# IDENTIFICATION OF HETEROTIC COMBINATIONS, USING OBCORDATE LEAF SHAPE CMS LINES IN PIGEONPEA [*Cajanus cajan* (L.) MILLSPAUGH]

**M.Sc. (Ag.) Thesis**

**by**

**Parsagoni Mallesh**

**DEPARTMENT OF GENETICS AND PLANT BREEDING**

**COLLEGE OF AGRICULTURE**

**FACULTY OF AGRICULTURE**

**INDIRA GANDHI KRISHI VISHWAVIDYALAYA**

**RAIPUR (Chhattisgarh)**

**2016**

# IDENTIFICATION OF HETEROTIC COMBINATIONS, USING OBCORDATE LEAF SHAPE CMS LINES IN PIGEONPEA [*Cajanus cajan* (L.) MILLSPAUGH]

**Thesis**

**Submitted to the**

**Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.)**

**by**

**Parsagoni Mallesh**

**IN PARTIAL FULFILMENT OF THE REQUIREMENTS**

**FOR THE DEGREE OF**

**Master of Science**

**In**

**Agriculture**

**(Genetics and Plant Breeding)**

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**JULY, 2016**

# CERTIFICATE – I

This is to certify that the thesis entitled **"Identification of heterotic combinations, using obcordate leaf shape CMS lines in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]"** submitted in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **PARSAGONI MALLESH** under my/our guidance and supervision. The subject of the thesis has been approved by Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma or has been published/ published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by him.

18/7/2016

**Co-Chairman** **Chairman**

Date: 18th July 2016

**THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE**

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# CERTIFICATE – II

This is to certify that the thesis entitled **"Identification of heterotic combinations, using obcordate leaf shape CMS lines in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]"** submitted by **PARSAGONI MALLESH** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur, in partial fulfillment of the requirements for the degree of **Master of Science** in the Department of **GENETICS AND PLANT BREEDING** has been approved by the external examiner and Student's Advisory Committee after an oral examination.

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**Signature External Examiner**

Date: 9-8-16

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**Major Advisor**

09/8/2016

**Head of the Department**

9.8.16.

**Faculty Dean**

**Approved/Not approved**

**Director of Instructions**

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**International Crops Research Institute for the Semi-Arid Tropics**

# CERTIFICATE - III

This is to certify that **Mr. Parsagoni Mallesh** has satisfactorily completed the research work related to this thesis entitled **"Identification of heterotic combinations, using obcordate leaf shape CMS lines in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]"**. His thesis contains results of original research work and it is of high standards to warrant its presentation to the examination. I also certify that neither the thesis nor its part, thereof, has been previously submitted by him for a degree at any other university.

**(Dr. C.V. Sameer Kumar)**

**Senior scientist, Pigeon pea Breeding,**

**ICRISAT, Patancheru, Hyderabad**

**Place: ICRISAT**

**Date;** 18 - 07 - 16

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**Place: Raipur**

**Date:18/07/2016**

**Parsagoni Mallesh**

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| DESCRIPTION | ABBREVIATION |
|---|---|
| Millimetre | mm |
| Centimetre | cm |
| Gram | g |
| Kilogram | kg |
| Litre | L |
| Acre | ac |
| Hectare | ha |
| Kilogram per hectare | kg ha-1 |
| Percent | % |
| Degree Celsius | °C |
| And others people | *et al*. |
| As such mean | per se |
| Namely | *viz.*, |
| Standard Deviation | SD |
| Analysis of Variance | ANOVA |
| Randomized completely Block Design | RBD |
| Critical Difference at 5, 1 and 0.1 per cent level of probability | CD (P=0.05, 0.01, 0.001) |
| Million | M |
| Meter | m |
| Meter square | $m^2$ |
| Mid parent heterosis | MPH |
| Better parent heterosis | BPH |
| Standard heterosis | SH |

| | |
|---|---|
| Serial Number | Sl.No or S.No. |
| Standard error | SE |
| Tonnes | t |
| Tonnes per hectare | t $ha^{-1}$ |
| Better parent heterosis | BPH |
| SPC | Seed protein content |
| DR% | Dal recovery% |
| PF% | Pollen fertility% |

# THESIS ABSTRACT

a) Title of the Thesis : Identification of heterotic combinations, using obcordate leaf shape CMS lines in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

b) Full Name of the Student: : Parsagoni Mallesh

c) Major Subject: : Genetics and Plant Breeding

d) Name and Address of the Major Advisor : Dr. H.C.Nanda, Principle scientist, Deptt. of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur, Chhattisgarh - 492012.

e) Degree to be Awarded: : M.Sc. (Ag.) Genetics and Plant Breeding

18/7/2016
Signature of Major Advisor

Signature of the Student

Date: 18/07/2016

18.07.2016
Signature of Head of the Department

## ABSTRACT

The present experiment was conducted in a Randomized Complete Block Design (RCBD) in three replications enrolling 14 $F_1$ hybrids, 4 B-lines, 5 R-lines and 5 standard checks of pigeonpea sown on 14 July 2015. Analysis of variance revealed that sufficient variability for all characters studied. Studies on per se performance of the 28 genotypes were revealed that the lower means for days to 50 per cent flowering, days to maturity. Higher means for pollen fertility, plant height, number of primary and secondary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, number of seeds plant$^{-1}$, 100 seed weight, biological yield plant$^{-1}$, seed yield (kg/ha),

harvest index, dal recovery, seed protein content and seed yield plant$^{-1}$ for hybrids compared with B and R lines were noticed.

