant, 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.

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% flowering, plant spread and pods per plant.

Sawant *et al.* (2009) studied 46 genotypes and revealed that the genotypic correlation coefficients were higher than corresponding phenotypic correlations. Seed yield showed significant positive correlation with plant spread, 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. Seed yield per plant had significant and positive association with days to 50% flowering, days to maturity, 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% flowering, plant height, primary and secondary branches per plant, pods per plant and raceme length.

Mittal *et al.* (2010) noted that seed yield was positively associated with plant height, branches per plant, pods per plant and harvest index in pigeonpea genotypes.

Linge *et al.* (2010) found that yield was positively and significantly correlated with all characters except for first primary branch from ground level and seeds per pod in 40 inter specific derivatives of pigeonpea.

Thanki and Sawargaonkar (2010) reported significant and positive correlation of pods per plant and harvest index with seed yield per plant in 28 different genotypes of pigeonpea.

Hamid *et al.* (2011) evaluated 100 germplasm lines of pigeonpea and noted high strong and positive correlation of seed yield with pods per plant followed by pod length.

Patel and Acharya (2011) found that yield was significantly and positively correlated with plant height, branches per plant, pods per plant, pod length, seeds per pod and 100-seed weight in 64 F₆ progenies of pigeonpea.

Rathore and Sharma (2011) found that seed yield per plant was positively correlated with seeds per plant in 25 erect groups whereas, pod clusters per plant, pods per plant and 100-seed weight in 25 semi-spreading groups of pigeonpea.

Devi *et al.* (2012) reported significant positive correlation of seed yield with pods per plant in parents (five lines and three testers) and plant height, pods per plant and harvest index in 15 crosses of pigeonpea.

Udensi and Ikpeme (2012) found that there were significant positive correlations between plant height and leaves per plant, leaf area per plant and seeds per plant, leaves per plant and pod length per plant.

Arbad *et al.* (2013) conducted characters association studies for seed yield and its components in pigeonpea and found that pods, secondary branches per plant, plant height, primary branches per plant showed

significantly positive correlation with seed yield at genotypic and phenotypic levels.

Birhan (2013) reported that seed yield had positive and significant phenotypic and genotypic association with plant height, biomass yield per plant, pods per plant, seeds per plant, days to maturity, days to flowering and seeds per pod.

Nagy *et al.* (2013) conducted association studies in 45 pigeonpea germplasm accessions and found that, seed yield per plant showed the highest significant positive correlation with pods per plant followed by pod cluster per plant, primary branches per plant and pod length.

Prasad *et al.* (2013) found that primary branches per plant, secondary branches per plant, pods per plant, pod bearing zone, harvest index and pollen viability exhibited positive and significant correlation with grain yield in pigeonpea.

Singh *et al.* (2013) showed that the seed yield per plant was found to be significant positively associated with seeds per pod, pod length and plant height at genotypic level in pigeonpea.

Rekha *et al.* (2013) reported strong positive association of seed yield with pods per plant, secondary branches per plant, primary branches per plant and plant height.

Saroj *et al.* (2013) revealed that the days to 50% flowering had significant and strongly positive association with yield per plant, primary branches per plant, pods per plant, days to maturity, 100-seed weight and plant height in both genotypic and phenotypic level.

Kothimbire *et al.* (2015) concluded the correlation analysis for yield per plant recorded highly significant and positive association with days to 50% flowering, days to maturity, plant height, primary branches, secondary branches and pods per plant.

Pandey *et al.* (2016) found that biological yield per plant, pods per plant, 100-seed weight, harvest index and secondary branches per plant showed positive and highly significant correlation with grain yield per plant to emerge as most important associates of seed yield.

2.5 PATH COEFFICIENT ANALYSIS

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 pods per plant, 100-seed weight and plant height. The indirect effects *via* these characters were also positive for all characters 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, primary branches, secondary branches, 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. 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 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 was 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 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 pods per plant and clusters per plant. Branches per plant, pods per plant, clusters per plant, 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 81 pigeon pea 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 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. Selection based on these attributes will be most advantageous in pigeonpea.

Mahajan *et al.* (2007) evaluated nine genotypes, 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 30 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 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% flowering, plant spread, primary and secondary branches per plant, pods and raceme length had moderate to low direct effect on seed yield.

Patel and Acharya (2011) found that pods per plant had the highest positive direct effect on grain yield per plant.

Rathore and Sharma (2011) indicated maximum positive direct effect on seed yield was exhibited by seeds per plant in erect group and days to 50% flowering in semi-spreading group.

Sreelakshmi *et al.* (2011) in their studies on pigeonpea revealed that maximum direct effect on seed yield was exhibited by primary branches per plant, days to 50% flowering and pods per plant.

Devi *et al.* (2012) showed that out of 14 characters, pods per plant, days to flowering, plant height and pod length in parents while pods per plant in crosses showed high positive direct effect on seed yield, indicating that these characters should be given due importance while making selection for increased seed yield in pigeonpea.

Nag and Sharma (2012) found that, pod clusters per plant had the highest direct effect on seed yield whereas, pods per plant and days to maturity had the highest indirect effect on seed yield *via* the characters pods per plant and days to 50% flowering, respectively.

Udensi and Ikpeme (2012) showed that 100-seed weight had the highest positive direct effect on yield. This was followed by the pod length per plant, leaves and leaf area, while plant height had very high negative direct effect.

Arbad *et al.* (2013) reported that, pods, secondary branches per plant, plant height, and primary branches per plant were the most important characters with high direct and positive indirect effect.

Birhan (2013) showed that, days to maturity had the highest positive direct effect on seed yield followed by plant height and seeds per plant whereas, genotypic path analysis revealed that, maximum direct effect on seed yield was exerted by days to flowering and days to maturity followed by seeds per plant and plant height. Thus, seeds per plant and plant height were the potent contributor to seed yield which could be used as indirect selection criteria.

Reddy and Rangare (2013) noticed from their path analysis of 27 genotypes of pigeonpea that harvest index had high positive direct effect on seed yield followed by biological yield per plant and days to 50% flowering. It also indicated that harvest index, biological yield per plant and days to 50% flowering are important characters in deciding the grain yield per plant.

Pahwa *et al.* (2013) reported that leaf area, specific leaf weight, pods per plant and plant height had direct positive contribution towards seed yield.

Prasad *et al.* (2013) found that primary branches per plant, secondary branches per plant, pods per plant, harvest index and pollen viability exhibited positive and high direct effects ranged from 0.060 to 0.430.

Rekha *et al.* (2013) showed that pods per plant exerted highest positive direct effect on seed yield whereas, primary branches per plant and 100-seed weight had moderate and low positive direct effects on seed yield, respectively.

Saroj *et al.* (2013) showed that pods per plant, 100-seed weight, days to 50% flowering, primary branches and secondary branches per plant had maximum direct effect on grain yield per plant.

Singh *et al.* (2013) showed that, seeds per pod exhibited the highest magnitude of direct effects on seed yield, followed by primary branches per

plant and pod length. Pod length and seeds per pod showed positive and significant correlation (0.529 and 0.794) with seed yield per plant and also exhibited positive and strong direct effects (0.531 and 0.266) on seed yield per plant.

Arbad *et al.* (2014) reported pods per plant, secondary branches per plant, plant height, and primary branches per plant were the most important character which can be used to improve yield in pigeonpea.

Pandey *et al.* (2016) identified biological yield per plant followed by harvest index, pods per plant, days to maturity, primary branches per plant, 100-seed weight and seeds per pod as most important direct yield contributing characters in pigeonpea.

Chapter – III

Material and Methods

Chapter – III

MATERIALS AND METHODS

The present study was undertaken with a view to evaluate heterosis and combing ability by adopting L x T analysis in pigeonpea during *kharif*, 2016 at ICRISAT, Hyderabad. The experimental site is situated at an altitude of 545 m above mean sea level, 17° 53'N latitude and 78° 27'E longitude geographically. The materials used and methods followed in the present investigation are described below.

3.1 MATERIALS

The experimental material comprised of nine parental genotypes *viz.*, five females (lines) namely, ICPB-2078, ICPB-2043, ICPB-2047, ICPB-2048 and ICPB-2092, four males (testers) namely, ICPL-87119, ICPL-20108, ICPL-20116 and ICPL-20123, 20 cross combinations obtained through line x tester mating design. The standard check included in the experiment was Maruti. Parents resistant to fusarium wilt and sterility mosaic and give higher yield. The details of parents and their source are furnished in the Table 3.1.

3.2 METHODS

3.2.1 Field Layout

The hybrids made during *kharif*, 2015 at ICRISAT, Hyderabad were evaluated during *kharif*, 2016 at ICRISAT, Hyderabad. The parents (five lines and four testers) and 20 cross combinations along with standard check were sown on 25th July, 2016 in a randomized block design with three replications. Each entry was grown in four rows of 4m length in each plot. The spacing adopted between row to row was 75 cm and 30 cm between plant to plant within a row. Five plants were tagged randomly for recording the data.

Table 3.1. Details of genotypes used in the present investigation:

S. No.	Genotype	Pedigree
1.	ICPH 3933	ICPA 2078 x ICPL 87119
2.	ICPH 2671	ICPA 2043 x ICPL 87119
3.	ICPH 2740	ICPA 2047 x ICPL 87119
4.	ICPH 2751	ICPA 2048 x ICPL 87119
5.	ICPH 3461	ICPA 2092 x ICPL 87119
6.	ICPH 4187	ICPA 2078 x ICPL 20108
7.	ICPH 3467	ICPA 2043 x ICPL 20108
8.	ICPH 3481	ICPA 2047 x ICPL 20108
9.	ICPH 3496	ICPA 2048 x ICPL 20108
10.	ICPH 3762	ICPA 2092 x ICPL 20108
11.	ICPH 4395	ICPA 2078 x ICPL 20116
12.	ICPH 3473	ICPA 2043 x ICPL 20116
13.	ICPH 4022	ICPA 2092 X ICPL 20116
14.	ICPH 3487	ICPA 2047 X ICPL 20116
15.	ICPH 3502	ICPA 2048 X ICPL 20116
16.	ICPH 4539	ICPA 2078 x ICPL 20123
17.	ICPH 3474	ICPA 2043 x ICPL 20123
18.	ICPH 3488	ICPA 2047 X ICPL 20123
19.	ICPH 3503	ICPA 2048 X ICPL 20123
20.	ICPH 4013	ICPA 2092 X ICPL 20123
21.	Maruti	Selection from landraces of Maharashtra.

Table 3.2. Description of female parental lines (CMS lines) used in the development of pigeonpea hybrids

S. No	CMS line	Pedigree	Days to 50% flowering	Days to maturity	Plant height (cm)	100 Seed weight (g)	Seed colour
1	ICPA 2043	ICPA 2043 (ICPA 2039 x ICPL 20176) x ICPL 20176 x ICPL 20176 x ICPL 20176 x ICPL 20176 x ICPL 20176	114	162	198	10	Brown
2	ICPA 2047	ICPA 2047 (ICPA 2039 x ICPL 99050) x ICPL 99050 x ICPL 99050 x ICPL 99050 x ICPL 99050 x ICPL 99050	112	165	242	10.8	Brown
3	ICPA 2048	ICPA 2048 (ICPA 2039 x ICPL 99052) x ICPL 99052 x ICPL 99052 x ICPL 99052 x ICPL 99052 x ICPL 99052	123	168	235	12.9	Brown
4	ICPA 2078	ICPA 2078 (ICPA 2039 x ICPL 118) x ICPL 118 x ICPL 118 x ICPL 118 x ICPL 118 x ICPL 118	103	146	132	13.7	Brown
5	ICPA 2092	ICPA 2092 (ICPA 2039 x ICPL 96058) x ICPL 96058 x ICPL 96058 x ICPL 96058 x ICPL 96058 x ICPL 96058	120	167	220	9.7	Light brown

Source: Pigeonpea Breeding Department, ICRISAT, Patancheru, (Telangana).

Table 3.3. Description of male parental lines (R lines) used in the development of pigeonpea hybrids

S. No	R line	Pedigree	Days to 50% flowering	Days to maturity	Plant height (cm)	100 Seed weight (g)	Seed colour
1	ICPL 87119	C 11 x ICP 1-6W3B	122	172	228	10.6	Brown
2	ICPL 20108	MS 3783 x ICPL 87119 (IPH 487 Inbred)	122	165	235	11.4	Cream
3	ICPL 20116	MS 3783 x ICPL 87119	125	181	275	10.8	Brown
4	ICPL 20123	MS 3783 x ICPL 87119 (IPH 487 Inbred)	122	168	228	10.8	Brown

Source: Pigeonpea Breeding Department, ICRISAT, Patancheru, (Telangana).

3.2.2 Crop Husbandry

The field was ploughed and harrowed to a fine tilth. The crop was raised during *khariif* 2016. 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. Recommended cultural practices and plant protection measures were taken to raise a good crop.

3.2.3 Data Recorded

3.2.3.1 Number of days to 50% 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 75% 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.

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.

3.2.3.8 100-seed weight (g):

One hundred dry seeds were counted and weighed in grams from each sample plant.

3.2.3.9 Seed yield per plant:

The seeds from each sample plant were dried and weighed in grams.

3.2.3.10 Harvest index (%):

The ratio of single plant seed yield to the total plant dry weight (roots and fallen leaves included) was taken and expressed in per cent.

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

3.2.3.11 Seed protein (%):

Protein content in this study refers to the total protein content in the seed. This 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 2N 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 up to 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 color 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 $Y = \text{OD}$ values of the sample and $X = \text{concentration of the protein } (\mu\text{g ml}^{-1})$. Then the concentration of protein in $\mu\text{g ml}^{-1}$ was converted in per cent for different entries.

3.3. STATISTICAL ANALYSIS OF DATA

Mean values were computed for the observations recorded in respect of 11 characters in each of the genotypes and were subjected to statistical analysis by SAS package.

3.3.1 Analysis of Variance:

The mean values of data recorded for 11 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	Degree of freedom	Sum of squares	Mean sum of squares	F ratio
Replication	(r-1)	RSS	Mr	Mr/Me
Genotypes	(g-1)	GSS	Mg	Mg/Me
Error	(r-1)(g-1)	ESS	Me	-
Total	(rg-1)	TSS		

Where,

r = Number of replications

t = Number of genotypes

Mr = Mean sum of squares due to replications

Mg = Mean sum of squares due to genotypes

Me = Mean sum of squares due to error.

3.3.2 Estimation of genetic parameters

Mean data of all characters is subjected to ANOVA and ANCOVA analysis to get the estimates of mean sum of squares and mean sum of products and were utilized for calculation of genetic parameters.

3.3.2.1 Phenotypic and genotypic variance:

The phenotypic and genotypic variances were estimated according the Lush (1940).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{\text{Number of replicaitons}}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where,

$$\sigma_g^2 = \text{Genotypic variance}$$

$$\sigma_e^2 = \text{Error variance}$$

3.3.2.2 Genotypic and phenotypic coefficient of variation:

Genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952).

$$\text{GCV (\%)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_g , σ_p and \bar{X} are genotypic standard deviation, phenotypic standard deviation and general mean of the character, respectively.

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

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

3.3.2.3 Heritability (Broad sense) $h^2_{(b)}$:

Heritability in broad sense was estimated using the formula of Allard (1960).

$$\text{Broad sense Heritability} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability estimates were categorized as suggested by Johnson *et al.* (1955).

- Less than 30% - Low
- 30 – 60 % - Moderate
- More than 60% - High

3.3.2.4 Genetic advance:

Estimated as per the formula proposed by Lush (1949) and Johnson *et al.* (1955).

$$GA = k \sigma_p H$$

where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

H = Heritability (broad sense)

k = Selection differential at 5% selection intensity

Genetic advance as percent of mean (GA as percent mean)

Genetic advance as percent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{\text{GA}}{\bar{X}} \times 100$$

where,

GA = Genetic advance

\bar{X} = Grand mean of the character

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

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

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.

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

Where,

F_1 = Mean of F_1

Mp = Mean of mid parent

3.3.3.2 Heterobeltiosis:

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

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

Where,

BP = 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.

$$\text{Standard Heterosis (\%)} = \frac{\bar{F}_1 - \bar{SC}}{\bar{SC}} \times 100$$

Where,

SC = Mean of standard check

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

$$\text{Relative heterosis} = \frac{\bar{F}_1 - \bar{MP}}{\sqrt{1.5EMS / r}}$$

$$\text{Heterobeltiosis} = \frac{\bar{F}_1 - \bar{BP}}{\sqrt{2EMS / r}}$$

$$\text{Standard heterosis} = \frac{\bar{F}_1 - \bar{SC}}{\sqrt{2EMS / r}}$$

Where,

EMS = Error mean squares

r = Number of replications

The calculated 't' value was compared with table 't' value at error degree of freedom.

3.3.4 Combining Ability Analysis

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

Table 3.3. ANOVA structure for combining ability

Source of variation	Degree of freedom	Mean sum of squares
Replications	(r-1)	
Genotypes	(g-1)	M_g
Parents	(p-1)	
Parents vs. Hybrids	1	
Hybrids	(c-1)	
Lines	(l-1)	M_l
Testers	(t-1)	M_t
Line x Testers	(l-1) (t-1)	M_{lt}
Error	(r-1) (a-1)	M_e

Where;

r, g, c, l, and t are number of replications, genotypes, parents, hybrids, lines and testers, respectively. M_l , M_t , M_{lt} , 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 x 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)th individual.

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

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

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

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

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 hybrids 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* effects of lines and testers and *sca* effects of different cross combinations were calculated as shown below.

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

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

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

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

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

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

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

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

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

$$\text{Cov. FS} = \frac{(M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4)}{3r} + \frac{6r\text{CovHS} - r(1+t)\text{CovHS}}{3r}$$

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

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

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

3.3.5 Character association

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

3.3.5.1 Genotypic correlation coefficient (r_g)

$$r_g (x_i x_j) = \frac{\text{Cov}_g(x_i x_j)}{\sqrt{V_g(x_i) \cdot V_g(x_j)}}$$

Where,

$r_g(x_i x_j)$ = Genotypic correlation between 'ith' and 'jth' characters

$V_g(x_i)$ = Genotypic variance of 'ith' character

$V_g(x_j)$ = Genotypic variance of 'jth' character

$Cov_{(g)}(x_i x_j)$ = Genotypic covariance between 'ith' and 'jth' characters.

3.3.5.2 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,

$V_p(x_i)$ = Phenotypic variance of 'ith' character

$V_p(x_j)$ = Phenotypic variance of 'jth' character

$Cov(x_i x_j)$ = Phenotypic covariance between 'ith' and 'jth' characters.

The significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1967)] at (n-2) degrees of freedom at 5% and 1% level where, 'n' denotes the number of treatments used in the calculations.

3.3.6 Path coefficient analysis

Path coefficient analysis was carried out by the procedure originally proposed by Wright (1921) which was subsequently elaborated by Dewey and Lu (1959) to estimate the direct and indirect effects of the individual characters on yield.

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

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

where,

r_{12} to r_{i-1} = 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 matrix forms as under:

$$\begin{matrix} \mathbf{A} \\ \left(\begin{array}{c} r_{1y} \\ r_{2y} \\ r_{3y} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ r_{iy} \end{array} \right) \end{matrix} = \begin{matrix} \mathbf{C} \\ \left(\begin{array}{cccc} 1 & r_{12} & r_{13} & \dots\dots\dots r_{1i} \\ r_{21} & 1 & r_{23} & \dots\dots\dots r_{2i} \\ r_{31} & r_{32} & 1 & \dots\dots\dots r_{3i} \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ r_{i1} & r_{i2} & r_{i3} & \dots\dots\dots 1 \end{array} \right) \end{matrix} \begin{matrix} \mathbf{B} \\ \left(\begin{array}{c} p_{1y} \\ p_{2y} \\ p_{3y} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ p_{iy} \end{array} \right) \end{matrix}$$

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

where,

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

Then, direct effects were calculated as follows:

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

$$P_{2y} = \sum_{i=1}^I C_{2i} r_{iy}$$

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

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:

$$\text{Residual effect (P}_{RY}) = \sqrt{1 - [P_{1y}r_{1y} + p_{2y}r_{2y} + \dots + p_{iy}r_{iy}]^2}$$

where,

P_{RY} = Residual effect

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

r_{iy} = Correlation coefficient of 'x_i' with 'y'.

