HETEROSIS IN CMS BASED HYBRIDS OF PIGEONPEA [*Cajanus cajan* (L.) Millsp.]

BY

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B.Sc. (Ag.)

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CHAIR PERSON: Dr. J DAYAL PRASAD BABU

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2016

DECLARATION

I**, NIDHI MOHAN** hereby declare that the thesis entitled "**HETEROSIS IN CMS 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 the original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place: **(NIDHI MOHAN)**

Date: **I.D.No. BAM-14-11**

CERTIFICATE

Ms. NIDHI MOHAN has satisfactorily prosecuted the course of research and that the thesis entitled **"HETEROSIS IN CMS 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:

(J. DAYAL PRASAD BABU)

Chairperson
Assistant Professor
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CERTIFICATE

This is to certify that the thesis entitled **"HETEROSIS IN CMS 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, Andhra Pradesh is a record of the bonafide original research work carried out by **Ms. NIDHI MOHAN** under our guidance and supervision.

No part of the thesis has been submitted 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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Place : ***Bapatla***

Date: ***(NIDHI MOHAN)***

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LIST OF SYMBOLS AND ABBREVIATIONS

A	:	A line (male sterile)
AKPH	:	Akola Pigeonpea Hybrid
ANOVA	:	Analysis of Variance
BC_1	:	First back cross generation
^0C	:	Degree Centigrade
CD	:	Critical Difference
CGMS	:	Cytoplasmic Genetic Male Sterile
CMS	:	Cytoplasmic Male Sterile
cm	:	Centimeter
CV	:	Coefficient of variation
DAS	:	Days after sowing
Df	:	Degrees of freedom
E	:	East
et al.	:	and coworkers
F_1	:	First filial generation of a cross
Fig	:	Figure
g	:	Grams
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic Coefficient of Variation
GMS	:	Genetic Male Sterile
GTH	:	Gujarat Tur Hybrid
ha	:	Hectare
h^2 (b)	:	heritability in broad sense
Hrs	:	Hours
ICAR	:	Indian Council of Agricultural Research
ICPH	:	ICRISAT Pigeonpea Hybrid
ICPL	:	ICRISAT Piheonea Lines
ICPA	:	ICRISAT Pigeonpea A-line
ICRISAT	:	International Crops Research Institute for Semi-Arid Tropics
Kg	:	Kilogram
kg ha^{-1}	:	Kilogram per hectare
Km/ hr	:	Kilometer per hour
m	:	Meter
M	:	Million
M_t	:	Mean sum of square of treatment
M_e	:	Mean sum of square of error
Millsp.	:	Millispaugh

Max	:	Maximum
Min	:	Minimum
N	:	North
No.	:	Number
PCV	:	Phenotypic Co-efficient of Variation
Per se	:	As such with mean
r	:	Number of replications
RBD	:	Randomized Block Design
Rel	:	Relative
SEd	:	Standard error of differences
SEm	:	Standard error of mean
S. K.	:	Sameer Kumar
S. No.	:	Serial Number
T	:	Tones
t ha^{-1}	:	Tones per hectare
%	:	per cent
viz.,	:	Namely
$\bar{X}$	:	Grand mean
/	:	per
@	:	at the rate of
➢	:	more than
σ^2_g	:	Variance due to genotypes

ABSTRACT

Name of the Author	:	**NIDHI MOHAN**
Title of the thesis	:	**HETEROSIS IN CMS BASED HYBRIDS OF PIGEONPEA [*Cajanus cajan* (L.) Millsp.]**
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An investigation on heterosis in CMS based hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.] was carried out during *kharif* 2015 at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru with 24 hybrids and four checks to elicit the information on magnitude of the genetic variability, heritability, genetic advance as *per cent* of mean, character association, path coefficient analysis, extent of fertility restoration and heterosis. Observations were recorded on ten characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod weight per plant, 100 seed weight (g), grain yield per plant (g) and mean pollen fertility %.

Analysis of variance showed significant differences among the hybrids for all the characters studied indicating a high degree of variability in the experimental material. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the influence of environment on expression of these traits. High genetic variability coupled with high heritability and genetic advance as *per cent* of mean were recorded for number of primary branches per plant, number of secondary branches per plant and pollen fertility % indicating the role of additive genes in governing the inheritance of these traits.

The correlation study indicated that grain yield per plant was significantly associated with days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of pods per plant and pod weight indicating their importance as selection criteria in pigeonpea yield improvement programmes.

Path coefficient analysis revealed that pod weight per plant and number of primary branches had positive direct effects on seed yield per plant. Hence, these traits should be considered as important selection criteria in all yield improvement programmes and direct selection for these traits is recommended.

Fertility restoration studies showed that 15 out of 24 hybrids recorded high (>80 %) pollen fertility and exhibited better fertility restoration. Nine out of 13 male lines

showed fertility restoration of more than 80% and were classified as restorers for corresponding CMS lines.

The present investigation also revealed high levels of heterosis *i.e*. over 50% in traits like number of pods per plant, pod weight per plant and grain yield per plant. ICPH 3762 and ICPH 4502, with high *per se* performance and high standard heterosis for grain yield per plant and for majority of yield attributes, were identified as promising hybrids.

Chapter- I

INTRODUCTION

Chapter I

INTRODUCTION

Once designated as an orphan crop, Pigeonpea has evolved over the time as life line for millions of resource poor farmers in the arid and semi-arid tropics, where it is cultivated for both subsistence and commercial purposes. This climate-smart crop is boon to farmers as it requires less water, enriches soil, withstands weather variability and is packed with nutrients. Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the sixth most important legume crop globally (FAO, 2015), grown predominantly in the tropical and sub-tropical regions of Asia, Africa and Latin America. Pigeonpea is an often cross-pollinated (0 - 70%, Saxena *et al.*, 1990) crop with 2n = 2x = 22 diploid chromosome number and a genome size of 833.07 Mb (Varshney, 2015). It is a short-lived perennial member of family Fabaceae and is invariably cultivated as an annual crop. India is considered as the center of origin of pigeonpea (Van der Maesen, 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country.

The global pigeonpea area, production and productivity in 2014 was approximately 6.23 M ha, 4.74 M T and 762.4 Kg ha^{-1}, respectively (FAOSTAT 2015). The major producers of pigeonpea are India (63.74% of global production), Myanmar (18.98%), Malawi (6.07%), Tanzania (4.42%) and Uganda (1.98%). In India pigeonpea was cultivated on 5.06 M ha with a total production of 3.29 M T and productivity of 649.9 Kg ha^{-1} during 2014 (FAOSTAT, 2015). The leading states in pigeonpea production are Maharashtra (0.259 M T), Karnataka (0.51 M T), Madhya Pradesh (0.39 M T), Uttar Pradesh (0.259 M T), Gujarat (0.258 M T) and Jharkhand (0.19 M T). These six states account for 84% of the total production in India during 2014 - 15 (E-Pulse Data Book, 2016.).

Pigeonpea is a hardy, widely adapted and drought tolerant crop. It has a range of maturity which helps in its adaption in a wide range of environments and cropping systems. It can be grown either as sole crop or intercrop with urdbean, mungbean, castor, sorghum, soybean, cotton, maize and groundnut in different states like Maharashtra, Karnataka, Andhra Pradesh, Telangana, Madhya Pradesh, Uttar Pradesh, Gujarat, Jharkhand, Rajasthan, Odisha, Punjab and Haryana. Pigeonpea is mostly consumed as dry split dhal besides several other uses of various parts of pigeonpea plant. Pigeonpea is

rich in essential amino acids and high in protein bioavailability (20 - 22%, Salunkhe *et al.,* 1986) among pulses. The high dietary fiber in pigeonpea lowers risk of diabetes, heart ailments and gastrointestinal diseases. Pigeonpea also provide substantial amount of micronutrients such as vitamin E, vitamin B_6, folic acid, iron, potassium, magnesium, calcium, phosphorous, sulfur and zinc. India is home to 194.6 million undernourished people, making malnutrition a national emergency. In such situation pigeonpea comes to the rescue of millions of people from clutches of chronic malnutrition as it is a cheap and easily accessible source of protein and micro nutrients for majority of vegetarian population. In addition to its nutritional advantage, pigeonpea has low carbon and water footprint which makes it an integral part of the sustainable farming system. Pigeonpea is also used as fodder, feed, fuel, functional utility (for making baskets, huts, fences, etc.), fertilizer (fixes atmospheric nitrogen and releases phosphorus), forest use (re-forestation, lac production), and even for pharmaceutical purposes (Mula and Saxena, 2010).

Stagnant productivity coupled with declining availability in the recent times has created substantial demand supply gap, forcing heavy import bill on the exchequer and affecting nutritional security of majority of the population for whom pulses are the one of the cheapest source of protein. Despite the fact that a large number of high yielding varieties have been released, productivity of the crop could not be improved over 750 kg ha^{-1} as compared to its potential yield (2500 - 3000 kg ha^{-1}). Non adoption of improved management practices and lack of proper scientific research have turned out to be the major culprits for low productivity and production.

Therefore, an alternative breeding approach such as hybrid technology, which has been profitably used in a number of cereals, fruits and vegetable crops was attempted in pigeonpea to enhance the yield. For commercially viable hybrid technology we require; a perfect male sterility system, efficient mass pollen transfer mechanism, hybrid vigor and large scale seed production system. But hybrid breeding technology remained elusive to pulse breeders due to unique pollination behavior in pulses which does not allow their economic hybrid seed production. Pigeonpea being an exception is unique in having both self and cross pollination systems operating simultaneously under natural conditions. This paved the way for advent of heterosis breeding in pigeonpea.

As such, before launching any breeding programme, a thorough knowledge of the nature and magnitude of genetic variability, heritability and genetic advance as per cent of mean is very essential. Heritability of a trait is a parameter of particular significance to

the breeder as it measures the degree of resemblance between the parents and the offsprings. Its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression while genetic advance aids in exercising the necessary selection pressure.

Seed yield, being a complex character, is very difficult to improve by selecting the genotypes for yield *per se*. Therefore identifying the characters which are closely related and have contributed to yield becomes highly essential in plant breeding programmes. The estimates of correlation coefficients mostly indicate the inter-relationships of the characters whereas, path analysis helps in partitioning the total correlations into direct and indirect contributions thereby suggesting the degree of contribution of each character towards the yield (Wright, 1921).

The development of commercial hybrid pigeonpea programme was innovated at ICRISAT in collaboration with ICAR (Indian Council of Agricultural Research). In 1974, a source of genetic male-sterility (GMS) was identified. As a consequence, a genetic male-sterility based pigeonpea hybrid ICPH 8 was released in 1991 in India (Saxena *et al*., 1992). It is considered a milestone in the history of crop breeding as ICPH 8 is the first ever commercial hybrid released in any food legume in the world. This hybrid, however, could not be commercialized due to its high seed cost and difficulties in maintaining the genetic purity.

Later on a new hybrid pigeonpea breeding technology i.e. CGMS based hybrids were developed jointly by the International Crops Research Institute for the Semi-arid Tropics (ICRISAT) and Indian Council of Agriculture Research (ICAR) which is capable of overcoming the shortcomings of GMS based hybrids, and thus offering hope of pulse revolution in the country (Saxena and Nadarajan, 2010). The different cytoplasmic male sterility sources derived from wild relatives of pigeonpea are given in Table 1.1. Of these, A2 and A4 systems derived from crosses involving wild relatives of pigeonpea and cultivated types have shown promise because of their stability under various agro-climatic conditions and availability of good maintainers and fertility restorers (Saxena and Nadarajan, 2010). By using A2 cytoplasm, a hybrid GTH-1, an early maturing one, was released by ICAR for commercial cultivation in Gujarat state. It demonstrated 57.40% yield superiority over the best GMS hybrid AKPH 4101 (1183 kg ha^{-1}) and 32% superiority over the best local variety GT 101 (1330 kg ha^{-1}).

Table 1.1. List of CMS sources derived from different wild relatives of pigeonpea

CMS System	Donor Species	Recipient Species	Remarks	References
A1	*Cajanus sericeus*	*Cajanus cajan*	CMS sensitive to temperature	Ariyanayagam *et al*., 1995
A2	*Cajanus scarabaeoides*	*Cajanus cajan*	Fertility restoration unstable	Saxena and Kumar, 2003
A3	*Cajanus volubilis*	*Cajanus cajan*	Large variation in expression	Wanjari *et al*., 1999
A4	*Cajanus cajanifolius*	*Cajanus cajan*	Stable, using in hybrid program	Saxena *et al*., 2005
A5	*Cajanus cajan*	*Cajanus acutifolius*	Uses cultivated pigeonpea cytoplasm	Mallikarjuna and Saxena, 2005
A6	*Cajanus lineatus*	*Cajanus cajan*		
A7	*Cajanus platycarpus*	*Cajanus cajan*	A new CMS using tertiary gene pool	Mallikarjuna *et al*., 2006
A8	*Cajanus reticulates*	*Cajanus cajan*	Searching fertility restoration	Saxena, 2013

Since the horizontal increase in the area under pigeonpea cultivation is implausible, the only option left for ever increasing production and productivity of pigeonpea is adoption of hybrids on a large scale under different agro-ecological zones. To sustain the achievements of this breakthrough, it is essential that superior hybrids are made available to farmers of different regions at an affordable cost and to achieve this, breeding of heterotic varieties i.e. CMS based hybrids becomes imperative. Thus, based upon the present context the present investigation is taken up with the following objectives.

1. To assess the magnitude of genetic variability present in the material.
2. To study the nature of association between yield and yield component traits.
3. To assess the magnitude of direct and indirect effects of component characters on yield.
4. To study the extent of fertility restoration in the hybrids derived from newly developed CMS lines.
5. To study extent of heterosis for yield and yield components in CMS based pigeonpea hybrids.

Chapter- II

REVIEW OF LITERATURE

Chapter II

REVIEW OF LITERATURE

The present investigation in CMS based pigeonpea hybrids was undertaken to study the magnitude of genetic variability present in the material, the nature of association between yield and yield component traits, the magnitude of direct and indirect effects of component characters on yield, the extent of fertility restoration in the hybrids derived from newly developed CMS lines and the extent of heterosis for yield and yield components.

The literature available on the main objectives of the present study has been comprehensively reviewed under the following headings:

2.1 Genetic Variability

2.2 Character Association

2.3 Path Analysis

2.4 Fertility Restoration

2.5 Heterosis

2.1 GENETIC VARIABILITY

An insight into the magnitude of variability present in a crop species is of utmost importance as it provides the basis for effective selection. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait.

The information on the nature and magnitude of variability of different quantitative and qualitative traits in any crop species plays a vital role while formulating efficient breeding programmes. Superior genotypes can be isolated by selection if considerable genetic variation exists within the population. Besides genetic variability, heritability and genetic advance also plays a crucial role in the improvement of any trait.

Heritability measures the relative amount of the heritable portion of variability. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. Basic information on heritability is a pre-requisite for planning any breeding programme.

Genetic advance helps to measure the amount of progress that could be expected with selection for a particular character. Estimates of heritability along with estimates of genetic advance are more useful in choice of selection method rather than heritability or genetic advance alone (Johnson *et al*., 1955).

A brief review of available literature on genetic variability, heritability and genetic advance in pigeonpea is presented here under.

Baskaran and Muthiah (2006) studied genetic parameters of 18 hybrids of pigeonpea synthesized from six female (CO 5, VBN 1, CORG 9407, CORG 9701, ICPL 87 and CORG 9904) and three male parents (APK 1, ICPL 83024 and ICPL 83027) during *kharif* 2003. Genetic variability was highest for the number of pod clusters per plant and number of pods per plant. Genotypic coefficient of variation was lowest for seed protein content, days to 50% flowering, days to maturity and pod length. The difference between PCV and GCV showed high variability for seed yield per plant, number of clusters per plant and number of branches per plant. Characters such as the number of clusters per plant, plant height, number of branches per plant, number of pods per plant and seed yield per plant had high heritability and genetic advance. However days to 50% flowering, days to maturity and seed protein content exhibited high heritability but low genetic advance.

Gohil (2006) conducted field experiments in Gujarat, India, during the 1999 *kharif* seasons, to study the performance, genetic variation, heritability and genetic advance of the yield and yield contributing characters, *i.e*. grain yield per plant, days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, pods per cluster, 100 seed weight, harvest index and protein content, of 39 pigeonpea genotypes. Significant variations were observed for all the characters in all the genotypes used in the experiment. Higher phenotypic coefficients of variation were observed for grain yield per plant, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster and harvest index. Grain yield per plant, days to 50% flowering, days to maturity, number of clusters per plant, number of pods per plant, number of pods per cluster and

harvest index showed high heritability. Considering high genetic advance, the percentage of mean was found for grain yield per plant, number of clusters per plant, number of pods per plant and harvest index.

Bhadru (2010) studied genetic parameters in 27 accessions of pigeonpea and recorded moderate to high PCV and GCV for number of pods, seed yield per plant and plant height. High heritability and genetic advance as % of mean was observed for number of pods, primary and secondary branches per plant, test weight and plant height.

Linge *et al.* (2010) screened 40 inter specific derivatives of pigeonpea along with five national checks derived from ICRISAT, Patancheru and one local checks screened to study the extent of genetic variability for yield and yield contributing character. The GCV of various characters varied from 5.15 to 73.02 and the highest GCV was recorded for trichome-A followed by trichome-B. Also the PCV values were higher than GCV values for all the characters. The high heritability estimates coupled with high expected genetic advance were observed for trichome type-A, B, number of secondary branches, trichome type-D, number of pods per plant, grain yield per plant, trichome type C, per cent pod setting, per cent pollen sterility, 100 seed weight, number of primary branches, height of first primary branch from ground level and seed per pod indicating the presence of additive gene action and phenotypic selection may be effective.

Bhadru (2011) evaluated 50 white seed coated lines of pigeonpea for studying the genetic variability, heritability and genetic advance for twelve yield related characters. High PCV and GCV were observed for number of pods per plant, seed yield per plant, plant height and raceme length, indicating the presence of high amount of variability. High genetic advance as % of mean was observed for number of pods, seed yield, primary and secondary branches per plant, plant height, raceme length, test weight, seeds per pod, pod length and plant spread.

Patel and Acharya (2011) recorded high GCV and PCV for grain yield per plant, pods per plant and branches per plant whereas low GCV and PCV were recorded for days to maturity, days to 50 per cent flowering, seeds per pod and pod length in 64 F_6 progenies of pigeonpea. High heritability coupled with moderate to high genetic advance for grain yield per plant, plant height, number of pods per plant, days to 50% flowering and days to maturity showed importance of additive gene effects and thereby higher selection value for these traits.

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 was noticed for seed yield, number of primary branches per plant and secondary branches per plant suggesting additive gene action controlling these traits.

Jaggal *et al.* (2012) computed the genetic variability, correlation and path coefficient analysis for 14 characters in 135 pigeonpea [*Cajanus cajan* (L.) Millsp.] accessions of mini core collection obtained from International Crops Research Institute for Semi-Arid Tropics, Hyderabad. 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 fifty per cent flowering, days to maturity and seed protein.

Nagy *et al*. (2013) studied 45 pigeonpea germplasm accessions received from ICRISAT, Patancheru, for genetic variability and correlation among yield and its attributes under rainfed conditions. Among the different yield attributing traits, number of pod clusters per plant had the highest magnitude of GCV and PCV followed by seed yield per plant and number of pods per plant which is an indicative of the substantial genetic variability exists in the pigeonpea germplasm accessions of Bastar origin. High heritability coupled with high genetic advance was recorded for the traits viz., number of pods per plant, number of pod clusters per plant, seed yield per plant and 100 seed weight.

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

Rangare *et al.* (2013) estimated genetic parameters for yield and its correspondent characters in 27 genotypes of pigeonpea, which were obtained from ICRISAT (Hyderabad), various parts of U.P and M.P. Low, moderate, and high genotypic and phenotypic coefficient of variations were observed. High genotypic and phenotypic co-efficient of variations were expressed by number of pods per plant,

harvest index, biological yield per plant and grain yield per plant. High heritability coupled with high genetic advance was exhibited by days to maturity, days to 50% flowering, days to initial flowering, plant height, number of pods per plant, biological yield per plant, grain yield per plant and harvest index

Saroj *et al.* (2013) estimated the PCV, GCV, heritability and genetic advance for yield and yield traits in 70 pigeonpea genotypes. The highest GCV was recorded for number of 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 number of primary branches per plant, number of secondary branches per plant, 100 seed weight, grain yield per plant, pods per plant, plant height and days to 50% flowering.

Singh *et al.* (2013) investigated genetic components like PCV, GCV, heritability and genetic advance in 21 diverse genotypes of short duration pigeonpea. The PCV was noted moderate for the characters like seed yield per plant (18.59%), pods per plant (18.04%) and primary branches per plant (12.22%). Genotypic coefficient of variation ranged from 3.24% to 17.84%. Maximum GCV was observed for seed yield per plant (17.84%), followed by pods per plant (17.80%) and primary branches per plant (10.94%). The estimate of broad sense heritability was the highest for pods per plant (97%), followed by days to 50% flowering (94%), grain yield per plant (92%), days to maturity (90%), primary branches per plant (80%) and plant height (78%). The estimated genetic advance was recorded as moderate for pods per plant (36%) and grain yield per plant (35%).

Rekha *et al.* (2013) studied the variability and heritability in 49 genotypes of pigonpea. Number of secondary branches per plant, number of pods per plant, seed yield per plant, phenol content, 100 seed weight and number of primary branches per plant showed higher estimates of PCV and GCV. High heritability with high genetic advance as per cent of mean recorded for all the characters except protein content, days to 50% per cent flowering and days to maturity.

Yerimani *et al.* (2013) studied genetic variability generated from the Gulyal white x Maruti cross in F_3 and F_4 generation to make effective selections for improving productivity. The study indicated that the higher magnitude of variability were recorded in F_3 and F_4 generation for 50 per cent flowering, number of secondary branches, number of seeds per pod, number of pod per plant, seeds yield per plant and seed yield (kg/ha)

and moderate variability observed in pod bearing length and test weight (gm). The higher heritability and genetic advance per mean were recorded in F_3 and F_4 generation for 50 per cent flowering, number of secondary branches, number of seeds per pod, number of pod per plant, seeds yield per plant and seed yield (kg/ha)

Ajay *et al.* (2014) evaluated F_2 and F_3 generations for yield and yield contributing traits to understand genetic variability and to identify transgressive segregants in three pigeonpea crosses. High variance, high heritability and high genetic advance were recorded for secondary branches per plant, number of pods per plant and seed yield in F_2 and F_3 generations.

Kumar *et al.* (2014) evaluated genetic variability and interrelationship for yield and yield contributing characters among 38 genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp]. Moderate to high PCV and GCV were recorded for days to fifty percent flowering (DFF), number of pods per plant, number of seed, grain yield and straw yield. High heritability and genetic advance was observed for number of pods (0.94, 27.14), plant height (0.90, 21.43), test weight, days to maturity (0.84, 23.02) and primary and secondary branches per plants (0.90, 11.32). Whereas the characters like DFF, test weight, pod length and number of primary branches showed high heritability along with moderate or low genetic advance.

Singh *et al.* (2014) studied the genetic variability of pigeonpea genotypes (102) in respect of days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, pods per plant, pod length (cm), seeds per pod, 100-seed weight and seed yield per plant were studied under rainfed conditions with terminal moisture stress. Genotypic coefficient of variation revealed seed yield per plant had greater range of variability followed by pods per plant and secondary branches per plant. Heritability in broad sense was moderate indicating influence of moisture stress on these traits. However, high genetic advance as per cent of mean indicated additive gene effects governing the traits providing ample scope of improvement.

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

Pandey *et al.* (2015) conducted study to determine nature and magnitude of genetic parameters and their utilization in development of superior varieties or hybrids of pigeonpea. Results showed that the sufficient amount of variability was found in the entire gene pool for all the traits studied. 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 in their inheritance.

2.2 CHARACTER ASSOCIATION

Plant yield is a complex and polygenically inherited trait. Therefore direct selection for yield is not much effective. But, it could be improved by selecting various component characters which are correlated to yield and are simple in inheritance with less environmental influence. Hence, correlation studies paved a path in order to find out the association between highly heritable independent characters and most economic but dependent character like yield which would help the breeder in obtaining improved yields.

The available literature on the association of component characters with grain yield per plant and the associations among the yield component characters are presented below:

Pandey and Singh (2001) observed positive correlations for seed yield per plot with seed yield per plant at both genotypic and phenotypic levels in pre-*rabi* pigeonpea. And positive and significant inter-association was observed between plant height, days to initial flowering, maturity and harvest index, during *kharif* and pre-*rabi.*

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

Baskaran and Muthiah (2007) assessed 27 pigeonpea genotypes and their correlation studies indicated that seed yield per plant had significant positive relationship

with number of pods per plant, number of clusters per plant, 100 seed weight and plant height.

Mahajan *et al.* (2007) evaluated nine pigeonpea genotypes to understand the contribution of various characters to 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 number of pods per plant in pigeonpea.

Sawant *et al.* (2009) studied 46 pigeonpea genotypes and revealed that the genotypic correlation coefficients were higher than corresponding phenotypic correlations. Seed yield showed significant positive correlation with plant spread, number of secondary branches per plant, pods per plant and days to maturity.