The results on correlation coefficient analysis revealed that seed yield plant$^{-1}$ was observed to be significantly and positively associated with primary branches plant$^{-1}$, secondary branches plant$^{-1}$, pods plant$^{-1}$, seeds pod$^{-1}$, biological yield plant$^{-1}$, seed yield (kg/ha) and harvest index indicating their importance as selection criteria in pigeonpea yield improvement programmes. The results on path co-efficient analysis showed that pollen fertility% had maximum direct effect fallowed by biological yield plant$^{-1}$, harvest index, pods plant$^{-1}$, number of secondary branches plant$^{-1}$ and dal recovery. In these traits, except pollen fertility% had also exhibited highly significant and positive association with seed yield plant$^{-1}$. High direct effects of these traits therefore appeared to be the main casual factor for yield plant$^{-1}$. Hence, these traits should be considered as important selection criteria in all yield improvement programmes and direct selection for these traits would be rewarded.

Studies on fertility restoration indicated that pollen fertility percent for the hybrids ranged from 83.00 to 87.33% with an average of 85.11%. Results showed that among R lines, ICPL 11229, ICPL 11237, ICPL 20116, ICPL 20093 and ICPL 20108 were good restorers with more than 80% fertility restoration in their hybrids.

The results on heterosis of 14 pigeonpea hybrids over mid-parent, better parent, and the standard check for seed yield and yield components revealed high heterosis over mid parent, better parent and standard check. Among these, for seed yield (kg/ha) was recorded higher heterosis followed by number of secondary branches plant$^{-1}$ and number of pods plant$^{-1}$. Further, ICPH 4679, ICPH 4571 and ICPH 4746 hybrids had uniformly recorded significant and desirable heterosis over mid and better parents compared to the check, Asha. ICPL 20116 and ICPL 20093 R lines, ICPB 2204, and ICPB 2200 B lines were observed to be superior for seed yield and other important yield attributes in the present study and are suggested for their exploitation in hybrid pigeonpea breeding programmes.

## शोधग्रंथ सारांश

| | | |
|---|---|---|
| शोध शीर्षक | : | अरहर में अबकार्डेट पत्ती आकार जीवपृत्यीम बंध्यता सी.एम.स. लाइन का उपयोग कर संकर संयोजनों का पहचान करना |
| छात्रा का पूरा नाम | : | परसागोनी मल्लेश |
| प्रमुख विभाग | : | आनुवंशिकी और पादप प्रजनन |
| सलाहकार का नाम व पता | : | डॉ. एच.सी. नंदा , प्रमुख वैज्ञानिक , एंव प्रभारी दलहन परियोजना , आनुवंशिकी और पादप प्रजनन विभाग, कृषि महाविद्यालय रायपुर (छत्तीसगढ़) 492012 |
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18/7/16

मुख्य सलाहकार के हस्ताक्षर

छात्र के हस्ताक्षर

दिनांक 18/07/2016

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विभागाध्यक्ष के हस्ताक्षर

## सारांश

वर्तमान प्रयोग में अरहर को यादृच्छिक पुर्ण खण्ड परिकल्पना में 14F, संकर 4B – प्रमेदे, 5R –प्रमेदे और 5 मानक किस्मों के साथ यादृच्छिक पुर्ण खण्ड परिकल्पना में तीन पुनर्रावृत्ति में लगाया गया था जिसकी बुआई 14 जुलाई 2015 को किया गया। विभिन्नता विश्लेषण से पता चला कि सभी लक्षणों के लिए अरहर

जैवप्रकारों में पर्याप्त भिन्नता पाई गइ थी। 28 जैव प्रकारों के औसत प्रदर्शन से पता चला की सबसे कम औसत 50% फूलों से भरा दिन और परिपक्वता का दिन के लिए थे। संकरों में B और R प्रमेदों की अपेक्षा अधिकत्म (अधिक) औसत पराग उर्वरता प्रतिशत, पौध उचाई, प्राथमिक और द्वितीय शाखाओं की संख्या प्रति पौधा, फलीयों की संख्या प्रति पौधा बीजों की संख्या प्रति पौधा, 100 बीजों का भार जैविक उपज प्रति पौधा, बीज उपज (किलोग्राम/हेक्टेयर), फसल सूचकांक, दाल प्राप्ति प्रतिशत, बीजों में उपस्थित प्रोटीन और बीज उपज प्रति पौधे के लिए पाया गया। सहसंबंध गुणांक विश्लेषण का परिणाम यह बताता हैं कि बीज उपज प्रति पौधा, प्राथमिक और द्वितीय शाखाओं की संख्या प्रति पौधा, फल्लियों की संख्या प्रति पौधा, बीजों की संख्या प्रति पौधा, जैविक उपज प्रति पौधा, बीज उपज (किलोग्राम/हेक्टेयर) और फसल सूचकांक के साथ महत्वपूर्ण एवं सकारात्मक रूप से संबंधित पाया गया यह अरहर के उपज संवर्धन कार्यक्रम में उनके महत्वपूर्ण चयन मापदण्ड के रूप से कार्य करता है।

पथ गुणांक विश्लेषण का परिणाम यह बतलाता है कि बीज उपज प्रति पौधे को सबसे अधिक सीधा पराग ऊर्वरता द्वारा उसके बाद जैविक उपज प्रति पौधा, फसल सूचकांक, फल्लीयों की संख्या प्रति पौधा, द्वितीय शाखाओं की संख्या प्रति पौधा और दाल प्राप्ति द्वारा दिया गया। पराग ऊर्वरता के अलावा अन्य सभी लक्षण भी बीज उपज प्रति पौध के साथ महत्वपूर्ण और सकरात्मक सीधा प्रभाव प्रदर्शित करते है। इस तरह से इन सभी लक्षणों का अधिक सीधा प्रभाव बीज उपज प्रति पौधा के साथ महबूत सबंध के लिए मुख्य कारक के रूप में दिखाई देता है। अतः यह सभी लक्षण सभी प्रकार के उपज कार्यक्रमों में महत्वपूर्ण चयन मापदण्ड के रूप में मानना चाहियें और इन लक्षणों को सीधा–सीधा चयन के लिए अनुशंसीत करना लाभदायक होगा। ऊर्वरता वापसी का अध्ययन यह बताता है कि पराग ऊर्वरता प्रतिशत संकरों के लिए 83.00 से 87.33 तक 85.11% औसत के साथ पाया गया।