The scales for path coefficients as proposed by Lenka and Mishra (1973) are as follows:

Value for Direct or Indirect effect	Rate or Scale
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
More than 1.00	Very high

Chapter – IV

Results & Discussion

Chapter - IV

RESULTS AND DISCUSSION

The results obtained on mean performance, genetic parameters, heterosis, combining ability and character association for 11 characters viz., days to 50% flowering, days to 75% maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, 100-seed weight, harvest index, seed protein, and seed yield per plant were discussed here under.

4.1 ANALYSIS OF VARIANCE

Analysis of variance for Randomized Block Design with respect to 11 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 days to 50% flowering, secondary branches per plant and seeds per pod.

4.2 MEAN PERFORMANCE

The mean performance of the parents, standard check (Maruti) and hybrids were presented in Tables 4.2 and 4.3, respectively. The results and discussions were furnished character wise hereunder.

4.2.1 Yield Attributes

4.2.1.1 Days to 50% flowering: Among the lines ICPB-2078 (100.00 days) and ICPB-2047 (122.33), among testers ICPL-20116 (118.67 days) and ICPL-20108 (123.00 days) were early and late in flowering, respectively with a mean of 117.70 days (Table 4.2). Among hybrids early flowering was observed in ICPA-2078 x ICPL-87119 (110.33 days) while ICPA-2047 x ICPL-20108 & ICPA-2047 x ICPL-20123 (121.33 days) and ICPA-2047 x ICPL-20116 (120.33 days) were very late (Table 4.3).

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

S. No.	Characters	Mean sum of squares		
		Replication (df = 2)	Treatments (df = 28)	Error (df = 56)
1	Days to 50% flowering	10.25**	84.06**	1.63
2	Days to 75% maturity	0.65	83.92**	2.02
3	Plant height (cm)	4.00	696.25**	2.59
4	Primary branches per plant	1.70	11.66**	1.51
5	Secondary branches per plant	12.86*	201.34**	3.15
6	Number of pods per plant	5.58	55906.25**	14.30
7	Number of seeds per pod	0.07**	0.18**	0.01
8	100-seed weight (g)	0.03	2.06**	0.36
9	Harvest index (%)	0.35	312.72**	1.38
10	Seed protein (%)	0.91	1.58**	0.61
11	Seed yield per plant (g)	0.80	4890.24**	1.37

** Significant at 0.01; * Significant at 0.05

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

Parents	Days 50% to flowering	Days 75% to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
LINES											
ICPB2078	100.00	160.33	84.33	10.00	16.00	52.40	3.20	11.63	17.70	16.81	13.74
ICPB2043	109.67	166.67	126.67	10.67	21.67	173.87	3.47	9.77	31.13	17.62	57.57
ICPB2047	122.33	175.67	159.50	15.33	31.00	406.40	4.13	9.07	40.47	18.03	114.07
ICPB2048	121.00	181.00	145.33	14.67	24.67	351.67	3.50	10.13	37.97	18.26	107.55
ICPB2092	121.67	175.67	127.33	14.00	29.00	325.80	3.40	9.80	38.97	19.35	93.29
TESTERS											
ICPL87119	122.67	183.33	137.50	13.00	15.67	572.53	3.60	10.27	42.57	17.35	179.57
ICPL20108	123.00	180.33	131.00	14.67	24.67	282.60	3.90	10.50	36.70	16.53	83.97
ICPL20116	118.67	174.67	128.67	10.67	16.00	351.40	3.63	9.73	44.77	17.23	89.40
ICPL20123	120.33	181.33	162.00	14.33	37.33	352.00	3.63	10.20	41.43	17.83	104.92
Mean of parents	117.70	175.44	133.59	13.04	24.00	318.74	3.61	10.12	36.86	17.67	93.79
Range (min)	100.00	160.33	84.33	10.00	15.67	52.40	3.20	9.07	17.70	16.53	13.74
Range (max)	123.00	183.33	162.00	15.33	37.33	572.53	4.13	11.63	44.77	19.35	179.57
Standard check (Maruti)	111.00	168.33	134.67	14.67	13.33	261.40	3.80	10.53	33.83	20.87	70.18
S.Em	1.37	1.68	13.94	1.62	4.98	37.33	0.20	0.58	0.92	0.08	14.13
C.D. (0.05)	4.16	5.08	42.28	4.91	15.10	113.24	0.62	1.75	2.79	0.24	42.87
C.V.(%)	2.11	1.76	11.48	17.26	38.96	15.79	8.89	8.00	7.72	0.57	24.12

Table 4.3. Mean performance of 20 hybrids for seed yield and yield components in pigeonpea

Crosses	Days 50% to flowering	Days 75% to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
ICPA 2078 x ICPL 87119	110.33	169.67	133.67	12.00	26.33	223.53	3.57	11.60	28.37	16.78	61.10
ICPA 2078 x ICPL 20108	111.33	171.33	134.17	11.00	25.33	158.73	3.90	12.20	36.90	16.50	53.91
ICPA 2078 x ICPL 20116	115.67	168.67	134.33	9.67	15.67	241.93	3.70	11.63	56.20	16.69	88.57
ICPA 2078 x ICPL 20123	112.33	175.33	140.00	9.67	23.67	192.67	3.40	11.93	25.70	17.77	51.37
ICPA 2043 x ICPL 87119	113.33	164.00	120.67	12.33	27.33	251.40	3.60	10.13	32.37	17.40	69.83
ICPA 2043 x ICPL 20108	113.67	171.67	125.53	13.00	25.33	352.27	3.83	10.77	42.57	18.28	104.28
ICPA 2043 x ICPL 20116	111.00	174.00	146.67	11.67	28.00	383.73	3.47	10.20	35.97	18.61	116.07
ICPA 2043 x ICPL 20123	113.33	169.67	125.33	12.67	29.33	252.67	3.80	9.87	30.93	16.69	68.12
ICPA 2047 x ICPL 87119	113.67	173.33	150.67	14.00	34.67	410.07	3.60	10.43	39.47	17.69	119.27
ICPA 2047 x ICPL 20108	121.33	178.67	144.33	15.67	37.00	294.27	3.90	10.00	66.37	16.62	143.57
ICPA 2047 X ICPL 20116	120.33	175.33	148.00	16.00	36.67	399.73	3.87	9.63	36.53	17.93	115.39
ICPA 2047 X ICPL 20123	121.33	175.00	152.63	15.67	27.33	335.67	4.10	10.63	36.30	16.91	92.57
ICPA 2048 x ICPL 87119	119.33	181.67	139.67	13.33	31.00	424.27	3.70	10.43	39.77	17.51	129.27
ICPA 2048 x ICPL 20108	116.67	176.33	128.17	13.67	28.00	252.07	3.83	10.50	31.37	17.01	74.92
ICPA 2048 X ICPL 20116	111.33	176.00	113.33	14.67	15.00	143.00	2.97	11.97	39.00	16.56	40.77
ICPA 2048 X ICPL 20123	116.67	173.33	136.93	16.33	47.33	337.33	3.67	10.07	33.27	18.13	93.10
ICPA 2092 x ICPL 87119	120.33	169.67	129.33	14.67	42.33	543.40	3.53	10.33	42.07	17.59	147.51
ICPA 2092 x ICPL 20108	118.67	176.00	148.00	15.00	37.00	712.07	3.80	10.17	64.73	17.20	200.86
ICPA 2092 X ICPL 20116	120.00	175.33	149.67	14.00	24.00	317.73	3.70	10.37	36.33	16.33	102.13
ICPA 2092 X ICPL 20123	119.33	177.00	134.67	12.00	21.67	197.27	3.80	12.07	29.13	17.70	61.06
Mean of hybrids	116.00	173.60	136.79	13.35	29.15	321.19	3.69	10.75	39.17	17.29	96.68
Range (Min)	110.33	164.00	113.33	9.67	15.00	143.00	2.97	9.63	25.70	16.33	40.77
Range (Max)	121.33	181.67	152.63	16.33	47.33	712.07	4.10	12.20	66.37	18.61	200.86
Standard check (Maruti)	111.00	168.33	134.67	14.67	13.33	261.40	3.80	10.53	33.83	20.87	70.18
S.Em	0.98	1.44	11.26	2.00	3.52	69.34	0.13	0.59	1.37	0.08	19.49
C.D (0.05)	2.84	4.18	32.63	5.81	10.19	200.84	0.38	1.71	3.97	0.24	56.44
C.V. (%)	1.52	1.58	8.92	19.97	24.11	18.37	5.62	8.58	10.99	0.55	21.31

4.2.1.2 Days to 75% maturity: The genotype, ICPB-2078 (160.33 days) among lines and ICPL-20116 (174.67 days) among testers were early to mature whereas the line ICPB-2048 (181.00 days) and the tester ICPL-87119 (183.33 days) were late to mature with a mean of 175.44 days (Table 4.2). Among hybrids it ranged from 164.00 days (ICPA-2043 x ICPL-87119) to 181.67 days (ICPA-2048 x ICPL-87119) with a mean of 173.60 days (Table 4.3).

4.2.1.3 Plant height (cm): The mean plant height for parents was 133.59 cm. The line ICPB-2047 (159.50 cm) and the tester ICPL-20123 (162.00cm) were the tallest, while the line ICPB-2078 (84.33 cm) and the tester ICPL-20116 (128.67 cm) were the shortest parents (Table 4.2). Among the hybrids ICPA-2047 x ICPL-20123 (152.63 cm) was the tallest, whereas ICPL-2048 x ICPL-20116 (113.33 cm) was the shortest with a mean plant height of 136.79 cm. Out of 20 hybrids, ten hybrids were observed to have higher plant height than the mean (Table 4.3).

4.2.1.4 Primary branches per plant: The line ICPB-2047 (15.33) and the tester ICPL-20108 (14.67) recorded more primary branches with a mean of 13.04. The line ICPB-2078 (10.00) and the tester ICPL-20116 (10.67) had lowest primary branches per plant among the parents (Table 4.2). Among the hybrids, ICPA-2048 x ICPL-20123 (16.33) and ICPB-2078 x ICPL-20116 (9.67), ICPB-2078 x ICPL-20123 (9.67) showed more and less primary branches per plant, respectively, with a cross mean of 13.35. Ten hybrids surpassed the mean of F₁ hybrids (Table 4.3).

4.2.1.5 Secondary branches per plant: The mean of the parents was 24.00. Among the parents, the line ICPB-2047 (31.00) and the tester ICPL-20123 (37.33) showed more secondary branches per plant whereas the line ICPB-2078 (16.00) and the tester ICPL-87119 (15.67) had lowest secondary branches per plant (Table 4.2). Among the hybrids, ICPA-2048 x ICPL-20123 (47.33) and ICPL-2048 x ICPL-20116 (15.00) showed highest and lowest values for this trait with a cross mean of 29.15, seven hybrids surpassed mean value out of 20 hybrids (Table 4.3).

4.2.1.6 Pods per plant: The genotype ICPB-2047 (406.40) among lines and ICPL-87119 (572.53) among testers recorded more pods per plant, whereas the line ICPB-2078 (52.40) and the tester ICPL-20108 (282.60) recorded less pod number per plant (Table 4.2). Among hybrids it ranged from 143.00 (ICPL-2048 x ICPL-20116) to 712.07 (ICPA-2092 x ICPL-20108) with a cross mean of 321.19. Nine hybrids recorded highest value than the mean (Table 4.3).

4.2.1.7 Seeds per pod: Among the lines ICPB-2047 (4.13) and ICPB-2078 (3.20), among the testers ICPL-20108 (3.90) and ICPL-87119 (3.60) showed maximum and minimum seeds per pod, respectively with the parental mean of 3.61 (Table 4.2). Among the hybrids, ICPA-2047 x ICPL-20123 (4.10) showed highest, whereas ICPL-2048 x ICPL-20116 (2.97) showed lowest values for this trait. Eleven hybrids were showed higher values than hybrid mean (3.69) (Table 4.3).

4.2.1.8 100-seed weight (g): Among the lines ICPB-2078 (11.63g) and ICPB-2047 (9.07g), among the testers ICPL-20108 (10.50g) and ICPL-20116 (9.73g) recorded maximum and minimum seed weight with a parental mean of 10.12 (Table 4.2). It was ranged from 9.63 (ICPA-2047 x ICPL-20116) to 12.20 (ICPA-2078 x ICPL-20108) among hybrids. Seven hybrids exceeded the mean seed weight (10.75) (Table 4.3).

4.2.1.9 Harvest index (%): Line ICPB-2047 (40.47) and the tester ICPL-20116 (44.77) recorded highest harvest index whereas the line ICPB-2078 (17.70) and the tester ICPL-20108 (36.70) had lowest harvest index with a mean of 36.86 (Table 4.2). In hybrids, it ranged from 25.70 (ICPA-2078 x ICPL-20123) to 66.37 (ICPA-2047 x ICPL-20108) with a mean of 39.17. Seven hybrids showed high harvest index than hybrid mean (Table 4.3).

4.2.1.10 Seed yield per plant (g): The genotype ICPB-2047 (114.07) among the lines and ICPL-87119 (179.57) among the testers showed highest seed yield per plant. The line ICPB-2078 (13.74) and the tester ICPL-20108 (83.97) had lowest seed yield among the parents with a mean of 93.79 (Table 4.2). In

hybrids, it ranged from 40.77 (ICPA-2048 x ICPL-20116) to 200.86 (ICPA-2092 x ICPL-20108) with a mean of 96.68. Nine hybrids recorded highest seed yield per plant over the F_1 mean (Table 4.3).

4.2.2 Quality Attributes

4.2.2.1 Seed protein (%): The line ICPB-2092 (19.35) and the tester ICPL-20123 (17.83) recorded superior protein percentage with a mean of 17.67. The line ICPB-2078 (16.81) and the tester ICPL-20108 (16.53) had low seed protein among the parents (Table 4.2). Seed protein in F_1 's ranged from 16.33 (ICPA-2092 x ICPL-20116) to 18.61 (ICPA-2043 x ICPL-20116) with a mean of 17.29 (Table 4.3).

Among the parents, the line ICPB-2047 was promising for seed yield and other yield contributing characters and the testers ICPL-20123 was found most desirable for yield and other yield contributing characters with high *per se* performance. The lines ICPB-2078 and ICPB-2043 were promising for earliness.

The hybrids ICPA-2092 x ICPL-20108 recorded high *per se* performance for yield. Cross combinations involving the lines ICPA-2078 and ICPA-2043 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. 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 is 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 genetic advance indicates the importance of additive gene effects in 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, 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 eleven characters in nine parents and 20 hybrids were furnished in the Table 4.4. The estimates of PCV and GCV for parents and hybrids were also presented in Fig. 4.1 and Fig. 4.2 respectively, whereas heritability and genetic advance as per cent of mean for parents and hybrids are given in Fig. 4.3. The results and discussion were presented on character wise hereunder.

4.3.1 Yield Attributes

4.3.1.1 Days to 50% flowering: Low Phenotypic co-efficient of variation (6.69) and genotypic co-efficient of variation (6.59) in parents was noted for the traits. Heritability estimate for this trait was high (97.07) with moderate genetic advance (15.75) and genetic advance as per cent of mean was 13.38 (Table 4.4).

Low PCV and GCV estimates observed for this trait were recorded among hybrids 3.25 and 3.42 respectively. Heritability estimate for this trait was high (90.61) with a low genetic advance (7.40) and genetic advance as per cent of mean (6.38) (Table 4.4).

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

Characters	Range		Mean		GCV		PCV		Heritability (%)		Genetic advance		Genetic advance as % of mean	
	Parents	Hybrids	Parents	Hybrids	Parents	Hybrids	Parents	Hybrids	Parents	Hybrids	Parents	Hybrids	Parents	Hybrids
Days 50% to flowering	100.00-123.00	110.33-121.33	117.70	116.00	6.59	3.25	6.69	3.42	97.07	90.61	15.75	7.40	13.38	6.38
Days to 75% maturity	160.33-183.33	164.00-181.67	175.44	173.60	4.29	2.26	4.36	2.40	96.54	88.18	15.22	7.57	8.68	4.36
Plant height (cm)	84.33-162.00	113.33-152.63	133.59	136.79	17.09	7.94	17.12	8.04	99.69	97.45	46.97	22.08	35.16	16.14
Primary branches per plant	10.00-15.33	9.67-16.33	13.04	13.35	14.81	13.84	17.44	16.65	72.13	69.07	3.38	3.16	25.91	23.70
Secondary branches per plant	15.67-37.33	15.00-47.33	24.00	29.15	31.29	27.65	31.75	28.47	97.08	94.35	15.24	16.13	63.50	55.33
Number of pods per plant	52.40-572.53	143.00-712.07	318.74	321.19	45.55	42.44	45.55	42.46	99.99	99.89	299.07	280.64	93.83	87.37
Number of seeds per pod	3.20-4.13	2.97-4.10	3.61	3.69	7.44	6.29	7.97	6.79	87.11	86.00	0.52	0.44	14.30	12.03
100-seed weight (g)	9.07-11.63	9.63-12.20	10.12	10.75	6.31	6.82	8.05	9.13	61.40	55.85	1.03	1.13	10.19	10.50
Harvest index (%)	17.70-44.77	25.70-66.37	36.86	39.17	22.14	28.33	22.25	28.54	99.05	98.59	16.73	22.70	45.40	57.95
Seed protein (%)	16.53-19.35	16.33-18.61	17.67	17.29	4.07	2.81	5.88	5.29	47.89	28.31	1.03	0.53	5.80	3.08
Seed yield per plant (g)	13.74-179.57	40.77-200.86	93.79	96.68	47.56	40.87	54.08	43.19	99.93	99.91	91.85	81.36	97.93	84.15

Fig. 4.1. Phenotypic co-efficient of variation for 11 characters in parents and hybrids of pigeonpea

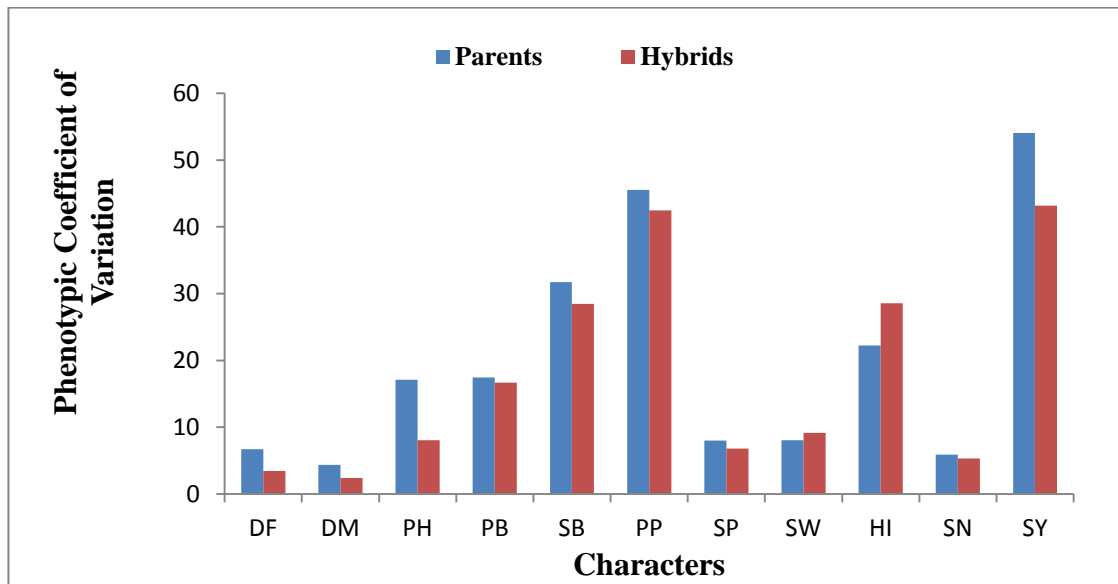
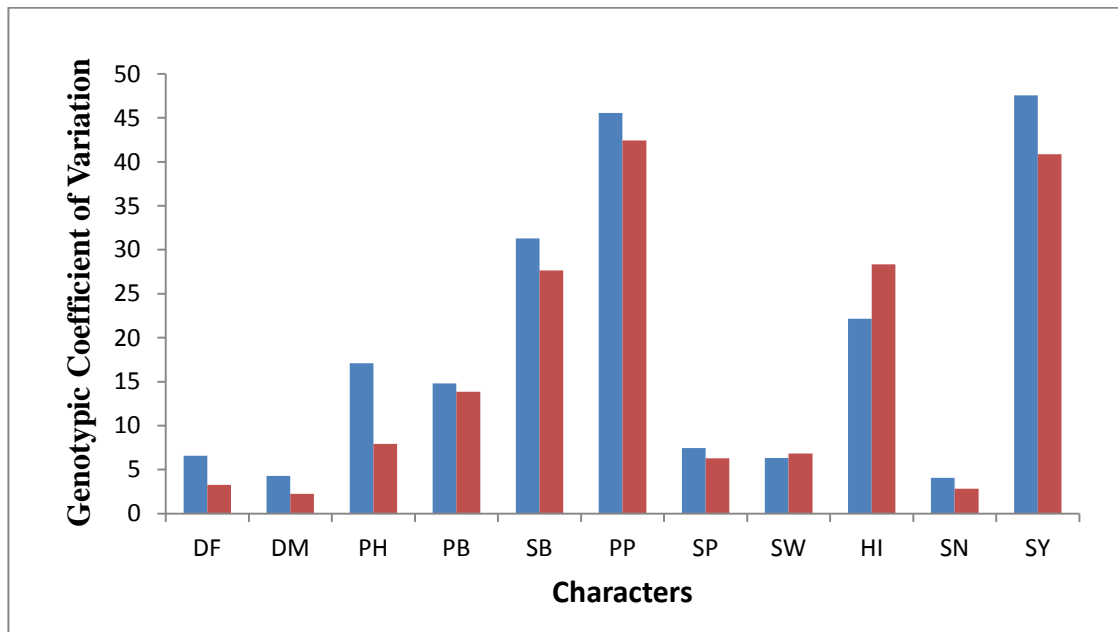