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

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

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

Linge *et al.* (2010) found that grain 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 number of pods per plant and harvest index with seed yield per plant in 28 different genotypes of pigeonpea.

Hamid *et al*. (2011) evaluated one hundred 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 grain yield was significantly and positively correlated with plant height, branches per plant, number of pods per plant, pod length, seeds per pod and 100 seed weight in 64 F_6 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 number of leaves per plant, leaf area per plant and number of seeds per plant, number of 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 number of pods, secondary branches per plant, plant height, number of primary branches per plant showed significantly positive correlation with seed yield at genotypic and phenotypic levels in pigeonpea.

Birhan (2013) reported that correlation coefficient results revealed 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 number of pods per plant followed by number of pod cluster per plant, number of primary branches per plant and pod length.

Prasad *et al.* (2013) found that number of primary branches per plant, number of secondary branches per plant, number of 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 number of pods per plant, number of secondary branches per plant, number of 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 grain yield per plant, primary branches per plan, pods per plant, days to maturity, 100 seed weight and plant height in both genotypic and phenotypic level.

Pandey *et al.* (2015) 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.

2.3 Path Analysis

The estimation of path coefficients gives an exact picture of relative importance of the direct and indirect contribution of the component characters to yield. Path analysis proposed by Dewey and Lu (1959) facilitates the partitioning of the correlation coefficients into direct and indirect effects of various characters on grain yield. Thus path analysis would give a better insight into the cause and effect relationship between the pairs of characters.

The literature on direct and indirect effects of yield components on grain yield is presented below:

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

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) reported that pods per plant, 100 seed weight and plant height were the major contributors for seed yield and selection based on these attributes would be most advantageous in pigeonpea in their path analysis studies on 27 genotypes.

Mahajan *et al.* (2007) evaluated nine pigeonpea genotypes and reported that 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 harvest index had a high positive direct effect on seed yield followed by seeds per pod and primary branches per plant.

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

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

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

Bhadru (2010) studied 27 accessions of pigeonpea and noticed that days to 50 % flowering, plant spread, primary and secondary branches per plant, number of pods and raceme length had moderate to low direct effect on seed yield.

Mittal *et al*. (2010) reported that branches per plant had maximum direct effect followed by pods per plant and seeds per pod upon seed yield per plant. Branches per plant and pods per plant also contributed indirectly via each other, thus concluding that seed yield in pigeonpea may be improved by selection of tall plants having more branches and pods per plant.

Thanki and Sawargaonkar (2010) revealed that number of pods per plant, 100 seed weight and harvest index made maximum direct contribution towards yield per plant in 28 different genotypes of pigeonpea.

Patel and Acharya (2011) found that pods per plant had the highest positive direct effect on grain yield per plant in 64 F_6 progenies of pigeonpea.

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 genotypic path analysis revealed that maximum direct effect on seed yield was exhibited by number of primary branches per plant, days to 50 per cent flowering and number of pods per plant.

Devi *et al.* (2012) showed that out of fourteen 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, the number of pod clusters per plant had the highest direct effect on seed yield. Whereas, the characters namely number of pods per plant and days to maturity had the highest indirect effect on seed yield via the characters number of pods per plant and days to 50% flowering respectively.

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

Arbad *et al.* (2013) reported that, the number of pods, secondary branches per plant, plant height, and primary branches per plant were the most important character

(high direct and positive indirect effect) which can be strategically used to improve yield in pigeonpea.

Birhan (2013) estimated correlation coefficients and path coefficients (partitioned into direct and indirect effects) of yield and its contributing traits. Phenotypic path analysis 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, number of pods per plant and plant height is having direct positive contribution towards seed yield.

Prasad *et al.* (2013) found that number of primary branches per plant, number of secondary branches per plant, number of 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 number of pods per plant exerted highest positive direct effect on seed yield. Whereas the characters viz., 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. The component characters namely, 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.

Pandey *et al.* (2015) identified biological yield per plant followed by harvest index, pods per plant, days to maturity, number of primary branches per plant, 100 seed weight and seeds per pod as most important direct yield contributing traits in pigeonpea.

2.4 Fertility Restoration

Presence of exploitable hybrid vigor, availability of cytoplasmic nuclear male sterility and fertility restoration system coupled with sound seed production techniques are the pre-requisites for the success of any hybrid breeding programme. In pigeonpea, both the genetic and cytoplasmic genetic male sterility systems were developed with the help of wide hybridization technology. High percentage of fertility restoration by male lines in F_1 hybrids is desirable for successful production of high yielding CMS based hybrids of pigeonpea. The relevant literature pertaining to extent of fertility restoration in hybrids derived from newly developed CMS lines has been provided below.

Dundas *et al*. (1981) studied microsporogenesis in genic male-sterile lines of pigeonpea. They reported that, in the sterile plants, pollen mother cell degeneration occurred at the young tetrad stage with the rupturing of nuclear membrane and callose of the outer cell wall. Conversely, in the fertile plants microsporogenesis proceeded quickly from pollen mother cells to mature bi-nucleate pollen grains.

Saxena and Kumar (2003) studied the fertility restoration system in A2 cytoplasm of pigeonpea. They developed the crosses between three CMS lines with A2 cytoplasm and 14 diverse pigeonpea lines. Among these, five crosses had 94 to 100% fertility restoration and these parents were preserved for direct use in breeding of high yielding restorer lines. Six crosses were male sterile and from this group one or two crosses were selected to develop maintainers by backcrossing. The remaining three crosses segregated for partial fertility and it was inferred that such pollinators need to be improved for their genetic purity for fertility restoration ability.

Chauhan *et al*. (2004) studied fertility restoration in cytoplasmic genic male sterile lines (CGMS) of pigeonpea derived from *C. scarabaeoides*. To identify perfect pollen fertility restorers, 543 derivative lines of *C. scarabaeoides* x *C. cajan* and 1365 germplasm accessions were used as pollen parent on stable cytoplasmic genic male

sterile line GT 288A during *kharif* 1997 to 2003. The F_1 progenies of all the crosses were evaluated from kharif 1998 to 2003 for their pollen fertility. The promising pollen fertility restoring parents were advanced and purified through selfing. Finally, eighteen fertility restorers were identified and characterized.

Gangwar and Bajpai (2005) studied pollen fertility in F_3 generation of interspecific hybrids in pigeonpea and reported that all male and female parents had complete pollen fertility (92.80 - 98.23%). The hybrids of *C. cajan* x *C. cajanifolius* however, showed wide variation for pollen fertility (68.69 - 89.20%) and the maximum fertility was seen in *C. cajan* x *C. scarabaeoides* (74.23 - 85.51 %). Further, poor fertility (8.02 - 36.50%) was seen in segregants of *C. cajan* x *C. acutifolius*.

Singh and Bajpai (2005) studied the relative pollen fertility in interspecific crosses. They found that, *C. cajan* × *C. acutifolius* hybrid showed low pollen fertility in F_1 generation, whereas high pollen fertility was found in crosses utilizing *C. cajanifolius* and *C. scarabaeoides*. They also noticed moderate variation in size of pollen grains among the parents and their hybrids.

Saxena *et al.* (2005) tested various testers for knowing fertility restoration and maintenance reaction of A4 cytoplasm of pigeonpea. They found ICPH 2470 as a promising medium duration experimental hybrid, which exhibited 77.5 % yield advantage over the control cultivar UPAS 120.

Singh *et al.* (2006) studied two cytoplasmic genetic male sterile (CGMS) lines of pigeonpea in BC_3F_1 namely, GT 288 A and CMS 1024 A along with their maintainers to confirm the nature of male sterility system. Pollen fertility test exhibited that only 50 and 35% plants of GT 288 A and B were completely male sterile and fertile, respectively, indicating that both A and B lines should be back crossed or selfed for a few more generations to obtain the perfect line. However CMS 1024 A appeared to have a mutated gene (s) with varying degree of fertility and the lack of pod setting after selfing was reported to be due to heterostyly nature of the flower.

Wanjari *et al*. (2007) studied 136 hybrids for anther dehiscence and pollen fertility and reported that, 11 had expressed high pollen fertility (> 80%) in all the plants.

Dalvi *et al*. (2008a) studied the fertility restoration in cytoplasmic-nuclear malesterile lines derived from three wild relatives of pigeonpea. To study the fertility

restoration of the CMS lines, three cytoplasmic-nuclear male-sterile (CMS) lines derived from *C. sericeus* (A1 cytoplasm), *C. scarabaeoides* (A2 cytoplasm), and *C. cajanifolius* (A4 cytoplasm) were crossed to seven pigeonpea cultivars in a line x tester mating scheme. The resultant 21 F_1 hybrid combinations were planted in three environments. The results revealed no effect of environment on the expression of fertility restoration. Further, it was observed that the pigeonpea cultivar, ICPL 129-3 restored fertility of A1 cytoplasm and maintained male sterility of the other two (A2 and A4) cytoplasms. Among crosses involving CMS line (of A4 cytoplasm) ICPA 2039, one hybrid combination was noticed to be male sterile and another male fertile. The remaining five combinations were observed to segregate for male fertility (66-84% fertility restoration). It was inferred that such testers could be purified for use in hybrid breeding programmes by selfing and single plant selection for 2-3 generations.

A medium duration hybrid, ICPH 2671, which has two dominant fertility restoring genes (Dalvi *et al.* 2008b) was observed to exhibit high stability for yield and fertility restoration in seven diverse states of India and three provinces of Myanmar (Saxena and Nadrajan, 2010). Further, among the medium duration hybrids with A4 cytoplasm, ICPH 2671 and ICPH 2740 were noticed to be the very promising. In multi-location trials conducted for four years, the hybrid ICPH 2740 had recorded 35.8% superiority over control. During 2009, the best performing hybrid, ICPH 2671 was evaluated in 1248 on farm trials in four Indian states (Saxena *et al*., 2010). In these trials ICPH 2671, on average, recorded 28.4% yield advantage over local control, and therefore, ICPH 2671 was released for commercial cultivation in Madhya Pradesh in 2010.

Nadarajan *et al*. (2008) studied the extent of fertility restoration for various cytoplasmic sources across germplasm lines, advanced breeding lines and cultivars. One hundred and sixty eight CGMS based hybrids were synthesized by adopting L x T mating design with 12 CGMS lines and 14 testers. The hybrids were tested for fertility restoration by observing the pollen fertility status. The results indicated fertility restoration in 19 hybrids out of 168 crosses evaluated accounting to 11.3%. The extent of restoration varied from 9.5 to 14.3 per cent across the three cytoplasmic sources, namely, A1, A2 and A4. Further, among the three sources of male parents selected, restoration was noticed to be maximum within the germplasm lines and inbreds as compared to advanced breeding lines and cultivars indicating need for intensive exploration across genetically and geographically diverse genetic resources.

Saxena *et al*. (2010) reported on the development of cytoplasmic nuclear male sterility, its inheritance, and fertility restoration for potential use in hybrid pigeonpea breeding. They searched for fertility restores and male sterility with wide diversity maintainers to produce heterotic hybrids for diverse environments. Among 251 F_1s evaluated, they reported that 30 (12.0%) maintained male sterility, 23 (9.2 %) restored fertility, and 198 (78.9 %) segregated for male-fertility and sterility traits due to heterozygosity within germplasm accessions. All 35 F_1 plants of hybrid ICPA 2067 x ICP 12320 were observed to be male fertile indicating the dominance of fertility restoring genes. Further, Out of the 359 F_2 plants grown, 303 were found to be fertile whereas only 56 exhibited male sterility. This segregation fits to a ratio of 13 fertile: 3 sterile (P = 0.01). In BC_1F_1 generation out of 175 plants, 121 were male fertile and 54 had male sterile anthers, which showed a good fit for a 3 fertile: 1 sterile (P = 0.01) ratio. These results suggested the presence of two dominant genes, with one basic and one inhibitory gene action for fertility restoration in ICPA 2067.

Kyu and Saxena (2011) studied fertility restoration system in five CMS based pigeonpea hybrids. They reported that two hybrids 'ICPH 2671' and 'ICPH 2740' which had the same male parent but different females segregated in F_2 in the ratio of 12 fertile (F): 3 partial fertile (PF):1 sterile (S), and in BC_1F_1 generation as 2 fertile: 1 partial fertile: 1 sterile, suggesting that fertility restoration in these hybrids was controlled by digenic dominant epistatic interaction. The progenies derived from hybrid 'ICPH 3359' fitted well to an F_2 ratio of 9 F : 6 PF : 1 S, and 1 F : 2 PF : 1 S in BC_1F_1 generation, indicating the involvement of two major genes with incomplete dominant epistasis. Progenies of the other two hybrids 'ICPH 4012' and 'ICPH 4344' segregated in F_2 in the ratio of 9 F: 3 PF: 4 S and 1 F: 1 PF: 2 S in BC_1F_1 generations, suggesting that pollen fertility was controlled by digenic recessive epistatic gene action. They concluded that the fertility restoration of A4 CMS system in pigeonpea was governed by two major genes but with different types of epistatic interactions in different crosses.

Saxena *et al*. (2011) studied the inheritance of the obcordate leaf trait and its fertility restoration ability using obcordate leaf line ICP 5529. The crosses were made between four CMS-lines (ICPA 2089, ICPA 2047, ICPA 2048 and ICPA 2049) and ICP 5529. All the F_1 plants of the obcordate donor were fully male fertile and had normal leaves suggested that the obcordate leaf trait was recessive and that fertility restoration was due to the effect of dominant gene (s).

Saxena *et al.* (2011) studied one extra-early (120 days), two early (150 days), and two late-maturing (180 days) pigeonpea hybrids to generate information on the genetics of fertility restoration of the A4 CMS system. In the extra early maturing hybrids, pollen fertility was controlled by a single dominant gene, whereas in the early and late maturing hybrids, male fertility was governed by two duplicate dominant genes. It was also observed that hybrids with two dominant genes produced a greater pollen load and expressed greater stability as compared with those carrying a single dominant gene. It was also concluded that for breeding hybrids with stable fertility restoration, the presence of two dominant genes is essential.

Sawargaonkar *et al.* (2012) reported that the fertility restoration in ICPH 2671 hybrid is high (95-100% pollen fertility), stable across environments and is controlled by two dominant genes.

Saxena *et al.* (2014) stated that fertility restoration of CMS based hybrids is an integral part of breeding hybrids and identified 25 male sterility maintainers and 179 fertility restorers of A4 cytoplasm in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Multi-location evaluation of hybrids exhibited high stability for fertility restoration across diverse environments. A total of 35 restorers were used to study stability of pollen fertility in hybrid combinations at diverse locations in different years. Of these, 20 were evaluated at 10 environments for three years. Their mean pollen fertility ranged from 88 to 99 %. The remaining 15 hybrids were evaluated in seven environments for two years and their pollen fertility ranged from 85.5 to 100 %.

Chaudhari *et al.* (2015) investigated the stability of male sterility of nine CGMS lines under three dates of sowing and the fertility restoration of 10 CGMS based pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids at three different locations. Significant variability existed for pollen fertility among hybrids and sterility among cytoplasmic male sterile (CMS) lines. All the hybrids except ICPH 3494 and ICPH 3491 exhibited high (>80%) pollen fertility across locations. Hybrids ICPH 2671, ICPH 2740, and ICPH 3933 had 100% male-fertile plants across locations. All the CMS lines had completely male-sterile plants across sowing dates. The CMS lines BRG1 A, Hy3C A, BRG3 A, and TTB7 A exhibited 100% pollen sterility at different sowing dates. The pooled analysis revealed a significant genotype × environment interaction for pollen fertility and sterility. The genotypic main effect + GE (GGE) biplot of hybrids showed that hybrids ICPH 2671, 2740, 3933, and 3461 were stable for fertility restoration. With the exception of

ICPA 2047 and ICPA 2051, all the CMS lines were highly stable with high mean performance and least distance from AEA (average environmental axis). Male sterility in A4 cytoplasm was independent of environmental conditions. Different dates of sowing did not affect expression of male sterility of these CMS lines.

Reddy *et al*. (2015) studied fertility restoration in newly developed CMS lines and extent of hybrid vigour in 24 pigeonpea hybrids for developing elite pigeonpea hybrids specifically suited for commercial exploitation. The study identified pigeonpea lines, ICPL 20098, ICPL 20123, ICPL 20137 and ICPL 87119 as complete restorers while ICPL 20108 and ICPL 20186 as partial restorers. Pollen fertility per cent for the hybrids ranged from 42.5 % (ICPH 4181) to 96.0 % (ICPH 2671) with an average of 83.1 %. Sixteen hybrids had recorded pollen fertility per cent more than 80 per cent and hence, were classified as fertile, while, seven hybrids with fertility per cent of 10-80 were classified as partially fertile. In addition to high pollen fertility per cent hybrids, ICPH 3762, ICPH 4500 and ICPH 3474 revealed high seed yield and yield attributes.

Saroj *et al.* (2015) studied segregation patterns for pollen fertility of five crosses were studied involving two CGMS lines and four restorers *viz*., ICPA 2043 / ICP 6399, ICPA 2043 / ICP 9149, ICPA 2043 / ICPR 4105, ICPA 2092 / ICPR 4105 and ICPA 2092 / KA 91-25 in F_2 and BC_1F_1 generations. All the 132 F_1 hybrids evaluated for the pollen fertility restoration, pod setting rate was considered main criteria, in which 12 F_1s showed 0-10 % pollen fertility with negligible pod setting, 94 F_1s were revealed 11-89 % pollen fertility with poor pod setting from all two CMS lines respectively. However, 26 crosses were exhibited > 90 % pollen fertility with good pod setting, associated with two CMS lines *viz.,* ICPA 2043 and ICPA 2092. All the lines and testers recorded 100% sterile and pollen fertility respectively and maintainers (B lines) revealed fertility ranged from 96.54-99.35. In the case of hybrids, all the plants were indicating fertile ranging from 94.74 to 98.67 over three years and each season had two (low and high) temperatures, in this event incorporated dominant fertility restoring genes from the restorer parent to the hybrids. Multi season evaluation of hybrids exhibited high stability for fertility restoration across diverse environments.

Choudhary and Singh (2015) studied fertility restoration efficiency in F_1 hybrids having either A2 or A4 cytoplasms. Four CMS lines namely Hy4A, H28A (each with A2 cytoplasm), ICP 2039A and ICP 2043A (both with A4 cytoplasm) were crossed with ten genotypes/restorers of long duration pigeonpea for two years. The F_1 hybrids so obtained

were assessed in the succeeding years for pollen fertility and pod setting. All the pollinators except IPA 203 restored fertility in F_1 hybrids derived from ICP 2039A and ICP 2043A (both having A4 cytoplasm). However, none of the restorers were effective in restoring fertility in hybrids derived from Hy4A and H28A (each with A2 cytoplasm).

Kumar *et al.* (2015) studied heterosis and pollen fertility status in 20 CGMS based pigeonpea hybrids. Among all hybrids, ICPA 2047 x ICPL 20108 recorded maximum pollen fertility (98.50%) followed by ICPA 2078 x ICPL 87113 (98.05%) and ICPA 2092 x ICPL 87119 (97.72%), whereas the minimum pollen fertility was recorded in ICPA 2048 x ICPL 20096 (59.22%) followed by ICPA 2047 x ICPL 20129 (74.46%).

2.5 HETEROSIS

The term “hybrid vigour” or “heterosis” means superiority of F_1 hybrid over its parents and it has been exploited commercially in a number of cereal and vegetable crops. Heterosis may be positive or negative. Depending upon the breeding objectives, both positive and negative heterosis are useful for crop improvement. In general, positive heterosis is desired for yield and negative heterosis for maturity. Heterosis is expressed in three ways, depending on the criteria used to compare the performance of a hybrid. These three ways are mid-parent, standard variety and better parent heterosis. Exploitation of heterosis in agriculture provides enhancing food security and represents a single greatest applied achievement in the discipline of genetics. In pigeonpea, a considerable amount of hybrid vigor with the mid-parent, standard variety and better parent has been reported by several workers for grain yield and other economic characters. The literature related to heterosis studies has been provided here under.

Solomon *et al*. (1957) were the first to report a study on heterosis in pigeonpea. Hybrid vigor up to a maximum of 24.51 % in grain yield, 13.04 % for plant height, 9.6 % for pod length were obtained in some of the crosses under his study. However, the fact that the best yielding hybrid had not been able to out yield the yielding type involved in one or more of the crosses.

Khorgade *et al*. (2000) reported heterosis over mid-parent and control cultivar (BDN 2) in 24 pigeon pea hybrids. Significant heterosis was observed for seven quantitative characters studied. Significant heterosis over the mid-parent and control cultivar was recorded for seed yield per plant in the hybrids AKMS 11 × AKT 9221, AKMS 11 × C11, and AKMS 21 × C11.

Chandirakala and Raveendran (2002) reported the heterosis for yield and yield components in 30 pigeonpea hybrids. Crosses with MS Prabhat DT showed marked heterosis for number of pods per plant, number of clusters per plant, 100 grain weight, and grain yield per plant. Significant negative heterosis over mid, better, and standard parents were observed in MS Prabhat DT x ICPL 88009 and MS CO 5 x ICPL 88009 for days to 50% flowering, and in MS Prabhat DT x ICPL 87104, MS Prabhat DT x ICPL 89020, MS Prabhat DT x ICPL 90012, and MS CO 5 x ICPL 87104 for plant height.

Pandey and Singh (2002) evaluated hybrids developed from crosses between three genetic male sterile lines (DAMS-1, ICPMS 3783 and KPMS 1050) and 12 diverse

genotypes of the long duration group of pigeonpea for standard heterosis. They observed that standard heterosis ranged from 144.32 % (KPMS 1050 x DA 94-6) to 8.75 % (MS 3783 x DA 37). Out of 36 combinations, 12 registered significant positive heterosis for seed yield per plant and number of primary and secondary branches per plant, clusters per plant and number of pods per plant.

Lohithaswa and Dharmaraj (2003) studied heterosis for yield and yield attributes. Observations were recorded for 12 quantitative characters. Non additive gene effects were predominant for all characters, except for days to 50% flowering, 100 seed weight and protein content, for which additive gene action was predominant. The heterosis values when considered alone were misleading as there was no correspondence with *per se* performance.

Sekhar *et al*. (2004) studied the heterosis in 36 early maturing pigeonpea hybrids involving 3 male sterile lines and 12 pollinator lines. Three crosses [QMS-1 x Sel 90307, QMS-1 x Sel 90311 and MS Prabhat (NDT) x Sel 90214] exhibited 51.3 to 171.6% heterosis for seed yield per plant over the standard check and better parent, respectively. Among the tested materials, the best five hybrids exceeded 40% standard heterosis for seed yield and its components.

Yadav and Singh (2004) reported the heterosis of pigeonpea in yield and its related traits. In their research finding, 20 to 49.8 % of standard heterosis for primary branches per plant was expressed in all the hybrids except MS UPAS 120 x Pant A 134. For seed per pod, significant positive heterosis was observed in seven hybrids. Number of pods per plant expressed up to 203.9% of standard heterosis. The highest standard heterosis for 100 seed weight was 12.1% in UPAS 120 x Pant A 169. The range of standard heterosis for grain yield over standard variety was -46.03 to 180%.

Wankhade *et al*. (2005) investigated the amount of heterosis for seed yield and its components by using three genetic male sterile lines (females) and eight testers (males) in a line x tester mating design. The heterosis was observed for most of the traits, except plant height. The cross AKMS 11 x AKT 9221 showed highest seed yield per plant and exhibited high heterosis (63.19%) and useful heterosis over BDN 2 (83.34%). The mean squares due to parents and crosses were highly significant for all the characters.

Aher *et al*. (2006) reported the range of heterosis for mid parent and better parent was from 3.25 to 2.25% and 2.50 to 10.50% for days to maturity, -1.10 to 3.15% and 2.9 to 2.4% for number of primary branches per plant, and -0.95 to 3.35% and -3.0 to 2.5%

for secondary branches per plant. For number of pods per plant, significant and positive heterosis over mid parent and better parent was observed in BDN 2 × BDN 201. Heterosis over mid parent and better parent ranged from -1.65 to 3.60% and -3.30 to 3.20%, respectively, for number of seeds per pod. Heterosis for 100 seed weight was from -0.51 to 0.22% and -1.97 to 0.03% for mid parent and better parent, respectively. For grain yield per plant, the range of heterosis over better was -20.66 to 23.79%.

Baskaran and Muthiah (2006) reported the magnitude of relative heterosis, heterobeltiosis and standard heterosis of 18 hybrids derived for seed yield and yield attributing characters. Significant positive heterotic effect over mid parent, better parent and standard control (CO 5) was recorded for seed yield per plant in hybrid VBN 1 x ICPL 83027 (81.74%, 66.57% and 68.36%) followed by CO 5 x ICPL 83027 (24.46%, 23.80% and 25.13%) and CORG 9904 × ICPL 83027 (56.47%, 17.77% and 19.03%).