इस प्रकार यह परिणाम बताता है कि R लाइन्स, आई.सी.पी.एल.–11229, आई.सी.पी. एल.–20093 और आईसी.पी.एल. 20108 अच्छे रीस्टोरर है जो उनके संकरो में 80% से अधिक ऊवर्रता वापसी प्रदर्शित करते है। 14 अरहर संकरों के संकरण का परिणाम मिड–पेरेन्ट (मध्य अभिभावक), बेटर पेरेंट (उन्नत सभिभावक) और मानक किस्म, बीज उपज और उपज करकों से अधिक था। जो यह प्रदर्शित करता है अधिकत्म संकरण भीड़ पैरन्टस (मध्य अभिभावक), उसके बाद बेटर पैरेंटस और मानक किस्मों के उपर था।

इन सभी लक्षणों में बीज उपज उससे अधिक **संकर ओज** प्रदर्शित करता है उसके बाद द्वितीय शाखाओं की संख्या प्रति पौधा द्वारा फल्लीयों की संख्या प्रति पौधा द्वारा दिया गया। इसके अलावा ICPH – 4679, ICPH 4571 और ICPH – 4746 संकर सभी लक्षणों के लिए सभी **संकर ओज** प्रारूपों में चेक्स से श्रेष्ठता तथा एकरूपता प्रदर्शित करता है। वर्तमान जाँच में ICPL - 20116 ICPL & 20093 R लाइन्स, ICPB & 2004 और ICPB & 22000 B लाइन्स को बीज उपज और दूसरे महत्वपूर्ण उपज घटकों के लिए श्रेष्ठ पाया गया और इस प्रकार इन सभी लाइन्स को संकर अरहर प्रजनन कार्यक्रमों में अनुशंसित किया जा सकता है।

# CHAPTER - 1

# INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an often cross pollinated crop with diploid (2n = 2x) chromosome number of 22 and genome size of 858 Mbp. It is an annual crop overlaps both k*harif* and *rabi* season. It is commonly known as redgram, tur, arhar, tuvarica, congobean (van der Maesen, 1986) and thogari in India. It is one of the major pulse crops of the tropics and sub-tropics, grown in approximately 50 countries in Asia, Africa and the America. It is the sixth most important pulse crop in the world with almost all production coming from the developing countries. Considering the vast natural genetic variability available in pigeonpea and presence of its wild relatives in the region, it has been postulated that India is the primary center of origin of pigeonpea (Vander Maesen, 1980).

Based on the crop duration pigeonpea cultivars were categorized into super early (70-75) cultivars, short-duration (100-140 days) cultivars, (early and short duration types) grown as sole crop, while the medium (160-180 days) and long-duration (> 200 days) types are invariably grown as intercrop or mixed crop with other short-duration crops. Pigeonpea has several advantages over other leguminous crops for broad scale agricultural production. These include drought tolerance, water logging, shattering resisting and perenniality, which allow the possibility of rationing. Being a pulse its main use as *dhal* (decupled split peas), its immature green seeds and pods are also consumed as vegetable. The crushed dry seeds are fed to animals, while green leaves form a quality fodder. The dry stems of pigeonpea are used as fuel wood. Pigeonpea enriches soil through symbiotic nitrogen fixation, releases soil-bound phosphorous, recycles the soil nutrients and adds organic matter. Seed and fodder contains 20-22% protein. Seeds are rich in iron, iodine and essential amino acids like lycine, cystine and arginine. Apart from these uses, perennial type pigeonpea is grown

on sloppy mountain and bunds for reducing soil erosion. In China, efforts are being made to use pigeonpea for lac production, fish cultivation and snacks preparation *etc*. (Saxena, 2006a).

The global production of pigeonpea is 4.32 Mt from an area of 5.32 Mha with a productivity of 813.2 kg/ha (FAO, 2012). In India, pigeonpea is cultivated in 264.02 lakh ha with average productivity of 789 kg/ha (Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India, 2013-14). The leading states in pigeonpea production are Maharashtra (1.30 Mha, 30%), Karnataka (0.89 Mha, 17%), Madhya Pradesh (0.49 Mha, 13%), Gujarat (0.28 Mha, 8%) and Andhra Pradesh (0.64 Mha, 8%). These six states account for over 70% of the total pigeonpea area and production in India. In order to meet this requirement, the Indian Government annually imports about 0.5 to 0.6 Mt of pigeonpea mainly from Myanmar and southern and eastern Africa (Saxena and Nadarajan, 2010). This is a matter of concern as the majority of the Indian population is vegetarian and their protein source directly depends on pulses.

In India, the pigeonpea area has recorded a significant rise from 2.3 Mha in 1950 to 3.67 Mha in 2015. However, the crop productivity has remained stagnant at around 600-789 kg/ha. The low yields in pigeonpea are due to many factors like decreasing per capita availability of pulses over the growing years, lack of high yielding varieties, better quality, disease and insect resistant varieties etc. The lack of high yielding cultivars alone has been identified as the major constraint underlying the stagnant productivity. Pigeonpea is unique among legumes as its floral morphology allows both self as well as insect-aided natural out crossing that range from 20 to 70% and vary from one place to another (Saxena *et al.* 1990). Efforts have been made in past to increase the average productivity by developing high yielding varieties. In spite of release of over 100 good varieties, yield levels did not increase significantly (Saxena, 2006b). In this endeavour, the use of hybrid pigeonpea technology has

potential. The stable male-sterility system in conjunction with natural out-crossing will make the hybrid pigeonpea seed production easy and affordable.