Fig. 4.2. Genotypic co-efficient of variation for 11 characters in parents and hybrids of pigeonpea



DF= Days to 50% flowering

DM= Days to 75% maturity

PH= Plant height

PB= Primary branches per plant

SB= Secondary branches per plant

PP= Pods per plant

SP= Seeds per pod

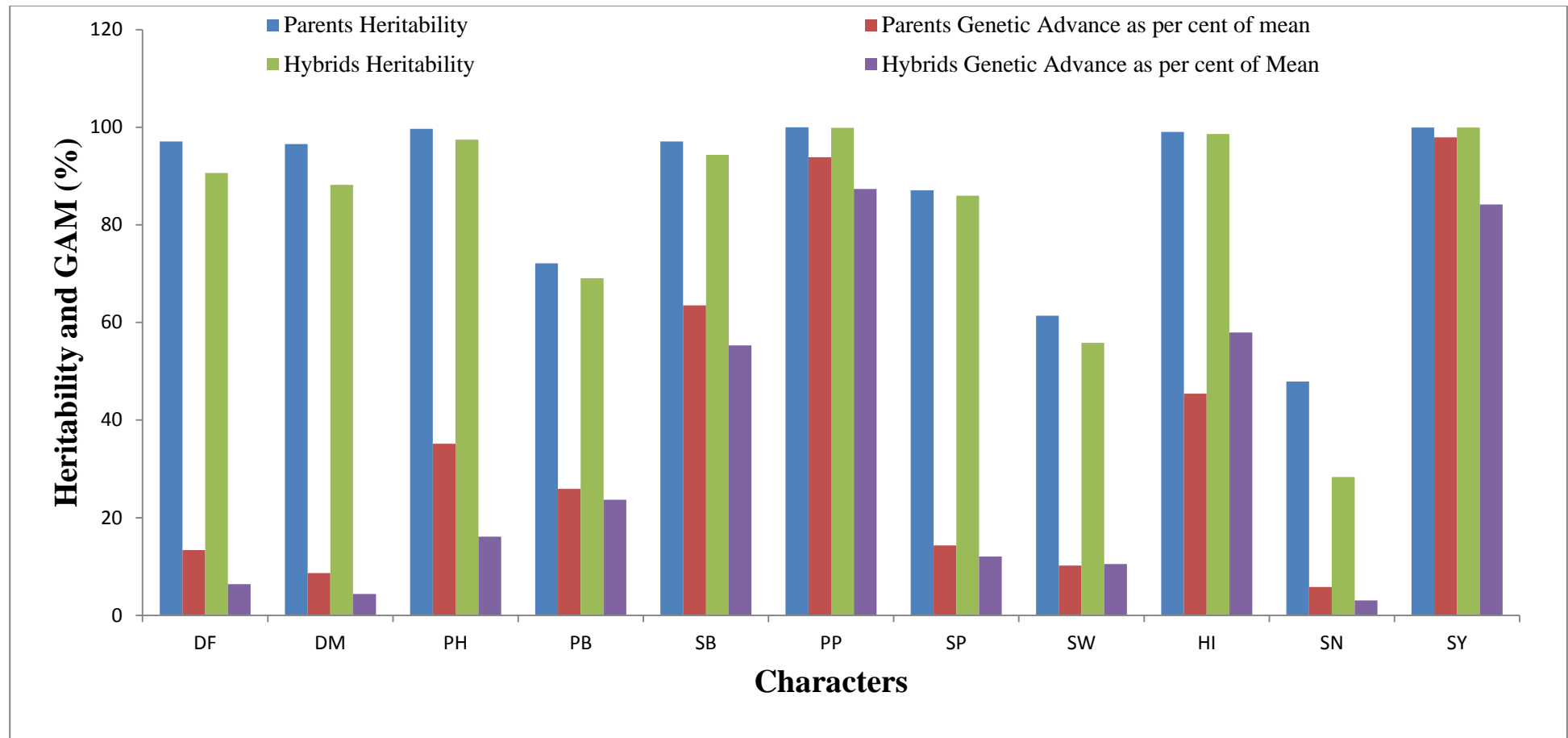
SW= 100-seed weight

HI= Harvest index

SN= Seed protein

SY= Seed yield per plant

Fig. 4.3. Heritability and genetic advance as per cent of mean for 11 characters in parents and hybrids of pigeonpea



DF= Days to 50% flowering
DM= Days to 75% maturity
PH= Plant height

SB= Secondary branches per plant
PP= Pods per plant

PB= Primary branches per plant
SP= Seeds per pod

SW= 100-seed weight
HI= Harvest index

SN= Seed protein
SY= Seed yield per plant

This trait exhibited low PCV and GCV in parents and hybrids indicating that the selection can be done at later generations. This is in conformity with Patil *et al.* (1989), Kapre and Nerker (1992), Aher *et al.* (1996) and Anantharaju and Muthaiah (2008). High heritability coupled with moderate genetic advance as per cent of mean in parents for this trait can be improved by simple selection methods. High heritability coupled with low genetic advance as per cent of mean in hybrids indicating the predominance of non-additive gene action. Similar results were reported by Patel and Acharya (2011) and Kumar *et al.* (2014).

4.3.1.2 Days to 75% maturity: Low PCV and GCV estimates of 4.29 and 4.36 in parents were observed for this trait. Heritability estimates for this trait was high (96.54) with moderate genetic advance (15.22) and low genetic advance as per cent of mean (8.68) (Table 4.4).

In hybrids, the PCV (2.40) and GCV (2.26) estimates were low. High heritability (88.18) estimates were recorded for this trait with a low genetic advance (7.57) and genetic advance as per cent of mean (4.36) (Table 4.4).

This trait exhibited low PCV and GCV both in parents and hybrids indicating that the selection can be done in later generations. This is in agreement with the results of Anantharaju and Muthaiah (2008), Aher *et al.* (1996), Patil *et al.* (1989) and Khapre and Nerker (1992). High heritability in parents and hybrids indicates less influence of environment on this trait. High heritability coupled with low genetic advance as per cent of mean indicate that it is controlled by non-additive gene action. Similar results were also reported by Aher *et al.* (1996) and Gohil (2006).

4.3.1.3 Plant height: In parents, plant height recorded moderate PCV (17.12) and GCV (17.09). High heritability (99.69), high genetic advance (46.97) and genetic advance as per cent of mean (35.16) were observed for this trait (Table 4.4).

Low PCV (8.04) and GCV (7.94) for this trait was observed in hybrids, while heritability estimates were high (97.45) with high genetic advance (22.08) and moderate genetic advance as per cent of mean (16.14) (Table 4.4).

Moderate PCV and GCV in parents and low PCV and GCV in hybrids indicates the selection may be effective in later generations for this trait. High heritability with high genetic advance as per cent of mean indicates importance of additive effects for this trait and is confirmed with the results of Vanisree and Sreedhar (2014), Kumar *et al.* (2014), Rnagare *et al.* (2013), and Jaggal *et al.* (2012).

4.3.1.4 Primary branches per plant: Moderate PCV (17.44) and GCV (14.81) was recorded in parents for this trait. Heritability estimate was high (72.13) with low genetic advance (3.38) and high genetic advance as per cent of mean (25.91) (Table 4.4).

This trait recorded moderate PCV (16.65) and GCV (13.84) values in hybrids. The heritability estimate (69.07) was high with a low genetic advance (3.16) and high genetic advance as per cent of mean (23.70) (Table 4.4).

This trait exhibited moderate variability among parents and hybrids indicating its amenability for selection in early generation. High heritability coupled with high genetic advance as per cent of mean was also reported for parents and hybrids by Sreelakhmi *et al.* (2011), Kumar *et al.* (2014), Lakhote *et al.* (2015), Jogendra Singh *et al.* (2008) and Bhadru (2010).

4.3.1.5 Secondary branches per plant: This trait recorded high PCV (31.75) and GCV (31.29) in parents. High heritability estimate (97.08) was observed with moderate genetic advance (15.24) and high genetic advance as per cent of mean (63.50) (Table 4.4).

This trait recorded high PCV (28.47) and GCV (27.65) values in hybrids. High heritability (94.35) with moderate genetic advance (16.13) and high genetic advance as per cent of mean (55.33) was recorded for this trait in hybrids (Table 4.4).

This trait exhibited high PCV and GCV both in parents and hybrids indicating existence of high variability for this character. This is in agreement with the results of Pandey *et al.* (2015), Lakhote *et al.* (2015), and Prasad *et al.* (2013). High heritability with high genetic advance as per cent of mean was observed in parents and hybrids indicating that the selection is effective because of additive gene action for this trait. These results are in confirmity with Aajay *et al.* (2014), Kumar *et al.* (2014), and Pandey *et al.* (2015).

4.3.1.6 Pods per plant: High PCV (45.55) and GCV (45.55) was recorded for this trait in parents. High heritability (99.99) estimates recorded with a high genetic advance (299.07) and genetic advance as per cent of mean (93.83). Hybrids recorded high PCV (42.46) and GCV (42.44). High heritability (99.89) was recorded with high genetic advance (280.64) and genetic advance as per cent of mean (87.37) (Table 4.4).

This trait showed high variability both in parents and hybrids. Hence this trait can be improved in early generations. High heritability coupled with high genetic advance as per cent of mean was recorded in parents and hybrids suggests the preponderance of additive gene action. This is in agreement with the results Vanisree and Sreedhar (2014), Saroj *et al.* (2013), Patel and Acharya (2011) and Nagy *et al.* (2013).

4.3.1.7 Seeds per pod: Low PCV (7.97) and GCV (7.44) and high heritability (87.11) estimates were recorded in parents with low genetic advance (0.52) and moderate genetic advance as per cent of mean (14.30) (Table 4.4).

In hybrids also low PCV (6.79) and GCV (6.29) was recorded. High heritability (86.00) coupled with low genetic advance (0.44) and moderate genetic advance as per cent of mean (12.03) was recorded (Table 4.4).

In this present study low variability observed both in parents and hybrids. 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 along with moderate genetic advance as per cent of

mean indicates that this trait can be improved by simple selection methods. These results are in conformity with the findings of Pandey *et al.* (2015), Kingshlin and Subbaraman (1999) and Magar (2003).

4.3.1.8 100-seed weight (g): In parents, low PCV (8.05) and GCV (6.31), high heritability (61.40) low genetic advance (1.03) and moderate genetic advance as per cent of mean (10.19) was recorded (Table 4.4).

In hybrids low variation recorded in terms of PCV (9.13) and GCV (6.82) was observed. Moderate heritability (55.85), with low genetic advance (1.13) and moderate genetic advance as per cent of mean (10.50) (Table 4.4).

This trait exhibited low PCV and GCV both in parents and hybrids indicating that the selection can be done in later generations. High heritability coupled with moderate genetic advance as per cent of mean was noticed, indicating that this trait is governed by additive and non-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).

4.3.1.9 Harvest index: High PCV (22.25) and GCV (22.14) was recorded in parents for this trait. High heritability (99.05), moderate genetic advance (16.73) and high genetic advance as per cent of mean (45.40) were also recorded (Table 4.4).

In hybrids high PCV (28.54) and GCV (28.33) values were recorded. High estimates of heritability (98.59) coupled with high genetic advance (22.70) and high genetic advance as per cent of mean (57.95) were recorded for this trait (Table 4.4).

Harvest index exhibited high variability both in parents and hybrids indicating the availability of variability for selection of this trait in early generations. High variability for harvest index was also reported earlier by Pansuriya *et al.* (1998), Prasad *et al.* (2013), Jaggal *et al.* (2012) and Khapre *et al.* (1993). High heritability and high genetic advance as per cent of mean was

observed in parents and hybrids, indicating this trait is controlled by additive gene action. This is in conformity with the results of Rangare *et al.* (2013), Jaggal *et al.* (2012) and Gohil (2006).

4.3.1.10 Seed yield per plant: In parents, high variability was recorded PCV (54.08) and GCV (47.56). Higher estimates of heritability (99.93), genetic advance (91.85) and genetic advance as per cent of mean (97.93) were observed (Table 4.4).

In case of hybrids higher estimates of PCV (43.19) and GCV (40.87) were recorded. High estimate of heritability (99.91) was registered along with high genetic advance (81.36) and genetic advance as per cent of mean (84.15) (Table 4.4).

Seed yield exhibited higher variability in parents and hybrids, indicating that selection can be recorded in early generations to improve this trait. High heritability coupled with high genetic advance as per cent of mean recorded for seed yield in the present study indicates that the trait is controlled by additive gene action and thus selection is effective. These results are in conformity of the findings of Pandey *et al.* (2015), Vanisree and Sreedhar (2014), Nagy *et al.* (2013) and Patel and Acharya (2011).

4.3.2 Quality Attributes

4.3.2.1 Seed protein: Low variability in terms of PCV (5.88) and GCV (4.07) was observed in parents. Moderate heritability (47.89) and also low genetic advance (1.03) and genetic advance as per cent of mean (5.80) were also observed for this trait (Table 4.4).

In case of hybrids a very low PCV (5.29) and GCV (2.81) values were recorded. Low heritability (28.31) with a very low genetic advance (0.53) and genetic advance as per cent of mean (3.08) were also observed for this trait (Table 4.4).

A Very low variability in parents and hybrids noticed for seed protein, indicates a limited scope of selection for this character. This is in conformity with the findings of Gohil (2006). Moderate heritability coupled with low genetic advance as per cent of mean in parents and low heritability coupled with low genetic advance as per cent of mean in hybrids, indicates that this trait is controlled by non-additive gene action. This is supported by the findings of Aher *et al.* (1996).

From the present study, it can be concluded that simple selection may be effective for secondary branches per plant, pods per plant, harvest index and seed yield per plant as these characters are under the control of additive gene action as evidenced by higher estimates of genetic parameters.

4.4 HETEROSIS

Estimation of the extent of heterosis in diverse cross combinations would always be useful in choosing the best performing hybrids 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, 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% higher than the standard variety. Hence, the heterosis over the standard parent was estimated and is termed as standard heterosis.

In present investigation, estimates of heterosis for 20 hybrids over mid parent, better parent and standard variety was presented in Table 4.5 and the relative merit of superior hybrids is discussed here under.

4.4.1 Yield Attributes

4.4.1.1 Days to 50% flowering: Heterosis for this trait ranged from -7.21% to 5.79% (ICPA-2078 x ICPL-20116) and -10.05% to -0.82% (ICPA-2047 x ICPL-20123) over mid parent and better parent, respectively, while for

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

Crosses	Days 50% to flowering			Days to 75% maturity			Plant height (cm)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPA 2078 x ICPL 87119	-0.9	-10.05**	-0.6	-1.26*	-7.45**	0.79	20.51**	-2.79**	-0.74
ICPA 2078 x ICPL 20108	-0.15	-9.49**	0.3	0.59	-4.99**	1.78**	24.61**	2.42*	-0.37
ICPA 2078 x ICPL 20116	5.79**	-2.53**	4.2**	0.7	-3.44**	0.2	26.13**	4.40**	-0.25
ICPA 2078 x ICPL 20123	1.97**	-6.65**	1.2	2.63**	-3.31**	4.16**	13.67**	-13.58**	3.96**
ICPA 2043 x ICPL 87119	-2.44**	-7.61**	2.1*	-6.29**	-10.55**	-2.57**	-8.64**	-12.24**	-10.4**
ICPA 2043 x ICPL 20108	-2.29**	-7.59**	2.4*	-1.06*	-4.81**	1.98**	-2.56**	-4.17**	-6.78**
ICPA 2043 x ICPL 20116	-2.77**	-6.46**	0	1.95**	-0.38	3.37**	14.88**	13.99**	8.91**
ICPA 2043 x ICPL 20123	-1.45*	-5.82**	2.1*	-2.49**	-6.43**	0.79	-13.16**	-22.63**	-6.93**
ICPA 2047 x ICPL 87119	-7.21**	-7.34**	2.4*	-3.44**	-5.45**	2.97**	1.46*	-5.54**	11.88**
ICPA 2047 x ICPL 20108	-1.09	-1.36	9.31**	0.37	-0.92	6.14**	-0.63	-9.51**	7.18**
ICPA 2047 X ICPL 20116	-0.14	-1.63*	8.41**	0.1	-0.19	4.16**	2.72**	-7.21**	9.9**
ICPA 2047 X ICPL 20123	0	-0.82	9.31**	-1.96**	-3.49**	3.96**	-5.05**	-5.78**	13.34**
ICPA 2048 x ICPL 87119	-2.05**	-2.72**	7.51**	-0.27	-0.91	7.92**	-1.24	-3.90**	3.71**
ICPA 2048 x ICPL 20108	-4.37**	-5.15**	5.11**	-2.40**	-2.58**	4.75**	-7.24**	-11.81**	-4.83**
ICPA 2048 X ICPL 20116	-7.09**	-7.99**	0.3	-1.03*	-2.76**	4.55**	-17.27**	-22.02**	-15.84**
ICPA 2048 X ICPL 20123	-3.31**	-3.58**	5.11**	-4.32**	-4.41**	2.97**	-10.89**	-15.47**	1.68
ICPA 2092 x ICPL 87119	-1.50*	-1.90**	8.41**	-5.48**	-7.45**	0.79	-2.33**	-5.94**	-3.96**
ICPA 2092 x ICPL 20108	-3.00**	-3.52**	6.91**	-1.12*	-2.40**	4.55**	14.58**	12.98**	9.9**
ICPA 2092 X ICPL 20116	-0.14	-1.37	8.11**	0.1	-0.19	4.16**	16.93**	16.32**	11.14**
ICPA 2092 X ICPL 20123	-1.38*	-1.92**	7.51**	-0.84	-2.39**	5.15**	-6.91**	-16.87**	0