Banu *et al*. (2007) investigated the relative heterosis and heterobeltiosis in 45 pigeonpea hybrids on days to 50% flowering, maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length and 100 seed weight and single plant yield. ICP 13201 × CO 5 was the best with the maximum heterosis for most of the yield attributing characters followed by ICP 11961 x ICP 7118 and ICP 11961 x CO 5, which showed higher heterobeltiosis and relative heterosis for most of the yield attributing characters.

Wanjari *et al*. (2007) evaluated the heterosis in a set of 136 CMS based pigeonpea hybrids in the background of A2 cytoplasm along with AKT 8811 as the control. Heterosis over male parent and the control was investigated. Among the 136 hybrids, 11 expressed high pollen fertility (>80%) in all the plants. The hybrids characterized by high pollen fertility varied in terms of heterosis. Six hybrids showed positive heterosis.

Dheva *et al*. (2008a) reported heterosis in CMS based pigeonpea hybrids. The highest heterosis was observed for number of pods per plant (79.43%) followed by grain yield per plant (68.06%) and plant height (37.89%) over the better parent. The highest heterosis over the better parent observed for days to 50% flowering (-23.84%) followed by days to maturity (-16.94%) was also in desirable negative directions.

Dheva *et al.* (2008b) evaluated heterosis in CMS based hybrid pigeonpea. They studied 31 hybrids showing fertility more than 80 per cent for heterosis over the mid parent, better parent and standard check. Among these, three hybrids showed heterosis

more than 40 per cent for number of pods and grain yield per plant. The range of heterosis over check for number of pods per plant is 0.84 to 87.68 per cent and 0.72 to 57.35 per cent for grain yield.

Kumar and Krishna (2008) reported heterosis in pigeonpea over superior and economic parent (T-7) for 13 quantitative characters. Eight hybrids KA-1 × KA32-1, K35 × Banda Palera, KA-1 × Banda Palera, KA26-8 × Banda Palera, KA26-8 × KA32-1, T7 × Banda Palera, K9125(B) × Banda Palera, and KA108 × KA32-1 were judged to be promising for grain yield per plant on the basis of their high heterosic response and *per se* performance.

Patel and Tikka (2008) reported heterosis for yield and yield components in 45 hybrids and 18 parental genotypes of pigeonpea. For number of pods per plant, 10 and 20 hybrids recorded significant positive heterosis over the better parent and control, respectively. Eight hybrids were superior over the better parent with respect to number of seeds per pod. Only two hybrids over the better parent and one hybrid over the control showed significant positive heterosis for protein content. For seed yield, two hybrids exhibited positive heterosis over the better parent. Hybrid MS 3783 × BSMR 853 (97.54%) recorded highest positive heterobeltiosis.

Bhavani and Bhalla (2009) analyzed the heterotic effects in 20 hybrid pigeonpea combinations involving five diverse parents belonging to different maturity groups (early, medium and late) for yield and its components. The average heterosis was maximum for yield per plant, followed by pods per plant and number of fruit bearing branches. Comparatively, the other yield components showed low average heterosis values. In general, early x late and medium x late combinations resulted in high heterosis for yield.

Dheva *et al*. (2009) reported heterosis in 31 hybrids. Three hybrids showed heterosis more than 40 per cent for the number of pods and grain yield per plant, respectively. The highest standard heterosis was observed for the number of pods per plant followed by grain yield per plant. The range of heterosis over check for number of pods per plant was observed to be from 0.84 to 87.68 per cent and the heterosis over check for the character grain yield per plant was noticed range from 0.72 to 57.35 per cent in desirable direction.

Kumar *et al*. (2009) reported the heterosis of pigeonpea for yield and its component traits. Significant and positive heterosis over better parent and standard check for seed yield per plant in four crosses was accompanied by significant and high positive heterosis for number of primary branches per plant, number of pods per plant, number of

pod clusters per plant and 100 seed weight. This study suggested that heterosis for yield should be through component trait heterosis. Hybrid vigor of individual yield components may have additive or synergistic effect on the yield.

Phad *et al*. (2009) reported the heterosis in pigeonpea by using 60 crosses in four different environments. The top 10 cross combinations recorded significant positive standard heterosis for number of secondary branches per plant, whereas nine cross combinations recorded standard heterotic effect for plant spread, number of primary branches per plant and number of pods per plant. Significant positive standard heterosis was recorded in seven cross combinations for harvest index, two cross combinations for plant height and only one cross combination for 100 seed weight. On the basis of pooled mean, the top 10 cross combinations showed superiority in different environments.

Sarode *et al*. (2009) estimated the heterosis in long duration pigeonpea for yield and yield traits using five lines and three testers. The maximum standard heterosis was recorded in the cross Pusa 9 x Bahar (52.11%), followed by Pusa 9 x ICPL 84023 (44.17%) and DA 11 x Bahar (42.03%) for number of pods per plant. Hybrid Pusa 9 x Bahar exhibited maximum economic heterosis (55.32%) for 100 seed weight, number of seeds per pod, pods per plant and number of primary and secondary branches.

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 two hybrids showed highly significant and positive heterosis over mid parent, better parent and standard check. The proportion of hybrids exhibiting significant heterotic effect for grain yield with genetic male sterile line MS Prabhat DT was greater as compared to lines, MS Prabhat NDT and MS CO5.

Shoba and Balan (2010) studied the magnitude of heterosis in 27 early maturing hybrids. They observed standard heterosis for single plant yield varied from -25.0 (CORG 990047 A x ICPL 87) to 325% (MS CO 5 x PA 128). The promising hybrids, CORG 990047 A x APK 1 manifested heterosis for days to 50% flowering (56.3%), days to maturity (92.47%), plant height (113.0%), number of pods per plant (106.0%), seed protein content (22.71%) and single plant yield (40.0%). MS CO5 x ICPL 83027 had significant standard heterosis for plant height (98.38%), number of branches per plant (128.2%), number of pods per plant (110.0%), number of seeds per pod (4.50%) and single plant yield (70.0%).

Lay *et al*. (2011) reported heterosis in CMS based pigeonpea hybrids. They evaluated 15 of ICRISAT's pigeonpea hybrids in Myanmar at three locations. Hybrids ICPH 2671, ICPH 2673, ICPH 2740 and ICPH 3497 were found stable over the three environments and produced 30.4 to 41.7 per cent standard heterosis. Hybrid ICPH 3461 was found suitable for one environment with 42.0 per cent standard heterosis. In 36 on farm trials, hybrid ICPH 2671 was 11.9 to 53.1 per cent superior in yield over the control. The other promising hybrid ICPH 2740 also exhibited 70.0 per cent standard heterosis in an on farm trial.

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 fourteen hybrids ranging from -85.06 to 33.74% and fifteen hybrids over standard variety ranging from -82.57 to 26.28%. Besides seed yield, substantial heterosis was also observed in negative as well as positive direction for remaining yield attributing characters. Among all the crosses, NDACMS1-64 x NDA98-6, NDACMS1-6 x NDA5-14, NDACMS1-4 x IPA208, NDACMS1-6 x ICP870 were found to be having more than 20% standard heterosis for seed yield recommended for commercial utilization.

Pawar *et al.* (2013) evaluated 64 pigeonpea hybrids, derived from crosses between four genetic male sterile lines and eight diverse testers, over three environments to estimate heterosis over mid parent, better parent, and standard check (ICPH 8). An appreciable amount of heterosis was noticed for almost all the traits. The magnitude of heterosis was high for seed yield per plant and pods per plant, medium for plant height, branches per plant, 100 seed weight and harvest index and low for days to flowering and protein content. The best three heterotic hybrids for seed yield per plant and its components like pods per plant, branches per plant and harvest index were MS 288 x SKNP 9256, MS 288 x SKNP 9219 and MS Pusa 33 x SKNP 9256.

Arbad *et al.* (2014) evaluated 4 lines, 23 testers, 92 crosses of pigeonpea, along with one check BSMR 736 and one promising hybrid ICPH 2671 to estimate variable components, standard heterosis for seed yield and its components, and to isolate better crosses. The heterosis study revealed that phenomenon of heterosis was of general occurrence for most of the characters. The cross ICPA 2092 x ICP 12057 showed highest seed yield per plant and exhibited highest heterosis (71.79%) followed by ICPA 2092 x ICP 12320 (45.74%) over standard check BSMR 736.

Gite and Madrap (2014) studied heterosis in 48 pigeonpea male sterile lines hybrids, along with their parents at Badnapur, Maharashtra, India, during the *kharif* season of 2008. ICPA 2043 x ICPR 2671, ICPA 2043 x ICPR 3473, ICPA 2043 x ICPR 3477, ICPA 2043 x ICPR 3514, and ICPA 2048 x ICPR 2671 had registered highest values for mid parent heterosis and heterobeltiosis for plant height, number of primary and secondary branches per plant, number of pods per plant and 100 seed weight.

Patel and Tikka (2014) crossed six newly converted cytoplasmic male sterile lines with 12 fertility restorer lines in line x tester mating design and these hybrids were evaluated with check Gujarat Tur Hybrid 1 at Sardarkrushinagar, Jagudan and Khedbrahma to study the extent of heterosis. High heterosis was recorded for grain yield per plant, pods per plant and harvest index, while, medium heterosis for plant height, number of branches per plant, 100-seed weight, protein content, biological yield and reproductive period. Days to flowering, days to maturity, number of seeds per pod and pod length recorded low magnitude of heterosis. Five hybrids, namely, CMS GT 087A x GTR 0525 (116.40%) CMS GT 087A x AGTR 0534 (108.93%), CMS GT 0307A x AGTR 0538 (99.21%), CMS GT 0301A x AGTR 0534 (95.51%) and CMS GT 0308A x AGTR 0536 (89.32%) showed standard heterosis for grain yield and its component characters.

Patil *et al.* (2014) under took investigation of heterobeltiosis for seed yield and its components with protein content in a set of 7 x 7 half diallel parent excluding reciprocals. Highly significant positive heterosis over better parent for seed yield and its component with protein content was recorded. 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) studied four pigeonpea crosses to understand the extent of heterosis over mid parent and better parent for grain yield and its attributing characters. Maximum positive heterosis over mid parent was observed for seed yield per plant (132.88%) and number of pods per plant (114.53%). In addition to it, maximum heterosis over better parent was observed for number of pods per plant (96.97%) followed by seed yield per plant (96.11%). And concluded that significant heterosis observed for branches per plant and pods per plant have resulted in increased yield of hybrids.

Kumar *et al.* (2015) evaluated 20 CGMS based pigeonpea hybrids to study yield potential with performance of their R-line. A majority of hybrids showed standard heterosis in desirable direction for yield and yield attributing characters over the standard checks (Asha and Maruti). The range of standard heterosis over Asha and Maruti for grain yield per plant ranged from -13.06 to 40.91% and 11.11 to 80.10 % respectively. And with respect to yield most of the hybrids showed positive standard heterosis for yield and it was up to 59.93%.

Mhasal *et al.* (2015) studied 11 genotypes; six females (CMS lines viz., AKCMS- 81A, AKCMS-82-2A, AKCMS-83A, AKCMS-12A, AKCMS-93A and ICPA-2047A) and five males (testers) viz., AKPR-303, AKPR-324, AKPR-364, AKPR-372, AKPR-057 and their 30 crosses along with two checks PKV-TARA and Asha with the objective of estimating the extent of heterosis and combining ability effects among parents and hybrids and to find out promising cross combinations for grain yield and its components. The cross ICPA-2047A × 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 × AKPR-372 also revealed high mean performance (33.00 g) and high magnitude of useful heterosis (15.38 % over check PKV-TARA and 20.73% over Asha).

Reddy *et al.* (2015) studied fertility restoration in newly developed CMS lines and extent of hybrid vigor in 24 pigeonpea hybrids for developing elite pigeonpea hybrids specifically suited for commercial exploitation. Maximum heterosis over mid parent, better parent and standard check were observed for seed yield per plant, followed by number of secondary branches and pods per plant. High heterosis, more than 100 per cent, over the check, 'Asha'; more than 50 per cent over mid parent; and more than 30 per cent over better parent, was noticed in the hybrids, 'ICPH 3762' and 'ICPH 3474'. These promising mid-late hybrids with improved *per se* performance, high fertility restoration and heterosis for seed yield and other major yield attributing traits are identified here for large scale commercial cultivation.

Singh and Singh (2016) developed 12 hybrids having diverse background to understand the heterosis and inbreeding depression in late maturity groups of pigeonpea [*Cajanus cajan* (L.) Millsp.]. More than 100% significant economic heterosis were revealed in crosses, MAL-17 × NDA 4906 (266.32%), BHUA 96-13-3 × NDA 49-6 (249.98%), BHUA 96-13-3 × MAL-19 (190.41%), MAL-17 × NDA 99-1 (136.27%) and

MAL-17 × MAL- 19 (103.46%) for seed yield per plant. The crosses, MAL-17 × NDA 49-6 and BHUA 96-13-3 × NDA 49-6, showed better performance in F_1, low/even negative inbreeding depression in F_2 and involved parents with high *per se* performance. Two crosses namely, BHUA 96-13-3 × MAL-19 and BHUA 96-21-4 × NDA 99-1 showing higher magnitude of heterosis were also associated with higher inbreeding depression. The cross, MAL-17 × NDA 49-6 (266.32%) showed maximum estimates of yield heterosis, also exhibited significant heterosis for days to 50% flowering, number of primary and secondary branches, pods per plant, pod length and harvest index.

Chapter- III

MATERIAL AND METHODS

Chapter III

MATERIAL AND METHODS

The present investigation on "Heterosis in CMS based hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.]" was carried out during *kharif* 2015. The material used and methods followed are presented in this chapter.

3.1 MATERIAL

The experimental material for present investigation comprised 24 F_1 hybrids and four standard checks; Asha, Maruti, LRG 41 and BDN 711, obtained from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru. The details of these lines are presented in table 3.1, table 3.2 and table 3.3.

3.2 METHOD

3.2.1 Experimental site and layout

The experimental site was located at ICRISAT, Patancheru, Telangana at an altitude of 545 m above mean sea level, latitude of 17º 53' N and longitude of 78º 27' E. The material consisting of 24 F_1 hybrids along with the standard checks, Asha, Maruti, LRG 41 and BDN 711 were evaluated in a randomized complete block design with three replications in three contiguous blocks. The experimental materials were line sown on July 24, 2015 with inter and intra row spacing of 150 and 60 cm respectively. The plot size for each genotype was 18.9 m^2 and consisted of three rows, each of 4.2 m in length. Only one plant was maintained after thinning at each hill. Border rows were planted around the experimental plot to increase the precision of study and to reduce border effect.

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	ICPA2047 x ICPL 287119
4.	ICPH 3477	ICPA 2047 x ICPL 20098
5.	ICPH 2751	ICPA 2048 x ICPL 87119
6.	ICPH 3461	ICPA 2092 x ICPL 87119
7.	ICPH 3762	ICPA 2092 x ICPL 20108
8.	ICPH 3337	ICPA 2043 x ICPL 20107
9.	ICPH 3473	ICPA 2043 x ICPL 20116
10.	ICPH 4395	ICPA 2078 x ICPL 20116
11.	ICPH 4485	ICPA 2078 x ICPL 20137
12.	ICPH 4187	ICPA 2078 x ICPL 20108
13.	ICPH 4539	ICPA 2078 x ICPL 20123
14.	ICPH 4275	ICPA 2078 x ICPL 20204
15.	ICPH 2680	ICPA 2043 x ICPL 20186
16.	ICPH 3816	ICPA 2043 x ICPL 20137
17.	ICPH 4488	ICPA 2043 x ICPL 20125
18.	ICPH 4500	ICPA 2199 x ICPL 20108
19.	ICPH 4502	ICPA 2199 x ICPL 20106
20.	ICPH 4540	ICPA 2078 x ICPL 20186
21.	ICPH 4542	ICPA 2078x ICPL 99046
22.	ICPH 4611	ICPA 2078 x SK Line
23.	ICPH 4671	ICPA 2199 x ICPL 20123
24.	ICPH 3474	ICPA 2043 x ICPL 20123
25.	Asha	ICPX 780143-EB-EB-EB-EB-E27-B
26.	Maruthi	Selection from landraces of Maharashtra.
27.	LRG 41	Selection from Chilakalurpet Local
28.	BDN 711	Selection from BPG 111

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	% Disease reaction in nursery	
								Wilt	SMD
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	19	-
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	11	-
6	ICPA 2199	ICPA 2101 x ICPL 96053	128	181	258	12.5	White	3.7	0

Where, SMD = sterility mosaic disease; 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	% Disease reaction in nursery	
								Wilt	SMD
1	ICPL 87119	C 11 x ICP 1-6W3B	122	172	228	10.6	Brown	-	-
2	ICPL 20098	ICPL 87119 x ICP12746 (Inbred)	130	174	235	14.3	Light brown	-	-
3	ICPL 20108	MS 3783 x ICPL 87119 (IPH 487 Inbred)	122	165	235	11.4	Cream	-	-
4	ICPL 20107	MS 3783 x ICPL 87119	130	185	283	11.6	Brown	1	1
5	ICPL 20116	MS 3783 x ICPL 87119	125	181	275	10.8	Brown	2	0
6	ICPL 20137	MA 3783 x ICP 8863	130	187	262	14.8	Cream	8	1
7	ICPL 20123	MS 3783 x ICPL 87119 (IPH 487 Inbred)	122	168	228	10.8	Brown	-	-
8	ICPL 20204	HPL 24-39	102	155	160	11.5	Brown	0	0
9	ICPL 20186	ICP 10928 Selection	145	188	242	9.4	Light brown	28	6
10	ICPL 20125	MS 3783 x GAUT85-19	137	190	257	11.8	Brown	0	1
11	ICPL 20106	MS 3783 x ICPL 87119 (IPH 487 Inbred)	128	175	215	10.5	Cream	86	49
12	ICPL 99046	ICPL 87119 x ICP13232	123	175	227	12.4	Brown	4.5	18.2
13	SK Line	Selection from local	110	160	180	13	-	20	27

Where, SMD = sterility mosaic disease; Source: Pigeonpea Breeding department, ICRISAT, Patancheru, (Telangana)

3.2.2 Cultural practices and weather conditions

The soil of the experimental site was black and classified as Vertisol. During early vegetative stage spray of herbicide Pendimethaline @ 3 liter per ha was carried out to control weeds. During reproductive stages one sprays of Indoxacarb @ 0.5 liter per ha and one sprays of Cypermethrin @ 0.5 liter per ha were used to control *Maruca* while two sprays of Spinosad @ 0.2 liter per ha was used to control *Helicoverpa*. The crop was irrigated at critical stages such as vegetative and pod filling stage. The weeds were controlled manually at various crop growth stages as per the intensity of the weeds. The mean meteorological data recorded during the crop growth period such as rainfall, temperature and relative humidity are presented in Appendix I and II.

3.2.3 Collection of Data

3.2.3.1 Yield and yield components

Ten competitive plants were randomly selected for recording observations on each hybrid and standard checks. The details of the observations recorded are as follows:

3.2.3.1.1 Days to 50 *per cent* flowering

Days taken from sowing to the flowering of 50 per cent plants in a plot were recorded.

3.2.3.1.2 Days to maturity

Days required from sowing to 75 *per cent* maturity were recorded for each plot.

3.2.3.1.3 Plant height (cm)

Height of the plant from ground level to the tip of the plant was measured (cm) at the time of maturity. Mean value of random sample of ten plants was computed.

3.2.3.1.4 Number of primary branches per plant

Total numbers of pod bearing branches on the main stem of a plant were counted. Mean value of random sample of ten plants was computed.

3.2.3.1.5 Number of secondary branches per plant

Total numbers of pod bearing branches on primary branches of a plant were counted. Mean value of random sample of ten plants was computed.

3.2.3.1.6 Number of pods per plant

The numbers of pods present on the sampled plants were counted at maturity. Mean value of random sample of ten plants was computed.

3.2.3.1.7 Pod weight per plant (g)

Total weight of the pods harvested from the sampled plant was weighed on electronic balance and measured in grams. Mean value of random sample of ten plants was computed.

3.2.3.1.8 100 Seed weight (g)

Fully grown 100 seeds of each entry were collected randomly in each plot and weighed on electric balance.

3.2.3.1.9 Grain yield per plant (g)

From each selected plant, dry pods were harvested and threshed separately. Grain weights were recorded after thorough sun drying. Mean value of random sample of ten plants was computed.

3.2.3.2 Pollen fertility percentage

For testing the pollen fertility in the hybrids two per cent aceto-carmine solution was used to stain and differentiate the fertile and sterile pollen grains. Ten plants were selected randomly from each hybrid and five buds from each plant were collected to record its pollen fertility. Anthers from each flower bud were squashed on a slide and the count of fertile pollen and sterile grains in three microscopic fields was noted. The round and well stained pollen grains were counted as fertile while shriveled hyaline pollen grains were scored as sterile. Percent pollen fertility of hybrids was calculated on mean of all the observations from a hybrid.

$$\text{Pollen fertility (\%)} = \frac{\text{Number of fertile pollens}}{\text{----------}} \times 100$$

Total number of pollens

Based on this data, the plants were classified into fertile (>80% pollen fertility), partial fertile (11 - 80% pollen fertility), and sterile (0 - 10% pollen fertility) (Kyu and Saxena 2011).

3.3 STATISTICAL ANALYSES

The following statistical techniques were used to analyze the data collected from the above mentioned experiments.

3.3.1 Analysis of Variance

The data was subjected to analysis of variance as per the method described by Fisher and Yates (1974).

The model for experimental design used in randomized block design can be expressed as follows.

$$\mathbf{Y_{ij} = \mu + g_i + r_j + e_{ij}}$$

Where,

Y_{ij} = Effect of i^{th} genotype in the j^{th} replication.

μ = general population mean

g_i = effect of i^{th} genotype.

r_j = effect of j^{th} replication.

e_{ij}= error associated with the experiment.

Aanalysis of variance for randomized complete block design.

Source of variation	df	SS	MSS	Expected MSS	'F' calculated
Replications	(r-1)	RSS	M_r	$\sigma^2e + t\,\sigma^2r$	M_r/ M_e
Treatments	(t-1)	TrSS	M_t	$\sigma^2e + r\,\sigma^2g$	M_t/ M_e
Error	(r-1) (t-1)	ESS	M_e	σ^2e	
Total	(rt-1)	TSS			

Where,

r = Number of replications

t = Number of genotypes

df = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

M_r = Mean sum of square of replication

M_t = Mean sum of square of treatment

M_e = Mean sum of square of error

σ^2_e = Environmental variance

σ^2_r = Variance due to replications

σ^2_g = Variance due to genotypes

3.3.1. 1 Test of significance

The mean sum of squares for genotypes and replications were tested against the error mean sum of squares for calculating F values which were compared with tabulated F value at 5 and 1 percent level of significance.

3.3.1.2 Mean

Mean was calculated using following conventional formula

$$\bar{x} = \frac{\sum x}{N}$$

Where,

$\bar{x}$ = mean of all the observations.

$\sum x$ = summation of all the observation.

N = number of observation.

3.3.1.3 Range

It is the range of lowest and highest values of each trait taken in the observations.

3.3.1.4 Standard error of mean

It was calculated as formula given below.

$$\text{SEm}\pm = \sqrt{\frac{MSe}{r}}$$

Where,

SEm± = standard error of mean.

MSe = mean sum of square due to error.

r = number of replication.

3.3.1.5 Standard error of differences

It was calculated as formula given below.

SEd ± = ? É? ?? ?

Where,

SEd± = standard error of differences.

MSe = mean sum of square due to error.

r = number of replications.

3.3.1.6 Critical difference

It was measured as formula mentioned below.

CD = SEd x t value at error degrees of freedom

Where,

CD = critical difference.

SEd = standard error of difference.

t = table value at 5% probability level of error degrees of freedom.

3.3.2 Estimation of Genetic Parameters

3.3.2.1 Phenotypic and genotypic variance

This was estimated according to the method given by Lush (1940).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + M_e = \frac{M_t - M_e}{r} + M_e$$

3.3.2.2 Coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\overline{X})} \times 100$$

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\overline{X})} \times 100$$

As suggested by Subramanian and Menon (1973), GCV and PCV were categorized into

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

3.3.2.3 Heritability in broad sense [$h^2_{(b)}$]

Heritability in broad sense was estimated as per the formula given by Allard (1960).

$$h^2_{(b)} = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

As suggested by Johnson *et al.* (1955), $h^2_{(b)}$ estimates were categorized into

Low	=	0 - 30 %
Moderate	=	31- 60 %
High	=	more than 60 %

3.3.2.4 Genetic advance as per cent of mean (GAM)

Genetic advance was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

$$\text{Genetic Advance (GA)} = K \times \sigma_p \times h^2 \text{ (b)}$$

Where,

K = Selection differential at 5% selection intensity (2.06).

h^2 (b) = heritability in broad sense.