The phenomenon of male-sterility was recorded as early as by Kolreuter (1763) where the plants are unable to reproduce through natural means because of their defective male-reproductive parts. Such plants reproduce only when fertile pollen from other plants is placed on the stigmatic surface of the male-sterile flowers through any mechanical means such as deliberate manual efforts, wind or insects. Male-sterility has been successfully used for enhancing yield in a number of cereal and vegetable crops. In food legumes, this technology could never been used either due to non-availability of natural out-crossing system, or an efficient male-sterility system or both. The development of commercial hybrid pigeonpea programme was initiated at ICRISAT in collaboration with ICAR (Indian Council of Agricultural Research). In 1974, a source of genetic male-sterility (GMS) was identified. The hybrid breeding programme using the improved genetic male sterility (GMS) lines resulted in the release of the world's first commercial pigeonpea hybrid ICPH-8 [MS Prabhat (DT) x ICPL 161] in 1991 in India (Saxena *et a*l. 1992). It is considered an important milestone in the history of crop breeding as ICPH 8 is the first ever-commercial hybrid released in any food legume in the world. However, the hybrid seed production with a genetically determined male-sterile sibs, time and labour intensive, accounting for 40-50% of the seed production cost (Muthiah *et al*. 1998).

To develop a CMS system, the pigeonpea genome was inserted into the cytoplasm of wild *cajanus* species through hybridization and backcrossing. It was believed that the interaction between wild cytoplasm and cultivated nuclear genome would result in male sterility effect. So far, eight such CMS systems have been bred (Table 1.1) in pigeonpea with varying degrees of success (Saxena *et al*., 2010). Of these, A2, A4 and A6 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). In the meantime, ICRISAT developed a number of experimental hybrids and tested in multi-location trials. They also developed genetically diverse CMS lines and their fertility restorers for developing widely adaptable hybrids to different agro-ecological areas and cropping systems. Among the medium duration hybrids with A4 cytoplasm, ICPH 2671 and ICPH 2740 are very promising in multi-location trials conducted for four years. During 2009, the best performing hybrid ICPH 2671 was evaluated in 1248 on-farm trials in four states of India (Saxena *et al*., 2010). In these trials ICPH 2671, recorded 28.4% yield superiority over local checks in farmer's fields and ICPH 2671 was released in Madhya Pradesh for commercial cultivation in 2010 (Saxena *et al.,* 2013).

Because pigeonpea is cultivated under diverse environments and cropping systems with specific maturity and plant-type requirements, the CMS trait from ICPA 2039 (A4 cytoplasm) was transferred to extra-early (ICPA 2089), early (ICPA 2039), and late maturing (ICPA 2043) lines to facilitate the development of hybrids in diverse maturity groups for different agro climatic zones. Efforts are being made at ICRISAT to develop new and promising CMS lines as well as restorers for use in hybrid pigeonpea research.

Recognizing the importance of hybrids in enhancing yield up to considerable extent, the present research work was taken up with the following objectives:

1. To study character association among various yield and yield contributing characters in pigeonpea.
2. To study the extent of fertility restoration in the hybrids derived from newly developed CMS lines.
3. To study extent of heterosis for yield and yield components in CMS-based pigeonpea hybrids.

# CHAPTER-II

# REVIEW OF LITERATURE

A literature review is an account of what has been published on a topic by accredited scholars and researchers. In writing the literature review, our purpose is to convey to our reader what knowledge and ideas have been established on the topic, and what are their strengths and weaknesses. The literature available on various aspects of the present investigation has been reviewed under the following heads:

**2.1 Character association**

**2.2 Fertility restoration**

**2.3 Heterosis in pigeonpea**

## 2.1 Character association studies

### 2.1.1 Correlation studies

Genetic improvement of yield is the primary concern to plant breeder as yield is a complex, quantitatively inherited character and is highly influenced by the environment. On the contrary, the yield component traits are not only less complex and relatively simply inherited and are influenced much less due to environmental deviations. Thus, effective improvement in yield may be brought about through selections in yield components (Grafius, 1956 and Srivastava *et al.*, 1972). Yield component characters show associations among themselves and with yield. Unfavorable associations between the desired attributes under selection may limit genetic advance. Hence, study of associations of component characters with yield enables a plant breeder to know how improvement of one character will bring about simultaneous improvement in other characters and aid in planning of an effective selection programme. Hence, a brief review of literature is presented hereunder.

Dahiya *et al*. (1976) found that grain yield and protein content were negatively correlated in $F_2$ plants from crosses between low to high protein content

lines. Grain yield and protein yield were highly correlated. It is suggested that for total protein production per unit area efforts should be directed towards increase seed yield while maintaining percent protein near average levels rather than by selecting for high protein in the grains alone.

Asawa *et al*. (1981) stated that yield was positively correlated with secondary branches, pods plant$^{-1}$, seeds plant$^{-1}$ and days to maturity.

Balyan and Sudhakar (1985) reported that seed yield plant$^{-1}$ had positive and significant association with plant height, days to maturity, primary branches, secondary branches, pods plant$^{-1}$, seeds pod$^{-1}$ and 100 seed weight in pigeonpea.

Saxena *et al*. (1986) noted that correlation coefficients among the crosses ranged from -0.30, ($P < 0.01$) to + 0.28 ($P < 0.01$). Of the five crosses examined, two had significant negative correlations, one showed a significant positive correlation, while in the remaining two crosses, no significant association was detected between seed size and protein percentage.