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Crosses	Primary branches per plant			Secondary branches per plant			Number of pods per plant		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPA 2078 x ICPL 87119	4.35	-7.69	-18.18**	66.32**	64.58**	97.5**	-28.46**	-60.96**	-14.49**
ICPA 2078 x ICPL 20108	-10.81	-25.00**	-25**	24.59**	2.7	90**	-5.23**	-43.83**	-39.28**
ICPA 2078 x ICPL 20116	-6.45	-9.38	-34.09**	-2.08	-2.08	17.5	19.83**	-31.15**	-7.45**
ICPA 2078 x ICPL 20123	-20.55**	-32.56**	-34.09**	-11.25*	-36.61**	77.5**	-4.71**	-45.27**	-26.29**
ICPA 2043 x ICPL 87119	4.23	-5.13	-15.91*	46.43**	26.15**	105**	-32.64**	-56.09**	-3.83**
ICPA 2043 x ICPL 20108	2.63	-11.36	-11.36	9.35	2.7	90**	54.34**	24.65**	34.76**
ICPA 2043 x ICPL 20116	9.38	9.38	-20.45**	48.67**	29.23**	110**	46.11**	9.20**	46.8**
ICPA 2043 x ICPL 20123	1.33	-11.63	-13.64*	-0.56	-21.43**	120**	-3.90**	-28.22**	-3.34**
ICPA 2047 x ICPL 87119	-1.18	-8.7	-4.55	48.57**	11.83**	160**	-16.22**	-28.38**	56.87**
ICPA 2047 x ICPL 20108	4.44	2.17	6.82	32.93**	19.35**	177.5**	-14.58**	-27.59**	12.57**
ICPA 2047 X ICPL 20116	23.08**	4.35	9.09*	56.03**	18.28**	175**	5.50**	-1.64*	52.92**
ICPA 2047 X ICPL 20123	5.62	2.17	6.82**	-20.00**	-26.79**	105**	-11.48**	-17.40**	28.41**
ICPA 2048 x ICPL 87119	-3.61	-9.09	-9.09	53.72**	25.68**	132.5**	-8.19**	-25.90**	62.31**
ICPA 2048 x ICPL 20108	-6.82	-6.82	-6.82	13.51**	13.51*	110**	-20.52**	-28.32**	-3.57**
ICPA 2048 X ICPL 20116	15.79**	0.00	0.00	-26.23**	-39.19**	12.5	-59.32**	-59.34**	-45.29**
ICPA 2048 X ICPL 20123	12.64*	11.36	11.36**	52.69**	26.79**	255**	-4.12**	-4.17**	29.05**
ICPA 2092 x ICPL 87119	8.64	4.76	0.00	89.55**	45.98**	217.5**	20.98**	-5.09**	107.88**
ICPA 2092 x ICPL 20108	4.65	2.27	2.27	37.89**	27.59**	177.5**	134.08**	118.56**	172.41**
ICPA 2092 X ICPL 20116	13.51*	0.00	-4.55	6.67	-17.24**	80**	-6.16**	-9.58**	21.55**
ICPA 2092 X ICPL 20123	-15.29**	-16.28**	-18.18**	-34.67**	-41.96**	62.5**	-41.79**	-43.96**	-24.53**

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Crosses	Number of seeds per pod			100-seed weight (g)			Harvest index (%)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC
ICPA 2078 x ICPL 87119	4.90**	-0.93	-6.14**	5.94	-0.29	10.13*	-5.86*	-33.36**	-16.16**
ICPA 2078 x ICPL 20108	9.86**	0	2.63**	10.24**	4.87	15.82**	35.66**	0.54	9.06**
ICPA 2078 x ICPL 20116	8.29**	1.83	-2.63	8.89*	0.00	10.44*	79.94**	25.54**	66.11**
ICPA 2078 x ICPL 20123	-0.49	-6.42**	-10.53**	9.31*	2.58	13.29**	-13.08**	-37.97**	-24.04**
ICPA 2043 x ICPL 87119	1.89	0.00	-5.26*	1.16	-1.3	-3.8	-12.17**	-23.96**	-4.33
ICPA 2043 x ICPL 20108	4.07**	-1.71	0.88	6.25	2.54	2.22	25.50**	15.99**	25.81**
ICPA 2043 x ICPL 20116	-2.35	-4.59*	-8.77**	4.62	4.44	-3.16	-5.23*	-19.66**	6.31*
ICPA 2043 x ICPL 20123	7.04**	4.59*	0.00	-1.17	-3.27	-6.33	-14.75**	-25.34**	-8.57**
ICPA 2047 x ICPL 87119	-6.90**	-12.90**	-5.26*	7.93	1.62	-0.95	-4.94*	-7.28**	16.65**
ICPA 2047 x ICPL 20108	-2.90*	-5.65**	2.63**	2.21	-4.76	-5.06	72.01**	64.00**	96.16**
ICPA 2047 X ICPL 20116	-0.43	-6.45**	1.75	2.48	-1.03	-8.54	-14.27**	-18.39**	7.98**
ICPA 2047 X ICPL 20123	5.58**	-0.81	7.89**	10.38*	4.25	0.95	-11.36**	-12.39**	7.29**
ICPA 2048 x ICPL 87119	4.23**	2.78	-2.63	2.29	1.62	-0.95	-1.24	-6.58**	17.54**
ICPA 2048 x ICPL 20108	3.60*	-1.71	0.88	1.78	0.00	-0.32	-15.98**	-17.38**	-7.29**
ICPA 2048 X ICPL 20116	-16.82**	-18.35**	-21.93**	20.47**	18.09**	13.61**	-5.72**	-12.88**	15.27**
ICPA 2048 X ICPL 20123	2.8	0.92	-3.51	-0.98	-1.31	-4.43	-16.20**	-19.71**	-1.67
ICPA 2092 x ICPL 87119	0.95	-1.85	-7.02**	2.99	0.65	-1.9	3.19	-1.17	24.33**
ICPA 2092 x ICPL 20108	4.11**	-2.56	0.00	0.16	-3.17	-3.48	71.10**	66.12**	91.33**
ICPA 2092 X ICPL 20116	5.21**	1.83	-2.63	6.14	5.78	-1.58	-13.22**	-18.84**	7.39**
ICPA 2092 X ICPL 20123	8.06**	4.59*	0.00	20.67**	18.30**	14.56**	-27.53**	-29.69**	-13.89**

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Crosses	Seed protein (%)			Seed yield per plant (g)		
	MP	BP	SC	MP	BP	SC
ICPA 2078 x ICPL 87119	-1.73	-3.27	-19.57**	-36.79**	-65.97**	-12.94**
ICPA 2078 x ICPL 20108	-1.02	-1.82	-20.93**	10.34**	-35.80**	-23.19**
ICPA 2078 x ICPL 20116	-1.94	-3.15	-20.02**	71.74**	-0.93	26.2**
ICPA 2078 x ICPL 20123	2.59	-0.36	-14.86**	-13.42**	-51.04**	-26.81**
ICPA 2043 x ICPL 87119	-0.49	-1.25	-16.61**	-41.10**	-61.11**	-0.49
ICPA 2043 x ICPL 20108	7.05*	3.75	12.4**	47.36**	24.19**	48.59**
ICPA 2043 x ICPL 20116	6.81*	5.64	10.8**	57.96**	29.84**	65.39**
ICPA 2043 x ICPL 20123	-5.82*	-6.38*	-20**	-16.15**	-35.07**	-2.94*
ICPA 2047 x ICPL 87119	0.01	-1.87	-15.22**	-18.77**	-33.58**	69.94**
ICPA 2047 x ICPL 20108	-3.84	-7.82*	-20.37**	44.99**	25.85**	104.57**
ICPA 2047 X ICPL 20116	1.68	-0.55	-14.09**	13.42**	1.15	64.42**
ICPA 2047 X ICPL 20123	-5.70*	-6.21*	-18.98**	-15.46**	-18.85**	31.9**
ICPA 2048 x ICPL 87119	-1.65	-4.09	-16.09**	-9.95**	-28.01**	84.2**
ICPA 2048 x ICPL 20108	-2.21	-6.83*	-18.48**	-21.76**	-30.34**	6.75**
ICPA 2048 X ICPL 20116	-6.66*	-9.28**	-20.62**	-58.60**	-62.10**	-41.91**
ICPA 2048 X ICPL 20123	0.5	-0.68	13.1**	-12.37**	-13.44**	32.66**
ICPA 2092 x ICPL 87119	-4.11	-9.06**	-15.69**	8.12**	-17.86**	110.18**
ICPA 2092 x ICPL 20108	-4.14	-11.11**	-17.59**	126.64**	115.31**	186.21**
ICPA 2092 X ICPL 20116	-10.73**	-15.61**	-21.76**	11.81**	9.48**	45.53**
ICPA 2092 X ICPL 20123	-4.8	-8.53**	-15.19**	-38.39**	-41.80**	-13**

** Significant at 1% level

* Significant at 5% level

standard heterosis it ranged from -0.6% (ICPA-2078 x ICPL-87119) to 9.31% (ICPA-2047 x ICPL-20123 & ICPA-2047 x ICPL-20108). The cross ICPA-2047 x ICPL-87119 recorded maximum negative significant heterosis over mid parent (-7.21%) and ICPA-2078 x ICPL-87119 for better parent (-10.05%), while the cross ICPA-2078 x ICPL-87119 recorded negative non-significant standard heterosis (-0.6%) (Table 4.5).

Heterosis for mid parent was negative and highly significant in 12 hybrids, heterobeltiosis in 17 hybrids and negative non-significant standard heterosis was observed in one cross only. The hybrids ICPA-2078 x ICPL-87119 (L x H), ICPA-2078 x ICPL-20108 (L x H), ICPA-2048 x ICPL-20116 (H x H) and ICPA-2043 x ICPL-87119 (L x H) exhibited desirable heterobeltiosis for earliness. The *per se* performance and heterosis were in same direction. These results are supported by Manivel *et al.* (1999) and Dheva *et al.* (2008).

4.4.1.2 Days to 75% maturity: The cross ICPA-2043 x ICPL-87119 recorded maximum negative significant relative heterosis (-6.29%), heterobeltiosis (-10.55%) and significant standard heterosis (-2.57%). Heterosis over mid parent ranged from -6.29% (ICPA-2043 x ICPL-87119) to 2.63% (ICPA-2078 x ICPL-20123), whereas over better parent, it ranged from -10.55% (ICPA-2043 x ICPL-87119) to -0.19% (ICPA-2047 x ICPL-20116, ICPA-2048 x ICPL-87119 and ICPA-2092 x ICPL-20116) and standard heterosis from -2.57% (ICPA-2043 x ICPL-87119) to 7.92% (ICPA-2048 x ICPL-87119) (Table 4.5).

Heterosis over mid parent was negative and significant in 11 hybrids, heterobeltiosis in 15 hybrids and standard heterosis in one cross ICPA-2043 x ICPL-87119 with desirable *per se* performance. The significant negative heterosis for this trait is advantageous in getting early maturing hybrids. Salanki *et al.* (2008) reported that most of the promising hybrids shown significant negative heterosis for days to 75% maturity suggesting that high yield in hybrids can be achieved along with early maturity. Similar results were documented by Aher *et al.* (2006), Bhanu *et al.* (2007), Dheva *et al.* (2008a),

Shoba and Balan (2010), Pandey *et al.* (2013), Kumar *et al.* (2015), Mahsal *et al.* (2015), Reddy *et al.* (2015) and Singh and Singh (2016).

4.4.1.3 Plant height: The cross ICPA-2078 x ICPL-20116 recorded high percentage of heterosis over mid parent (26.13%), ICPA-2092 x ICPL-20116 over better parent (16.32%) and standard heterosis was high in the cross ICPA-2047 x ICPL-20123 (13.34%). Relative heterosis ranged from -17.27% (ICPA-2048 x ICPL-20116) to 26.13% (ICPA-2078 x ICPL-20116), heterobeltiosis ranged from -22.63% (ICPA-2043 x ICPL-20123) to 16.32% (ICPA-2092 x ICPL-20116) and standard heterosis ranged from -15.84% (ICPA-2048 x ICPL-20116) to 13.34% (ICPA-2047 x ICPL-20123) (Table 4.5).

Heterosis over mid parent was positive and significant in nine hybrids, heterobeltiosis in five hybrids and standard heterosis in nine hybrids. Standard heterosis was positive and significant in the cross combinations ICPA-2047 x ICPL-20123 (H X H), ICPA-2047 x ICPL-87119 (H x H) and ICPA-2092 x ICPL-20116 (L x L) with high *per se* performance and thus it can be utilized in breeding programme to obtain tall plants. Negative and significant heterosis was observed in ICPA-2048 x ICPL-20116 (H x L) and ICPA-2043 x ICPL-87119 (L x H) cross combinations over mid, better and standard parent, indicating the possibility of utilization of these hybrids in breeding programme to obtain dwarf plants. In present study, tall plants recorded high yield and hence, positive heterosis is desirable. Present results are in close agreement with earlier reports of several workers like Mehetre *et al.* (1993), Hooda *et al.* (1999), Khorgade *et al.* (2000a), Shoba and Balan (2010), Shoba and Balan (2010), Gite and Madrap (2014), Patel and Tikka (2014), Kumar *et al.* (2015), Reddy *et al.* (2015) and Singh and Singh (2016).

4.4.1.4 Primary branches per plant: The cross ICPA-2047 x ICPL-20116 recorded maximum value for relative heterosis (23.08%), ICPA-2048 x ICPL-20123 over better parent (11.36%) and standard heterosis (11.36%) for this trait. Heterosis over mid parent ranged from -20.55% (ICPA-2078 x ICPL-20123) to 23.08%, heterobeltiosis ranged from -32.56% (ICPA-2048 x ICPL-

20123) to 11.36% and standard heterosis ranged from -34.09% (ICPA-2048 x ICPL-20123) to 11.36% (Table 4.5).

Four hybrids recorded positive significant heterosis over mid parent, positive and non-significant heterobeltiosis was observed in seven hybrids and positive significant standard heterosis was observed in three hybrids. The hybrids *viz.*, ICPA-2048 x ICPL-20123 (H x H), ICPA-2047 x ICPL-20116 (H x L) and ICPA-2047 x ICPL-20123 (H x H) exhibited high standard heterosis in desirable direction along with high *per se* performance. Similar results were reported by Chaudhary *et al.* (1980), Narladkar and Khapre (1996), Hooda *et al.* (1999), Khorgade *et al.* (2000a), Pandey and Singh (2002), Sarode *et al.* (2009), Singh and Singh (2016), Patel and Tikka (2014), Gite and Madrap (2014). Pandey (1999), Shoba and Balan (2010) and Kumar *et al.* (2015) reported significant positive standard heterosis for this trait.

4.4.1.5 Secondary branches per plant: The cross ICPA-2092 x ICPL-87119 recorded high percentage of heterosis over mid parent (89.55%). Heterobeltiosis in ICPA-2078 x ICPL-87119 (64.58%) and standard heterosis in ICPA-2048 x ICPL-20123 (255.0%) were recorded for this trait. Relative heterosis ranged from -34.67% (ICPL-2092 x ICPL-20123) to 89.55%, heterobeltiosis ranged from -41.96% (ICPL-2092 x ICPL-20123) to 64.58% and standard heterosis ranged from 62.5% (ICPL-2092 x ICPL-20123) to 255.0% (Table 4.5).

Twelve hybrids recorded positive significant heterosis over mid parent, 11 hybrids over better parent, whereas 19 hybrids out of 20 hybrids showed positive significant heterosis over the standard check. The hybrids *viz.*, ICPA-2048 x ICPL-20123 (H X H), ICPA-2092 x ICPL-87119 (H X L), ICPA-2092 x ICPL-20108 (H X H), ICPA-2047 x ICPL-20108 (H X H), ICPA-2047 x ICPL-20116 (H X L) and ICPA-2047 x ICPL-87119 (H X L) exhibited high standard heterosis in desirable direction along with high *per se* performance. The six hybrids involving ICPA-2048, ICPA-2092 and ICPA-2047 as parents showed highest desirable standard heterosis along with high mean performance

for this trait. These results are in accordance with the results reported by Pandey and Singh (2002), Sarode *et al.* (2009), Chandirakala *et al.* (2010), Gite and Madrap (2014), Patel and Tikka (2014), Reddy *et al.* (2015) and Singh and Singh (2016).

4.4.1.6 Pods per plant: The cross ICPA-2092 x ICPL-20108 recorded maximum relative heterosis (134.08%), heterobeltiosis (118.56%) and standard heterosis (172.41%). Heterosis over mid parent ranged from -59.32% (ICPA-2048 x ICPL-20116) to 134.08%, heterobeltiosis from -60.96% (ICPA-2078 x ICPL-87119) to 118.56% and standard heterosis from -45.29% (ICPA-2048 x ICPL-20116) to 172.41% (Table 4.5).

Heterosis in positive direction is desirable for this trait as more pods can lead to higher seed yield per plant. Out of 20 hybrids, six hybrids showed positive significant relative heterosis, three hybrids showed heterobeltiosis and 11 hybrids showed positive significant standard heterosis. The two hybrids involving ICPA-2092 as one of the parent showed highest desirable standard heterosis along with high performance for this trait. 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), Sarode *et al.* (2009), Ajay *et al.* (2015), Patel and Tikka (2008), Sekhar *et al.* (2004) and Gite and Madrap (2014) over better parent, whereas Pandey (1999), Sekhar *et al.* (2004), Patel and Tikka (2008), Shoba and Balan (2010) and Reddy *et al.* (2015) for desirable heterosis over standard check.

4.4.1.7 Seeds per pod: The cross ICPA-2078 x ICPL-20108 recorded highest positive significant heterosis over mid parent (9.86%). Heterobeltiosis in ICPA-2092 x ICPL-20123 (4.59%) and standard heterosis in ICPA-2047 x ICPL-20123 (7.89%) were recorded for this trait. Relative heterosis ranged from -16.82% (ICPA-2048 x ICPL-20116) to 9.86%, heterobeltiosis from -18.35% (ICPA-2048 x ICPL-20116) to 4.59% and standard heterosis ranged from -21.93% (ICPA-2048 x ICPL-20116) to 7.89% for this trait (Table 4.5).

Heterosis over mid parent was positive and significant in 11 hybrids, heterobeltiosis in two hybrids and standard heterosis in three cross. The cross ICPA-2047 x ICPL-20123, ICPA-2078 x ICPL-20108 and ICPA-2047 x ICPL-20108 which involved high x high and low x high parental combinations showed high desirable standard heterosis with high mean performance for this trait. High heterosis was also reported earlier by Sarode *et al.* (2009) and Shoba and Balan (2010).

4.4.1.8 100-seed weight (g): The cross ICPA-2092 x ICPL-20123 recorded highest positive significant heterosis over mid parent (20.67%) and better parent (18.30%). Standard heterosis was recorded for ICPA-2078 x ICPL-20108 (15.82%). Relative heterosis ranged from -1.17% (ICPA-2043 x ICPL-20123) to 20.67%, heterobeltiosis from -4.76% (ICPA-2047 x ICPL-20108) to 18.30% and standard heterosis from -8.54% (ICPA-2047 x ICPL-20116) to 15.82% for this trait (Table 4.5).

Heterosis over mid parent was positive and significant in six hybrids, heterobeltiosis in two hybrids and standard heterosis in six hybrids. The cross ICPA-2078 x ICPL-20108, ICPA-2092 x ICPL-20123 and ICPA-2048 x ICPL-20116 which involved high x high, low x high and high x low parental combinations showed higher desirable standard heterosis with high mean performance 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) and Patel and Tikka (2014), while Chaudary *et al.* (1980), Manivel *et al.* (1999) and Gite and Madrap (2014) reported significant positive heterobeltiosis.

4.4.1.9 Harvest index: The cross ICPA-2078 x ICPL-20116 recorded maximum positive and significant heterosis over mid parent (79.94%). Heterobeltiosis was recorded for ICPA-2092 x ICPL-20108 (66.12%) and standard heterosis for ICPA-2047 x ICPL-20108 (96.16%). Relative heterosis ranged from -27.53% (ICPA-2092 x ICPL-20123) to 79.94%, heterobeltiosis from -37.97% (ICPA-2078 x ICPL-20123) to 66.12% and standard heterosis

ranged from -24.04% (ICPA-2078 x ICPL-20123) to 96.16% for this trait (Table 4.5).

Positive and significant values observed in five, four and 13 hybrids 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. High heterosis over mid-parent, better parent and standard check recorded in three hybrids (ICPA-2047 x ICPL-20108, ICPA-2092 x ICPL-20108 and ICPA-2078 x ICPL-20116) along with high *per se* performance. These hybrids can be exploited in hybrids production. The significant positive heterosis was also reported by Singh *et al.* (1983), Patel and Tikka (2014) and Singh and Singh (2016).