σ_p = phenotypic standard deviation.

$$GAM = \frac{GA}{\text{Grand mean } (\overline{X})} \times 100$$

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

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

3.3.3 Correlations

Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

Phenotypic coefficient of correlation (r_p)

$$r(x_i.x_j)_p = \frac{Cov(x_i.x_j)_p}{\sqrt{V(x_i)p.V(x_j)p}}$$

Where,

$r(X_i.X_j)_p$ = Phenotypic correlation between i^{th} and j^{th}character

$Cov(X_i.X_j)_p$ = Phenotypic covariance between $i^{th}$and j^{th} character

$V(X_i)p$ = Phenotypic variance of i^{th} character

$V(X_j)p$ = Phenotypic variance of j^{th} character

Genotypic coefficient of correlation (r_g)

$$r(x_i.x_j)_g = \frac{Cov(x_i.x_j)_g}{\sqrt{V(x_i)g.V(x_j)g}}$$

Where,

$r(X_i.X_j)_g$ = Genotypic correlation between i^{th} and j^{th} character

$COV(X_i.X_j)_g$ = Genotypic covariance between i^{th} and j^{th}character

$V(X_i)g$ = Genotypic variance of i^{th} character

$V(X_j)g$ = Genotypic variance of j^{th} character

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5 per cent and 1 per cent level, where 'n' denotes the number of paired observations used in the calculation.

3.3.4 Path coefficient Analysis

Phenotypic and genotypic correlation coefficients were utilized for path coefficient analysis. The direct and indirect contribution of various traits were calculated through path coefficient analysis as suggested by Wright (1921) and later elaborated by Dewey and Lu (1959).

For estimation of various direct and indirect effects, a set of simultaneous equations were formed:

$$r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \ldots + r_{1k} P_{ky}$$

$$r_{2y} = r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \ldots + r_{2k} P_{ky}$$

$$r_{iy} = r_{i1} P_{1y} + r_{i2} P_{2y} + r_{i3} P_{3y} + \ldots + r_{ik} P_{ky}$$

$$r_{ky} = r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \ldots + r_{kk} P_{ky}$$

Where,

r_{1y} to r_{ky} = Coefficient of correlations between causal factors 1 to K and dependent character Y.

r_{12} to $r_{k-1,k}$ = Coefficient of correlations among causal factors.

P_{1y} to P_{ky} = Direct effects of characters 1 to k on character y

The above equations were written in a matrix form as under:

$$A = C B$$

$$\begin{pmatrix} r_{1Y} \\ r_{2Y} \\ . \\ . \\ . \\ . \\ r_{iY} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{1i} \\ r_{21} & 1 & r_{2i} \\ . & . & . \\ . & . & . \\ r_{i1} & r_{i2} & 1 \end{pmatrix} \begin{pmatrix} P_{1Y} \\ P_{2Y} \\ . \\ . \\ . \\ . \\ P_{iY} \end{pmatrix}$$

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

Where

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

Then direct effect were calculated as follows,

$P_{1y} = \sum C_{1i} \, . \, r_{iy}$

$P_{2y} = \sum C_{2i} \, . \, r_{iy}$

$P_{ky} = \sum C_{ki} \, . \, r_{iy}$

In the same way equations for r_{1y}, r_{3y}, r_{4y} up to r_{ky} indirect effects were calculated by solving the simultaneous equations. Besides the direct and indirect effects, the residual effect was computed by using the formula:

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

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)

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

3.3.5 Estimation of Standard Heterosis

Standard heterosis was expressed as per cent increase or decrease observed in F_1 over standard check as per the following formula given by Liang *et al.* (1971).

$$\text{Standard heterosis (\%)} = \frac{\overline{F_1} - \text{Mean of superior check}}{\text{Mean of superior check}} \times 100$$

Where,

$\overline{F_1}$ = Mean performance of first filial generation (hybrid).

Chapter- IV

RESULTS AND DISCUSSION

Chapter IV

RESULTS AND DISCUSSION

In India, the area under pigeonpea has increased significantly from 2.3 M ha in 1950 to 5.06 M ha in 2014 (FAOSTAT, 2015). However, the crop productivity has remained stagnant at around 750 kg/ha. Thus to break this yield plateau hybrid development was attempted in pigeonpea, which is unique in having both self and cross pollination systems operating simultaneously under natural conditions. This led to the development of GMS and CMS based hybrids, later one being a commercially viable option. CMS based hybrids have revolutionized the pigeonpea farming sector and demands further research and innovation to make it more accessible to farmers of different agro-climatic zones at an affordable cost.

The present investigation entitled "Heterosis in CMS based hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.]"carried out at ICRISAT, Hyderabad is a step forward towards research and development of pigeonpea hybrids. The main objective of the experiment is to ascertain the standard heterosis and fertility restoration among CMS based hybrids along with genetic studies and correlation studies.

The results obtained from the statistical analysis of the data from twenty four hybrids and four checks of pigeonpea for yield, yield component characters and mean pollen fertility percentage arepresented and discussed here under the following heads:

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 Character association

4.4 Path coefficient analysis

4.5 Fertility restoration studies in pigeonpea

4.6 Heterosis

4.1 ANALYSIS OF VARIANCE

The data collected from the experimental material was subjected to analysis of variance and data was presented in the Table 4.1. The mean performance of the genotypes for different characters is presented in Table 4.2. It is discernible from the table that the treatment differences for yield, yield related characters and pollen fertility % were significant for all the genotypes. Thus the experimental material chosen for the present study was highly variable in nature.

4.2 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Genetic variability is essential for initiating an effective and successful breeding programme and it becomes imperative to study the level of genetic variability available in the existing genotypes. Genetic improvement of a crop through breeding relies solely on the utilization of available or created genetic variability. Depending on the trait, variability in a population can arise from genotype or environment or genotype x environment interaction effects. If variability in the population is largely due to genetic cause with least environmental effect, the probability of isolating superior genotype through selection will be more.

In genetic studies, character with high genotypic coefficient of variation indicates the potential for an effective selection (Sadiq *et al.,* 1986). Determining the components of variability in yield and its components enable us to know the extent of environmental influence on yield, taking into consideration of the fact that yield and its component traits are quantitativecharacters that are affected by environments (Ahmed *et al.,* 2007). Thus to improve selection efficiency it becomes necessary to have an understanding of parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance which helps to further clarify the nature of character.

Heritability is a measure of observed phenotypic differences for a trait due to genetic differences (Klug and Cummings, 2005). It provides information about the extent to which a particular genetic character can be transmitted to the successive generations (Mangi *et al.,* 2010). High heritability indicates less environmental influence in the observed variation (Mohanty, 2003 and Eid, 2009). However, heritability value alone cannot provide information on the amount of genetic progress that would result from selection of best individuals. Johnson *et al.* (1955) reported that heritability estimates

along with genetic advance would be more successful in predicting the effectiveness of selecting the best individuals.

Genetic advance, which estimates the degree of gain in a trait obtained under a given selection pressure, is an important parameters that guides the breeder in choosing a selection program (Hamid *et al.,* 2003). Heritability and genetic advance is a useful tool for breeders in determining the direction and magnitude of selection. High heritability and high genetic advance for a given trait indicates it is governed by additive gene action and, therefore, provides the most effective condition for selection (Tazeen *et al.,* 2009).

The estimates of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2 broad sense) and genetic advance as *per cent* of mean (GAM) are presented in Table 4.3 and described character wise here under.

4.2.1 Yield component characters and pollen fertility (%)

4.2.1.1 Days to 50% flowering

The range of variation for days to 50 % flowering was 86.66 (ICPH 4611) to 101 (Maruti) with a mean value of 93.92 days. The PCV (3.98) and GCV (3.75) estimates are low indicating less variation for days to 50% flowering among the hybrids studied. Similar results were obtained by Deshmukh *et al.* (2000), Kumar (2005), Gohil (2006), Bhaskaran and Muthiah (2006), Gupta *et al.*(2008), Bhadru (2010), Linge *et al.* (2010), Prakash (2011), Patel and Acharya (2011), Nagy *et al.* (2013), and Prasad *et al.* (2013).

High heritability (88.9%) coupled with low genetic advance as *per cent* of mean (6.84) was noticed for days to 50% flowering, which indicates non-additive gene action and selection for such trait may not be rewarding. These findings were similar to those of Aher *et al.* (1996), Patel and Patel (1998), Srinivas *et al.* (1999), Kingshlin and Subbaraman (1999), Prakash (2011), Singh *et al.* (2013), Prasad *et al.* (2013), Rekha *et al.* (2013) and Kumar *et al.* (2014).

4.2.1.2 Days to maturity

The variation for days to maturity ranged from 152 (BDN 711) to 177 (ICPH 4502) with a mean value of 165.16 days. The estimates of PCV (5.0) and GCV (4.43) are

low indicating less variation for days to maturity among the hybrids studied.This result is in agreement with the results obtained by Deshmukh *et al.* (2000), Venkateshwarlu (2001), Kumar (2005), Bhaskaran and Muthiah (2006), Gohil (2006), Bhadru (2010), Linge *et al.* (2010), Prakash (2011), Patel and Acharya (2011), Nagy *et al.* (2013), Prasad *et al.* (2013), Rekha *et al.* (2013) and Saroj *et al.* (2013).

High heritability (78.6%) with low genetic advance as *per cent* of mean (8.1) was seen for days to maturity indicating non-additive gene action and thus selection for days to maturity will not be effective. Similar findings were reported by Kumar (2005), Bhadru (2010) and Rekha *et al.* (2013).

4.2.1.3 Plant height (cm)

The range of variation for this character varied from 141.06 (BDN 711) to 194.4 (ICPH 4542) with a mean value of 170.66 cm. Low PCV (5.96) and GCV (9.07) indicates less variation among the hybrids studied. Such a result was earlier reported by Deshmukh *et al.* (2000), Linge *et al.* (2010) and Prasad *et al.* (2013) too.

Moderate heritability (43.1%) along with low genetic advance as *per cent* of mean (8.05) was observed for this trait indicating the predominance of non-additive gene action in the inheritance of this trait. Moderate heritability for plant height was earlier reported by Venkateshwarlu (2001) and Prasad *et al.* (2013). Meanwhile low genetic advance as per cent of mean was encountered by Deshmukh *et al.* (2000) and Prasad *et al.* (2013).

4.2.1.4 Number of primary branches per plant

Variation for number of primary branches per plant ranged from 12.13 (BDN 711) to 31.2 (ICPH 2740) with a mean value of 22.48. High PCV (24.79) and GCV (22.76) were recorded for this character, indicating the presence of substantial variability for selection. Similar results were reported by Kumar (2005), Gupta *et al.* (2008), Vange and Moses (2009), Prakash (2011), Patel and Acharya (2011), Rekha *et al.* (2013), Saroj *et al.* (2013) and Lakhote *et al.* (2015).

High heritability (84.2%) with high genetic advance as *per cent* of mean (43.02) was seen which indicates that most likely the heritability is due to additive gene effects and the desired results may be obtained by simple selection. These results are in accordance with the results obtained by Kumar (2005), Vange and Moses (2009), Bhadru

(2010), Linge *et al.* (2010), Prakash (2011), Sreelakshmi *et al.* (2011), Nagy *et al.* (2013), Rekha *et al.* (2013) and Saroj *et al.* (2013).

4.2.1.5 Number of secondary branches per plant

The range of variation for this character is from 19.6 (BDN 711) to 84.6 (ICPH 4671) with a mean value of 53. High PCV (32.22) and GCV (30.36) were recorded. Similar results were reported by Venkateshwarlu (2001), Linge *et al.* (2010), Prakash (2011), Rekha *et al.* (2013), Yerimani *et al.* (2013), Singh *et al.* (2014), Ajay *et al.* (2014) and Pandey *et al.* (2015).

High heritability (88.8%) and high genetic advance (58.92) was observed for this trait which revealed the importance of additive gene action. This indicates that this character can be improved through simple selection procedures. This is in accordance with the results obtained by Sreelakshmi *et al.* (2011), Saroj *et al.* (2013), Rekha *et al.* (2013), Yerimani *et al.* (2013), Ajay *et al.* (2014), Kumar *et al.* (2014) and Pandey *et al.* (2015).

4.2.1.6 Number of pods per plant

Number of pods per plant showed variation in the range of 363.66 (ICPH 4542) to 769.9 (ICPH 3762) with a mean value of 520.26. Moderate PCV (19.51) and GCV (15.78) were recorded for this character. These results are in accordance with the findings of Deshmukh *et al.* (2000) and Venkateshwarlu (2001).

In case of heritability and genetic advance as a *per cent* of mean, both were high (65.4%, 26.29) for this trait indicating the predominance of additive gene action and hence simple selection may be rewarding. Similar results were obtained by Gohil (2006), Kalaimagal *et al.* (2008), Vange and Moses (2009), Rao (2009), Bhadru (2010), Prakash (2011), Nagy *et al.* (2013), Prasad *et al.* (2013), Rekha *et al.* (2013), Saroj *et al.* (2013), Yerimani *et al.* (2013), Ajay *et al.* (2014) and Pandey *et al.* (2015).

4.2.1.7 Pod weight per plant (g)

The variation for pod weight per plant varied from 152.16 (ICPH 2751) to 337.65 (ICPH 3762) and recorded a mean value of 222.27 g. The PCV (20.13) and GCV (17.4) were high and moderate respectively.

High heritability (74.7) along with high genetic advance as *per cent* of mean (30.99) was seen, therefore additive gene effect is responsible for heritability and simple selection will be effective for pod weight per plant.

4.2.8 100 Seed weight (g)

Variation for this character ranged from 9.38 (ICPH 2680) to 15.74 (ICPH 4542) with a mean value of 11.77 g. Moderate PCV (13.08) and GCV (12.72) were seen for this character. Similar results were reported by Kumar (2005), Gohil (2006), Rao (2009), Linge *et al.* (2010), Prakash (2011), Nagy *et al.* (2013), Yerimani *et al.* (2013) and Pandey *et al.* (2015).

High heritability (94.6%) along with high genetic advance as *per cent* of mean (25.49) for this character implied that heritability is due to additive gene effects and simple selection should be attempted. Similar results were reported by Kumar (2005), Kalaimagal *et al.* (2008), Linge *et al.* (2010), Prakash (2011), Nagy *et al.* (2013), Rekha *et al.* (2013), Saroj *et al.* (2013) and Pandey *et al.* (2015).

4.2.1.9 Grain yield per plant (g)

Variation for grain yield per plant ranged from 102.24 (ICPH 4611) to 229.68 (ICPH 3762) with a mean value of 141.65 g. High PCV (21.15) and moderate GCV (18.45) was seen for grain yield per plant. These findings are similar to those of Bhadru (2011), Patel and Acharya (2011), Sreelakshmi *et al.* (2011), Jaggal *et al.* (2012) and Yerimani *et al.* (2013).

High heritability (76.1) along with high genetic advance as *per cent* of mean (33.16) signifies that heritability is because of additive gene effect and hence simple selection will be rewarding. Similar results were reported by Rao (2009), Linge *et al.* (2010), Bhadru (2011), Prakash (2011), Sreelakshmi *et al.* (2011), Nagy *et al.* (2013), Rekha *et al.* (2013) and Saroj *et al.* (2013).

4.2.1.10 Mean pollen fertility percentage

The variation for this character ranged from 15.66 (ICPH 4611) to 92.77(ICPH 4275) with a mean value of 76.22 %. High PCV (26.61) and GCV (24.89) were recorded, which was similar to the result obtained by Prasad *et al.* (2013).

High heritability (87.5%) along with high genetic advance as *per cent* of mean (47.97) shows that heritability is due to additive gene effect and simple selection will be effective for this trait. High value of genetic advance as *per cent* of mean was also observed by Prasad *et al.* (2013).

The perusal of above findings reveal that PCV estimates of all the characters (except plant height) were slightly higher than that of GCV, indicting the less influence of environment in expression of these characters. Thus, the selection of these traits on the basis of the phenotypic value may be effective.

The magnitude of PCV and GCV indicates the level of variation among the hybrids. Higher is the value of PCV and GCV higher is the variation and *vice versa.* Low PCV and GCV were recorded for days to 50% flowering, days to maturity and plant height. High PCV and GCV were recorded for number of primary branches per plant, number of secondary branches per plant and mean pollen fertility %. Also high PCV was recorded for pod weight per plant and grain yield per plant. Meanwhile medium PCV and GCV were observed in number of pods per plant and 100 seed weight. Also medium value of GCV was recorded in pod weight per plant and grain yield per plant.

Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain (Saroj *et al.,* 2013).

High heritability in conjunction with high genetic advance as *per cent* of mean was observed for number of primary and secondary branches per plant, number of pods per plant, pod weight per plant, 100 seed weight, grain yield per plant and mean pollen fertility % which indicates the preponderance of additive gene action governing the inheritance of these characters and offers the best possibility of improvement through simple selection procedures.

Moderate heritability coupled with low genetic advance as *per cent* of mean was observed in plant height indicating the role of both additive and non additive gene action governing the inheritance of this trait and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects.

Low heritability coupled with low genetic advance as *per cent* of mean was observed for days to 50% flowering and days to maturity, indicating the presence of non-additive gene action in the inheritance and further selection for its improvement will be ineffective.

4.3 CHARACTER ASSOCIATION

Yield is a complex and polygenically inherited character resulting from multiplicative interaction of its component traits. The cumulative effect of such traits determines the yield. These traits play an important role in modification of yield as a whole in magnitude as well as in direction. The change in one character brings about a series of changes in the other characters, since they are interrelated.

Therefore, the correlation studies are of considerable importance in any selection programme as they provide degree and direction of relationship between two or more component traits.

If the value of correlation (r) is significant, the association between two characters is high. If the value of r bears negative sign, it means that increase in the value of one character will lead to decrease in second character and *vice versa*. Similarly if it bears a positive sign, it means that increase in one variable will lead to increase in second character.

If value of genotypic correlation coefficient is higher than phenotypic correlation coefficient, it means that there is strong association between these two characters genetically and the true phenotypic value is lessened by the significant interaction of environment.

If the value of phenotypic correlation coefficient is greater than genotypic correlation coefficient, it shows that the apparent association of two characters is not due to genes, but also favorable influence of environment.

If the value of r is zero or insignificant, it means that these two characters are independent. But, if the values of genotypic and phenotypic correlation coefficients are also insignificant, it further indicates the independent nature of two characters.

The results obtained on character associations for yield and yield components are presented in Table 4.4 (Phenotypic correlations) and Table 4.5 (Genotypic correlations)

and a perusal of these results revealed that in general phenotypic and genotypic correlations to be of similar direction. Further, the genotypic correlations were noticed to be in general higher than phenotypic correlation values for almost all the characters, indicating the masking effect of environment on these traits (Johnson *et al.,* 1955).

4.3.1 Days to 50% flowering

This character recorded significant positive association with days to maturity (0.5261**), number of primary branches per plant (0.4439**), number of secondary branches per plant (0.4198**) and grain yield per plant (0.2531*) at phenotypic level.

At genotypic level, this trait showed significant positive association with days to maturity (0.6257**), number of primary branches per plant, number of secondary branches per plant (0.4896**), pod weight per plant (0.2265*), grain yield per plant (0.3574**) whereas significant negative association with 100 seed weight (-0.2227*).

Earlier studies too have indicated such association of days to 50% flowering with days to maturity (Prakash, 2011; Hamid *et al.,* 2011; Nagy *et al.,* 2013; Prasad *et al.,* 2013; Rekha *et al.,* 2013 and Saroj *et al.,* 2013), number of primary branches per plant (Anuradha *et al.,* 2007; Das *et al.,* 2007; Prakash, 2011 and Saroj *et al.,* 2013), number of secondary branches per plant (Bhadru, 2010; Linge *et al.,* 2010; Prakash, 2011 and Rekha *et al.,* 2013), 100 seed weight (Chattopadyay and Dhiman, 2005) and grain yield per plant (Bhaskaran and Muthaiah, 2007; Gupta *et al.,* 2008; Sodavadiya *et al.,* 2009; Bhadru, 2010; Rao *et al.,* 2010; Prakash, 2011; Hamid *et al.,* 2011 and Saroj *et al.*, 2013).

Days to 50% flowering exhibited significant positive association with days to maturity, number of primary branches per plant, number of secondary branches per plant, pod weight per plant and grain yield per plant at phenotypic and genotypic levels. This type of desirable association would be helpful for simultaneous improvement of all these characters. This trait also showed significant negative association with 100 seed weight at genotypic level, indicating that simultaneous improvement is not possible.

4.3.2 Days to maturity

Days to maturity show significant positive association with number of primary branches per plant (0.3546**), number of secondary branches per plant (0.5035**), pod weight (0.3007**) and grain yield per plant (0.3915**) at phenotypic level.

At genotypic level, this trait showed significant positive association with plant height (0.2176*), number of primary branches per plant (0.5198**), number of secondary branches per plant (0.5866**), pod weight per plant (0.3019**) and grain yield per plant (0.4565**).

Previous studies too have indicated such association of days to maturity with plant height (Vange and Moses,2009; Rao *et al*., 2010; Hamid *et al.*, 2011; Prakash, 2011 and Rekha *et al.,* 2013), number of primary branches per plant (Anuradha *et al.*, 2007; Das *et al.*, 2007; Vange and Moses, 2009 and Saroj *et al.*, 2013), number of secondary branches per plant (Anuradha *et al.*, 2007; Linge *et al.*, 2010; Prakash, 2011 and Rekha *et al.*, 2013) and grain yield per plant (Sodavadiya *et al.,* 2009; Rao *et al.,* 2010; Prakash, 2011 and Hamid *et al.,* 2011).

Significant positive correlation at phenotypic and genotypic level for days to maturity with plant height, number of primary branches per plant, number of secondary branches per plant, pod weight per plant and grain yield per plant will translate into successful improvement of all these characters.

4.3.3 Plant height (cm)

At phenotypic level this character recorded significant positive association with number of primary branches per plant (0.2972**) and 100 seed weight (0.2816**).

At genotypic level, this trait showed significant positive association with number of primary branches per plant (0.4087**) and 100 seed weight (0.3812**). While significant negative association with number of pods per plant (-0.2355*) was recorded.

Similar results of association were reported earlier for plant height with number of primary branches per plant (Bhadru *et al.*, 2010; Linge *et al.*, 2010; Nagy *et al.*, 2013; Rekha *et al.*, 2013 and Saroj *et al.*, 2013) and 100 seed weight (Bhadru, 2010; Prakash, 2011 and Rekha *et al.,* 2013).

Thus, concurrent improvement in plant height, number of primary branches per plant and 100 seed weight can be observed as they recorded significant positive phenotypic and genotypic inter character association.

4.3.4 Number of primary branches per plant

This trait showed significant positive association at phenotypic level with number of secondary branches per plant (0.7391**) and grain yield per plant (0.2554*) along with significant negative association with 100 seed weight (-0.4035**).

At genotypic level, this trait showed significant positive association with number of pods per plant (0.3632**) and grain yield per plant (0.28**), whereas significant negative association with 100 seed weight (-0.4531**).

These results are in concurrence with earlier work on association of number of primary branches per plant with number of secondary branches per plant (Prakash, 2011; Devi *et al.,* 2012; Rekha *et al.*, 2013 and Saroj *et al.,*2013), number of pods per plant (Bhadru, 2010; Linge *et al*., 2010; Prakash, 2011; Rekha *et al.,* 2013 and Saroj *et al.,* 2013), 100 seed weight (Linge *et al.*, 2010; Prakash, 2011 and Rekha *et al.*, 2013) and grain yield per plant (Gupta *et al.,* 2008; Bhadru, 2010; Nagy *et al.,* 2013; Prasad *et al.,* 2013; Rekha *et al.,* 2013 and Saroj *et al.*, 2013).

The increase in number of primary branches per plant resulted in more number of productive branches having more number of photosynthetically active leaves there by increasing the source capacity which is associated with simultaneous increase in number of secondary branches per plant, number of pods per plant and grain yield. Hence selection of this character may improve yield directly.

4.3.5 Number of secondary branches per plant

This trait showed significant positive association at phenotypic level with number of pods per plant (0.4623**), pod weight per plant (0.3112**) and grain yield per plant (0.435**), whereas significant negative association with 100 seed weight (-0.3949**) was recorded.

At genotypic level, this trait showed significant positive association with number of pods per plant (0.5543**), pod weight per plant (0.3304**) and grain yield per plant (0.4614**), whereas significant negative association with 100 seed weight (-0.43**) was recorded.

Similar results were earlier reported for association of number of secondary branches per plant with number of pods per plant (Linge *et al.*, 2010; Prakash, 2011; Prasad *et al.*, 2013; Rekha *et al.*, 2013 and Saroj *et al.*, 2013), 100 seed weight (Marekar and Nerkar, 1987; Linge *et al.*, 2010 and Rekha *et al.*, 2013) and grain yield per plant (Anuradha *et al.,* 2007; Bhadru, 2010; Prakash, 2011; Prasad *et al.,* 2013; Rekha *et al.,* 2013; Saroj *et al.*, 2013 and Pandey *et al.,* 2015).

Number of secondary branches per plant exhibited significant positive association with number of pods per plant, pod weight per plant and grain yield per plant at both phenotypic and genotypic levels. This indicates that selection of genotypes with more secondary branches is an indirect selection for grain yield improvement.

4.3.6 Number of pods per plant

This trait showed significant positive association at phenotypic level with pod weight per plant (0.4899**) and grain yield per plant (0.4753**), whereas significant negative association was recorded with 100 seed weight (-0.4699**).

At genotypic level, this trait showed significant positive association with pod weight per plant (0.4915**) and grain yield per plant (0.4582**), whereas significant negative association was recorded with 100 seed weight (-0.5832**).