Bhongale and Raut (1987) found that plant height; branches plant$^{-1}$, pod number, pod weight and seeds per pod were positively correlated with each other and with seed yield in pigeonpea.

Angadi *et al*. (1988) noted that pod yield was significantly correlated with seed yield, pods plant$^{-1}$, days to 50% flowering and plant height.

Balakrishnan and Natarajaratnam (1989) revealed that seed yield had a positive correlation with number of pods plant$^{-1}$ and pod setting in pigeonpea genotypes. Among the yield components, 100 seed weight was positively correlated with number of pods plant$^{-1}$.

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

Paul and Upadhaya (1991) found the positive correlation of yield per hectare with total number of branches plant$^{-1}$, number of pods plant$^{-1}$, number of

pods per cluster and yield plant$^{-1}$ in pigeonpea. The correlation between number of pods plant$^{-1}$ and yield plant$^{-1}$ was found to be positively significant and the length of pod was significant but negatively correlated with yield plant$^{-1}$ as well as with the number of pods plant$^{-1}$.

Dhameliya *et al.* (1994) reported significant and positive association of seed yield with plant height and pods plant$^{-1}$, whereas significant and negative association of seed yields with pod length and seeds per pod in pigeonpea genotypes. They also reported that days to 50% flowering, days to maturity, plant height, primary branches plant$^{-1}$, pod length, seeds per pod and 100 seed weight were highly correlated with one another.

Salunke *et al.* (1995) observed in a study of 54 diverse genotypes of pigeonpea that seed yield was significantly and positively associated with pods plant$^{-1}$, primary and secondary branches, plant spread, plant height and 100seed weight. It had a strong negative association with seeds per pod. The yield components like days to 50% flowering, days to maturity, plant height, plant spread, number of primary and secondary branches and 100-seed weight were positively associated with each other.

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

Chandrakala and Raveendran (1998) reported that seed yield was significantly and positively correlated with number of branches plant$^{-1}$, pods plant$^{-1}$, clusters plant$^{-1}$, seeds per pod and 100-seed weight in pigeonpea.

Vikas and Singh (1998) found that seed yield plant$^{-1}$ had positive and significant correlation with days to 75% flowering and number of pods plant$^{-1}$ in extra early semi determinate group and with days to maturity in early indeterminate group of pigeonpea.

Srinivas *et al.* (1999) reported that seed yield plant$^{-1}$ had significant and positive association with plant height, number of primary branches, secondary branches and pods plant$^{-1}$ in pigeonpea.

Basavarajaiah *et al.* (1999) studied 81 genotypes of pigeonpea and their association studies indicated significant positive correlation of seed yield with pods plant$^{-1}$ and branches plant$^{-1}$.

Pandey and Singh (2001) observed positive correlations for seed yield per plot, with seed yield plant$^{-1}$ at both genotypic and phenotypic levels in pre-*rabi* pigeonpea and positive and significant association between plant height at initial flowering, maturity and harvest index was observed 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 plant$^{-1}$ had significant positive relationship with number of pods plant$^{-1}$, number of clusters plant$^{-1}$, 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 plant$^{-1}$, pod length, plant height and days to maturity had significant positive association with yield.

Jogendra Singh *et al.* (2008) studied 29 genotypes of pigeonpea and reported that seed yield plant$^{-1}$ exhibited positive and significant correlation with pods plant$^{-1}$ 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 plant$^{-1}$ 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 plant$^{-1}$, pods plant$^{-1}$ and days to maturity.

Sodavadiya *et al.* (2009) observed that genotypic correlation coefficients were higher than phenotypic correlation coefficients in pigeonpea. The seed yield plant$^{-1}$ had significant and positive association with days to 50% flowering, days to maturity, number of branches plant$^{-1}$, pods plant$^{-1}$ and 100-seed weight at both genotypic and phenotypic levels.

Bhadru (2010) reported that seed yield was significantly and positively associated with days to 50% flowering, plant height, primary and secondary branches plant$^{-1}$ and pods plant$^{-1}$ in pigeonpea.

Mittal *et al*. (2010) noted that seed yield was positively associated with plant height, branches plant$^{-1}$, pods plant$^{-1}$ and harvest index in pigeonpea genotypes.

Hamid *et al*. (2011) evaluated one hundred germplasm lines of pigeonpea and noted high strong and positive correlation of seed yield with pods plant$^{-1}$ followed by pod length.

Rama Devi *et al*. (2012) noticed that seed yield plant$^{-1}$ had significant positive correlation with plant height, pods plant$^{-1}$ and harvest index in pigeonpea.

Udensi and Ikpeme (2012) studied the correlation results, revealed that there was significant positive correlations between plant height and number of leaves plant$^{-1}$, leaf area plant$^{-1}$ and number of seeds plant$^{-1}$. It also showed that the number of leaves plant$^{-1}$ was positively correlated with the pod length plant$^{-1}$ and number of seeds plant$^{-1}$. Additionally, pod length plant$^{-1}$ correlated positively with the number of seed plant$^{-1}$ while number of nodules plant$^{-1}$ correlated positively with 100seed weight. Additionally, genotypic correlation coefficient with yield showed very high coefficients, especially for pod length plant$^{-1}$, 100-seed weight, number of leaves plant$^{-1}$, plant height plant$^{-1}$and leaf area plant$^{-1}$, respectively. Number of nodules plant$^{-1}$ had the lowest genotypic correlation coefficient followed by number of flowers plant$^{-1}$.

Birhan *et al.* (2013) reported that correlation coefficient results revealed that seed yield had positive and significant phenotypic and genotypic association

with plant height, biomass yield plant$^{-1}$, pods plant$^{-1}$, seeds plant$^{-1}$, days to maturity, and days to flowering and seeds per pod.