4.4.1.10 Seed yield per plant: Out of 20 hybrids, the cross ICPA-2092 x ICPL-20108 recorded maximum heterosis over mid parent (126.64%), better parent (115.31%) and standard check (186.21%) coupled with high *per se* performance. Relative heterosis for seed yield ranged from -58.60% (ICPL-2048 x ICPL-20116) to 126.64%, heterobeltiosis from -65.97% (ICPA-2078 x ICPL-87119) to 115.31% and standard heterosis from -41.91% (ICPL-2048 x ICPL-20116) to 186.21% (Table 4.5).

Nine hybrids showed positive significant heterosis over their mid parent, five hybrids over better parent and 13 hybrids over standard heterosis. The hybrids ICPA-2092 x ICPL-20108 and ICPA-2047 x ICPL-20108 may throw superior segregants for seed yield in the succeeding generations for selection and isolation of superior genotypes as they also had significant positive heterobeltiosis. These results are in conformity with the findings of Narladker and Kapre (1996), Manivel *et al.* (1999), Khorgade *et al.* (2000a), Pandey and Singh (2002), Sekhar *et al.* (2004), Aher (2006), Patel and Tikka (2008), Shoba and Balan (2010), Chandirakala *et al.* (2010), Vaghela *et al.* (2011), Pandey *et al.* (2013), Patil *et al.* (2014), Kumar *et al.* (2015), Reddy *et al.* (2015) and Singh and Singh (2016).

4.4.2 Quality attributes

4.4.2.1 Seed protein: The cross ICPA-2043 x ICPL-20108 recorded positive significant heterosis over mid parent (7.05%). The cross ICPA-2043 x ICPL-20116 recorded positive heterosis over better parent (5.64%), but standard heterosis was negative and significant (13.1%). Heterosis over mid parent ranged from -10.73% (ICPA-2092 x ICPL-20116) to 7.05%, heterobeltiosis from -15.61% (ICPA-2092 x ICPL-20116) to 5.64% and standard heterosis from -21.76% (ICPA-2092 x ICPL-20116) to 13.1% (Table 4.5).

Three hybrids (ICPA 2048 X ICPL 20123, ICPA 2043 x ICPL 20123 and ICPA 2043 x ICPL 20116) recorded positive significant heterosis over standard parent, along with high *per se* performance. Significant positive heterosis was also observed earlier by Khorgade *et al.* (2000a), Patel and Tikka (2014) and Patil *et al.* (2014), while negative heterosis was noticed by Pankaja Reddy *et al.* (1979) for seed protein.

In present investigation, the cross combinations, ICPA-2092 x ICPL-20108, ICPA-2047 x ICPL-20108, ICPA-2047 x ICPL-20116 and ICPA-2047 x ICPL-20123 showed positive significant heterosis in desirable direction for most of the traits along with seed yield. The differences in the magnitude of positive and negative heterosis in hybrids for different characters indicates presence of dominance or positive action of genes. Wide range of heterosis recorded for different characters can be exploited due to non-allelic interaction.

In most of the cross combinations the significant positive heterosis was observed for seed yield per plant was mainly due to the manifestation of heterosis for its component characters *viz.*, plant height, secondary branches per plant, pods per plant, harvest index. This clearly indicates that heterosis for seed yield was through heterosis for individual component characters.

4.5 COMBINING ABILITY

Combining ability studies help 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 11 characters and mean sum of squares are presented in Table 4.6. Treatments (genotypes) registered highly significant differences for all the characters. The parents and hybrids exhibited significant differences for all the characters, while parents vs. hybrids also showed significant differences for all the characters except primary branches per plant.

The effects of hybrids were partitioned into lines, testers and their interactions. The lines were found to be significant for days to 50% flowering, primary branches per plant and 100-seed weight(g). Among testers, the differences were non-significant for all the characters. The interaction effects (lines x testers) were found to be significant for all the characters.

Estimates of the relative contribution of *gca* and *sca* in a population are of interest to plant breeders, as selection of breeding methods most appropriate for specific objectives may differ appreciably based on type of gene action. 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 in the study (Table 4.7 and Fig. 4.4). Estimates of additive and dominance variance indicated that the dominance variance was predominant for all the characters.

Non-additive gene action was found high for pods per plant followed by seed yield per plant, harvest index and plant height.

In the present investigation, the combining ability analysis was carried out based on mean value of five plants for nine parents and twenty hybrids derived from 5 lines x 4 testers programme. General combining ability effects of the parents and specific combining ability effects of hybrids are presented in the Table 4.8 and Table 4.9 for parents and hybrids, respectively, and the results and discussion are presented character wise hereunder.

4.5.1 Yield Attributes

4.5.1.1 Days to 50% flowering: The lines ICPB-2078 (-3.58) and ICPB-2043 (-3.17) had highly significant negative *gca* effect which is related to earliness. None of the testers recorded significant *gca* effects for this trait, indicating there is limited variability for improving this character. The lines ICPB-2092 (3.58) and ICPB-2047 (3.17) showed positive significant *gca* effects (Table 4.8).

Five hybrids *viz.*, ICPA-2047 x ICPL-87119 (-4.90), ICPA-2048 x ICPL-20116 (-4.33), ICPA-2043 x ICPL-20116 (-1.50), ICPA-2078 x ICPL-87119 (-1.48) and ICPA-2078 x ICPL-20108 (-1.42) recorded negative and highly significant *sca* effects indicating the possibility of improvement for early flowering. On contrary, the hybrids *viz.*, ICPA-2048 x ICPL-87119 (3.93), ICPA-2078 x ICPL-20116 (3.58), ICPA-2047 x ICPL-20108 (1.83), ICPA-2047 x ICPL-20123 (1.57) and ICPA-2047 x ICPL-20116 (1.50) registered positive and highly significant *sca* effects, indicating that these hybrids late in flowering (Table 4.9).

Non-additive gene action recorded for days to 50% flowering in the present investigation was in confirmity with the results reported by Pandey (1999), Jayamala and Rathnaswamy (2000), Pandey and Singh (2002), Sekhar *et al.* (2004), Patel *et al.* (2010) and Patel and Tikka (2015).

Table 4.6. Analysis of variance for combining ability in Line x Tester design for 11 characters in pigeonpea

Source of variation	Df	Days 50% to flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
Replications	2	10.25**	0.65	4.00	1.70	12.86**	5.58	0.07**	0.03	0.35	0.91	0.80
Treatments	28	84.06**	83.92**	696.25**	11.66**	201.34**	55906.25**	0.18**	2.06**	312.72**	1.58**	4890.24**
Parents	8	182.45**	171.67**	1565.96**	12.62**	170.83**	63237.60**	0.23**	1.48**	200.47**	2.11**	5969.87**
Parents vs Hybrids	1	54.04**	63.35**	190.17**	1.82	493.87**	111.70**	0.12**	7.26**	99.46**	2.58*	156.17**
Hybrids	19	44.21**	48.06**	356.70**	11.77**	198.78**	55755.92**	0.17**	2.04**	371.20**	1.31*	4684.82**
Lines	4	137.21**	104.73	800.29	42.31**	216.64	93235.74**	0.17	5.34*	227.56	1.03	8098.74
Testers	3	4.71	27.33	41.88	0.68	202.37	37248.83	0.31	0.27	804.63	0.33	4982.43
Line x Tester	12	23.09**	34.35**	287.53**	4.36**	191.94**	47889.42**	0.14**	1.37**	310.73**	1.65**	3472.45**
Error	56	1.63	2.02	2.59	1.51	3.15	14.30	0.10	0.36	1.38	0.60	1.37

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

Table 4.7. Magnitude of genetic variance due to general and specific combining abilities for 11 characters in 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 50% to flowering	0.62	7.20	0.09	1.23	7.20	0.17
2	Days to 75% maturity	0.40	10.76	0.04	0.80	10.76	0.07
3	Plant height (cm)	2.02	94.81	0.02	4.04	94.81	0.04
4	Primary branches per plant	0.22	0.95	0.23	0.43	0.95	0.46
5	Secondary branches per plant	0.20	62.68	0.00	0.40	62.68	0.01
6	Number of pods per plant	229.59	15956.63	0.01	459.18	15956.63	0.03
7	Number of seeds per pod	0.00	0.04	0.02	0.00	0.04	0.04
8	100-seed weight (g)	0.02	0.32	0.06	0.04	0.32	0.12
9	Harvest index (%)	1.77	102.99	0.02	3.53	102.99	0.03
10	Seed protein (%)	0.01	0.35	0.03	0.02	0.35	0.06
11	Seed yield per plant (g)	35.38	1157.02	0.03	70.77	1157.02	0.06

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

Parents	Days to 50% flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
LINES											
ICPB2078	-3.58**	-2.35**	-1.25*	-2.77**	-6.40**	-116.97**	-0.04	1.10**	-2.38**	-0.36	-32.95**
ICPB2043	-3.17**	-3.77**	-7.24**	-0.93**	-1.65**	-11.17**	-0.01	-0.50**	-3.71**	0.45*	-7.11**
ICPB2047	3.17**	1.98**	12.12**	1.98**	4.77**	38.74**	0.18**	-0.57**	5.50**	-0.01	21.01**
ICPB2048	0.00	3.23**	-7.26**	1.15**	1.18*	-32.02**	-0.14**	-0.00	-3.32**	0.01	-12.17**
ICPB2092	3.58**	0.90*	3.63**	0.57	2.10**	121.43**	0.02	-0.01	3.90**	-0.09	31.21**
SE	0.35	0.41	0.51	0.36	0.57	1.28	0.03	0.19	0.38	0.22	0.34
(gi-g)	0.50	0.58	0.72	0.50	0.80	1.80	0.04	0.27	0.54	0.32	0.48
TESTERS											
ICPL87119	-0.60	-1.93**	-1.99**	-0.08	3.18**	49.34**	-0.09**	-0.16	-2.76**	0.10	8.71**
ICPL20108	0.33	1.20**	-0.75	0.32	1.38**	32.69**	0.17**	-0.02	9.22**	-0.17	18.82**
ICPL20116	-0.33	0.27	1.61**	-0.15	-5.28**	-23.96**	-0.15**	0.01	1.64**	-0.07	-4.10**
ICPL20123	0.60	0.47	1.13*	-0.08	0.72	-58.07**	0.07**	0.17	-8.10**	0.14	-23.44**
SE	0.31	0.37	0.45	0.32	0.51	1.14	0.02	0.17	0.34	0.20	0.30
(gi-gj)	0.44	0.52	0.64	0.45	0.72	1.61	0.03	0.24	0.48	0.28	0.43

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

Table 4.9. Estimation of specific combining ability (*sca*) effects in hybrids for yield and yield components in pigeonpea

Crosses	Days 50% to flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
ICPA 2078 x ICPL 87119	-1.48*	0.35	0.11	1.50*	0.40	-30.03**	0.01	-0.08	-5.66**	-0.25	-11.35**
ICPA 2078 x ICPL 20108	-1.42*	-1.12	-0.63	0.10	1.20	-78.17**	0.09	0.38	-9.11**	-0.26	-28.65**
ICPA 2078 x ICPL 20116	3.58**	-2.85**	-2.82**	-0.77	-1.80	61.68**	0.20**	-0.22	17.77**	-0.17	28.93**
ICPA 2078 x ICPL 20123	-0.68	3.62**	3.33**	-0.83	0.20	46.52**	-0.31**	-0.08	-2.99**	0.69	11.07**
ICPA 2043 x ICPL 87119	1.10	-3.90**	-6.90**	0.00	-3.35**	-107.96**	0.01	0.05	-0.33	-0.45	-28.46**
ICPA 2043 x ICPL 20108	0.50	0.63	-3.27**	0.27	-3.55**	9.56**	-0.01	0.54	-2.11**	0.71	-4.12**
ICPA 2043 x ICPL 20116	-1.50*	3.90**	15.50**	-0.60	5.78**	97.68**	-0.06	-0.05	-1.13	0.94*	30.59**
ICPA 2043 x ICPL 20123	-0.10	-0.63	-5.34**	0.33	1.12	0.72	0.06	-0.54	3.57**	-1.20**	1.98**
ICPA 2047 x ICPL 87119	-4.90**	-0.32	3.75**	-1.25	-2.43*	0.79	-0.18**	0.42	-2.44**	0.30	-7.14**
ICPA 2047 x ICPL 20108	1.83**	1.88*	-3.83**	0.02	1.70	-98.36**	-0.13*	-0.15	12.48**	-0.49	7.05**
ICPA 2047 X ICPL 20116	1.50*	-0.52	-2.52*	0.82	8.03**	63.76**	0.15**	-0.55	-9.77**	0.71	1.79**
ICPA 2047 X ICPL 20123	1.57*	-1.05	2.60*	0.42	-7.30**	33.80**	0.17**	0.29	-0.27	-0.52	-1.69*
ICPA 2048 x ICPL 87119	3.93**	6.77**	12.13**	-1.08	-2.52*	85.76**	0.24**	-0.15	6.68**	0.11	36.04**
ICPA 2048 x ICPL 20108	0.33	-1.70*	-0.61	-1.15	-3.72**	-69.79**	0.12*	-0.22	-13.70**	-0.12	-28.42**
ICPA 2048 X ICPL 20116	-4.33**	-1.10	-17.80**	0.32	-10.05**	-122.20**	-0.43**	1.21**	1.51*	-0.67	-39.65**
ICPA 2048 X ICPL 20123	0.07	-3.97**	6.28**	1.92**	16.28**	106.24**	0.06	-0.84*	5.52**	0.68	32.02**
ICPA 2092 x ICPL 87119	1.35	-2.90**	-9.10**	0.83	7.90**	51.44**	-0.09	-0.24	1.76*	0.29	10.90**
ICPA 2092 x ICPL 20108	-1.25	0.30	8.33**	0.77	4.37**	236.76**	-0.08	-0.55	12.45**	0.17	54.15**
ICPA 2092 X ICPL 20116	0.75	0.57	7.64**	0.23	-1.97	-100.92**	0.14*	-0.38	-8.37**	-0.81	-21.66**
ICPA 2092 X ICPL 20123	-0.85	2.03*	-6.88**	-1.83*	-10.30**	-187.28**	0.02	1.17**	-5.83**	0.35	-43.39**
S.E	0.70	0.83	1.01	0.71	1.14	2.55	0.05	0.38	0.77	0.45	0.68
Sij-Sjk	2.98	3.51	4.31	3.03	4.83	10.83	0.23	1.60	3.25	1.90	2.88

The lines *viz.*, ICPB-2078 and ICPB-2043 were found to be good combiners for earliness as indicated by significant negative *gca* effects and may be used in crop improvement programmes in the development of genotypes with earliness. Five hybrids recorded significant negative *sca* effects *viz.*, ICPA-2047 x ICPL-87119 (H x H), ICPA-2048 x ICPL-20116 (H x H), ICPA-2043 x ICPL-20116 (L x H), ICPA-2078 x ICPL-87119 (L x H) and ICPA-2078 x ICPL-20108 (L x H). Out of five hybrids, three hybrids 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 cross combinations.

4.5.1.2 Days to 75% maturity: The lines ICPB-2043 (-3.77) and ICPB-2078 (-2.35) and the tester ICPL-87119 (-1.93) showed significant negative *gca* effect indicating their use as general combiners in getting early maturing types. Among the lines ICPB-2048 (3.23), ICPB-2047 (1.98), ICPB-2092 (0.90) and the testers ICPL-20108 (1.20) recorded positive significant *gca* effects (Table 4.8).

The hybrids, ICPA-2048 x ICPL-20123 (-3.97), ICPA-2043 x ICPL-87119 (-3.90), ICPA-2092 x ICPL-87119 (-2.90), ICPA-2078 x ICPL-20116 and ICPA-2048 x ICPL-20108 (-1.70) showed significant and negative *sca* effects indicating that the possibility to get early maturing hybrids whereas, ICPA-2048 x ICPL-87119 (6.77), ICPA-2043 x ICPL-20116 (3.90), ICPA-2078 x ICPL-20123 (3.62), ICPA-2092 x ICPL-20123 (2.03) and ICPA-2047 x ICPL-20108 (1.88) recorded positive and highly significant *sca* effect indicating late maturity (Table 4.9).

High magnitude of *sca* variance than *gca* variance indicates non-additive gene action for this trait. The predominance of non-additive gene action in the inheritance of days to 75% 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), Raju and Muthiah (2007), Patel *et al.* (2010) and Patel and Tikka (2015).

The lines ICPB-2043 and ICPB-2078 and the tester ICPL-87119 displayed negative significant *gca* effects for days to 75% maturity. Hence, they can be utilized as good donor sources in breeding for earliness. The resulted cross combinations between them also showed significant negative *sca* effects for early maturity. Five hybrids recorded significant negative *sca* effects *viz.*, ICPA-2048 x ICPL-20123 (H x H), ICPA-2043 x ICPL-87119 (L x H), ICPA-2092 x ICPL-87119 (H x H) and ICPA-2078 x ICPL-20116 (L x L). ICPA-2048 x ICPL-20108 (H x H) Out of five hybrids, two hybrids 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.

4.5.1.3 Plant height: The lines ICPB-2047 (12.12), ICPB-2092 (3.63) and the testers ICPL-20116 (1.61), ICPL-20123 (1.13) recorded significant positive effect for plant height, whereas the line ICPB-2048 (-7.26), ICPB-2043 (-7.24), ICPB-2078 (-1.25) and the testers ICPL-87119 (-1.99) (Table 4.8) showed highly significant negative *gca* effect indicating the possibility of obtaining dwarf plants. The high *sca* effect than *gca* effect indicated the importance of non-additive gene action for plant height.

Eight out of 20 hybrids ICPA-2043 x ICPL-20116 (15.50), ICPA-2048 x ICPL-87119 (12.13), ICPA-2092 x ICPL-20108 (8.33), ICPA-2092 x ICPL-20116 (7.64), ICPA-2048 x ICPL-20123 (6.28), ICPA-2047 x ICPL-87119 (3.75), ICPA-2078 x ICPL-20123 (3.33) and ICPA-2047 x ICPL-20123 (2.60) recorded positive significant *sca* effects with high *per se* performance for this trait (Table 4.9).

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), Patel *et al.* (2010) and Patel and Tikka (2015).

4.5.1.4 Primary branches per plant: Positive significant *gca* effects were observed in the lines ICPB-2047 (1.98) and ICPB-2048 (1.15) along with high *per se* performance. On contrary, the line ICPB-2078 (-2.77) and ICPB-2043 (-0.93) recorded negative significant *gca* effects. None of the testers were positive significant for this trait (Table 4.8).

Only one cross ICPA-2048 x ICPL-20123 (H X H) recorded significant *sca* effect with high performance (Table 4.9), indicating the operation of additive gene action and can be exploited through pedigree method. 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), Yadav *et al.* (2008), Phad *et al.* (2009) and Patel and Tikka (2015) in the inheritance of primary branches per plant.

4.5.1.5 Secondary branches per plant: The lines ICPB-2047 (4.77), ICPB-2092 (2.10) and ICPB-2048 (1.18) and the testers ICPL-87119 (3.18) and ICPL-20108 (1.38) recorded highly significant positive *gca* effect. On contrary, the lines ICPB-2078 (-6.40) and ICPB-2043 (-1.65) and the testers ICPL-20116 (-5.28) showed significant and negative *gca* effects (Table 4.8).

Out of 20 hybrids, five hybrids recorded positive and significant and eight hybrids recorded negative and significant *sca* effects for this trait indicating operation of non-additive gene action.

Lines, *viz.*, ICPB-2047, ICPB-2092 and ICPB-2048 recorded positive significant *gca* effect along with high mean performance and they were found to be best general combiners. Out of 20 hybrids, five hybrids *viz.*, ICPA-2048 x ICPL-20123 (H x H), ICPA-2047 x ICPL-20116 (H x L), ICPA-2092 x ICPL-87119 (H x L) and ICPA-2092 x ICPL-20108 (H x H) with high *per se* performance. The second cross involved one parent with significant *gca* effect and the other with poor negative *gca* effects and may throw the desirable

transgressive segregants if additive genetic system present in good combiners and the epistatic effects present in cross acts in a complementary fashion to maximize desirable plant attributes which could be exploited for further breeding purposes. Hence these combinations may be handled through diallel mating or intermating in segregating populations followed by cyclic selections for improving this character.

Srinivas *et al.* (1998), Jahagirdar (2003), Sunilkumar *et al.* (2003), Pandey (2004), Raju and Muthiah (2007), Vaghela *et al.* (2009) and Yamunura *et al.* (2014) also reported similar results.