Earlier studies too have indicated such association of number of pods per plant with 100 seed weight (Linge *et al.*, 2010; Prakash, 2011 and Rekha *et al.*, 2013) and grain yield per plant (Prakash, 2011; Hamid *et al.,* 2011; Devi *et al.,* 2012; Prasad *et al.,* 2013; Rekha *et al.,* 2013; Saroj *et al.*, 2013 and Pandey *et al.,* 2015).

Number of pods per plant exhibited significant positive association with pod weight per plant and grain yield per plant at both phenotypic and genotypic levels. These results suggest that, as the number of pods per plant increases there is an increase in yield, hence selection of this character may improve yield directly.

4.3.7 Pod weight per plant (g)

Pod weight per plant shows significant positive association with grain yield per plant (0.9327**) at phenotypic level.

At genotypic level, it showed positive correlation with grain yield per plant (0.9539**).

This indicates that increase in pod weight per plant can translate into increased grain yield per plant. Thus simultaneous selection of pod weight per plant and grain yield per plant may be effective.

4.3.8 100 Seed weight (g)

100 seed weight showed insignificant negative association with grain yield per plant (-0.0173) at phenotypic level.

At genotypic level, it showed insignificant positive correlation with grain yield per plant (0.0028). The results were in concurrence with the findings of Anuradha *et al.* (2007), Gupta *et al.* (2008), Kalaimagal *et al.* (2008) and Prakash (2011).

The scrutiny of result revealed that, genotypic correlations were higher in magnitude than the phenotypic correlation indicating strong inherent relationship among the characters. Genotypic correlation provides a measure of genotypic association among different traits and help in identifying the traits for selection.

Grain yield is the result of expression and association of several plant growth components, which contribute additively or help in some conditions in modifying the expression of other traits directly or indirectly (Udensi and Ikpeme, 2012). Association studies showed that grain yield per plant showed very strong significant positive correlation with pod weight per plant followed by moderately weak correlation with number of pods per plant, number of secondary branches per plant, days to maturity and days to 50% flowering and very weak correlation with number of primary branches per

plant (Searle, 1965). Further, a significant positive association was observed among these individual components. Hence simultaneous selection based on these characters could be suggested for improvement in grain yield.

Association of grain yield per plant with other characters, namely, plant height (0.053, 0.0984) and 100 seed weight (-0.0173, 0.0028) at phenotypic and genotypic levels respectively, was found to be insignificant. This is in concurrence with the results obtained by Das *et al.* (2007), Kalaimagal *et al.* (2008), Sodavadiya *et al.* (2009), Vange and Moses (2009), Nagy *et al.* (2013) and Prasad *et al.* (2013) for plant height and Singh and Gumber (1995), Anuradha *et al.* (2007), Gupta *et al.* (2008), Kalaimagal *et al.* (2008) and Prakash (2011) for 100 seed weight.

Meanwhile, negative and significant inter character association were observed for plant height with number of pods per plant, number of primary branches per plant with 100 seed weight, number of secondary branches with 100 seed weight and number of pods per plant with 100 seed weight, which indicates the presence of competition for a common possibility, such as nutrient supply (Adams, 1967; Adams and Grafius, 1971) and the need for balanced selection, while attempting for improvement of these characters. Rest all other relationships were found to be insignificant in the present investigation.

4.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation into the measures of direct and indirect effects. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. In these cases, direct selection on the basis of correlated response may not be fruitful. For critical evaluation, the correlation coefficient need to be split into direct and indirect effects using path coefficient analysis since, many characters affect a given trait. Thus, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of character. As a guideline for interpretation of path analysis results, the following broad points may be kept in view (Singh and Chaudhary,1977):

If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.

If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.

Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, 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.

If the correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on that character.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

Hence, the study of phenotypic and genotypic direct and indirect effects of yield components on grain yield per plant was undertaken in the present investigation for 24 hybrids and the results obtained are presented in Tables 4.6 and 4.7 and discussed here under.

4.4.1 Days to 50% flowering

The direct contribution (0.0676, -0.0378) of this character to grain yield per plant is positive and negative at phenotypic and genotypic levels, respectively. The indirect effect through days to maturity (0.0356, -0.0236), plant height (0.0044, -0.0014), number of primary branches (0.03, -0.0201), number of secondary branches (0.0284, -0.0185), number of pods per plant (-0.001, 0.0009), pod weight per plant (0.0084, -0.0086) and 100 seed weight (-0.0137, 0.3574) at phenotypic and genotypic levels nullifies the negligible and negative direct effect to result into significant positive correlation (0.2531*, 0.3574**) at both the levels. Thus these indirect causal factors are to be considered during selection process for improving grain yield per plant. These

results were in conformity with the findings of Chattopadhyay and Dhiman (2005), Anuradha *et al*. (2007), Sodavadiya *et al.* (2009), Prakash (2011) and Saroj *et al.* (2013).

4.4.2 Days to maturity

This trait showed significant positive association (0.3915**, 0.4565**) and negligible positive direct effect (0.033, 0.0852) on grain yield per plant at phenotypic and genotypic levels. Here the contribution of negligible direct effect is nullified by indirect effects. In such situations, positive indirect causal factors *viz.,* days to 50% flowering (0.0175, 0.0533), plant height (0.001, 0.0185), number of primary branches per plant (0.0118, 0.0443), number of secondary branches per plant (0.0168, 0.05), number of pods per plant (0.0028, -0.0008), pod weight per plant (0.01, 0.0257) and 100 seed weight (0.0006, 0.0041) are to be considered during selection process for improving grain yield per plant. Similar results were recorded by Bhadru (2010), Rao *et al.* (2010), Prakash (2011), Devi *et al.* (2012), Rekha *et al.* (2013) and Saroj *et al.* (2013).

4.4.3 Plant height (cm)

Plant height exhibited negligible positive and negative direct effect (0.0448, -0.0624) along with insignificant association (0.053, 0.0984) with grain yield per plant at phenotypic and genotypic levels, respectively. Thus, selection foreither plant height or indirect causal factors like days to 50% flowering (0.0029, -0.0024), days to maturity (0.0014, -0.0136), number of primary branches per plant (0.0133, -0.0255), number of secondary branches per plant (0.004, -0.0064), number of pods per plant (-0.0057, 0.0147), pod weight per plant (-0.0014, -0.0009) and 100 seed weight (0.0126, -0.0238) will be ineffective in improving grain yield as plant height is independent of grain yield per plant.

4.4.4 Number of primary branches per plant

This trait showed moderate positive direct effect (0.0858, 0.2636) along with significant positive association (0.2554*, 0.28**) with grain yield per plant at phenotypic and genotypic level. This is in agreement with the results obtained by Anuradha *et al.* (2007), Bhadru (2010), Prakash (2011), Prasad *et al.* (2013) and Rekha *et al.* (2013). Also the indirect effect through days to 50% flowering (0.0381, 0.1406), days to maturity (0.0304, 0.137), plant height (0.0255, 0.1077), number of secondary branches (0.0634, 0.2172), number of pods per plant (0.0175, 0.0957) and pod weight per plant (0.008,

0.0252) was positive at phenotypic and genotypic levels. Whereas negative indirect effect was recorded for 100 seed weight (-0.0346, -0.1195) at phenotypic and genotypic level**.** These results for indirect effect is in accordance with the results obtained by Prasad *et al.* (2013) and Rekha *et al.* (2013). As the correlation coefficient is positive and almost equivalent to the direct effect, direct selection through number of primary branches per plant will be effective for improving grain yield per plant.

4.4.5 Number of secondary branches per plant

This trait recorded negligible positive and negative direct effect (0.0449, -0.0442) and significant positive association (0.435**, 0.4614**) with grain yield per plant at phenotypic and genotypic level. Therefore, this trait affected the grain yield per plant *via* indirect causal factors *viz.,* days to 50% flowering (0.0188, -0.0216), days to maturity (0.0226, -0.0259), plant height (0.004, -0.0046), number of primary branches (0.0332, -0.0364), number of pods per plant (0.0208, 0.0245), pod weight per plant (0.014, -0.0146) and 100 seed weight (-0.0177, 0.019). Because the negligible direct effect is nullified by indirect effects to produce significant positive association. Similar results were earlier reported by Prakash (2011), Devi *et al.* (2012) and Saroj *et al.* (2013).

4.4.6 Number of pods per plant

Number of pods per plant manifested positive and negative direct effect (0.0095, -0.1111) on grain yield at phenotypic and genotypic level along with significant positive association (0.4753**, 0.4582**) with grain yield per plant. The negligible and negative direct effect at genotypic level has been nullified by the indirect effect of causal factors *viz.,* days to 50% flowering (-0.0001, 0.0027), days to maturity (0.0008, 0.001), plant height (-0.0012, 0.0262), number of primary branches (0.0019, -0.0403), number of secondary branches (0.0044, -0.0616), pod weight per plant (0.0046, -0.0546) and 100 seed weight (-0.0045, 0.0648). Similar findings were also observed by Anuradha *et al*. (2007) and Prasad *et al.* (2013).

4.4.7 Pod weight per plant

This trait recorded high positive direct effect (0.8889, 0.9817) towards grain yield per plant and also exhibited significant and positive association with grain yield per plant (0.9327**, 0.9539**) at phenotypic and genotypic level. It also showed positive indirect

effect *via* days to 50% flowering (0.1101, 0.2223), days to maturity (0.2673, 0.2964), plant height (-0.0279, 0.0147), number of primary branches per plant (0.0828, 0.094), number of secondary branches (0.2766, 0.3244), number of pods per plant (0.4355, 0.4825) and 100 seed weight (0.0314, 0.0508) at phenotypic (except in plant height) and genotypic levels. Here, the correlation coefficient between pod weight per plant and grain yield per plant is almost equal to its direct effect, thus, the correlation explains the true relationship and a direct selection through this trait will be effective. Hence, pod weight per plant should be considered as important selection criterion in all improvement programmes and direct selection for this trait is recommended for yield improvement in pigeonpea.

4.4.8 100 Seed weight

100 seed weight recorded negligible positive and negative direct effect (0.0085, -0.0012) at phenotypic and genotypic level along with insignificant association (-0.0173, 0.0028) with grain yield per plant. This indicates that 100 seed weight is independent of grain yield per plant. Therefore selection for either 100 seed weight or indirect causal factors *viz.,* days to 50% flowering (-0.0017, 0.0003), days to maturity (0.0002,-0.0001), plant height (0.0024, -0.0004), number of primary branches (-0.0034, 0.0005), number of secondary branches (-0.0034, 0.0005), number of pods per plant (-0.004, 0.0007) and pod weight per plant (0.0003, -0.0001) for improvement in grain yield will be ineffective.

Thus from the present investigation it can be inferred that major emphasis should be laid on selection process with more pod weight per plant and number of primary branches per plant and there should be economic balance among these traits to harness higher grain yield per plant.

The results also revealed low residual effect for both phenotypic (0.3043) and genotypic (0.2043) path coefficients respectively indicating that variables studied in the present investigation explained about 69.57 (phenotypic) and 79.57 (genotypic) *per cent* of the variability in yield. This indicates that most of the yield and yield contributing traits were studied in the present investigation and very few of them are yet to be studied. This result is in concurrence with the findings of Prasad *et al.* (2013).

In path analysis, a line diagram which is constructed with the help of simple correlation coefficients among various characters included under study is referred to as

path diagram. The path diagram constructed using the phenotypic and genotypic correlation coefficients among grain yield per plant and eight of its component traits are shown in Fig 4.1 and Fig 4.2. It depicts the cause and effect situation in a simple manner and makes the presentation of results more attractive. It depicts the association between various characters. It also helps in understanding the direct and indirect contribution of various independent variables towards dependent variable i.e. grain yield per plant.

4.5 FERTILITY RESTORATION IN CMS BASED HYBRIDS

Pollen fertility (%) is an important character for evaluation of extent of fertility restoration in the hybrids derived from newly developed CMS lines. High percentage of fertility restoration is desirable for successful production of high yielding CMS-based hybrids of pigeonpea. In present investigation, hybrids were classified into three categories *viz.* fertile (> 80% pollen fertility), partial fertile (11-80% pollen fertility) and sterile (0-10% pollen fertility) as suggested by Kyu and Saxena, 2011. The mean pollen fertility percentage of hybrids and checks ranged from 15.66 to 92.77 % (Table 4.2). Among hybrids ICPH 4275 recorded maximum pollen fertility (92.77%) followed by ICPH 2671 (90.33%) and ICPH 2740 (88.66%), whereas minimum pollen fertility was recorded in ICPH 4611 (15.66%) followed by ICPH 4542 (26.32%) and ICPH 4502 (50.77%) (Table 4.8). Out of 24 CMS based hybrids 15 (ICPH 3933, ICPH 2671, ICPH 2740, ICPH 2751, ICPH 3461, ICPH 3477, ICPH 3762, ICPH 4500, ICPH 4500, ICPH 3473, ICPH 4485, ICPH 4671, ICPH 3474, ICPH 4275, ICPH 3816 and ICPH 4488) showed high fertility restoration, while rest nine showed partial fertility restoration (Table 4.9.). Nine (ICPL 87119, ICPL 20098, ICPL 20108, ICPL 20116, ICPL 20137, ICPL 20123, ICPL 20204, ICPL 20137 and ICPL 20125) out of 13 male lines effected fertility restoration of more than 80% and were classified as restorer for corresponding CMS line. Similar results for fertility restoration were reported earlier by Wanjari *et al.* (2007), Dalvi *et al.* (2008), Saxena *et al.* (2010), Sawargaonkar *et al.* (2012), Saxena *et al*. (2014), Kumar *et al*. (2015), Reddy *et al.* (2015) and Saroj *et al*. (2015).

Three line system of hybrid technology, which is based on cytoplasmic nuclear male sterility, is expected to result in quantum increase in yield and production of pigeonpea and usher an era of pulse revolution. Cytoplasmic male sterility is under extranuclear genetic control (mitochondrial genome). They show non mendelian inheritance and are under the regulation of cytoplasmic factors. In this system, male sterility is inherited maternally and is never lost or diluted in the succeeding generations. The success in development of pigeonpea hybrids largely depends on availability of

effective restorers. Such male lines possess fertility restorer (*Rf* or*Fr*) genes in their nucleus which is subsequently transferred to F_1 hybrids. These genes in F_1 hybrids' nucleus suppresses the malesterile phenotype and allows the production of high yielding CMS based hybrids. Therefore the incorporation of fertility restorer gene(s) into the CMS lines is essential in hybrid pigeonpea breeding technology.

The perusal of above results revealed that 62.5% of the hybrids have good fertility restoration and 69.2% of the male lines are good fertility restorers for their respective CMS lines. The range of fertility restoration is 15.66 to 92.77%, with ICPH 4275, ICPH 2671 and ICPH 2740 being the top three hybrids in terms of mean pollen fertility %.

4.6 HETEROSIS

Commercial exploitation of heterosis in crop plants is regarded a major breakthrough in the realm of plant breeding. Hybrid gives an opportunity to break yield barrier of conventional varieties and have already been successfully used in rice, maize, pearl millet and sorghum. A considerable additive and non-additive gene action which can be exploited in heterosis breeding of pigeonpea was reported by Saxena and Sharma, (1990). Further, Saxena *et al*. (2006) reported 50 to 100% of standard heterosis in medium duration pigeonpea hybrids over the popular varieties and local checks. A substantial degree of heterosis for yield and related traits standard check variety has also been reported in pigeonpea hybrids based on male sterile lines. Heterosis refers to the superiority of F_1 hybrid in one or more characters over its parents. The term hybrid vigor is frequently used as synonym for heterosis. Generally, it is believed that increased vigour in plant growth and a higher seed production are usually realized in the first filialgeneration. Heterosis may be positive or negative. Depending upon breeding objectives, both positive and negative heterosis is useful for crop improvement. In general, positive heterosis is desired for yield and negative heterosis for early maturity. A study of this phenomenon is necessary to explore possibility of the exploiting of heterosis in the CMS based pigeonpea hybrids at commercial level.

The present investigation alsorevealed significant levels of heterosis for yield and yield components. The results on heterosis of 24 pigeonpea hybrids over the checks: Asha, Maruti, LRG 41 and BDN 711 for seed yield and yield components are presented in Table 4.10 and are discussed here under.

4.6.1 Yield component characters

4.6.1.1 Days to 50 % flowering

Early flowering and early maturity are desirable traits in hybrid pigeonpea as it helps in escaping drought. Therefore negative heterosis is what we are looking for when it comes to days to 50% flowering and days to maturity. All the twenty four hybrids were compared with four checks: Asha, Maruti, LRG 41 and BDN 711 for estimating standard heterosis.Heterosis over the standard check Asha ranged from -12.46% to -0.34% while it ranged from -14.19% to -2.31% in Maruti, -12.45% to -0.33% in LRG 41 and -6.81% to 6.09% in BDN 711. Among all, the maximum value of negative standard heterosis for days to 50% flowering was recorded in ICPH 4611 (-12.46%, -14.19%, -12.46% and -6.81% over Asha, Maruti, LRG 41 and BDN 711, respectively). This was followed by ICPH 4395 (-9.76%,-11.55%, -9.76% and -4.94% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 3816 (-9.1%, -10.89%, -9.1% and -3.22% over Asha, Maruti, LRG 41 and BDN 711, respectively). Other hybrids like ICPH 3933, ICPH 2671, ICPH 3473, ICPH 4539, ICPH 4275, ICPH 2680, ICPH 4540, ICPH 4542 and ICPH 3474 also recorded negative standard heterosis over the four checks. While ICPH 2740, ICPH 3477, ICPH 2751, ICPH 4461 ICPH 3762 ICPH 3337, ICPH 4485, ICPH 4187, ICPH 4488, ICPH 4500 ICPH 4502 and ICPH 4671 showed negative standard heterosis over Asha, Maruti and LRG 41. Heterosis in both negative and positive directions for days to 50% flowering have been reported by Wankhade *et al.* (2005), Bhaskaran and Muthiah (2006), Wanjari *et al.* (2007), Patel and Tikka (2008), Sarode *et al.* (2009), Chadirkala *et al.* (2010), Vaghela *et al.* (2011), Pandey *et al.*(2013), Kumar *et al.*(2015) and Mahasal *et al.* (2015).

4.6.1.2 Days to maturity

Early maturing hybrids are generally preferred therefore, negative heterosis for days to maturity is considered as useful parameter. Heterosis for days to maturity over standard checks ranged from -13.26% to 0.57% (Asha), -5.18% to 9.94% (Maruti), -12.09% to 1.92% (LRG 41) and 0.44% to 16.45% (BDN 711). The maximum value of negative standard heterosis was recorded for ICPH 4275 (-13.26%, -5.18% and -12.09% over Asha, Maruti and LRG 41, respectively), followed by ICPH 4542 (-13.07%,-4.97% and -11.90% over Asha, Maruti and LRG 41, respectively) and ICPH 3473 (-11.55%, -3.31% and -10.36% over Asha, Maruti and LRG 41, respectively).

Other hybrids like ICPH 3933, ICPH 2671, ICPH 680 and ICPH 3474 also recorded negative standard heterosis over Asha, Maruti and LRG 41. Rest of the hybrids showed negative heterosis over Asha and LRG 41, while none of the 24 hybrids showed negative heterosis for days to maturity over BDN 711. Salanki *et al.* (2008) reported that most of the promising hybrids depicted significant negative heterosis for days to maturity, there by 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).

4.6.1.3 Plant height (cm)

In pigeonpea plant height is desirable character for achieving high yield as vigor in plant height may lead to increase in biomass as well as source - sink capacity for obtaining optimum yield. Heterosis for plant height over four standard checks was observed to range from -15.41% to 8.57% (Asha), 0.57% to 29.08% (Maruti), -14.68% to 9.50% (LRG 41) and 7.38% to 37.81% (BDN 711). The maximum heterosis was recorded in ICPH 4542 (8.57%, 29.08%, 9.50% and 37.81% over Asha, Maruti, LRG 41 and BDN 711, respectively), followed by ICPH 4485 (6.70%, 26.87%, 7.62% and 35.45% over Asha, Maruti, LRG 41 and BDN 711, respectively), ICPH 2740 (6.66%, 26.82%, 7.59% and 35.40% over Asha, Maruti, LRG 41 and BDN 711, respectively), and ICPH 3477 (2.39%, 21.74%, 3.27% and 29.96% over Asha, Maruti, LRG 41 and BDN 711, respectively). Rest of the hybrids showed negative heterosis over Asha and LRG 41 baring ICPH 4488 in case of Asha and ICPH 4539 and ICPH 4488 in case of LRG 41. Meanwhile high positive standard heterosis over Maruti and BDN 711 was seen in rest of the hybrids. Present observations are in close agreement with earlier report of several workers like Wankhade *et al*. (2005), Bhaskaran and Muthiah (2006), Patel and Tikka (2008), Sarode *et al*.(2009), Chandirakala *et al*. (2010), Pandey *et al*. (2013), Gite and Madrap (2014), Patel and Tikka (2014), Kumar *et al*. (2015), Reddy *et al*. (2015) and Singh and Singh (2016).

4.6.1.4 Number of primary branches per plant

Number of primary branches per plant is believed to be closely associated with high grain yield per plant thus, resulting in high productivity. Therefore, the hybrids with more primary branches per plant were to be identified. The range of standard heterosis over the four checks for number of primary branches was found to be -54.73% to

16.42% (Asha), -42.77% to 47.17% (Maruti), -49.44% to 30% (LRG 41) and -6.66% to 140% (BDN 711). Maximum heterosis was recorded for ICPH 2740 (16.42%, 47.17%, 30% and 140% over Asha, Maruti, LRG 41 and BDN 711, respectively), followed by ICPH 3461 (9.45%, 38.36%, 22.22% and 125.64% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 3337 (7.09%, 35.38%, 19.58% and 120.77% over Asha, Maruti, LRG 41 and BDN 711, respectively). ICPH 3762, ICPH 2680 and ICPH 4488 also showed positive standard heterosis over all the checks. In addition to it all the hybrids recorded very high heterosis over BDN 711 for number of primary branches per plant.

These results are in accordance with the findings of Kumar *et al.* (2009), Phad *et al.* (2009), Shobha and Balan (2010), Pandey *et al*. (2013), Gite and Madrap (2014), Patel and Tikka (2014), Kumar *et al*. (2015) and Singh and Singh (2016).

4.6.1.5 Number of secondary branches per plant

High number of secondary branches is desirable as these are the pod bearing branches, and thus have a direct bearing on the seed yield per plant. Therefore positive standard heterosis is desirable for number of secondary branches per plant in pigeonpea. Standard heterosis over four checks for number of secondary branches was recorded in the range of -65.90% to 26.91% (Asha), -45.61% to 102.39% (Maruti), -61.47% to 43.39% (LRG 41) and 15.99% to 331.63% (BDN 711). The highest heterosis was recorded in ICPH 4671 (26.91%, 102.39%, 43.39% and 331.63% over Asha, Maruti, LRG 41 and BDN 711, respectively), followed by ICPH 3762 (26.16%, 101.20%, 42.54% and 329.08% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 3461 (11.61%, 77.99%, 26.10% and 279.59% over Asha, Maruti, LRG 41 and BDN 711, respectively). ICPH 4488 and ICPH 4500 also showed positive heterosis over the checks.

These results are in accordance with the results obtained by Bhaskaran and Muthiah (2006), Patel and Tikka (2008), Phad *et al.* (2009), Sarode *et al.* (2009), Chandirakala *et al.* (2010), Vaghela *et al.* (2011), Gite and Madrap (2014), Patel and Tikka (2014), Kumar *et al.* (2015), Reddy *et al.*(2015) and Singh and Singh (2016).

4.6.1.6 Number of pods per plant

The hybrids with positive heterosis for number of pods per plant are desirable to increase the yield. Heterosis over standard checks for number of pods per plant ranged

from -27.34% to 53.82% (Asha), -35.63% to 36.27% (Maruti), -21.72% to 65.71% (LRG 41) and -21.82% to 65.50% (BDN 711). Highest heterosis was seen in ICPH 3762 (53.83%, 36.27%, 65.71% and 65.50% over Asha, Maruti, LRG 41 and BDN 711, respectively), followed by ICPH 3816 (27.87%, 13.27%, 37.75% and 37.40% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 2680 (27.71%, 13.13%, 37.58% and 37.40% over Asha, Maruti, LRG 41 and BDN 711, respectively). ICPH 4671, ICPH 3473, ICPH 4488, ICPH 3474 and ICPH 4395 also showed positive heterosis.

Similar results were obtained by Dheva *et al.* (2009), Kumar *et al.* (2009), Phad *et al.* (2009), Sarode *et al.* (2009), Chandirakala *et al.* (2010), Sobha and Balan (2010) and Vaghela *et al.* (2011). They concluded that heterosis in yield was primarily due to increased number of pods per plant in pigeonpea. Also, both positive and negative heterosis for number of pods per plant was recorded by Pandey *et al.* (2013), Mhasal *et al.* (2015) and Singh and Singh (2016).