Saroj *et al.* (2013) found that phenotypic and genotypic variances, correlation and path coefficient, heritability and genetic advances were estimated for grain yield and yield traits in 70 pigeonpea genotypes. The highest GCV was recorded for number of secondary branches plant$^{-1}$ followed by pods/plant. Correlation and Path coefficient analysis (genotypic and phenotypic) revealed that pods plant$^{-1}$, 100-seed weight, days to 50% flowering, primary branches and secondary branches had maximum direct effect resulted significantly positive correlation with grain yield plant$^{-1}$. These traits can be used to improve the grain yield of pigeonpea.

Guruvendra Reddy *et al.* (2014) found that seed yield plant$^{-1}$ was observed to be significantly and positively associated with days to maturity, plant height, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$ and number of pods plant$^{-1}$ indicating their importance as selection criteria in pigeonpea yield improvement programmes.

### 2.1.2 Path coefficient analysis

Knowledge on the association of quantitative characters, especially yield and its attributes will be of immense practical value in crop improvement programme. Correlation, which is the primary tool of a plant breeding programme only provides the degree of association of the characters, while path coefficient analysis which is a standard partial regression coefficient, measures the direct influence of one variable upon another and permits the separation of correlation coefficient into components of direct and indirect effects (Dewey & Lu, 1959). Direct selection for yield is not a reliable approach since it is highly influenced by the environment. Therefore, it is essential to identify the component characters through which yield can be improved. Thus, correlation in conjunction with path analysis would give better insight into the cause and effect relationship between

different character pairs. The available literature on path coefficient analysis is furnished here under.

Dumbre *et al.* (1985) revealed that days to 50% flowering had highest positive direct effect on seed yield followed by number of pods plant$^{-1}$, 100-seed weight and plant height in pigeonpea. The indirect effects via these traits were also positive for all traits except seeds per pod, which had negative indirect effect via 100-seed weight.

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

Angadi *et al*. (1988) noticed that pod yield was the only character with a direct effect on seed yield in pigeonpea. Characters like pods plant$^{-1}$, plant height, branches plant$^{-1}$ and days to flower influenced seed yield through pod yield, which alone had direct influence on seed yield.

Balakrishnan and Natarajaratnam (1989) found that pods plant$^{-1}$ had the highest positive direct effect on seed yield followed by harvest index and dry matter efficiency in pigeonpea genotypes.

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

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

Salunke *et al.* (1995) noticed that pods plant$^{-1}$, seeds per pod, and 100-seed weight had direct positive effects on seed yield. The pods plant$^{-1}$ and 100-seed weight also exhibited high positive indirect effects on seed yield through most of the other characters. It was suggested that pods plant$^{-1}$, seeds per pod and 100-seed weight could prove useful as selection criteria for early pigeonpea.

Paul *et al.* (1996) revealed that out of six independent characters having positive direct effect on seed yield, maximum contribution was number of pods plant$^{-1}$, followed by dry matter at maturity and 100-seed weight in pigeonpea.

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

Musaana and Nahdy (1998) indicated that pod clusters plant$^{-1}$, pods plant$^{-1}$, seeds per pod and seed weight were the main yield components having maximum direct effects on yield in pigeonpea genotypes.

Chandirakala and Raveendran (1998) in their studies on 13 Pigeonpea genotypes reported that 100-seed weight had the highest positive direct effect on seed yield followed by number of pods plant$^{-1}$ and number of clusters plant$^{-1}$. Number of branches plant$^{-1}$, number of pods plant$^{-1}$, number of clusters plant$^{-1}$, number of seeds per pod and 100-seed weight also showed high positive indirect effect on seed yield.

Vikas and Singh (1998) revealed that days to 75% flowering and days to maturity had positive direct effect on seed yield at both genotypic and phenotypic levels in pigeonpea.

Srinivas *et al.* (1999) observed high and positive direct effect of pods plant$^{-1}$, plant height and secondary branches on seed yield in pigeonpea.

Basavarajaiah *et al.* (1999) evaluated 81 pigeonpea genotypes and reported that plant height, branches plant$^{-1}$ and pods plant$^{-1}$ showed maximum direct effects on seed yield.

According to Chattopadyay and Dhiman (2005), the plant height and number of seeds per pod contributed positive and direct effect on seed yield in pigeonpea.

Mittal *et al.* (2006) found from a study of 21 diverse progenies of pigeonpea the seeds per pod, followed by pods plant$^{-1}$ and plant height had high positive direct effect on seed yield.

Baskaran and Muthiah (2007) reported that pods plant$^{-1}$, 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 27genotypes.

Mahajan *et al. (*2007) evaluated nine pigeonpea genotypes and reported that maximum direct positive and negative contribution to yield was observed from pods plant$^{-1}$ 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 plant$^{-1}$.

Jogendra Singh *et al.* (2008) noticed from their path coefficient studies of 29 pigeonpea genotypes that pods plant$^{-1}$, 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 plant$^{-1}$ 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 plant$^{-1}$ through most of the characters.

Bhadru *et al*. (2010) studied 27 accessions of pigeonpea and noticed that days to 50 % flowering, plant spread, primary and secondary branches plant$^{-1}$, number of pods and raceme length had moderate to low direct effect on seed yield.

Mittal *et al*. (2010) reported that branches plant$^{-1}$ had maximum direct effect followed by pods plant$^{-1}$ and seeds per pod upon seed yield plant$^{-1}$. Branches plant$^{-1}$ and pods plant$^{-1}$ 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 plant$^{-1}$.

Sreelakshmi *et al.* (2011) in their studies on pigeonpea genotypic path analysis revealed that number of primary branches plant$^{-1}$ exhibited maximum direct effect on seed yield, days to 50 % flowering and number of pods plant$^{-1}$.