4.5.1.6 Pods per plant: The lines ICPB-2092 (121.43) and ICPB-2047 (38.74) and the testers ICPL-87119 (49.34) and ICPL-20108 (32.69) recorded highly significant positive *gca* effect for this trait indicating their use as good general combiners to get maximum pods per plant. On contrary, the genotypes, ICPB-2078 (-116.97), ICPB-2048 (-32.02), ICPB-2043 (-11.17) and ICPL-20123 (-58.07) and ICPL-20116 (-23.96) recorded negative significant *gca* effects (Table 4.8).

Ten hybrids recorded positive significant *sca* effects for this trait and eight hybrids recorded negative non-significant *sca* effects indicating that the trait controlled by non-additive gene action.

Non-additive gene action was predominant for pods per plant in the present study and is in agreement with earlier reports of Pandey (1999), Jayamala and Rathnaswamy (2000), Ajay Kumar *et al.* (2001), Sunilkumar *et al.* (2003), Sekhar *et al.* (2004), Raju and Muthiah (2007), Yadav *et al.* (2008), Vaghela *et al.* (2009), Phad *et al.* (2009), Gupta *et al.* (2011), Patil *et al.* (2015) and Patel and Tikka (2015).

Among the lines, ICPB-2092 and ICPB-2047 and the tester ICPL-87119 were found to be best general combiners. The cross combinations, ICPA-2092 x ICPL-20108 (H X L), ICPA-2048 x ICPL-20123 (H X H) and ICPA-2043 x ICPL-20116 (L X H), ICPA-2048 x ICPL-87119 (H x H), ICPA-2047 x ICPL-

20116 (H x H), ICPA-2092 x ICPL-87119 (H x H), ICPA-2047 x ICPL-20123 (H x H), ICPA-2043 x ICPL-20108 (L x L) recorded significant *sca* effects. These results clearly indicated that the hybrids showing H X H combinations may be exploited through the simple pedigree method while H X L and L X L cross combinations through diallel selective mating or intermating in segregating populations followed by cyclic selections for improvement this character.

4.5.1.7 Seeds per pod: The line ICPB-2047 (0.18) and the testers ICPL-20108 (0.17) and ICPL-20123 (0.07) showed positive significant *gca* effect with high *per se* performance and it can be utilized as good general combiner in breeding programmes for improving this trait. The lines ICPB-2048 (-0.14) and the testers ICPL-20116 (-0.15) and ICPL-87119 (-0.09) showed negative significant *gca* effects (Table 4.8).

Among hybrids, ICPA-2048 x ICPL-87119 (0.24), ICPA-2078 x ICPL-20116 (0.20), ICPA-2047 x ICPL-20123 (0.17), ICPA-2047 x ICPL-20116 (0.15), ICPA-2092 x ICPL-20116 (0.14) and ICPA-2048 x ICPL-20108 (0.12) showed significant positive *sca* effect with high *per se* performance and were found to be good specific combiners, while seven hybrids, ICPA-2048 x ICPL-20116 (-0.43), ICPA-2078 x ICPL-20123 (-0.31), ICPA-2047 x ICPL-87119 (-0.18) and ICPA-2047 x ICPL-20108 (-0.13) recorded negative significant *sca* effects (Table 4.9).

Non-additive gene action was found to be important in controlling this character, which is in agreement with the results of Patel *et al.* (1992), Ajay Kumar *et al.* (2001), Lohithaswa and Dharmaraj (2003), Sekhar *et al.* (2004), Raju and Muthiah (2007), Yadav *et al.* (2008), Patel *et al.* (2010) and Patel and Tikka (2015).

4.5.1.8 100-seed weight (g): The line ICPB-2078 (1.10) showed positive and significant *gca* effect (Table 4.8) and it can be utilized as good general combiner in breeding programmes for improving this trait. None of the testers

were found to be the good combiners. The lines ICPB-2047 (-0.57) and ICPB-2043 (-0.50) showed negative significant *gca* effects.

Among hybrids, ICPA-2048 x ICPL-20116 (1.21) and ICPA-2092 x ICPL-20123 (1.17) recorded desirable positive and significant *sca* effects for this trait (Table 4.9). ICPA-2048 x ICPL-20123 (-0.84) had negative significant *sca* effect. The hybrids, ICPA-2048 x ICPL-20116 (H X L) and ICPA-2092 x ICPL-20123 (L X H) were found to be good specific combiners. The importance of non-additive gene action for 100-seed weight as recorded in this present study 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), Vaghela *et al.* (2009), Gupta *et al.* (2011), Patel *et al.* (2010) and Patel and Tikka (2015).

4.5.1.9 Harvest index: Among parents, the lines ICPB-2047 (5.50) and ICPB-2092 (3.90) and the testers ICPL-20108 (9.22) and ICPL-20116 (1.64) recorded highly significant positive *gca* effect. On contrary, the genotypes, ICPB-2043 (-3.71), ICPB-2048 (-3.32), ICPB-2078 (-2.38), ICPL-20123 (-8.10) and ICPL-87119 (-2.76) recorded negative significant *gca* effects (Table 4.8).

Out of 20 hybrids, eight hybrids recorded positive significant and nine hybrids recorded negative significant *sca* effects and thus it is evident that harvest index is under the control of non-additive gene action.

This type results were reported by Patel *et al.* (1992), Sekhar *et al.* (2004) and Patel and Tikka (2015).

Among the lines, ICPB-2047 and ICPB-2092 and the tester ICPL-20116 were found to be best general combiners. The cross combinations, ICPA-2078 x ICPL-20116 (L x H), ICPA-2047 x ICPL-20108 (H x L), ICPA-2092 x ICPL-20108 (H x L), ICPA-2048 x ICPL-87119 (H x H) and ICPA-2092 x ICPL-87119 (H x H) exhibited positive significant *sca* effects besides high *per se* performance. The superiority of hybrids 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 and high x high cross combination may be exploited through the simple pedigree method.

4.5.1.10 Seed yield per plant (g): The lines ICPB-2092 (31.21) and ICPB-2047 (21.01) and the testers ICPL-20108 (18.82) and ICPL-87119 (8.71) recorded highly significant positive *gca* effects. On contrary, the lines ICPB-2078 (-32.95), ICPB-2048 (-12.17) and ICPB-2043 (-7.11) and the tester ICPL-20123 (-23.44), ICPL-20116 (-4.10) reported highly significant negative *gca* effects (Table 4.8).

Out of 20 hybrids, 10 hybrids recorded positive significant *sca* effects while 10 hybrids recorded negative significant *sca* effects.

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), Patel *et al.* (2010), Gupta *et al.* (2011), Parmar *et al.* (2012), Meshram *et al.* (2013), Yamunura *et al.* (2014), Patil *et al.* (2015), Patel and Tikka (2015) and Tikle *et al.* (2016).

For seed yield per plant, the lines ICPB-2047 and the tester ICPL-87119 were found to be good general combiners for their utility in breeding programmes in the improvement of seed yield. The hybrids ICPA-2043 x ICPL-20116 (L X L), ICPA-2047 x ICPL-20108 (H X L), ICPA-2047 x ICPL-20116 (H x L), ICPA-2048 x ICPL-87119 (H x H), ICPA-2092 x ICPL-87119 (L x H) and ICPA-2092 x ICPL-20108 (L X L) recorded significant *sca* effects. These results clearly indicates that the hybrids showing H X H combination may be exploited through the simple pedigree method while the other combinations (H X L or L X L) 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, only one line ICPB-2043 (0.45) showed positive significant *gca* effect and among hybrids, one cross ICPA-2043 x ICPL-20116 (0.94) showed positive significant *sca* effect with high *per se* performance. The superiority of cross (ICPA-2043 x ICPL-20116) with low x low combination may be due to complementary gene action. 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.

Low *gca* / *sca* variance ratio, indicated that seed protein is controlled by non-additive gene action, which was also reported by Patel *et al.* (2010) and Patel and Tikka (2015)

Based on the overall *gca* effects, the hybrids were classified as H X H, H X L, L X H combinations. 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 hybrids indicating major role of non-additive gene action. So these hybrid combinations are suitable for heterosis breeding. The combinations of H X H or L X L can be utilized to get useful transgressive segregants in the subsequent segregating generations.

From the results of study, it is concluded that based on *per se* performance and *gca* effects of the parents, ICPB-2078 and ICPB-2043 were the best general combiners for days to 50% flowering and days to 75% maturity, while ICPB-2047 for plant height, primary branches per plant, secondary branches per plant, seeds per pod, harvest index and seed yield per

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

S. NO	Character(s)	Best performing parents	Good general combiner	Best performing crosses	Crosses with high <i>sca</i> effect	Crosses with high standard heterosis
1	Days 50% to flowering	ICPB-2078 ICPB-2043	ICPB-2078 ICPB-2043 ICPL-87119	ICPA-2078 x ICPL-87119 ICPA-2043 x ICPL-20116 ICPA-2078 x ICPL-20108	ICPA-2047 x ICPL-87119 ICPA-2048 x ICPL-20116 ICPA-2043 x ICPL-20116	ICPA-2078 x ICPL-87119
2	Days to 75% maturity	ICPB-2078 ICPB-2043 ICPL-20116	ICPB-2043 ICPB-2078 ICPL-87119	ICPA-2043 x ICPL-87119 ICPA-2078 x ICPL-20116 ICPA-2078 x ICPL-87119	ICPA-2048 x ICPL-20123 ICPA-2043 x ICPL-87119 ICPA-2092 x ICPL-87119	ICPA-2043 x ICPL-87119
3	Plant height (cm)	ICPL-20123 ICPB-2047 ICPB-2048	ICPB-2047 ICPB-2092 ICPL-20116	ICPA-2047 x ICPL-20123 ICPA-2047 x ICPL-87119 ICPA-2092 x ICPL-20116	ICPA-2043 x ICPL-20116 ICPA-2048 x ICPL-87119 ICPA-2092 x ICPL-20108	ICPA-2047 x ICPL-20123 ICPA-2047 x ICPL-87119 ICPA-2092 x ICPL-20116
4	Primary branches per plant	ICPB-2047 ICPB-2048 ICPL-20108	ICPB-2047 ICPB-2048	ICPA-2048 x ICPL-20123 ICPA-2047 x ICPL-20116 ICPA-2047 x ICPL-20123	ICPA-2048 x ICPL-20123 ICPA-2078 x ICPL-87119	ICPA-2048 x ICPL-20123 ICPA-2047 x ICPL-20116 ICPA-2047 x ICPL-20123
5	Secondary branches per plant	ICPL-20123 ICPB-2047 ICPB-2092	ICPB-2047 ICPL-87119 ICPB-2092	ICPA-2048 x ICPL-20123 ICPA-2092 x ICPL-87119 ICPA-2092 x ICPL-20108	ICPA-2048 x ICPL-20123 ICPA-2047 x ICPL-20116 ICPA-2092 x ICPL-87119	ICPA-2048 x ICPL-20123 ICPA-2092 x ICPL-87119 ICPA-2092 x ICPL-20108 ICPA-2047 x ICPL-20108
6	Number of pods per plant	ICPL-87119 ICPB-2047 ICPL-20123	ICPB-2092 ICPL-87119 ICPB-2047	ICPA-2092 x ICPL-20108 ICPA-2092 x ICPL-87119 ICPA-2048 x ICPL-87119	ICPA-2092 x ICPL-20108 ICPA-2048 x ICPL-20123 ICPA-2043 x ICPL-20116	ICPA-2092 x ICPL-20108 ICPA-2092 x ICPL-87119 ICPA-2048 x ICPL-87119

Cont...

S. NO	Character	Best performing parents	Good general combiner	Best performing crosses	Crosses with high sca effect	Crosses with high standard heterosis
7	Number of seeds per pod	ICPB-2047 ICPL-20108 ICPL-20116	ICPB-2047 ICPL-20108	ICPA-2047 x ICPL-20123 ICPA-2047 x ICPL-20108 ICPA-2078 x ICPL-20108	ICPA-2048 x ICPL-87119 ICPA-2047 x ICPL-20123 ICPA-2047 x ICPL-20116	ICPA-2047 x ICPL-20123 ICPA-2047 x ICPL-20108 ICPA-2078 x ICPL-20108
8	100-seed weight (g)	ICPB-2078 ICPL-20108 ICPL-87119	ICPB-2078	ICPA-2078 x ICPL-20108 ICPA-2092 x ICPL-20123 ICPA-2048 x ICPL-20116	ICPA-2048 x ICPL-20116 ICPA-2092 x ICPL-20123	ICPA-2078 x ICPL-20108 ICPA-2092 x ICPL-20123 ICPA-2048 x ICPL-20116
9	Harvest index (%)	ICPL-20116 ICPL-87119 ICPB-2047	ICPL-20108 ICPB-2047 ICPB-2092	ICPA-2047 x ICPL-20108 ICPA-2092 x ICPL-20108 ICPA-2078 x ICPL-20116	ICPA-2078 x ICPL-20116 ICPA-2047 x ICPL-20108 ICPA-2092 x ICPL-20108	ICPA-2047 x ICPL-20108 ICPA-2092 x ICPL-20108 ICPA-2078 x ICPL-20116
10	Seed protein (%)	ICPB-2092 ICPB-2048 ICPB-2047 ICPL-20123	ICPB-2043	ICPA-2043 x ICPL-20116 ICPA-2043 x ICPL-20108 ICPA-2048 x ICPL-20123	ICPA-2043 x ICPL-20116	ICPA-2043 x ICPL-20116 ICPA-2043 x ICPL-20108 ICPA-2048 x ICPL-20123
11	Seed yield per plant (g)	ICPL-87119 ICPB-2047 ICPB-2048	ICPB-2092 ICPB-2047 ICPL-20108	ICPA-2092 x ICPL-20108 ICPA-2092 x ICPL-87119 ICPA-2047 x ICPL-20108	ICPA-2092 x ICPL-20108 ICPA-2048 x ICPL-87119 ICPA-2043 x ICPL-20116	ICPA-2092 x ICPL-20108 ICPA-2092 x ICPL-87119 ICPA-2047 x ICPL-20108

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

S.No.	Hybrids	Mean seed yield (g)	Heterosis		Gca effect		sca effect	Useful and significant heterosis for component traits in desired direction
			BP	SC	Line	Tester		
1	ICPA-2092 x ICPL-20108	200.86	115.31**	186.21**	31.21**	18.82**	54.15**	PH, SB, PP, HI, SY
2	ICPA-2092 x ICPL-87119	147.51	-17.86**	110.18**	31.21**	8.71**	10.90**	SB, PP, HI, SY
3	ICPA-2047 x ICPL-20108	143.57	25.85**	104.57**	21.01**	18.82**	7.05**	PH, SB, PP, HI, SY
4	ICPA-2048 x ICPL-87119	129.27	-28.01**	84.2**	-12.17**	8.71**	36.04**	PH, SB, PP, HI, SY
5	ICPA-2047 x ICPL-87119	119.27	-33.58**	69.94**	21.01**	8.71**	-7.14**	PH, SB, PP, HI, SY
6	ICPA-2043 x ICPL-20116	116.07	29.84**	65.39**	-7.11**	-4.10**	30.59**	PH, SB, PP, HI, SY
7	ICPA-2047 x ICPL-20116	115.39	1.15	64.42**	21.01**	-4.10**	1.79**	PH, SB, PP, HI, SY
8	ICPA-2043 x ICPL-20108	104.28	24.19**	48.59**	-7.11**	18.82**	-4.12**	SB, PP, HI, 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	Lines x Testers interaction
1	Days 50% to flowering	65.34	1.68	32.98
2	Days to 75% maturity	45.88	8.98	45.14
3	Plant height (cm)	47.23	1.85	50.91
4	Primary branches per plant	75.67	0.92	23.41
5	Secondary branches per plant	22.94	16.07	60.98
6	Number of pods per plant	35.20	10.55	54.25
7	Number of seeds per pod	20.79	28.39	50.82
8	100-seed weight (g)	55.24	2.09	42.67
9	Harvest index (%)	12.91	34.23	52.87
10	Seed protein (%)	16.51	4.00	79.50
11	Seed yield per plant (g)	36.39	16.79	46.81

plant. ICPB-2092, ICPB-2078 and ICPB-20123 were the promising parents for pods per plant, 100-seed weight and seed protein.

Critical observation of *per se* performance, standard heterosis and *sca* effects of hybrids, indicated ICPA-2078 x ICPL-20116, ICPA-2048 x ICPL-20116 and ICPA-2092 x ICPL-20123, were the promising hybrids for harvest index and 100-seed weight, while ICPA-2043 x ICPL-20116 and ICPA-2048 x ICPL-87119 for plant height, pods per plant, seed protein and seed yield per plant. Whereas ICPA-2047 x ICPL-20116 and ICPA-2048 x ICPL-20123 for primary and secondary branches per plant, pods per plant, seeds per pod and seed yield per plant, ICPA-2078 x ICPL-87119 for days to 50% flowering and ICPA-2043 x ICPL-87119 for days to 75% maturity. Similarly, the hybrids *viz.*, ICPA-2092 x ICPL-87119 and ICPA-2092 x ICPL-20108 were found to be most rewarding for pods per plant, harvest index, secondary branches per plant and seed yield (Table 4.10). The details of the hybrids 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 (%) was presented in Table 4.12. The contribution of lines towards total variation was maximum in respect of days to 50% flowering, days to 75% maturity, primary branches per plant. Plant height, secondary branches per plant, pods per plant, seeds per pod, harvest index, seed protein and seed yield per plant which are attributable highly by the line x tester interaction.

4.6 CHARACTER ASSOCIATION

Generally, direct selection for yield is not aimed at, as it is a complex and quantitatively inherited character and is highly influenced by environment. 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 obtained revealed that the genotypic correlation coefficients were higher than phenotypic correlation coefficients and in the same direction. Significant phenotypic correlations will be useful when coupled with significant genotypic correlations. Here, phenotypic and genotypic correlation coefficients were computed separately for parents and hybrids 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. 4.5 and 4.6, respectively.

4.6.1 Association of Yield Components with Seed Yield in Parents and hybrids

Seed yield per plant showed significant and positive association with days to 50% flowering (0.798**, 0.543**), days to 75% maturity (0.845**, 0.264*), plant height (0.684**, 0.521**), primary branches per plant (0.494**, 0.430**), pods per plant (0.987**, 0.933**), seeds per pod (0.428*, 0.274*) and harvest index (0.799**, 0.710**). Further, secondary branches per plant, and seed protein recorded positive correlations with seed yield per plant. 100-seed weight showed significant and negative association with seed yield (Table 4.13).

Seed yield per plant was associated significantly and positively with all characters except 100-seed weight and seed protein. 100-seed weight was associated significantly and negatively with seed yield. Seed protein showed positive association at phenotypic level and positive and significant association at genotypic level with seed yield per plant.