4.6.1.7 Pod weight per plant (g)

Hybrids with positive heterosis for pod weight per plant are desirable, because it directly affects the grain yield per plant. Heterosis over four standard checks for pod weight per plant was found to be in the range of -28.76% to 58.08% (Asha), -32.94% to 48.81% (Maruti), -16.49% to 85.32% (LRG 41) and -17.96% to 82.05 (BDN 711). Maximum heterosis was observed in ICPH 3762 (58.08%, 48.81%, 85.32% and 82.05% over Asha, Maruti, LRG 41 and BDN 711, respectively), followed by ICPH 4502 (44.77%, 36.28%, 69.72% and 66.72% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 4395 (24.43%, 17.13%, 45.87% and 43.30% over Asha, Maruti, LRG 41 and BDN 711, respectively). ICPH 3477, ICPH 3337, ICPH 4485, ICPH 4187, ICPH 4539 ICPH 3816, ICPH 4671 and ICPH 3474 also recorded positive heterosis over the standard checks.

Dalvi (2007) and Sawargaonkar (2010) also observed positive heterosis for pod weight per plant in pigeonpea.

4.6.1.8 100 Seed weight (g)

The 100 seed weight is one of the important traitwhich influences the grain yield. Heterosis for 100 seed weight over four standard checks were observed to be in the range of -20.90% to 32.64% (Asha), -8.33% to 53.71% (Maruti), -6.51% to 56.77% (LRG 41)

and -9.92 to 51.06% (BDN 711). Maximum standard heterosis was recorded in ICPH 4542 (32.64%, 53.71%, 56.77% and 51.06% over Asha, Maruti, LRG 41 and BDN 711, respectively), followed by ICPH 4611 (28.65%, 49.09%, 52.06% and 46.51% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 4502 (12.08%, 29.88%, 32.47% and 27.64% over Asha, Maruti, LRG 41 and BDN 711, respectively). ICPH 3933, ICPH 2740, ICPH 3477, ICPH 4395, ICPH 4485, ICPH 4187, ICPH 4539, ICPH 4500 and ICPH 4671 also recorded positive standard heterosis over the checks.

Heterosis with respect to 100 seed weight in positive and negative direction have also been reported by Wankhade *et al.* (2005), Bhaskaran and Muthiah (2006), Patel and Tikka (2008), Kumar *et al.*(2009), Sarode *et al.* (2009), Chandirakala *et al.* (2010), Vaghela *et al.* (2011), Pandey *et al.* (2013), Kumar *et al.* (2015), Mhasal *et al.* (2015) and Singh and Singh (2016).

4.6.1.9 Grain yield per plant (g)

Grain yield is a complex trait and end product of a number of components, most of which are under polygenic control. All changes in yield must be accompanied by changes in one or more of the components have been pointed out by Grafius (1956). A wide range of estimates of standard heterosis in positive and negative direction was observed for grain yield per plant. Standard heterosis for grain yield over four checks was recorded in the range of -30.90% to 55.23% (Asha), -21.02% to 77.43% (Maruti), -14.72% to 91.58% (LRG 41) and -17.19% to 86.02% (BDN 711). Maximum heterosis was seen in case of ICPH 3762 (55.23%, 77.43%, 91.58% and 86.02% over Asha, Maruti, LRG 41 and BDN 711, respectively), which was followed by ICPH 4502 (35.41%, 54.77%, 67.11% and 62.27% over Asha, Maruti, LRG 41 and BDN 711, respectively) and ICPH 4395 (15.37%, 31.87%, 42.38% and 38.25% over Asha, Maruti, LRG 41 and BDN 711, respectively). ICPH 3477, ICPH 3461, ICPH 3337, ICPH 4485, ICPH 4539, ICPH 3816, ICPH 4500, ICPH 4671 and ICPH 3474 also recorded positive heterosis over the checks.

Similar results were obtained by Pandey and Singh (2002), Wankhade *et al.* (2005), Bhaskaran and Muthiah (2006), Wanjari *et al.* (2007), Solanki *et al.* (2008), Patel and Tikka (2008), Dheva *et al.* (2009), Kumar *et al.* (2009), 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).

The perusal of above results has shown that out of 24 hybrids three hybrids i.e. ICPH 3762, ICPH 4502 and ICPH 4395, possess high favorable standard heterosis (55.23%, 35.41% and 15.37%, respectively) for grain yield per plant and most of the yield components. And out of these three, ICPH 3762 and ICPH 4502 were found to have more than 30% standard heterosis and thus can be recommended for commercial utilization in Telangana and Andhra Pradesh after successful field trials.

Table 4.1. Analysis of Variance for yield, yield components and pollen fertility in pigeonpea hybrids

Mean sum of squares											
Source of variation	**d.f.**	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**No. of primary branches / plant**	**No. of secondary branches / plant**	**No. of pods / plant**	**Pod weight / plant (g)**	**100 Seed weight (g)**	**Grain yield / plant (g)**	**Pollen fertility (%)**
Replication	2	24.14	9.48	1303.74	16.29	22.86	2289.73	127.62	0.75	162.35	486.06
Genotypes	27	38.72**	175.44**	446.42**	83.42**	809.50**	23776.05**	4995.56**	6.86**	2264.05**	1131.25**
Error	54	1.55	14.59	136.42	4.89	32.7	3560.4	506.15	0.13	214.33	51.34

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

Table 4.2. Mean performance of pigeonpea genotypes for yield, yield components and pollen fertility (%)

S. No.	Genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches / plant	No. of secondary branches / plant	No. of pods / plant	Pod weight / plant (g)	100 Seed weight (g)	Grain yield / plant (g)	Pollen fertility %
1	ICPH 3933	91.00	159.00	174.00	19.73	39.40	429.53	196.13	13.22	119.37	86.33
2	ICPH 2671	90.00	155.66	160.80	23.00	51.70	560.60	198.26	11.07	121.62	90.33
3	ICPH 2740	95.33	166.66	191.00	31.20	50.60	523.66	192.93	12.04	135.19	88.66
4	ICPH 3477	98.33	173.66	183.33	25.93	54.00	480.06	235.69	12.46	162.40	84.21
5	ICPH 2751	95.33	172.66	172.00	25.60	62.26	402.00	152.16	11.62	109.16	86.99
6	ICPH 3461	97.00	176.33	168.80	29.33	74.40	493.86	219.20	10.45	149.80	86.99
7	ICPH 3762	96.33	173.00	168.53	27.60	84.10	769.90	337.65	10.89	229.68	86.44
8	ICPH 3337	94.00	164.66	163.00	28.70	62.20	495.66	247.70	10.40	151.83	55.55
9	ICPH 3473	91.00	155.66	163.53	18.13	51.50	614.13	214.00	10.28	131.36	87.77
10	ICPH 4395	89.33	162.66	168.86	14.86	44.06	583.53	265.77	12.96	170.70	59.99
11	ICPH 4485	93.33	167.33	191.06	21.20	43.26	466.06	254.04	12.80	160.58	82.22
12	ICPH 4187	93.66	162.66	163.66	16.73	43.96	463.46	232.97	12.93	143.04	59.22
13	ICPH 4539	90.66	162.66	178.20	16.86	41.20	562.13	264.00	12.83	150.90	76.66
14	ICPH 4275	91.00	152.66	176.66	22.06	54.33	507.73	196.94	11.62	122.12	92.77
15	ICPH 2680	92.00	160.66	170.66	27.60	52.26	639.20	174.40	9.38	118.64	68.33
16	ICPH 3816	90.00	164.33	174.20	25.00	53.33	542.60	252.33	10.69	153.61	87.55
17	ICPH 4488	93.33	166.00	180.46	27.50	74.00	605.93	197.92	10.79	122.47	82.55
18	ICPH 4500	98.66	168.66	174.33	25.60	69.66	441.00	224.20	12.48	151.76	87.44
19	ICPH 4502	98.33	177.00	168.93	22.80	53.90	484.80	309.23	13.30	200.35	50.77
20	ICPH 4540	92.33	164.33	165.40	15.00	35.80	552.73	211.06	11.25	119.52	72.77

Table 4.2. (cont.).

S. No.	Genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches / plant	No. of secondary branches / plant	No. of pods / plant	Pod weight / plant (g)	100 Seed weight (g)	Grain yield / plant (g)	Pollen fertility %
21	ICPH 4542	92.66	153.00	194.40	18.13	29.20	363.66	192.86	15.74	119.40	26.32
22	ICPH 4611	86.66	169.33	157.53	12.13	22.73	396.43	172.83	15.26	102.24	15.66
23	ICPH 4671	96.66	175.00	151.46	25.13	84.60	625.86	241.70	11.94	150.11	79.99
24	ICPH 3474	91.00	158.33	169.60	25.33	64.66	609.93	231.54	10.56	149.65	86.99
25	Asha	99.00	176.00	179.06	26.80	66.66	500.50	213.60	11.86	147.96	89.33
26	Maruti	101.00	161.00	150.60	21.20	41.80	564.33	226.90	10.41	129.44	87.90
27	LRG 41	99.00	173.66	177.53	24.00	59.00	458.33	182.20	10.14	119.88	82.20
28	BDN 711	93.00	152.00	141.06	12.33	19.60	429.66	185.46	10.30	123.46	92.16
	Mean	93.92	165.16	170.66	22.48	53.00	520.26	222.27	11.77	141.65	76.22
	CV	1.32	2.31	6.84	9.84	10.78	11.46	10.12	3.04	10.33	9.40
	SE±	0.72	2.20	6.74	1.28	3.30	34.45	12.99	0.21	8.45	4.14
	CD (0.05)	2.04	6.25	19.12	3.62	9.36	97.67	36.83	0.58	23.96	11.73

Table 4.3. Estimates of variability, heritability and genetic advance as per cent of mean for yield, yield components and pollen fertility (%) among hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.].

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV(%)		
1	Days to 50% flowering	93.92	86.66	101.00	3.98	3.75	88.90	7.28
2	Days to maturity	165.16	152.00	177.00	5.00	4.43	78.60	8.10
3	Plant Height (cm)	170.66	141.06	194.40	9.07	5.96	43.10	8.05
4	No. of primary branches / plant	22.48	12.13	31.20	24.79	22.76	84.20	43.02
5	No. of secondary branches / plant	53.00	19.60	84.60	32.22	30.36	88.80	58.92
6	No. of pods / plant	520.26	363.66	769.90	19.51	15.78	65.40	26.29
7	Pod weight / plant (g)	222.27	152.16	337.65	20.13	17.40	74.70	30.99
8	100 Seed weight	11.77	9.38	15.74	13.08	12.72	94.60	25.49
9	Grain yield / plant (g)	141.65	102.24	229.68	21.15	18.45	76.10	33.16
10	Pollen fertility (%)	76.22	15.66	92.77	26.61	24.89	87.50	47.97

Table 4.4. Phenotypic correlation among yield and yield components in pigeonpea hybrids

S. No.	Character	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods / plant	Pod weight / plant	100 Seed weight	Grain yield / plant
1	Days to 50% flowering	1	0.5261**	0.0646	0.4439**	0.4198**	-0.0151	0.1239	-0.2034	0.2531*
2	Days to maturity		1	0.0312	0.3546**	0.5035**	0.0833	0.3007**	0.0193	0.3915**
3	Plant Height			1	0.2972**	0.0896	-0.1269	-0.0314	0.2816**	0.053
4	No. of primary branches / plant				1	0.7391**	0.2046	0.0932	-0.4035**	0.2554*
5	No. of secondary branches / plant					1	0.4623**	0.3112**	-0.3949**	0.435**
6	No. of pods / plant						1	0.4899**	-0.4699**	0.4753**
7	Pod weight / plant (g)							1	0.0354	0.9327**
8	100 Seed weight (g)								1	-0.0173
9	Grain yield / plant (g)									1

*Significant at 5% level

**Significant at 1% level

Table 4.5. Genotypic correlation among yield and yield components in pigeonpea hybrids

S. No.	Character	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods / plant	Pod weight / plant	100 Seed weight	Grain yield / plant
1	Days to 50% flowering	1	0.6257**	0.0378	0.5333**	0.4896**	-0.0245	0.2265*	-0.2227*	0.3574**
2	Days to maturity		1	0.2176	0.5198**	0.5866**	-0.0092	0.3019**	0.0486	0.4565**
3	Plant Height			1	0.4087**	0.1033	-0.2355*	0.015	0.3812**	0.0984
4	No. of primary branches / plant				1	0.824	0.3632**	0.0957	-0.4531**	0.28**
5	No. of secondary branches / plant					1	0.5543**	0.3304**	-0.43**	0.4614**
6	No. of pods / plant						1	0.4915**	-0.5832**	0.4582**
7	Pod weight / plant (g)							1	0.0518	0.9539**
8	100 Seed weight (g)								1	0.0028
9	Grain yield / plant (g)									1

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

Table 4.6. Phenotypic path coefficients (direct and indirect effect) for yield components and grain yield in pigeonpea hybrids

S. No.	Character	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods / plant	Pod weight / plant	100 seed weight
1	Days to 50% flowering	**0.0676**	0.0356	0.0044	0.03	0.0284	-0.001	0.0084	-0.0137
2	Days to maturity	0.0175	**0.0333**	0.001	0.0118	0.0168	0.0028	0.01	0.0006
3	Plant Height	0.0029	0.0014	**0.0448**	0.0133	0.004	-0.0057	-0.0014	0.0126
4	No. of primary branches / plant	0.0381	0.0304	0.0255	**0.0858**	0.0634	0.0175	0.008	-0.0346
5	No. of secondary branches / plant	0.0188	0.0226	0.004	0.0332	**0.0449**	0.0208	0.014	-0.0177
6	No. of pods / plant	-0.0001	0.0008	-0.0012	0.0019	0.0044	**0.0095**	0.0046	-0.0045
7	Pod weight / plant	0.1101	0.2673	-0.0279	0.0828	0.2766	0.4355	**0.8889**	0.0314
8	100 seed weight	-0.0017	0.0002	0.0024	-0.0034	-0.0034	-0.004	0.0003	**0.0085**
9	Grain yield / plant	0.2531*	0.3915**	0.053	0.2554*	0.435**	0.4753**	0.9327**	-0.0173

*Significant at 5% level
**Significant at 1% level
R Square = 0.9074, Residual Effect = 0.3043
Diagonal bold letters indicate direct effects.

Table 4.7. Genotypic path coefficients (direct and indirect effect) for yield components and grain yield in pigeonpea hybrids

S. No.	Character	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods / plant	Pod weight / plant	100 seed weight
1	Days to 50% flowering	**-0.0378**	-0.0236	-0.0014	-0.0201	-0.0185	0.0009	-0.0086	0.0084
2	Days to maturity	0.0533	**0.0852**	0.0185	0.0443	0.05	-0.0008	0.0257	0.0041
3	Plant Height	-0.0024	-0.0136	**-0.0624**	-0.0255	-0.0064	0.0147	-0.0009	-0.0238
4	No. of primary branches / plant	0.1406	0.137	0.1077	**0.2636**	0.2172	0.0957	0.0252	-0.1195
5	No. of secondary branches / plant	-0.0216	-0.0259	-0.0046	-0.0364	**-0.0442**	-0.0245	-0.0146	0.019
6	No. of pods / plant	0.0027	0.001	0.0262	-0.0403	-0.0616	**-0.1111**	-0.0546	0.0648
7	Pod weight / plant	0.2223	0.2964	0.0147	0.094	0.3244	0.4825	**0.9817**	0.0508
8	100 seed weight	0.0003	-0.0001	-0.0004	0.0005	0.0005	0.0007	-0.0001	**-0.0012**
9	Grain yield / plant	0.3574**	0.4565**	0.0984	0.28*	0.4614**	0.4582**	0.9539**	0.0028

*Significant at 5% level
**Significant at 1% level
R Square = 0.9582, Residual Effect = 0.2043
Diagonal bold letters indicate direct effects.

Table 4.8. List of fertile and partially fertile hybrids of pigeonpea

S. No.	Fertile Hybrids	Mean pollen fertility %	Partially fertile hybrids	Mean pollen fertility %
1	ICPH 4275	92.77	ICPH 4539	76.66
2	ICPH 2671	90.33	ICPH 4540	72.77
3	ICPH 2740	88.66	ICPH 2680	68.33
4	ICPH 3473	87.77	ICPH 4395	59.99
5	ICPH 3816	87.55	ICPH 4187	59.22
6	ICPH 4500	87.44	ICPH 3337	55.55
7	ICPH 2751	86.99	ICPH 4502	50.77
8	ICPH 3461	86.99	ICPH 4542	26.32
9	ICPH 3474	86.99	ICPH 4611	15.66
10	ICPH 3762	86.44		
11	ICPH 3933	86.33		
12	ICPH 3477	84.21		
13	ICPH 4488	82.55		
14	ICPH 4485	82.22		

Table 4.9. Fertility restoration studies in pigeonpea hybrids

S. No.	R line	No. of crosses made	Pollen fertility status of the hybrids	Extent of fertility restoration (%)	Hybrids produced
1	ICPL 87119	5	Fully fertile - 5	86.33 - 90.33	ICPH 3933, ICPH 2671, ICPH 2740, ICPH 2751 and ICPH 3461
2	ICPL 20098	1	Fully fertile - 1	84.21	ICPH 3477
3	ICPL 20108	3	Fully fertile - 2 Partially fertile - 1	59.22 - 87.55	ICPH 3762, ICPH 4187 and ICPH 4500
4	ICPL 20107	1	Partially fertile - 1	55.55	ICPH 3337
5	ICPL 20116	2	Fully fertile - 1 Partially fertile - 1	59.99 - 87.77	ICPH 3473 and ICPH 4395
6	ICPL 20137	2	Fully fertile - 2	82.22 – 87.55	ICPH 4485 and ICPH 3816
7	ICPL 20123	3	Fully fertile - 2 Partially fertile - 1	76.66 - 89.33	ICPH 4539, ICPH 4671 and ICPH 3474
8	ICPL 20204	1	Fully fertile - 1	92.77	ICPH 4275
9	ICPL 20186	2	Partially fertile - 2	68.33 - 72.77	ICPH 2680 and ICPH 4540
10	ICPL 20125	1	Fully fertile - 1	82.55	ICPH 4488
11	ICPL 20106	1	Partially fertile - 1	50.77	ICPH 4502
12	ICPL 99046	1	Partially fertile - 1	26.32	ICPH 4542
13	SK Line	1	Partially fertile - 1	15.66	ICPH 4611

Table 4.10. Standard heterosis for yield and yield contributing characters in CMS based hybrids of pigeonpea

S. No.	Hybrid	Days to 50 % flowering				Days to maturity				Plant height (cm)			
		Asha	Maruti	LRG 41	BDN 711	Asha	Maruti	LRG 41	BDN 711	Asha	Maruti	LRG 41	BDN 711
1	ICPH 3933	-8.08	-9.90	-8.08	-2.15	-9.66	-1.24	-8.44	4.61	-2.83	15.54	-1.99	23.35
2	ICPH 2671	-9.09	-10.89	-9.09	-3.23	-11.55	-3.31	-10.36	2.41	-10.19	6.77	-9.42	13.99
3	ICPH 2740	-3.70	-5.61	-3.70	2.51	-5.30	3.52	-4.03	9.65	6.67	26.83	7.59	35.40
4	ICPH 3477	-0.67	-2.64	-0.67	5.74	-1.33	7.87	0.004	14.25	2.39	21.74	3.27	29.97
5	ICPH 2751	-3.70	-5.61	-3.70	2.51	-1.89	7.24	-0.57	13.59	-3.94	14.21	-3.12	21.93
6	ICPH 3461	-2.02	-3.96	-2.02	4.30	0.18	9.52	1.54	16.01	-5.73	12.09	-4.92	19.66
7	ICPH 3762	-2.69	-4.62	-2.69	3.58	-1.70	7.45	-0.38	13.82	-5.88	11.91	-5.07	19.48
8	ICPH 3337	-5.05	-6.93	-5.05	1.07	-6.434	2.28	-5.18	8.33	-8.97	8.23	-8.18	15.55
9	ICPH 3473	-8.08	-9.90	-8.08	-2.15	-11.55	-3.31	-10.36	2.41	-8.67	8.59	-7.88	15.93
10	ICPH 4395	-9.76	-11.55	-9.76	-3.94	-7.57	1.04	-6.33	7.02	-5.69	12.13	-4.88	19.71
11	ICPH 4485	-5.72	-7.59	-5.72	0.36	-4.92	3.93	-3.64	10.09	6.71	26.87	7.63	35.45
12	ICPH 4187	-5.38	-7.26	-5.38	0.72	-7.57	1.04	-6.33	7.02	-8.59	8.68	-7.81	16.03
13	ICPH 4539	-8.41	-10.23	-8.42	-2.51	-7.57	1.04	-6.33	7.02	-0.48	18.33	0.38	26.33
14	ICPH 4275	-8.08	-9.90	-8.08	-2.15	-13.26	-5.17	-12.09	0.44	-1.34	17.31	-0.49	25.24
15	ICPH 2680	-7.07	-8.91	-7.07	-1.07	-8.71	-0.21	-7.48	5.70	-4.69	13.32	-3.87	20.99
16	ICPH 3816	-9.09	-10.89	-9.09	-3.22	-6.63	2.07	-5.37	8.11	-2.71	15.67	-1.88	23.49
17	ICPH 4488	-5.72	-7.59	-5.72	0.36	-5.68	3.11	-4.41	9.21	0.79	19.83	1.65	27.94
18	ICPH 4500	-0.33	-2.31	-0.33	6.09	-4.17	4.76	-2.88	10.96	-2.64	15.76	-1.80	23.59
19	ICPH 4502	-0.67	-2.64	-0.67	5.73	0.57	9.94	1.92	16.45	-5.65	12.17	-4.84	19.76
20	ICPH 4540	-6.73	-8.58	-6.73	-0.71	-6.63	2.07	-5.37	8.11	-7.63	9.83	-6.83	17.25
21	ICPH 4542	-6.39	-8.25	-6.39	-0.35	-13.07	-4.97	-11.89	0.66	8.57	29.08	9.50	37.81
22	ICPH 4611	-12.45	-14.19	-12.45	-6.81	-3.79	5.17	-2.49	11.40	-12.02	4.60	-11.26	11.68
23	ICPH 4671	-2.35	-4.29	-2.35	3.94	-0.57	8.69	0.77	15.13	-15.41	0.57	-14.68	7.38
24	ICPH 3474	-8.08	-9.90	-8.08	-2.15	-10.04	-1.66	-8.83	4.17	-5.28	12.62	-4.47	20.23

Table 4.10.(cont.)

S. No.	Hybrid	No. of primary branches / plant				No. of secondary branches / plant				No. of pods / plant			
		Asha	Maruti	LRG 41	BDN 711	Asha	Maruti	LRG 41	BDN 711	Asha	Maruti	LRG 41	BDN 711
1	ICPH 3933	-26.37	-6.91	-17.78	51.79	-40.89	-5.74	-33.20	101.02	-14.18	-23.98	-7.55	-7.67
2	ICPH 2671	-14.18	8.49	-4.16	76.92	-22.44	23.68	-12.37	163.78	12.01	-0.78	20.66	20.51
3	ICPH 2740	16.42	47.17	30.00	140.00	-24.09	21.05	-14.24	158.16	4.63	-7.32	12.72	12.57
4	ICPH 3477	-3.23	22.33	8.06	99.48	-18.99	29.19	-8.47	175.51	-4.08	-15.03	3.33	3.19
5	ICPH 2751	-4.48	20.75	6.67	96.92	-6.59	48.96	5.53	217.69	-19.68	-28.85	-13.47	-13.58
6	ICPH 3461	9.45	38.36	22.22	125.64	11.61	77.99	26.10	279.59	-1.32	-12.59	6.29	6.16
7	ICPH 3762	2.99	30.18	15.00	112.31	26.16	101.19	42.54	329.08	53.82	36.26	65.71	65.49
8	ICPH 3337	7.09	35.37	19.58	120.77	-6.69	48.80	5.424	217.35	-0.96	-12.27	6.68	6.55
9	ICPH 3473	-32.34	-14.46	-24.44	39.49	-22.74	23.21	-12.71	162.75	22.70	8.69	32.18	32.01
10	ICPH 4395	-44.53	-29.87	-38.05	14.36	-33.89	5.42	-25.31	124.83	16.59	3.28	25.59	25.43
11	ICPH 4485	-20.89	0.00	-11.67	63.08	-35.09	3.51	-26.67	120.75	-6.88	-17.51	0.32	0.19
12	ICPH 4187	-37.56	-21.07	-30.28	28.72	-34.04	5.18	-25.48	124.32	-7.39	-17.97	-0.24	-0.37
13	ICPH 4539	-37.06	-20.44	-29.72	29.74	-38.19	-1.44	-30.17	110.20	12.31	-0.51	20.99	20.84
14	ICPH 4275	-17.66	4.09	-8.06	69.74	-18.49	29.98	-7.91	177.21	1.44	-10.14	9.28	9.14
15	ICPH 2680	2.99	30.19	15.00	112.31	-21.59	25.04	-11.41	166.67	27.71	13.13	37.58	37.40
16	ICPH 3816	-6.72	17.92	4.17	92.31	-19.99	27.59	-9.60	172.11	27.87	13.27	37.75	37.57
17	ICPH 4488	2.61	29.72	14.58	111.54	11.01	77.03	25.42	277.55	21.06	7.24	30.42	30.25
18	ICPH 4500	-4.48	20.75	6.67	96.92	4.51	66.67	18.08	255.44	-11.88	-21.95	-5.08	-5.20
19	ICPH 4502	-14.923	7.55	-5.00	75.38	-19.14	28.95	-8.64	175.00	-3.13	-14.19	4.35	4.21
20	ICPH 4540	-44.03	-29.24	-37.50	15.38	-46.29	-14.35	-39.32	82.60	10.44	-2.17	18.97	18.82
21	ICPH 4542	-32.34	-14.47	-24.44	39.49	-56.19	-30.14	-50.51	48.98	-27.34	-35.63	-21.72	-21.83
22	ICPH 4611	-54.73	-42.77	-49.44	-6.66	-65.89	-45.61	-61.47	15.99	-20.79	-29.83	-14.67	-14.78
23	ICPH 4671	-6.22	18.55	4.72	93.33	26.91	102.39	43.3	331.63	25.05	10.77	34.71	34.54
24	ICPH 3474	-5.47	19.49	5.55	94.872	-2.99	54.71	9.60	229.93	21.86	7.95	31.28	31.11

Table 4.10. (cont.)