Rama Devi *et al.* (2012) noticed that pods plant$^{-1}$ had the highest positive direct effect on seed yield followed by days to flowering, plant height and pod length. It indicates that these characters should be given due importance while making selection for increased seed yield in pigeonpea.

Yogesh Kumar Nag and Sharma (2012) revealed from their studies on 45 pigeonpea genotypes that number of pod clusters plant$^{-1}$ had the highest positive direct effect on seed yield, while number of pods plant$^{-1}$ and days to maturity had the highest indirect effect on seed yield.

Udensi and Ikpeme (2012) reported that path coefficient results showed that 100-seed weight had the highest direct effect on yield, which was positive. This was followed by the pod length plant$^{-1}$, number of leaves, and leaf area while plant height had negative direct effect but very high. Number of pods plant$^{-1}$ had the lowest direct effect on yield.

Birhan *et al.* (2013) found that correlation coefficients and path coefficients (partitioned into direct and indirect effects) were estimated on 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 plant$^{-1}$ whereas; genotypic path analysis revealed that, maximum direct effect on seed yield was exerted by days to flowering and reproductive phase followed by seeds plant$^{-1}$ and plant height. Thus, seeds plant$^{-1}$ and plant height were the potent contributor to seed yield that could be used as indirect selection criteria.

Kuma *et al.* (2013) noticed from their path analysis of 27 genotypes of pigeonpea showed that harvest index had high positive direct effect on seed yield followed by biological yield plant$^{-1}$ and days to 50% flowering. The present study indicated that harvest index, biological yield plant$^{-1}$ and days to 50% flowering are important characters in deciding the grain yield plant$^{-1}$.

Guruvendra Reddy *et al*. (2014) reported that negligible direct effects on seed yield plant$^{-1}$ was recorded by days to maturity and plant height. However, their association with seed yield plant$^{-1}$ was observed to be significant and positive indicating a major role of indirect effects. In addition, days to 50% flowering had recorded high negative direct effects on seed yield plant-1. Association of this trait with seed yield plant$^{-1}$ was however, non-significant indicating the indirect effect of this trait, mostly through days to maturity on seed yield plant$^{-1}$.

Singh and Singh (2016) found from this study of segregating and non-segregating pigeonpea populations namely parents, $F_1$s and $F_2$s. In parents pods plant$^{-1}$ were positively and significantly associated with seed yield. However, harvest index, number of secondary branches and 100- seed weight exhibited comparatively higher correlation values with seed yield through they were non-significant. In $F_1$s, seed yield was positively and significantly correlated with pods per plant whereas number of secondary branches, harvest index and number of primary branches though had high correlation values with seed yield but were observed to be non-significant. In $F_2$s populations, pods plant$^{-1}$ and plant height revealed positively significant associations with seed yield whereas 100-seed weight, seeds pod$^{-1}$ and harvest index had positive and high correlation values with seed yield but were statistically non-significant.

**2.2 Fertility restoration**

The various approaches considered with continued attention to break the existing yield barriers in pigeonpea to feed the increasing population, hybrid technology is considered as one of the promising, sustainable and eco-friendly technologies. Impressive progress and success made by ICRISAT in this regard has encouraged the global pigeonpea production and productivity by adopting the CMS-based hybrid technology. Presence of exploitable hybrid vigour, availability of cytoplasmic nuclear male sterility and fertility restoration system and sound seed production techniques are the pre-requisites for the success of any hybrid breeding programme. In the exploitation of heterosis from potential crosses, the level of fertility restoration would likely be the key for added yield advantages. As

a result, a precise understanding of the fertility restoration is necessary for improving the efficiency and quality of restorers used in hybrid pigeonpea breeding. The literature on fertility restoration in pigeonpea is briefly reviewed here under:

Dundas *et al*. (1981) studied microsporogenesis in genetic 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.

Reddy *et al*. (2000) noted that hybrids between *Cajanus cajan* × *C. reticulates* var.*gradifolius.* Moreover, reported that meiotic cells of the hybrid had quadrivalents, trivalents, univalents and showed chromosome pairing as revealed by the increased number of rod bivalents per cell at metaphase-I and stickiness and precocious movement of chromosome to poles in the second division. Further, the hybrids, comparison to parents, had fewer pods and seeds.

Mallikarjuna and Saxena (2002) in their study found that the interspecific hybrid seed obtained by cross between *Cajanus acutifolius* and *Cajanus cajan* were semi shriveled. Very few seeds germinated to give rise to $F_1$ plants. Backcrossing of the hybrid plants was done by saving the aborting embryos in vitro. The $BC_1$ plants thus produced showed normal meiotic pairing, but had low pollen fertility. The reason for embryo abortion and low pollen fertility in spite of normal meiosis was attributed to the effects of wild species cytoplasm.

Saxena and Kumar (2003) assessed the fertility restoration system in A2 cytoplasm of pigeonpea. They developed the crosses between 3 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 genetic 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 genetic male sterile line GT20 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) reported that 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) noticed 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 short-duration experimental hybrid, which exhibited 77.5 % yield advantage over the control cultivar UPAS 120.

Singh *et al.* (2006) examined two cytoplasmic genetic male sterile (CMS) 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 and selfed for a few more generations to obtain the perfect line. However CMS 1024A appeared to have a mutated gene 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*. (2008) noted that fertility restoration in cytoplasmic-nuclear male sterile 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. 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).

According to Nadrajan *et al*. (2008) 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 % across the three cytoplasmic sources, namely, $A_1$, $A_2$ and $A_4$.

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 $F_1$s evaluated, the 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.

Lay 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 F: 3 PF: 1 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*. (2011a) observed 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.

Saxena *et al.* (2011b) studied one extra-early (120 days), two early (150 days), and two late mature (180 days) pigeonpea hybrids to generate information on the genetics of fertility restoration of the A4 CMS system. In the extra early

maturing hybrids, a single dominant gene controlled pollen fertility, whereas in the early and late-maturing hybrids, two duplicate dominant genes governed male fertility.