Seed yield had positive significant association with all the characters except secondary branches per plant, 100-seed weight and seed protein in parents, while in hybrids, all the characters had positive significance with seed yield except 100-seed weight and seed protein. Seed yield can be increased with an increase in days to 50% flowering, days to 75% maturity, plant height, primary branches per plant, pods per plant, seeds per pod and harvest index in

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

Characters		Days 50% to flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
Days 50% to flowering	P	1.0000	0.913**	0.788**	0.729**	0.425*	0.832**	0.602**	-0.541**	0.892**	0.268	0.798**
	G	1.0000	0.936**	0.803**	0.844**	0.439*	0.844**	0.682**	-0.689**	0.910**	0.418*	0.811**
Days to 75% maturity	P		1.0000	0.759**	0.675**	0.363	0.843**	0.461*	-0.313	0.822**	0.140	0.845**
	G		1.0000	0.755**	0.805**	0.377*	0.858**	0.527**	-0.429*	0.839**	0.258	0.859**
Plant height (cm)	P			1.0000	0.682**	0.681**	0.700**	0.656**	-0.622**	0.792**	0.312	0.684**
	G			1.0000	0.801**	0.695**	0.702**	0.705**	-0.804**	0.799**	0.424*	0.685**
Primary branches per plant	P				1.0000	0.653**	0.496**	0.509**	-0.331	0.462*	0.354	0.494**
	G				1.0000	0.767**	0.585**	0.712**	-0.486**	0.567**	0.445*	0.587**
Secondary branches per plant	P					1.0000	0.134	0.376*	-0.369*	0.303	0.379*	0.122
	G					1.0000	0.136	0.406*	-0.428*	0.315	0.619**	0.126
Number of pods per plant	P						1.0000	0.477**	-0.456*	0.857**	0.206	0.987**
	G						1.0000	0.511**	-0.584**	0.861**	0.301	0.987**
Number of seeds per pod	P							1.0000	-0.451*	0.551**	-0.015	0.428*
	G							1.0000	-0.735**	0.576**	-0.185	0.455*
100-seed weight (g)	P								1.0000	-0.608**	-0.324	-0.402*
	G								1.0000	-0.809**	-0.717**	-0.520**
Harvest index (%)	P									1.0000	0.260	0.799**
	G									1.0000	0.384*	0.801**
Seed protein (%)	P										1.0000	0.197
	G										1.0000	0.283
Seed yield per plant (g)	P											1.0000
	G											1.0000

** Significant at 0.01; * Significant at 0.05

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

Characters		Days 50% to flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
Days 50% to flowering	P	1.0000	0.417**	0.436**	0.508**	0.397**	0.448**	0.486**	-0.360**	0.369**	-0.070	0.543**
	G	1.0000	0.484**	0.473**	0.653**	0.422**	0.467**	0.563**	-0.491**	0.391**	-0.076	0.569**
Days to 75% maturity	P		1.0000	0.401**	0.279*	0.072	0.153	0.073	0.002	0.170	0.072	0.264*
	G		1.0000	0.438**	0.396**	0.097	0.165	0.089	-0.048	0.190	0.005	0.282*
Plant height (cm)	P			1.0000	0.228	0.335**	0.450**	0.434**	-0.252	0.234	0.107	0.521**
	G			1.0000	0.250	0.343**	0.457**	0.456**	-0.358**	0.238	0.180	0.528**
Primary branches per plant	P				1.0000	0.597**	0.419**	0.172	-0.475**	0.240	-0.060	0.430**
	G				1.0000	0.677**	0.503**	0.210	-0.739**	0.280*	-0.002	0.519**
Secondary branches per plant	P					1.0000	0.627**	0.261*	-0.605**	0.181	0.241	0.608**
	G					1.0000	0.645**	0.286*	-0.766**	0.188	0.537**	0.627**
Number of pods per plant	P						1.0000	0.193	-0.509**	0.491**	0.241	0.933**
	G						1.0000	0.205	-0.682**	0.495**	0.461**	0.933**
Number of seeds per pod	P							1.0000	-0.255*	0.194	-0.075	0.274*
	G							1.0000	-0.367**	0.209	-0.101	0.294*
100-seed weight (g)	P								1.0000	-0.194	-0.037	-0.524**
	G								1.0000	-0.257*	-0.553**	-0.702**
Harvest index (%)	P									1.0000	-0.147	0.710**
	G									1.0000	-0.303*	0.714**
Seed protein (%)	P										1.0000	0.163
	G										1.0000	0.299*
Seed yield per plant (g)	P											1.0000
	G											1.0000

** Significant at 0.01; * Significant at 0.05

Fig. 4.5. Phenotypic correlation of yield components with seed yield of pigeonpea

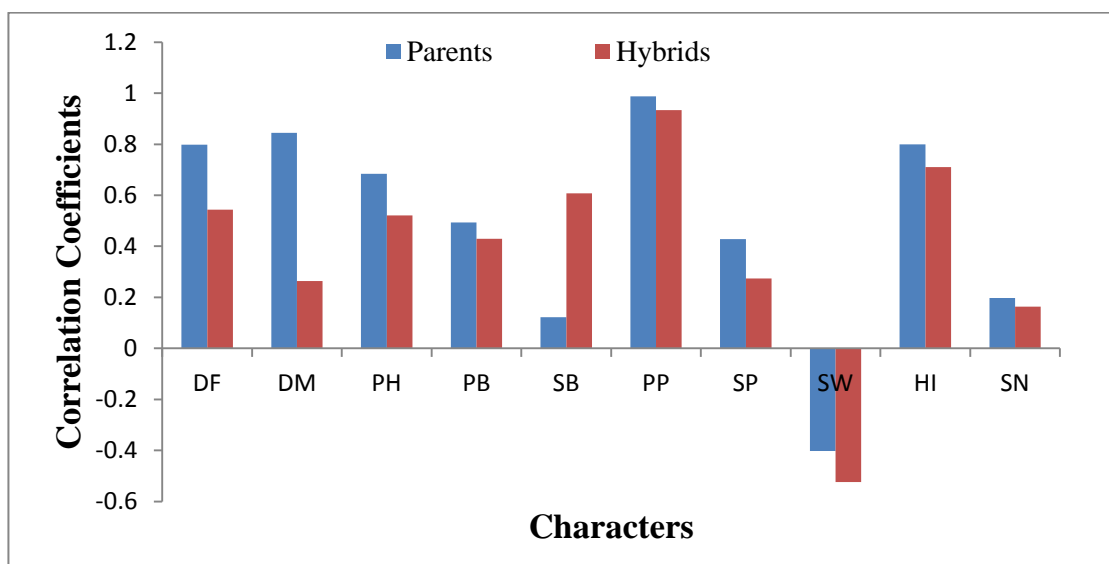
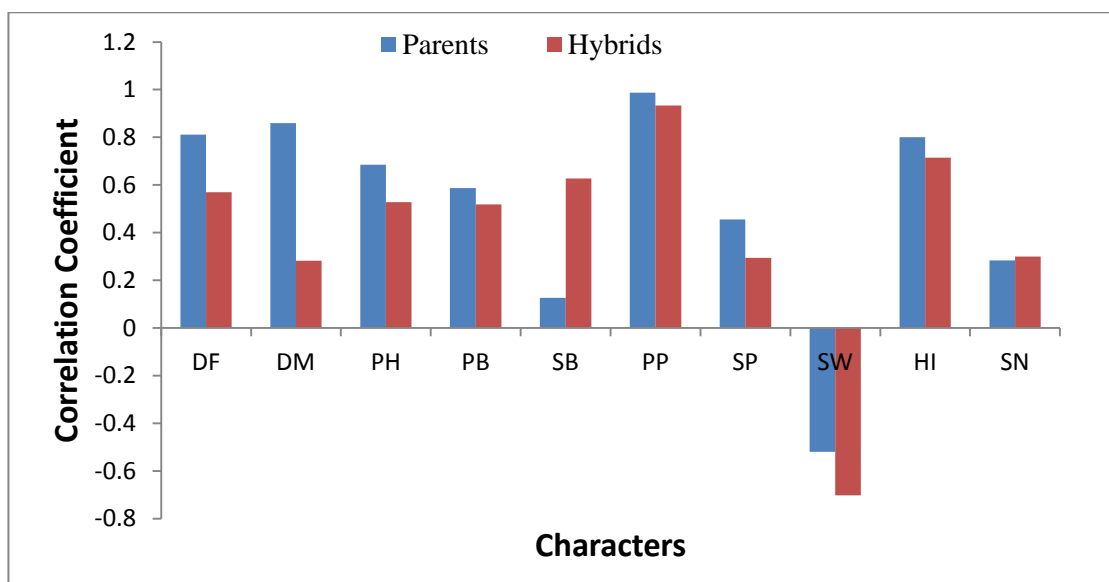


Fig. 4.6. Genotypic correlation of yield components with seed yield of pigeonpea



DF= Days to 50% flowering	SB= Secondary branches per plant	HI= Harvest index
DM= Days to 75% maturity	PP= Pods per plant	SN= Seed protein
PH= Plant height	SP= Seeds per pod	
PB= Primary branches per plant	SW= 100-seed weight	

parents and hybrids and secondary branches per plant in hybrids. Hence, these characters can be considered as selection criteria for selection of higher yielding genotypes as these are directly associated with seed yield. Similar results were reported 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), Mahajan *et al.* (2007), Jogendra Singh *et al.* (2008), Dodake *et al.* (2009), Balyan and Sudhakar (1985), Bhongale and Raut (1987), Salunke *et al.* (1995), Srinivas *et al.* (1999) and Bhadru (2010).

4.6.2. Association among Yield Components in Parents and hybrids

In parents, pods per plant showed significant and positive association with plant height (0.700**), days to 75% maturity (0.843**) and days to 50% flowering (0.832**) and primary branches per plant (0.496**), while the association was positive non-significant with secondary branches per plant. It was indicated that increase in plant height, days to 75% maturity, days to 50% flowering and primary branches per plant will increase pods per plant, finally the total seed yield. In hybrids, pods per plant was associated positively and significantly with plant height (0.450**), days to 50% flowering (0.448**), primary branches per plant (0.419**) and secondary branches per plant (0.627**), while its association with days to 75% maturity was non-significant and positive. It was indicated that increase in plant height, days to 50% flowering, primary branches per plant and secondary branches per plant 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 Vanisree and Sreedhar (2014), Saroj *et al.* (2013) and Kothimbire *et al.* (2015) for days to 50% flowering, Chandhirikala and Subbaraman (2010) and Kothimbire *et al.* (2015) for days to 75% maturity, Bhadru (2010), Linge *et al.* (2010), Prakash (2011), Rekha *et al.* (2013) and Saroj *et al.* (2013) for primary branches per plant, Linge *et al.* (2010), Prakash (2011), Prasad *et al.* (2013), Rekha *et al.* (2013), Saroj *et al.* (2013) and Arbad *et al.* (2014) for plant height.

Secondary branches per plant displayed significant and positive association with days to 50% flowering (0.425*, 0.397**), plant height (0.681**, 0.335**) and primary branches per plant (0.653**, 0.597**) and positive non-significant association with days to 75% maturity in parents and hybrids. This is in confirmity with the results of Bhadru (2010), Linge *et al.* (2010), Prakash (2011) and Rekha *et al.* (2013) for days to 50% flowering, Anuradha *et al.* (2007), Linge *et al.* (2010), Prakash (2011) and Rekha *et al.* (2013) for days to 75% maturity, Prakash (2011), Devi *et al.* (2012), Rekha *et al.* (2013) and Saroj *et al.* (2013) for primary branches per plant and Rekha *et al.* (2013), Arbad *et al.* (2014), Pandey *et al.* (2015) for Plant height.

Plant height manifested significant positive association with days to 50% flowering (0.788**, 0.436**) and days to 75% maturity (0.759**, 0.401**) in parents and hybrids. These results were in accordance with the findings of Rekha *et al.* (2013) for days to 75% maturity and Bharathi and Saxena (2013) and Saroj *et al.* (2013) for days to 50% flowering.

Primary branches per plant had significant positive association with days to 50% flowering (0.729**), plant height (0.682**) and days to 75% maturity (0.675**) in parents, while in hybrids it had positive significant association with days to 50% flowering (0.508**) and days to 75% maturity (0.279*). The results indicated that increase in days to 50% flowering, plant height and days to 75% maturity in parents and days to 50% flowering and days to 75% maturity in hybrids will increase pods per plant, finally it will result in improvement of seed yield. These results were in accordance with the results of Anuradha *et al.* (2007), Das *et al.* (2007), Prakash (2011), Vange and Moses (2009) and Saroj *et al.* (2013) for days to 50% flowering and days to 75% maturity, while Bhadru *et al.* (2010), Linge *et al.* (2010), Nagy *et al.* (2013), Rekha *et al.* (2013) and Saroj *et al.* (2013) for Plant height.

Days to 75% maturity expressed significant and positive association with days to 50% flowering (0.913**, 0.417**) in parents and in hybrids, indicated that delay in flowering will increase in crop duration. This was also

supported by Prakash (2011), Hamid *et al.* (2011), Nagy *et al.* (2013), Prasad *et al.* (2013), Rekha *et al.* (2013) and Saroj *et al.* (2013).

Harvest index exhibited significant positive association with days to 75% maturity (0.822**), days to 50% flowering (0.892**), primary branches per plant (0.462*), plant height (0.792**), pods per plant (0.857**) and seeds per pod (0.551**), while it had positive non-significant correlation with secondary branches per plant suggesting that increase in days to 75% maturity, days to 50% flowering, primary branches per plant, plant height, pods per plant and seeds per pod will increase harvest index. In hybrids, harvest index had high and positive and significant association with days to 50% flowering (0.369**), pods per plant (0.491**), while it had positive and non-significant correlation with days to 75% maturity, plant height, secondary branches per plant and seeds per pod indicating that increase in days to 50% flowering and pods per plant will increase the harvest index. Similar results were also reported earlier by Mittal *et al.* (2010), Pandey *et al.* (2016), Sodavadiya *et al.* (2009), Kothimbire *et al.* (2015) and Pandey *et al.* (2015).

Seeds per pod expressed positive and significant association with days to 50% flowering, days to 75% maturity, plant height, primary and secondary branches per plant and pods per plant in parents, while it had positive and significant association with days to 50% flowering, plant height and secondary branches per plant revealing that increase in these characters may increase in seeds per pod. This trait showed positive non-significant association with days to 75% maturity, primary branches per plant and pods per plant in hybrids. These results were in agreement with the reports of Nethravathi and patil (2014), Pandey *et al.* (2016), Vijayalakshmi *et al.* (2013), Arbad *et al.* (2014), Ajay *et al.* (2016), Sodavadiya *et al.* (2009), Pandey *et al.* (2015), Bhadru (2010), Kothimbire *et al.* (2015) and Saroj *et al.* (2013).

The trait, 100-seed weight exhibited significant and negative association with days to 50% flowering (-0.541**), plant height (-0.622**), secondary branches per plant (-0.369*), pods per plant (-0.456*) and seeds per pod

(-0.451*). In hybrids, 100-seed weight exhibited significant and negative association with days to 50% flowering (-0.360**), primary branches per plant (-0.475**), secondary branches per plant (-0.605**), pods per plant (-0.509**) and seeds per pod (-0.255*). These results in tune with the findings of Patel *et al.* (2011), Singh *et al.* (2013), Vanisree *et al.* (2013), Rao *et al.* (2013), Patel and Acharya (2011), Pandey *et al.* (2015), Saroj *et al.* (2013), Nagy *et al.* (2013) and Rekha *et al.* (2013).

Seed protein had positive and non-significant association with days to 50% flowering (0.268), days to 75% maturity (0.140), plant height (0.312), primary branches per plant (0.354), pods per plant (0.206) and harvest index (0.260), it had positive and significant association with secondary branches per plant (0.379*). In hybrids, the trait exhibited positive and non-significant association with days to 75% maturity and plant height, secondary branches per plant and pods per plant. None of the characters showed positive and significant association with seed protein. These results are in close agreement with Baskaran and Muthiah (2007), Rekha *et al.* (2013) and Devi *et al.* (2012).

It was evident from the present investigation that highly significant and positive association of pods per plant, days to 50% flowering, days to 75% maturity, plant height, primary branches per plant, pods per plant, seeds per pod, harvest index with seed yield per plant in parents and hybrids. Seed protein had non-significant and positive association with seed yield in parents and hybrids. The positive and non-significant association of secondary branches per plant with seed yield in parents became positive and significant in hybrids.

Non-significant and positive associations observed among the yield components in parents *viz.*, were secondary branches per plant with pods per plant become significant and positive in hybrids. The positive and significant association in parents between character pairs *viz.*, plant height with primary branches per plant; days to 75% maturity with pods per plant and seeds per pod; days to 75% maturity, plant height, primary branches per plant, seeds per

pod with harvest index; seeds per pod with pods per plant, primary branches per plant and seed protein with secondary branches per plant became non-significant in hybrids.

Negative and significant association of among character pairs in parents became negative and significant in hybrids *viz.*, 100-seed weight with plant height and harvest index. Negative non-significant association of 100-seed weight with primary branches per plant in parents became negative and significant in hybrids.

Positive and non-significant association of harvest index with seed protein and seed protein with primary branches per plant in parents became negative and non-significant in hybrids. Negative and non-significant association of 100-seed weight with days to 75% maturity in parents became Positive and non-significant in hybrids. These changes in correlations between pairs of characters in parents and hybrids might have resulted due to the modifications in the linkages as a result of re-combinations in the populations.

In general, the yield component traits which showed significant and positive association with seed yield in parents and hybrids are of prime importance in determining the seed yield. Such a situation is favourable to a plant breeder as it helps in simultaneous improvement of the characters along with seed yield *per se*. Hence, the emphasis should be given on days to 50% flowering, days to 75% maturity, plant height, primary branches per plant, pods per plant, seeds per pod and harvest index for obtaining higher yield in pigeonpea.

4.7 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and a particular yield component is the net result of direct effect of component traits 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 sometimes may be not fruitful. If the direct effect is equal to correlation co-efficient, then correlation explains the true relationship and simple and direct selection will be effective for this traits.

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 nine parents and 20 hybrids was worked out and furnished in Tables 4.14 and 4.15 respectively. The results and discussion are presented hereunder.

4.7.1 Direct and Indirect Effects of Yield Attributes

4.7.1.1 Days to 50% flowering

In parents, days to 50% flowering exhibited negligible positive direct effect on seed yield (0.0225). It had positive indirect effects through days to 75% maturity (0.1592), plant height (0.0763) and pods per plant (0.8531) which resulted in positive correlation with seed yield (0.798**). In hybrids this trait exhibited direct positive effect on seed yield (0.0507). Its positive indirect effects through days to 75% maturity (0.0305), plant height (0.0333), secondary branches per plant (0.0372), pods per plant (0.2773), 100-seed weight (0.0317) and harvest index (0.1302) resulted in positive correlation with seed yield (0.543**). Its positive direct effect on seed yield was also reported earlier by Bhadru (2010), Rathore and Sharma (2011), Sreelakshmi *et al.* (2011), Reddy and Rangare (2013) and Saroj *et al.* (2013).