S. No.	Hybrid	Pod weight / plant (g)				100 seed weight (g)				Grain yield / plant (g)			
		Asha	Maruti	LRG 41	BDN 711	Asha	Maruti	LRG 41	BDN 711	Asha	Maruti	LRG 41	BDN 711
1	ICPH 3933	-8.17	-13.59	7.64	5.75	11.45	29.16	31.74	26.94	-19.32	-7.78	-0.43	-3.312
2	ICPH 2671	-7.18	-12.61	8.82	6.89	-6.68	8.14	10.29	6.27	-17.79	-6.04	1.45	-1.49
3	ICPH 2740	-9.67	-14.96	5.89	4.02	1.45	17.58	19.92	15.55	-8.63	4.43	12.76	9.49
4	ICPH 3477	10.34	3.87	29.36	27.08	5.05	21.74	24.17	19.64	9.75	25.45	35.46	31.53
5	ICPH 2751	-28.76	-32.93	-16.48	-17.96	-2.02	13.54	15.80	11.58	-26.22	-15.67	-8.95	-11.59
6	ICPH 3461	2.62	-3.39	20.31	18.18	-11.91	2.08	4.11	0.32	1.24	15.72	24.95	21.32
7	ICPH 3762	58.07	48.81	85.32	82.05	-8.20	6.38	8.49	4.54	55.23	77.43	91.57	86.02
8	ICPH 3337	15.96	9.16	35.95	33.55	-12.30	1.63	3.65	-0.13	2.62	17.29	26.64	22.97
9	ICPH 3473	0.18	-5.68	17.45	15.38	-13.31	0.45	2.45	-1.28	-11.22	1.47	9.57	6.39
10	ICPH 4395	24.43	17.13	45.87	43.29	9.21	26.56	29.08	24.37	15.37	31.86	42.38	38.25
11	ICPH 4485	18.93	11.96	39.43	36.97	7.92	25.06	27.55	22.90	8.53	24.05	33.94	30.06
12	ICPH 4187	9.07	2.67	27.86	25.61	8.98	26.30	28.81	24.12	-3.32	10.50	19.31	15.85
13	ICPH 4539	23.59	16.35	44.89	42.34	8.14	25.32	27.82	23.16	1.99	16.57	25.86	22.22
14	ICPH 4275	-7.79	-13.20	8.09	6.18	-2.02	13.54	15.80	11.58	-17.46	-5.66	1.86	-1.09
15	ICPH 2680	-18.35	-23.14	-4.28	-5.96	-20.90	-8.33	-6.50	-9.92	-19.812	-8.35	-1.04	-3.91
16	ICPH 3816	18.13	11.21	38.49	36.05	-9.89	4.43	6.50	2.62	3.82	18.66	28.13	24.41
17	ICPH 4488	-7.34	-12.77	8.63	6.71	-9.04	5.40	7.50	3.58	-17.23	-5.39	2.15	-0.81
18	ICPH 4500	4.96	-1.18	23.05	20.88	5.16	21.87	24.30	19.77	2.57	17.23	26.58	22.91
19	ICPH 4502	44.77	36.28	69.72	66.73	12.07	29.88	32.47	27.64	35.41	54.77	67.11	62.26
20	ICPH 4540	-1.18	-6.97	15.84	13.80	-5.17	9.89	12.08	7.99	-19.22	-7.66	-0.30	-3.19
21	ICPH 4542	-9.71	-14.99	5.85	3.98	32.64	53.71	56.77	51.05	-19.30	-7.76	-0.41	-3.29
22	ICPH 4611	-19.08	-23.83	-5.14	-6.81	28.65	49.08	52.06	46.51	-30.90	-21.02	-14.72	-17.19
23	ICPH 4671	13.15	6.52	32.66	30.32	0.67	16.66	18.99	14.65	1.45	15.96	25.21	21.58
24	ICPH 3474	8.40	2.05	27.08	24.84	-10.96	3.19	5.24	1.41	1.14	15.60	24.82	21.21

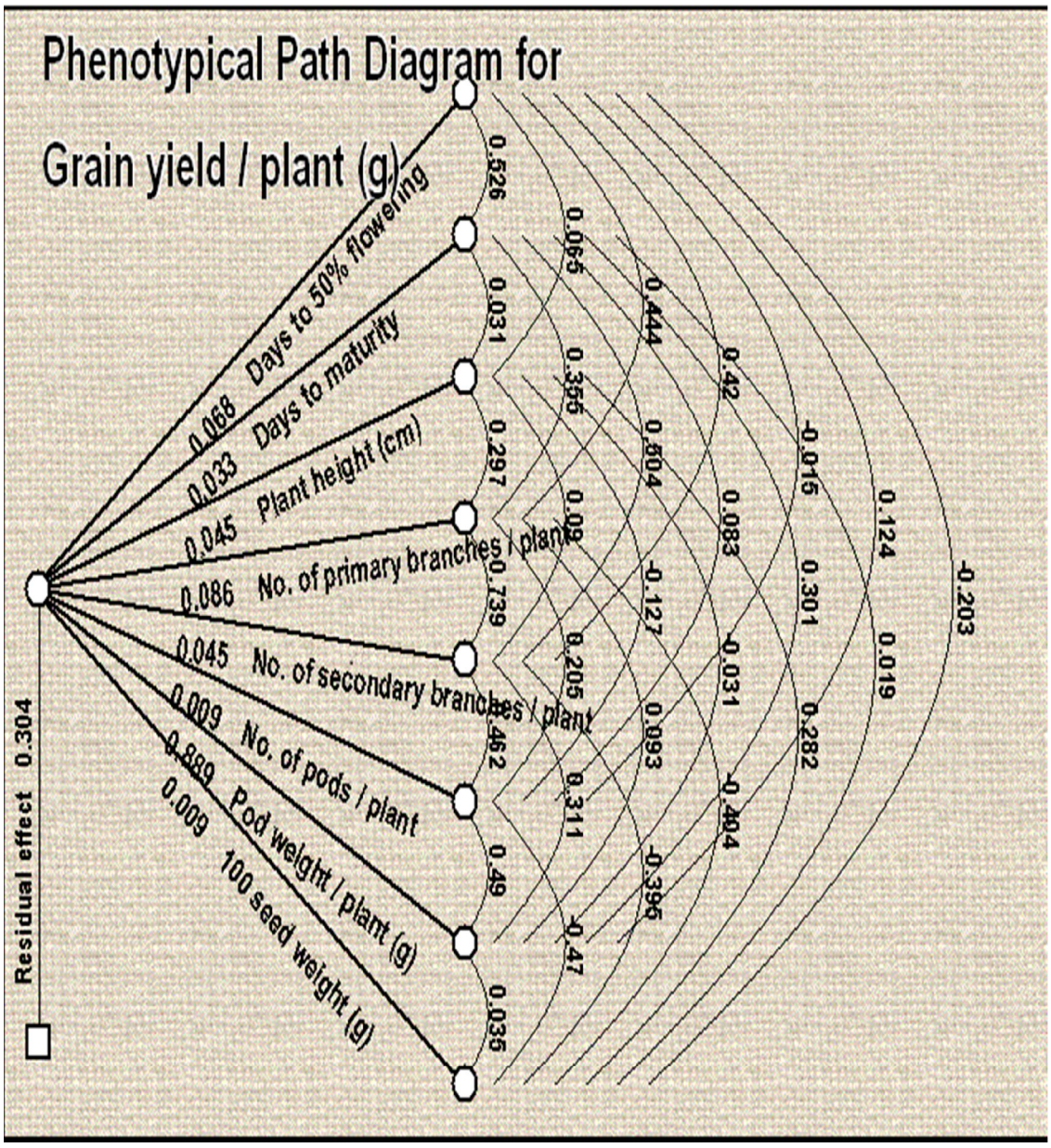


Fig. 4.1. Phenotypic path diagram showing direct and indirect effects of yield components on grain yield per plant in pigeonpea

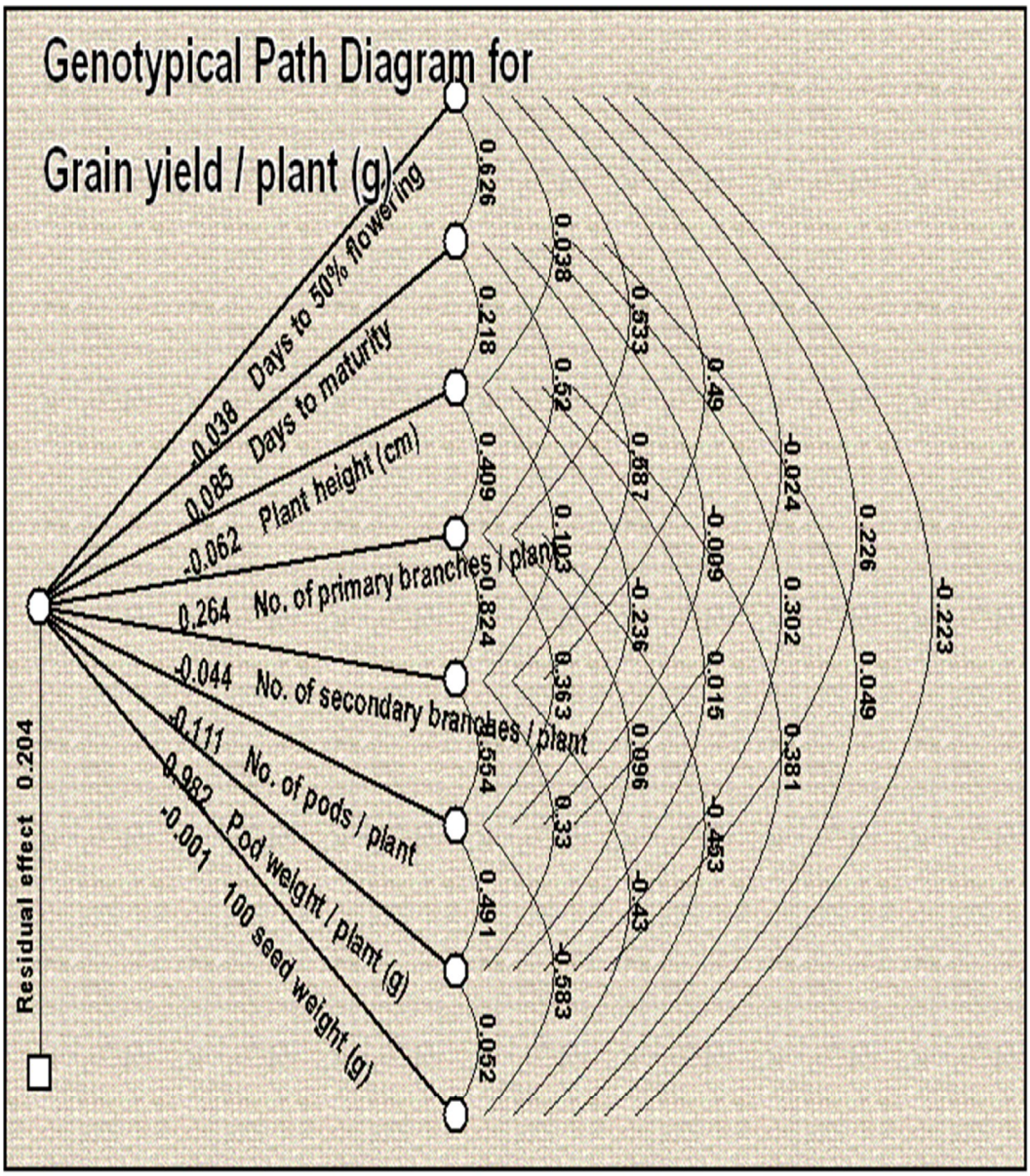


Fig. 4.2. Genotypic path diagram showing direct and indirect effects of yield components on grain yield per plant in pigeonpea

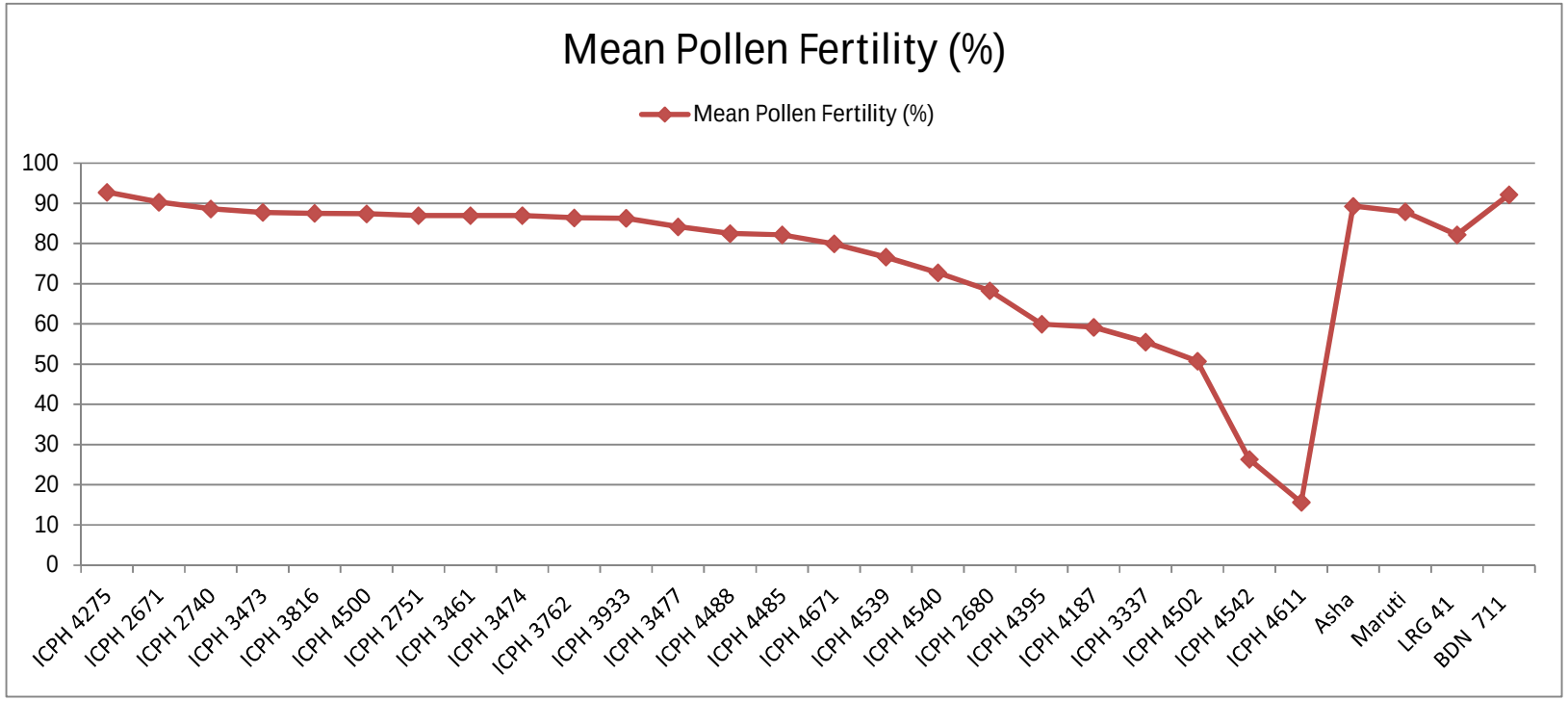
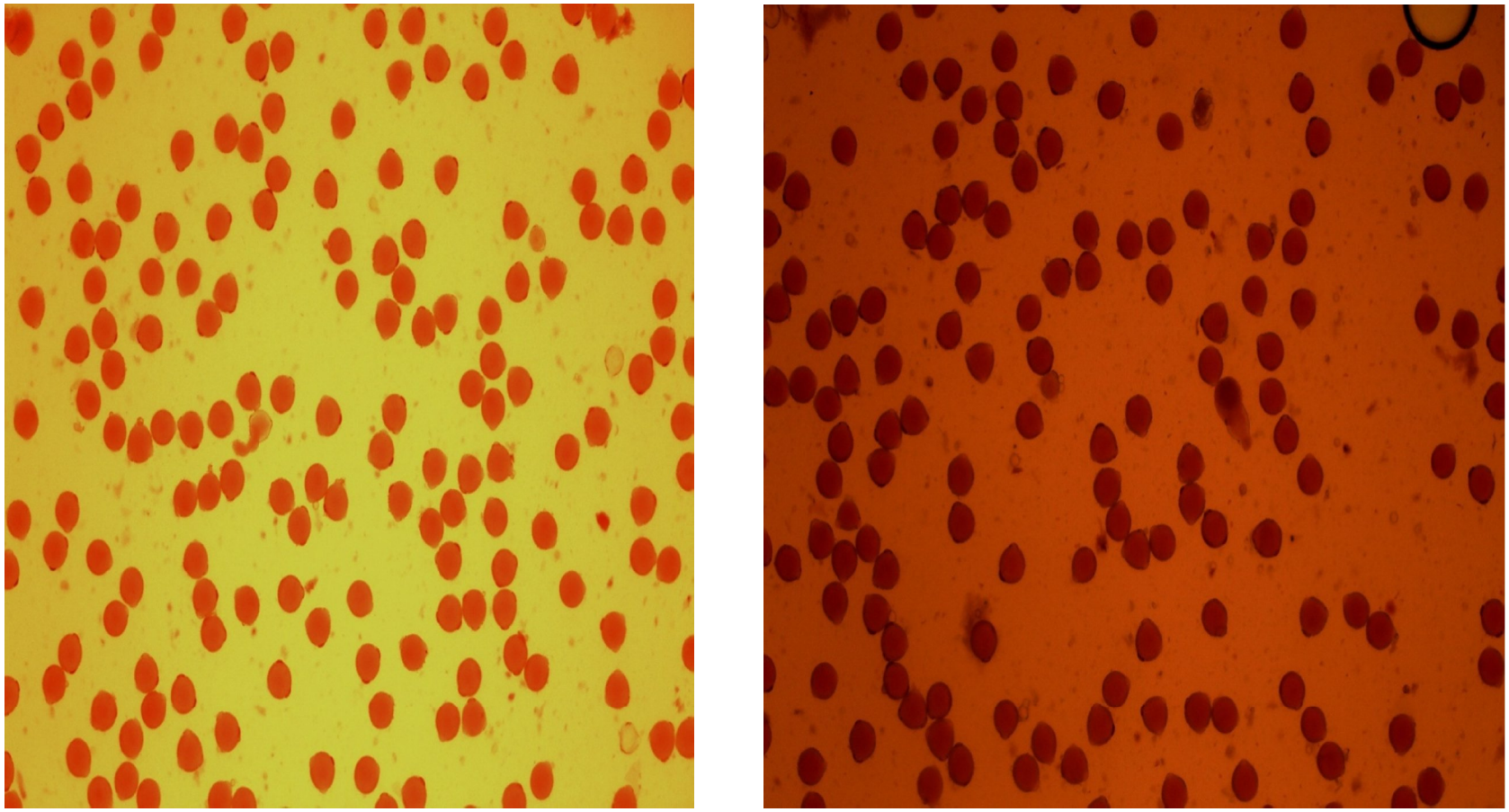
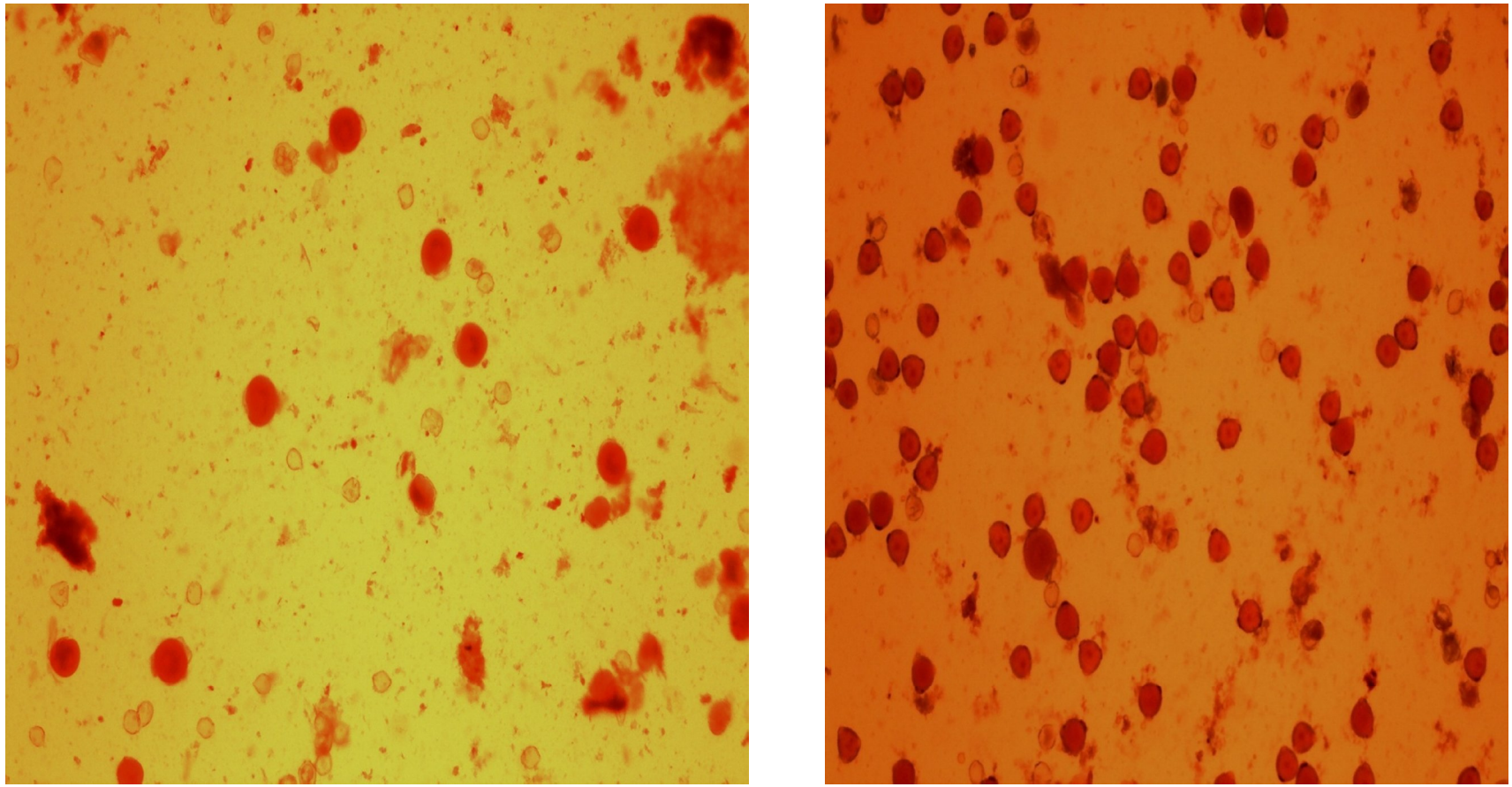


Fig. 4.3. Mean pollen fertility percentage of twenty four hybrids and checks of pigeonpea



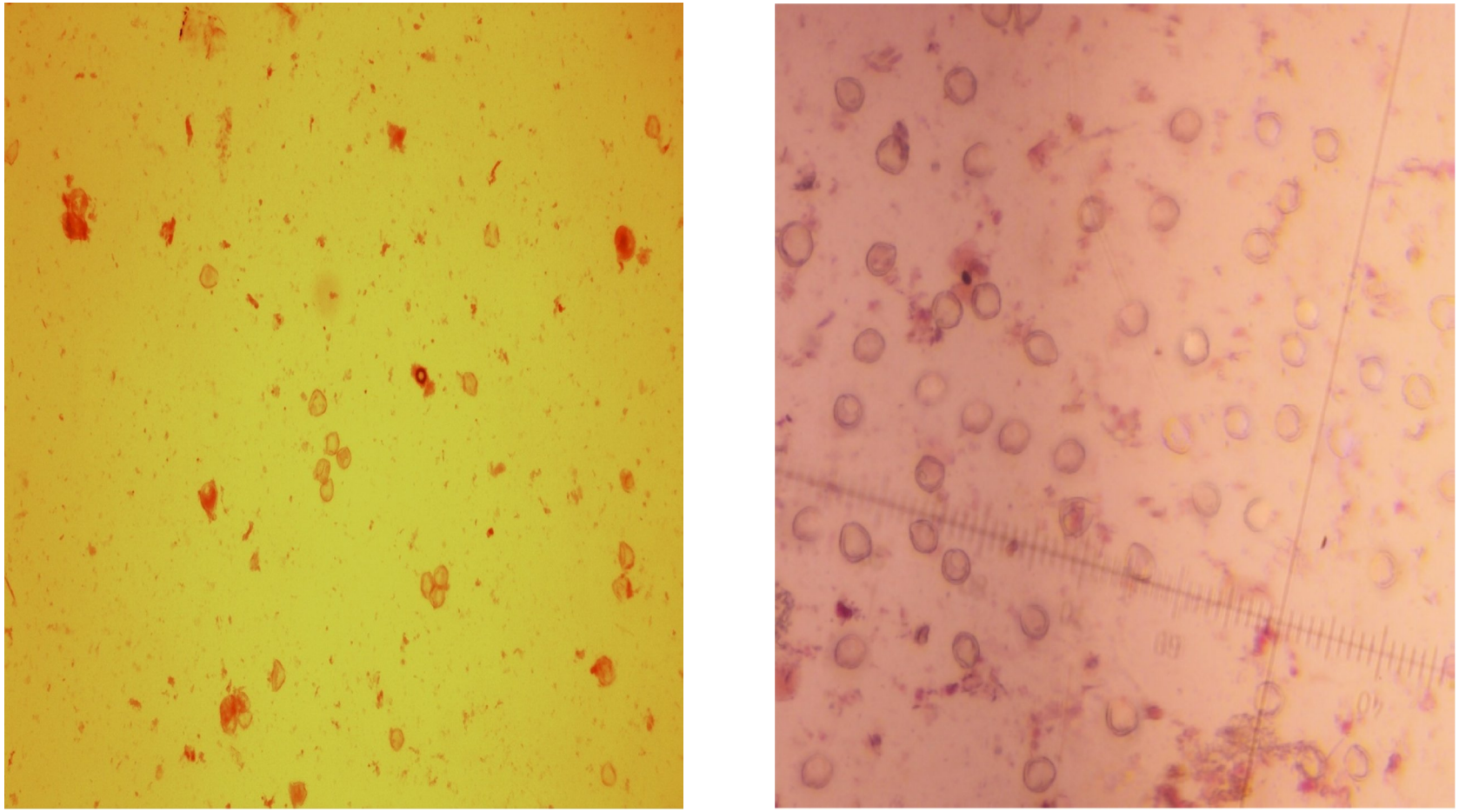
(a) **(b)**

Fig. 4.4. Microscopic view (a and b) of pollen grains in fertile hybrids



(a) **(b)**

Fig. 4.5. Microcsopic view (a and b) of pollen grains in partially fertile hybrids



(a) **(b)**

Fig. 4.6. Microscopic view (a and b) of pollen grains in sterile hybrids.