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

Characters		Days 50% to flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
Days 50% to flowering	P	0.0225	0.1592	0.0763	-0.0473	-0.0104	0.8531	-0.0057	-0.0051	-0.2991	-0.0004	0.798**
	G	-0.0946	0.1908	0.0588	0.0152	-0.0232	0.8218	-0.0029	-0.0187	-0.2849	0.0002	0.811**
Days to 75% maturity	P	0.0207	0.1733	0.0729	-0.0425	-0.0094	0.8622	-0.0041	-0.0032	-0.2758	-0.0024	0.845**
	G	-0.0891	0.2026	0.0563	0.0142	-0.0211	0.8316	-0.0021	-0.0122	-0.2624	0.0030	0.859**
Plant height (cm)	P	0.0170	0.1248	0.1013	-0.0510	-0.0130	0.7127	-0.0072	-0.0056	-0.2655	0.0045	0.684**
	G	-0.0725	0.1486	0.0767	0.0168	-0.0287	0.6778	-0.0036	-0.0206	-0.2496	-0.0065	0.685**
Primary branches per plant	P	0.0138	0.0958	0.0672	-0.0769	-0.0101	0.4574	-0.0058	-0.0025	-0.1409	0.0081	0.494**
	G	-0.0668	0.1336	0.0596	0.0216	-0.0254	0.5133	-0.0038	-0.0107	-0.1606	-0.0120	0.587**
Secondary branches per plant	P	0.0110	0.0762	0.0617	-0.0366	-0.0213	0.1809	-0.0026	-0.0037	-0.1097	-0.0013	0.122
	G	-0.0473	0.0921	0.0476	0.0119	-0.0463	0.1739	-0.0013	-0.0124	-0.1057	0.0012	0.126
Number of pods per plant	P	0.0186	0.1451	0.0701	-0.0341	-0.0037	1.0298	-0.0048	-0.0043	-0.2909	0.0010	0.987**
	G	-0.0795	0.1723	0.0532	0.0113	-0.0082	0.9776	-0.0024	-0.0156	-0.2726	-0.0015	0.987**
Number of seeds per pod	P	0.0113	0.0627	0.0646	-0.0396	-0.0050	0.4413	-0.0113	-0.0036	-0.1694	0.0028	0.428*
	G	-0.0543	0.0849	0.0531	0.0161	-0.0120	0.4540	-0.0051	-0.0173	-0.1675	-0.0026	0.455*
100-seed weight (g)	P	-0.0124	-0.0595	-0.0614	0.0208	0.0084	-0.4789	0.0044	0.0093	0.2073	-0.0020	-0.402*
	G	0.0673	-0.0943	-0.0603	-0.0088	0.0219	-0.5824	0.0034	0.0262	0.2572	0.0056	-0.520**
Harvest index (%)	P	0.0199	0.1412	0.0795	-0.0320	-0.0069	0.8850	-0.0056	-0.0057	-0.3385	0.0018	0.799**
	G	-0.0854	0.1684	0.0607	0.0110	-0.0155	0.8442	-0.0027	-0.0214	-0.3157	-0.0028	0.801**
Seed protein (%)	P	-0.0004	-0.0210	0.0232	-0.0315	0.0014	0.0494	-0.0016	-0.0010	-0.0312	0.0199	0.197
	G	0.0007	-0.0231	0.0191	0.0100	0.0022	0.0556	-0.0005	-0.0057	-0.0345	-0.0259	0.283

** Significant at 0.01; * Significant at 0.05

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

Characters		Days 50% to flowering	Days to 75% maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Harvest index (%)	Seed protein (%)	Seed yield per plant (g)
Days 50% to flowering	P	0.0507	0.0305	0.0333	-0.0327	0.0372	0.2773	-0.0005	0.0317	0.1302	-0.0023	0.543**
	G	0.0834	-0.0189	0.0491	0.0880	-0.0210	0.2146	0.0103	-0.0374	0.1920	-0.0218	0.569**
Days to 75% maturity	P	0.0211	0.0732	0.0307	-0.0160	0.0066	0.0948	-0.0001	0.0001	0.0599	0.0024	0.264*
	G	0.0404	-0.0389	0.0454	0.0491	-0.0047	0.0759	0.0018	-0.0038	0.0936	0.0014	0.282*
Plant height (cm)	P	0.0221	0.0294	0.0765	-0.0133	0.0309	0.2789	-0.0005	0.0223	0.0827	0.0035	0.521**
	G	0.0394	-0.0170	0.1038	0.0306	-0.0169	0.2101	0.0086	-0.0272	0.1167	0.0519	0.528**
Primary branches per plant	P	0.0255	0.0180	0.0157	-0.0649	0.0580	0.2730	-0.0002	0.0440	0.0879	0.0012	0.430**
	G	0.0540	-0.0140	0.0234	0.1359	-0.0352	0.2400	0.0041	-0.0573	0.1426	0.0024	0.519**
Secondary branches per plant	P	0.0199	0.0051	0.0250	-0.0398	0.0946	0.3865	-0.0003	0.0536	0.0615	0.0078	0.608**
	G	0.0348	-0.0036	0.0348	0.0951	-0.0504	0.2945	0.0053	-0.0587	0.0888	0.1536	0.627**
Number of pods per plant	P	0.0227	0.0112	0.0345	-0.0286	0.0590	0.6194	-0.0002	0.0452	0.1733	0.0080	0.933**
	G	0.0390	-0.0064	0.0475	0.0710	-0.0323	0.4594	0.0036	-0.0523	0.2429	0.1331	0.933**
Number of seeds per pod	P	0.0244	0.0056	0.0336	-0.0119	0.0244	0.1124	-0.0011	0.0219	0.0647	-0.0026	0.274*
	G	0.0464	-0.0039	0.0485	0.0299	-0.0145	0.0891	0.0185	-0.0274	0.0959	-0.0215	0.294*
100-seed weight (g)	P	-0.0184	-0.0001	-0.0195	0.0327	-0.0580	-0.3201	0.0003	-0.0874	-0.0685	-0.0014	-0.524**
	G	-0.0411	0.0019	-0.0372	-0.1027	0.0390	-0.3167	-0.0067	0.0759	-0.1262	-0.1573	-0.702**
Harvest index (%)	P	0.0187	0.0124	0.0179	-0.0162	0.0165	0.3043	-0.0002	0.0170	0.3528	-0.0049	0.710**
	G	0.0326	-0.0074	0.0247	0.0395	-0.0091	0.2272	0.0036	-0.0195	0.4910	-0.0876	0.714**
Seed protein (%)	P	-0.0035	0.0053	0.0082	-0.0024	0.0224	0.1496	0.0001	0.0036	-0.0523	0.0331	0.163
	G	-0.0063	-0.0002	0.0187	0.0011	-0.0268	0.2118	-0.0014	-0.0413	-0.1490	0.2887	0.299*

** Significant at 0.01; * Significant at 0.05

4.7.1.2 Days to 75% maturity

Days to 75% maturity had high positive direct effect on seed yield (0.1733) but its positive indirect effects *via* days to 50% flowering (0.0207), plant height (0.0729) and pods per plant (0.8622) nullified indirect negative effects and resulted high positive correlation with seed yield (0.845**). In hybrids this trait exhibited negligible positive direct effect on seed yield (0.0732). But its positive indirect effects *via* days to 50% flowering (0.0211), plant height (0.0307), secondary branches per plant (0.0066), pods per plant (0.0948), 100-seed weight (0.001), harvest index (0.0599) and seed protein (0.0024) suppressed negative indirect effects and resulted in positive correlation with seed yield (0.264**). Positive direct effect of days to 75% maturity on seed yield was supported by Mahajan *et al.* (2007), Birhan (2013), Nag and Sharma (2012) and Pandey *et al.* (2016).

4.7.1.3 Plant height (cm)

Plant height exhibited high direct positive effect on seed yield (0.1013). The low positive indirect effects through days to 50% flowering (0.0170), days to 75% maturity (0.1248), pods per plant (0.7127) and seed protein (0.0045) suppressed negative indirect effects and resulted in positive correlation with seed yield (0.684**). In hybrids plant height had negligible positive direct effect on seed yield (0.0765). The indirect positive effects *via* days to 50% flowering (0.0221), days to 75% maturity (0.0294), secondary branches per plant (0.0309), pods per plant (0.2789), 100-seed weight (0.0223), harvest index (0.0827) and seed protein (0.0035) suppressed negative indirect effects and resulted in positive correlation with seed yield (0.521**). The positive direct effect on seed yield was confirmity with the results of Chattopadyay and Dhiman (2005) and Baskaran and Muthiah (2007).

4.7.1.4 Primary branches per plant

In parents, primary branches per plant had low negative direct effect on seed yield (-0.0769). The indirect positive effects *via* days to 50% flowering

(0.0138), days to 75% maturity (0.0958), plant height (0.0672), pods per plant (0.4574) and seed protein (0.0081) suppressed negative direct and indirect effects and resulted in positive correlation with seed yield (0.494**). In hybrids, primary branches per plant showed negative direct effect on seed yield (-0.0649). Its positive indirect effects *via* days to 50% flowering (0.0255), days to 75% maturity (0.0180), plant height (0.0157), secondary branches per plant (0.0580), pods per plant (0.2730), 100-seed weight (0.0440), harvest index (0.0879) and seed protein (0.0012) nullified negative direct and indirect effects and resulted in high positive correlation with seed yield (0.430**). Its negative direct effect on seed yield was also reported earlier by Saroj *et al.* (2013) and Vijayalakshmi *et al.* (2013).

4.7.1.5 Secondary branches per plant

In parents, secondary branches per plant had low negative direct effect on seed yield (-0.0213). Its positive indirect effects *via* days to 50% flowering (0.0110), days to 75% maturity (0.0762), plant height (0.0617) and pods per plant (0.1809) nullified direct and indirect negative effects and resulted high positive correlation with seed yield (0.122). In hybrids, it had positive direct effect on seed yield (0.0946). Its positive indirect effects *via* days to 50% flowering (0.0199), days to 75% maturity (0.0051), plant height (0.0250), pods per plant (0.3865), 100-seed weight (0.0536), harvest index (0.0615) and seed protein (0.0078) suppressed negative indirect effects and produced high positive correlation with seed yield (0.608**). Negative direct effect on seed yield in parents was supported by Vijayalakshmi *et al.* (2013), Arbad *et al.* (2014), Pandey *et al.* (2016), Saroj *et al.* (2013), Ram *et al.* (2016), Pandey *et al.* (2015) and Sreelakshmi *et al.* (2010). Its positive direct effect on seed yield in hybrids was also reported by Bhadru (2010), Kothimbire *et al.* (2015), Singh *et al.* (2010) and Devi *et al.* (2012).

4.7.1.6 Pods per plant

In parents, pods per plant had high direct effect of this trait on seed yield was high and positive (1.0298). Its positive indirect effects *via* days to 50%

flowering (0.0186), days to 75% maturity (0.1451), plant height (0.0701) and seed protein (0.0010) nullified the negative indirect effects and resulted in highly significant positive correlation with seed yield (0.987**). In hybrids, pods per plant had high positive direct effect on seed yield (0.6194). It also exerted positive indirect effects *via* days to 50% flowering (0.0227), days to 75% maturity (0.0112), plant height (0.0345), secondary branches per plant (0.0590), 100-seed weight (0.0452), harvest index (0.1733) and seed protein (0.0080). These positive direct and indirect effects were high enough to nullify negative indirect effects and resulted in significant positive correlation with seed yield (0.933**). The high positive direct effect on seed yield in parents and hybrids was also reported by Mittal *et al.* (2010), Jogendra Singh *et al.* (2008), Sawant *et al.* (2009), Pahwa *et al.* (2013), Saroj *et al.* (2013), Arbad *et al.* (2014) and Pandey *et al.* (2016).

4.7.1.7 Seed per pod

In parents, seeds per pod exhibited negative direct effect on seed yield (-0.0113). However, its positive effects *via* days to 50% flowering (0.0113), days to 75% maturity (0.0627), plant height (0.0646), pods per plant (0.4413) and seed protein (0.0028) suppressed negative direct and indirect effects and resulted high positive correlation with seed yield (0.428**). In hybrids, it had negative direct effect on seed yield (-0.0011). Its positive indirect effects *via* days to 50% flowering (0.0244), days to 75% maturity (0.0056), plant height (0.0336), secondary branches per plant (0.0244), pods per plant (0.1124), 100-seed weight (0.0219) and harvest index (0.0647), nullified negative direct and indirect effects and finally resulted in high positive association with seed yield (0.274**). Its negative direct effect on seed yield in parents and hybrids was earlier reported by Vanisree *et al.* (2013), Bhadru (2010) and Rekha *et al.* (2013).

4.7.1.8 100-seed weight (g)

In parents, direct effect of 100-seed weight on seed yield was very low and positive (0.0093). It had negative indirect effect *via* days to 50% flowering

(-0.0124), days to 75% maturity (-0.0595), plant height (-0.0614), pods per plant (-0.4789) and seed protein (-0.0020) suppressed positive direct and indirect effects and resulted in high negative correlation with seed yield (-0.402*). In hybrids, it exerted negative direct effect on seed yield (-0.0874). Its negative indirect effects through days to 50% flowering (-0.0184), days to 75% maturity (-0.0001), plant height (-0.0195), secondary branches per plant (-0.0580), pods per plant (-0.3201), harvest index (-0.0685) and seed protein (-0.0014) suppressed positive indirect effects and resulted in high negative correlation with seed yield (-0.524**). Negative direct effect of this trait on seed yield was in confirmity with the results of Vijayalakshmi *et al.* (2013) and Singh *et al.* (2013).

4.7.1.9 Harvest index (%)

In parents, harvest index exerted negative direct effect on seed yield (-0.3385). Its positive indirect effects through days to 50% flowering (0.0199), days to 75% maturity (0.1412), plant height (0.0795), pods per plant (0.8850) and seed protein (0.0018) suppressed negative direct and indirect effects and finally resulted in positive correlation with seed yield (0.799**). In hybrids, direct effect of this character on seed yield was positive and high (0.3528). It also exerted positive indirect effects through days to 50% flowering (0.0187), days to 75% maturity (0.0124), plant height (0.0179), secondary branches per plant (0.0165), pods per plant (0.3043) and 100-seed weight (0.0170). These positive direct and indirect effects were high enough to nullify the negative indirect effects and resulted in significant positive correlation with seed yield (0.710**). The negative direct effect of harvest index on seed yield in parents was supported by Mittal *et al.* (2010). The positive direct effect of harvest index on seed yield in hybrids was reported by Prasad *et al.* (2013), Reddy and Rangare *et al.* (2013) and Pandey *et al.* (2016).

4.7.2 Direct and Indirect Effects of Quality Attributes

4.7.2.1 Seed protein (%)

In parents, direct effect of seed protein on seed yield was positive (0.0199). Its correlation on seed yield was also positive (0.197) indicating the existence of positive indirect effects *via* plant height (0.0232), secondary branches per plant (0.0014) and pods per pod (0.0494). In hybrids, it exerted positive direct effect on seed yield (0.0331). Its positive indirect effects *via* days to 75% maturity (0.0053), plant height (0.0082), secondary branches per plant (0.0224), pods per plant (0.1496), seeds per pod (0.0001) and 100-seed weight (0.0036) suppressed negative indirect effects and resulted in positive correlation with seed yield (0.163). The positive direct effect of seed protein on seed yield was also reported by Bharadwaj and Gupta (2004) and Anuradha *et al.* (2007).

From the findings of path analysis, it is evident that pods per plant had high direct effect on seed yield and found to be the main factor. It had strong positive correlation with seed yield in parents and hybrids. Hence, direct selection for pods per plant would be effective. Similarly, days to 75% maturity and plant height also exerted high direct effects on seed yield followed by days to 50% flowering and seed protein in parents in the decreasing order. Though 100-seed weight had positive direct effect, 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 in parents. Whereas in hybrids, days to 50% flowering, days to 75% maturity, plant height, secondary branches per plant, harvest index and seed protein, exhibited positive direct effect and positive association on seed yield.

In parents, the character primary branches per plant followed by secondary branches per plant, seeds per pod and harvest index had negative direct influence on seed yield but they had significant and positive association with seed yield. In hybrids, similar results were observed for primary branches

per plant, seeds per pod and 100-seed weight. This may be due to their high positive indirect contribution *via* pod per plant except for 100-seed weight. Hence, the indirect effects of most of the characters were found positive and high *via* pods per plant both in parents and hybrids.

The genotypic residual effect was 0.0047 in parents and 0.0197 in hybrids, while phenotypic residual effects were 0.0094 and 0.0187 in parents and hybrids, 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 & Conclusions

Chapter - V

SUMMARY AND CONCLUSIONS

The present investigation entitled "Combining ability and heterosis studies in CGMS based hybrids of 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 parameters correlations between yield and yield components and direct and indirect effects of yield contributing traits on seed yield. The experiment was carried out in Randomized Block Design with three replications during *Kharif*, 2016 with five lines *viz.*, ICPB-2078, ICPB-2043, ICPB-2047, ICPB-2048 and ICPB-2092, four testers *viz.*, ICPL-87119, ICPL-20108, ICPL-20116 and ICPL-20123 and their 20 hybrids of pigeonpea obtained by L x T mating design along with a standard check (Maruti) at ICRISAT, Hyderabad, Telangana. Data was collected on days to 50% flowering, days to 75% maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, 100-seed weight, harvest index, seed protein and seed yield per plant.

An overall view of mean performance of parents revealed that the no single genotype was superior in respect of all the traits studied. However, among the lines, ICPB-2078 and ICPB-2043 were found to be the best for earliness, while ICPB-2047 was found promising for seed yield and other yield contributing characters except 100-seed weight. Among the testers, ICPL-87119 emerged as the best for days to 50% flowering, days to 75% maturity, plant height, pods per plant, 100-seed weight, harvest index and seed yield per plant, which can be utilised in the breeding programmes.

The genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were high for secondary branches per plant, pods per plant, harvest index and seed yield per plant both in parents and hybrids. Heritability (broad sense) estimates were high for all the characters except seed

protein and 100-seed weight both in parents and hybrids. Genetic advance as per cent of mean was high for primary branches per plant, secondary branches per plant, pods per plant, harvest index and seed yield per plant in both parents and hybrids. High GCV and PCV, heritability and genetic advance as per cent mean were observed for the characters secondary branches per plant, pods per plant, harvest index and seed yield per plant both in parents and hybrids, 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 11 characters varied among themselves. The magnitude of standard heterosis was high for secondary branches per plant, pods per plant, harvest index and seed yield per plant, whereas for seeds per pod and days to 75% maturity it was very low. Out of 20 hybrids, the hybrids *viz.*, ICPA- 2092 x ICPL-20108, ICPA-2047 x ICPL-20108, ICPA-2047 x ICPL-20116 and ICPA-2047 x ICPL-20123 had recorded significant and maximum heterosis for most of the characters.

Studies on heterosis suggested that higher and significant heterosis was contributed through characters studied except days to 75% maturity, days to 50% flowering, primary branches per plant, seeds per pod, 100-seed weight and seed protein in ICPA-2092 x ICPL-20108, ICPA-2047 x ICPL-20108 and ICPA-2047 x ICPL-20116 and through the traits except days to 75% maturity, days to 50% flowering, primary branches per plant, 100-seed weight and seed protein in ICPA-2047 x ICPL-20123. Hence, significant positive heterosis observed for seed yield per plant was mainly due to the manifestation of heterosis for its component characters *viz.*, plant height, secondary branches per plant, pods per plant and harvest index. This would clearly indicate that heterosis for seed yield was through heterosis for individual component characters.

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 and significant variances due to line x tester interaction components indicated differential behaviour of lines with testers across the characters.

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 days to 50% flowering, days to 75% maturity, primary branches per plant. Plant height, secondary branches per plant, pods per plant, seeds per pod, harvest index, seed protein and seed yield per plant, which were contributed highly by the line x tester interaction.

Predominance of non-additive gene action for all the characters was noticed from the ratio of *gca* / *sca* variance suggesting that there is a good scope for heterotic breeding. 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.

Based on *per se* performance and *gca* effects, the parents ICPB-2078 and ICPB-2043 was the best general combiners for days to 50% flowering and days to 75% maturity, while ICPB-2047 for plant height, primary branches per plant, secondary branches per plant, seeds per pod, harvest index and seed yield per plant. ICPB-2092, ICPB-2078 and ICPB-20123 were the promising parents for pods per plant, 100-seed weight and seed protein. Based on *sca* effects, *per se* performance and heterosis, the hybrids *viz.*, ICPA-2092 x ICPL-87119 and ICPA-2092 x ICPL-20108 were identified as the best specific hybrids for hybrid breeding programme, while the hybrids ICPA-2092 x ICPL-20123, ICPA-2048 x ICPL-20116, ICPA-2078 x ICPL-20108, ICPA-2043 x ICPL-87119, ICPA-2048 x ICPL-20108, ICPA-2092 x ICPL-20116, ICPA-2092 x ICPL-87119, ICPA-2078 x ICPL-87119, ICPA-2047 x ICPL-87119,

ICPA-2043 x ICPL-20108 and ICPA-2047 x ICPL-20123 were identified for advancing through recombination breeding programme.

Character association studies revealed that selection based on all the characters except secondary branches per plant, seed protein, 100-seed weight in parents and seed protein, 100-seed weight in hybrids will be effective for bringing improvement in seed yield as they had significant and positive correlation with seed yield per plant. In parents, inter-se association between days to 50% flowering with days to 75% maturity; plant height, primary branches per plant with days to 50% flowering and days to 75% maturity; pods per plant, seeds per pod with plant height, days to 75% maturity and days to 50% flowering with primary branches per plant; harvest index with days to 50% flowering and pods per plant was significant positive among themselves in both the parents and hybrids, whereas the association between character pair secondary branches per plant with pods per plant was positive non-significant in parents become significant positive in hybrids. Positive non-significant association of harvest index with seed protein and seed protein with primary branches per plant in parents became negative non-significant in hybrids. Negative non-significant association of 100-seed weight with days to 75% maturity in parents became Positive non-significant in hybrids. These changes in correlations between pairs of characters from parents to hybrids might have resulted due to the modifications in the linkages as a result of re-combinations in those populations. Thus simultaneous selection for one trait brings considerable improvement in another trait and finally 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 100-seed weight had positive direct effects, it had recorded negative correlation with seed yield which may be due to indirect effects mainly *via* pods per plant in parents. Days to 50% flowering, days to 75% maturity, plant height, secondary branches per plant, harvest index and seed protein, exhibited positive direct effect and positive association on seed yield. Hence direct and

indirect effects of pods per plant on seed yield indicated that the selection for pods per plant will be effective in the improvement of seed yield.

Based on the study, it is suggested that inter-mating of superior segregants followed by recurrent selection or multiple crossing in a judicious approach would be rewarding to harness both additive and non-additive 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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