Chapter- V

SUMMARY AND CONCLUSIONS

Chapter V

SUMMARY AND CONCLUSIONS

In the present investigation entitled "Heterosis in CMS based hybrids of pigeonpea" an attempt was made to study standard heterosis and extent of fertility restoration in newly developed CMS based hybrids to ascertain their worth over the national checks and probable adoption for cultivation in near future. Genetic variability and character association was also studied to further help in hybrid breeding programs. Twenty four F_1 hybrids along with standard checks, Asha, Maruti, LRG 41 and BDN 711 were evaluated in a randomized complete block design with three replications in three contiguous blocks at ICRISAT, Patancheru, Hyderabad, in *Kharif* 2015. An inter and intra row spacing of 150 and 60 cm was followed and crop was line sown. The plot size was 18.9 m^2 and consisted of three rows, each of 4.2 m in length. The main characters under focus in this study were days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod weight per plant (g), 100 seed weight (g), grain yield per plant (g) and mean pollen fertility %.

The analysis of variance for 24 hybrids revealed significant differences among the hybrids for all the characters studied, indicating the presence of sufficient variation. The genotypic coefficients of variation for all the characters studied were slightly lesser than the phenotypic coefficients of variation indicating the less influence of environment on expression of these traits. High PCV and GCV were recorded for number of primary branches per plant, number of secondary branches per plant and pollen fertility %. Meanwhile medium PCV and GCV were recorded for number of pods per plant, pod weight per plant, 100 seed weight and grain yield per plant. Low value of PCV and GCV was recorded for days to 50% flowering, days to maturity and plant height. This indicates that there is considerable amount of variability for majority of the characters studied.

The estimates of heritability and genetic advance as per cent of mean were high for the characters *viz.,* number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod weight per plant, 100 seed weight, grain yield per plant and mean pollen fertility %. High heritability with low genetic advance as *per cent* of mean was seen in days to 50% flowering and days to maturity. While, moderate heritability and low genetic advance as per cent of mean was recorded in plant height.

The results on character associations for yield and yield components revealed that the genotypic correlations were noticed to be higher than phenotypic correlation values for almost all the characters, indicating the masking effect of environment on these traits. Further, grain yield per plant was found to be significantly associated with days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, number of pods per plant and pod weight indicating their importance as selection criteria in pigeonpea yield improvement programmes. Association of grain yield per plant with other characters, namely, plant height and 100 seed weight was found to be insignificant. Studies on inter-character associations among the yield components studied had revealed significant and positive association of days to 50% flowering with days to maturity, number of primary branches per plant and number of secondary branches per plant; days to maturity with number of primary branches per plant, number of secondary branches per plant and pod weight per plant; plant height with number of primary branches per plant and 100 seed weight; number of primary branches per plant with number of secondary branches per plant; number of secondary branches with number of pods per plant and pod weight per plant; number of pods per plant with pod weight per plant, indicating the possibility of simultaneous improvement of these characters through selection. However negative and significant inter character association was observed for number of primary branches per plant with 100 seed weight; number of secondary branches with 100 seed weight and number of pods per plant with 100 seed weight, indicating the need for balanced selection, while attempting for improvement of these traits.

A perusal of the results on path coefficient analysis revealed genotypic and phenotypic path coefficients to be of different direction and magnitude in general. Further, the genotypic path coefficients were observed to be of higher magnitude, compared to phenotypic path coefficients in most of the traits indicating the masking effect of environment. The results also revealed lowresidual effect for both phenotypic (0.3043) and genotypic (0.2043) path coefficients respectively indicating that variables studied in the present investigation explained about 69.57 (phenotypic) and 79.57 (genotypic) per cent of the variability in yield indicating the possibility of addition of some more parameters inthe study. A detailed analysis of the direct and indirect effects also revealed high positive direct effect of pods weight per plant, followed by number of primary branches. Pod weight per plant also exhibited highly significant and positive association with grain yield per plant. High direct effects of this trait therefore appeared

to be the main factor for their strong association with grain yield per plant. Hence, this trait should be considered as important selection criterion in all yield improvement programmes and direct selection for this trait is recommended.

Complete fertility restoration in hybrids is an important prerequisite for the development of successful high yielding hybrid varieties. And pollen fertility (%) is an important character for evaluation of extent of fertility restoration in the hybrids derived from newly developed CMS lines. ICPH 4275 recorded highest pollen fertility (92.77%). Fifteen out of 24 hybrids recorded high (>80 %) pollen fertility i.e. showed better fertility restoration. Nine out of 13 male lines showed fertility restoration of more than 80% and were classified as restorer for corresponding CMS lines.

The present investigation also revealed high levels of heterosis for yield and yield component characters. Among all four checks Asha is the best performing one with mean value of 147.96 g for grain yield per plant. Considerable amount of negative heterosis was recorded for days to 50% flowering and days to maturity, which is desirable for breeding varieties which can escape drought and moisture stress conditions. Low standard heterosis over Asha was recorded for plant height, number of primary branches per plant, number of secondary branches per plant and 100 seed weight. Meanwhile, high standard heterosis i.e. over 50% was recorded in traits like number of pods per plant, pod weight per plant and grain yield per plant. ICPH 3762 and ICPH 4502 with high *per se* performance of 229.68 g and 200.55 g, respectively and high standard heterosis (55.23% and 35.41%, respectively) for grain yield per plant and majority of yield attributes are identified as promising hybrids for large scale commercial cultivation in states like Telangana and Andhra Pradesh. However, performance of above hybrids; ICPH 3762 and ICPH 4502 need to be evaluated over the seasons and locations for knowing stability in their performance, prior to their large scale recommendation and adoption.

Future line of work

The hybrid ICPH 3762 along with ICPH 4502 possess great potential for wide scale adoption in Telangana and Andhra Pradesh, and it can be done by taking up multi location trials and on farm trials to further ascertain the findings .

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Note : The pattern of Literature Cited presented above is in accordance with the guidelines for thesis presentation, Acharya N. G. Ranga Agricultural University, Hyderabad

APPENDICES

APPENDIX I

Weather Data recorded at ICRISAT, Patancheru.
Latitude :17.53^{o}N Longitude : 78.27^{o}E Altitude : 545m

Monthly Weather Data for the Year - 2015

Year	Month	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity1 at 07:17 (in %)	Rel Humidity2 at 14:17 (in %)	Wind Velocity (in Kmph)	Solar Radiation (in mj / m^2)	Bright Sunshine (in Hrs)
2015	7	45.79	248.09	33.61	23.4	79.93	50.03	12.2	18.6	6.46
2015	8	139.39	134.79	30.69	22.32	89.58	65.48	7.95	15.1	4.47
2015	9	172.99	121	31.08	21.79	91.76	63.89	6.49	16.97	5.29
2015	10	63.6	141.9	32.32	19.68	89.54	45.22	3.96	18.31	7.99
2015	11	0.3	141.99	30.91	17.03	87.66	42.23	4.7	16.55	7.68
2015	12	2.2	136.39	31.29	14.54	89.41	36.7	4.77	15.71	8.01

Where mm = millimeter
Source: Meteorological department, ICRISAT, Patancheru, Hyderabad.

APPENDIX II

Daily weather data during the crop season recorded at ICRISAT, Patancheru, 2015.
Latitude: 17°53'N, Longitude: 78°27' E, Altitude: 545 m

Date	Rain (in mm)	Evap (in mm)	Max Temp (in °C)	Min Temp (in °C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr)	Solar Radiation (in mi/ m^2)	Bright Sunshine (in Hrs)
7/24/2015	0	4.4	32	23	84	63	9.3	13.7	0.4
7/25/2015	0	7.4	32.8	23.2	82	53	11.4	20.4	5.5
7/26/2015	0.4	6.6	33.2	22.6	77	49	12.6	18.3	8.2
7/27/2015	0	7.1	31.8	22.8	82	57	11.6	18.1	5.7
7/28/2015	0	9.4	33.8	22	83	48	11.7	22.3	9.6
7/29/2015	0	9.9	34.6	21.8	82	41	14.9	22.8	11.1
7/30/2015	0	9.4	34	21.8	83	47	13.8	19.4	9.8
7/31/2015	0	5.6	31.2	22	85	61	9.5	13.3	1.1
8/1/2015	0	6	32.8	22.2	87	51	11.4	18.6	6.5
8/2/2015	0	7.4	33.4	23.4	82	48	10	20.2	10.7
8/3/2015	2.2	7	33.7	22.8	85	46	8.6	18.5	8.9
8/4/2015	0	5.8	33.2	23	78	50	9.3	15.2	4.3
8/5/2015	0.4	5.7	30	22.8	82	59	13.4	14.3	0
8/6/2015	0	6.3	33	21.2	85	45	11.8	16.5	6.2
8/7/2015	0.6	7	31.7	23	84	54	12.1	13.9	5.5
8/8/2015	1.6	5.3	32.2	22.2	93	54	10.7	14.7	4.2
8/9/2015	0	5.4	32.4	23.2	85	57	9.1	15.9	5
8/10/2015	0	2.7	28.8	23.6	86	76	7.7	10.2	0
8/11/2015	20	3.8	30.8	22.4	97	97	6.8	11.6	3

Date	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr)	Solar Radiation (in mi/ m^2)	Bright Sunshine (in Hrs)
8/12/2015	3.4	3.1	30.2	21.8	97	71	8.7	11.3	1.9
8/13/2015	10	1.4	26.4	22.2	87	84	8	7.9	0
8/14/2015	0.2	1.6	26.4	22.2	87	84	8	7.9	0
8/15/2015	3.2	4.1	30.6	21.6	97	71	7.3	15.2	6.7
8/16/2015	30.4	6.4	31.8	20.4	98	62	8.1	20.2	9.9
8/17/2015	1.6	1.5	28	22.6	92	76	4.6	9.4	0
8/18/2015	0	4.3	31.2	23.2	95	58	7.2	19.6	8.1
8/19/2015	0	2.9	30.6	22.8	90	66	3.9	13.1	0.2
8/20/2015	7	3.6	33.2	21.4	98	61	6.6	14.6	6.7
8/21/2015	17.6	3.5	30.6	22	97	67	4.6	14.3	0.8
8/22/2015	0.2	3.7	30.6	22.2	87	66	6.4	17.2	5.4
8/23/2015	13.8	3.5	29	22	92	71	5.4	13.7	2.1
8/24/2015	0	4.8	30	22.2	87	64	6.9	18.4	8.8
8/25/2015	0	4.5	30.2	22.2	88	63	6.3	19.6	8.1
8/26/2015	0	5.3	30.8	21.6	91	60	6.6	19.5	9.3
8/27/2015	0	5.4	31.4	22.6	90	59	5.9	19.8	7.2
8/28/2015	0	4.6	30.4	22.2	85	69	7.8	16.5	2.8
8/29/2015	26.2	1.8	29.2	22.2	93	98	8.2	11.5	2
8/30/2015	0	2.7	29.2	22.8	92	74	7.5	13.5	2.1
8/31/2015	1	3.7	29.6	22.2	90	69	7.8	15.3	2.4
9/1/2015	0	3.5	29.8	22.8	84	64	6.2	14.8	1.2
9/2/2015	0	5.4	31.6	21.2	85	59	5.9	20.1	8.9
9/3/2015	0	4	31.4	22.4	87	60	5.6	19.4	7.6
9/4/2015	0	5.8	33.2	24	86	51	50	22.8	8.8

Date	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr)	Solar Radiation (in mi/ m^2)	Bright Sunshine (in Hrs)
9/5/2015	0	5.4	34	22.4	88	51	5.6	19	7
9/6/2015	0	5.5	33	21.6	93	56	3.8	20.8	8
9/7/2015	1	4.5	33.2	22	97	60	5.4	15.9	5.9
9/8/2015	10	3.1	31.6	21	97	59	5.5	17.6	6.2
9/9/2015	21	4	31	22	84	60	3.9	18.4	4.8
9/10/2015	4.4	2.8	31.2	21	97	66	4.1	15.9	5.2
9/11/2015	6.2	3.6	29.5	21.5	98	75	4.3	14.7	6.2
9/12/2015	9.2	2	29.8	20.6	98	73	4.4	11.1	1.1
9/13/2015	0	2.1	28.4	21.4	91	76	5.3	11.8	0.4
9/14/2015	0	3.4	29.6	22	92	71	6	13.5	2.6
9/15/2015	9.6	2.1	29.8	21.4	97	72	6.2	10.6	1.9
9/16/2015	65.8	1.5	26.6	22	95	98	5.2	6.5	0
9/17/2015	33.6	3.8	29.8	21.6	97	78	8.8	13	1
9/18/2015	10.6	3.1	29.4	22.2	92	75	9.5	12.2	1.5
9/19/2015	0	2.5	31.2	21.2	95	69	5.4	18	5.8
9/20/2015	0.6	4.8	31.2	21.6	91	69	5	20.6	6.5
9/21/2015	0	3.5	30.2	21.4	90	65	5.3	16.6	2.4
9/22/2015	0	4.4	31	21.4	91	58	4.8	20.6	6.5
9/23/2015	0	4.8	31.6	21.6	90	59	4.1	21.1	9.2
9/24/2015	0	4.7	32.6	23.6	88	50	2.8	21.4	9
9/25/2015	0	5.2	33	23	89	54	4	19.2	8
9/26/2015	0.6	5.3	33.6	22	93	56	3.9	18.3	6.8
9/27/2015	0	3.3	30.8	22.2	95	65	2.4	15.4	3.2
9/28/2015	0	6.2	31	19.4	91	65	3.9	22.8	8.7

Date	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr	Solar Radiation in mi/ m^2)	Bright Sunshine (in Hrs)
9/29/2015	0	5.2	32	21.4	90	48	2.1	19.4	8.5
9/30/2015	0.4	5.5	31.4	22	92	55	5.3	17.6	5.8
10/1/2015	0	4	30.6	22.2	95	62	5.4	15.5	4.2
10/2/2015	0	5	31.2	21.6	93	57	6.1	15.9	5.6
10/3/2015	0	4.3	31.8	21.6	93	56	3.8	17.5	6.3
10/4/2015	13	4.4	32.8	21.6	93	56	4.6	16.2	6
10/5/2015	0.6	3	31.8	21.4	97	66	3	14	3.6
10/6/2015	0	4.6	32.2	19.4	93	46	2.4	19.9	8.7
10/7/2015	0	5.2	33	19.6	84	39	2.8	21.6	9.3
10/8/2015	0	6	33.6	18.6	82	36	2.4	22.1	10.3
10/9/2015	0	4.4	33.6	21.2	75	34	2.6	21.1	9
10/10/2015	0	5.8	31.6	23	79	29	3	20.3	9.6
10/11/2015	40	5	31.6	20.5	91	43	5.4	16.6	8.3
10/12/2015	0	3.6	31.3	20	83	42	4.3	15.8	4.6
10/13/2015	0	5	33.6	18.2	87	36	1	19.9	8.7
10/14/2015	0	3.6	33.4	18	87	47	2.4	17.8	8.6
10/15/2015	0	3.4	33.2	19.6	88	36	2	20	9.1
10/16/2015	0	4.3	33.4	20.6	91	40	3.2	20.1	9.1
10/17/2015	0	5.2	32.4	20.6	95	50	4.1	18.5	8.7
10/18/2015	0	4.2	31.6	20.6	95	57	4.1	17.5	8
10/19/2015	0	4.8	32.2	19	95	53	3.7	18.8	8.3
10/20/2015	0	4.8	32.4	18.2	87	40	3.5	18.8	9.7
10/21/2015	0	4.2	32.6	18	87	40	4.4	19	9.1
10/22/2015	0	5.2	32.6	18.2	89	38	4.3	19.9	9.8

Date	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr)	Solar Radiation (in mi/ m^2)	Bright Sunshine (in Hrs)
10/23/2015	0	5	33.2	17.4	91	38	3.9	19.6	9.8
10/24/2015	0	4.2	33	18	91	38	3.7	19.1	9.5
10/25/2015	0	5.6	32.8	19.2	91	44	4.9	18.2	8.3
10/26/2015	0	4.8	32.6	18.2	91	42	6	18.3	8.9
10/27/2015	0	4.8	31.2	17.2	91	44	4.4	18.1	7.9
10/28/2015	0	5.1	32	16.4	90	36	3.6	18.9	9.3
10/29/2015	10	5.9	31.2	21.4	91	47	7.6	18.1	7.4
10/30/2015	0	3	31.8	21.4	90	58	5.9	16.5	7.7
10/31/2015	0	3.5	31.8	19.2	91	52	4.3	14.1	4.5
11/1/2015	0	4.6	31.6	19.2	96	46	2.6	19	9.3
11/2/2015	0	4.6	31.6	17.6	94	47	2.5	19.1	8.7
11/3/2015	0	4.4	32	20.6	88	39	2.7	18.9	9.2
11/4/2015	0	3.7	30.6	18.8	95	51	3	12	5.1
11/5/2015	0	4.3	32.2	17.2	91	38	3.4	18	9.7
11/6/2015	0	4.4	31.4	17	91	40	3.3	17.2	8.6
11/7/2015	0	5.6	32.6	16.8	89	33	3.3	17.6	8.8
11/8/2015	0	4.9	31.4	19.2	89	40	5.3	17.4	9
11/9/2015	0	6	31.6	14	88	38	6.2	17	8.4
11/10/2015	0	5.4	30.7	16.8	78	37	5	14.9	4.7
11/11/2015	0	5.9	30.8	18.4	79	40	5.9	16.4	6.9
11/12/2015	0	7.5	31.8	14.6	86	24	5.8	19	9.4
11/13/2015	0	5.2	32	12.6	87	37	3	18.2	9.5
11/14/2015	0	5.6	32	13.8	84	29	2.6	18.3	8.5
11/15/2015	0	4.8	30.8	13.8	90	35	4.3	17.1	8

Date	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr)	Solar Radiation (in mi/ m^2)	Bright Sunshine (in Hrs)
11/16/2015	0	5.7	32.6	17.6	87	31	4.6	26.6	7.2
11/17/2015	0	2.6	26.4	15.2	92	58	3.8	7.1	0
11/18/2015	0	4.7	30	14	94	44	3.8	16.4	7
11/19/2015	0	4.6	30.8	16.4	67	44	2.7	18.9	9.5
11/20/2015	0	5.1	29.8	19.8	83	50	8.4	15.5	7.5
11/21/2015	0.3	2.5	26.4	19.2	76	82	6.7	8.8	0.1
11/22/2015	0	5.6	29.6	19.8	89	52	9.6	14.4	7
11/23/2015	0	4.2	30.2	19.2	91	54	5.2	13.9	6.8
11/24/2015	0	5	31	18.4	94	45	5.8	16.9	8.6
11/25/2015	0	3.7	30.6	15.8	94	53	3.3	14.4	7
11/26/2015	0	4.3	30	13.2	92	43	4.2	16	8.5
11/27/2015	0	3.2	31.4	14.6	94	35	3.8	17.1	9
11/28/2015	0	4.7	32.4	16.2	90	31	5.4	16.8	9.5
11/29/2015	0	5	31.8	19.6	80	35	7.1	17.2	9.4
11/30/2015	0	4.2	31.2	21.8	82	36	7.9	16.6	9.6
12/1/2015	2.2	1.8	28.4	19.2	91	78	4.8	8.1	0
12/2/2015	0	4.6	30.4	18.8	96	39	5.7	14.7	9.6
12/3/2015	0	3.5	28	16.8	85	59	6.4	10.5	1
12/4/2015	0	5	31.2	15	90	40	4.2	16.8	9.2
12/5/2015	0	3.4	31.2	15.6	88	45	3.5	14.6	7.4
12/6/2015	0	3.6	30.2	14.2	90	39	4.9	16.1	9.2
12/7/2015	0	3.5	29.2	13	92	35	4.8	15.7	6.7
12/8/2015	0	3.5	29.8	13.2	89	57	3.8	15.2	5.4
12/9/2015	0	4.6	30	14.2	96	33	4.9	16.6	8.3

Date	Rain (in mm)	Evap (in mm)	Max Temp (in ^{o}C)	Min Temp (in ^{o}C)	Rel Humidity 1 at 07:17 (in %)	Rel Humidity 2 at 14: 17 (in %)	Wind Velocity (in km/ hr)	Solar Radiation (in mi/ m^2)	Bright Sunshine (in Hrs)
12/10/2015	0	3.2	28.4	13.6	96	40	4.1	13.8	5
12/11/2015	0	4.4	33	18.4	91	31	6.2	17.4	9.4
12/12/2015	0	2.7	32	18.7	89	42	5.3	13.4	5.4
12/13/2015	0	3.7	34.6	18.8	94	41	4.4	15.5	8.7
12/14/2015	0	4.7	34	17.4	91	42	6	13.6	8.3
12/15/2015	0	5.7	33.2	17.2	94	38	5	16	9.2
12/16/2015	0	5	33.8	15.2	86	21	4	16.2	9.7
12/17/2015	0	6.1	33.8	16.2	94	21	6.6	17.8	10.2
12/18/2015	0	5.3	33.4	15.7	96	22	6.3	18.3	9.9
12/19/2015	0	4.6	33.2	14.4	88	32	4.3	17.7	9.5
12/20/2015	0	5.3	31.4	17.2	96	38	7.5	16.7	9.5
12/21/2015	0	4.2	32	19.6	83	39	6.5	15.6	7.6
12/22/2015	0	4.7	32.2	16.2	90	40	5.9	15.4	7.8
12/23/2015	0	4.6	32.8	15.4	96	36	5	15.2	8.3
12/24/2015	0	4.8	31.8	15	79	37	3.8	15.1	8.5
12/25/2015	0	4.2	30	14	68	42	3.8	16.4	9
12/26/2015	0	4.6	27.4	6.6	82	29	2	15.8	7.3
12/27/2015	0	4	28.7	7.4	82	29	2.6	17.6	9.4
12/28/2015	0	4.5	29	8	83	20	2.5	16	8.7
12/29/2015	0	5.4	31.4	8.2	93	25	4.5	18.2	9.8
12/30/2015	0	5	33	8.4	93	22	3.9	18.8	10.2
12/31/2015	0	6.2	32.6	9.4	91	26	4.8	18.3	10.2

Where mm-millimeter
Source: Meteorological department, ICRISAT, Patancheru, Hyderabad.