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.

Guruvendra reddy *et al.* (2015) studied pollen fertility in the hybrids was noticed to range from 42.5 (ICPH 4181) to 96.0 (ICPH 2671) with an average of 83.1. Based on pollen fertility % of the hybrids, R lines of 24 hybrids studied in the present investigation were categorized for fertility restoration % in their hybrids. A perusal of these results revealed ICPL 20098, ICPL 20123, ICPL 20137, ICPL 87119 to be good restorers with more than 80 % fertility restoration in their hybrids, while ICPL 20108 and ICPL 20186 were noticed to be partial restorers with extent of fertility restoration between 10-80 % in their hybrids.

Sunil chaudhary *et al*. (2015) reported that the extent of pollen fertility among hybrids ranged from 58.5% to 98.3% across locations. High pollen fertility indicated higher fertility restoration and vice versa. Among hybrids, the highest pollen fertility was recorded in ICPH 2740 (96.5%) at Patancheru, whereas ICPH 2671 recorded the highest pollen fertility (96.2% and 95.9%) at Ranchi and Sehore.

Choudhary and Singh (2015) noted that variable expression of fertility restoration could be attributed to different genetic backgrounds of the F1 plants, arising from male parents of different genetic constitution. Alternatively, differences observed in segregation patterns also could be due to the presence of some modifier genes that influence the process of penetrance and expressivity of the fertility-restoring genes.

Sudhir Kumar *et al*. (2016) found that the restoring capacities of restorer lines are very important to quality seed production and for yield potential. The variability for pollen fertility ranged from 59.22 to 99.76%. Among the hybrids, ICPA 2047 x ICPL 20108 recorded maximum pollen fertility (98.50%) followed by ICPA 2078 x ICPL 87119 (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%).

**2.3 Heterosis in Pigeonpea**

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 is 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. The 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, several workers for grain yield and other economic characters have reported a considerable amount of hybrid vigour with the mid-parent, standard variety and better parent. The literature related to heterosis studies has been provided hereunder.

Solomon *et al*. (1957) were the first to report a study on heterosis in pigeonpea. Hybrid vigour up to a maximum of 24.5% 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.

Shrivastava *et al*. (1976) noted heterosis in pigeonpea. They studied heterosis in 17 $F_1$ hybrid combinations involving 14 genotypes of pigeonpea. Heterotic effects were analyzed for yield, its components and some growth factors. Mean heterosis of 67% was obtained for seed yield, 96% for secondary branches and 80% for number of pods plant$^{-1}$. In general, medium x medium and low x medium crosses had resulted in high heterotic performance indicating that genetic diversity was the key to obtaining hybrid vigour.

Patel *et al*. (1991) reported high degree of standard heterosis for various morphological physiological traits in short and medium duration genetic male-sterility based pigeonpea hybrids. Short duration hybrid, MS Prabhat x DL 78-1 showed 71.9% standard heterosis and it was due to significant and positive heterosis for morpho-physiological traits such as plant height, harvest index, per day productivity and reproductive period. Hybrid MS 3A x ICPL 8504 in medium group had highest heterosis (74.90%) over standard variety S5 and BDN 2, respectively. In medium duration group, delayed flowering, taller plant height and high per day productivity were observed and were attributed as the main cause of high heterotic response noticed for seed yield plant$^{-1}$.

Saxena *et al.* (1992) stated that GMS hybrids showed 25-30% heterosis for seed yield in farmer's fields with wide adaptation, but various seed production difficulties and seed quality concerns did not permit commercialization of these hybrids.

Patel and Patel (1992) reported heterosis in 30 hybrids derived from six lines and five testers in pigeonpea for yield and important yield contributing traits. Maximum heterosis response over better parent was obtained for number of pods plant$^{-1}$ (169.31%) and it was followed by seed yield plant$^{-1}$ (136.49%). None of the hybrids exhibited significant heterobeltiosis in any direction for pod length and seeds pod$^{-1}$.

Gumber and Singh (1996) studied the phenomenon of heterosis in pigeonpea crosses involving genotypes of three different growth habits (DT: determinate; SDT: semi determinate, and IDT: indeterminate). They observed that heterosis over better parent was from -16.3 to 19.3% for seed yield plant$^{-1}$, 36.0 to 78.0% for plant height and -4.0 to 20.30% for pods plant$^{-1}$. They also indicated that, the cross combinations involving parents of different growth habits expressed greater heterosis while the cross combinations involving parents of similar growth habit (DTxDT or IDTxIDT) exhibited low heterosis over better parent.

Srinivas (1996) in his studies in pigeonpea reported that expression of heterosis was most evident for yield plant$^{-1}$, pods plant$^{-1}$ and number of secondary

branches. Further, maximum heterosis was reported in mid-late x medium crosses, followed by early x medium crosses. The hybrids, ICP MS 288 x ICP 7349, ICP MS 3783 x BDN1, ICP MS3783 x LRG 30 and ICP MS 3783 x ICP 8863 were identified as promising heterotic hybrids for commercial exploitation.

Kumar and Srivastava (1998) studied heterosis in relation to combining ability in a line x tester mating design involving three male sterile lines and 12 male fertile lines of long duration pigeonpea for yield and its components. Heterosis over better parent for seed yield ranged from -77.91 to 110.07 %. Pods plant$^{-1}$ and primary branches plant$^{-1}$ contributed substantially towards the expression of heterosis for seed yield.

Hooda *et al*. (1999) provided information on heterosis of pigeonpea in seven yield related traits in the parents and 40 hybrids from a four line × ten tester crosses. Maximum heterosis over the best standard check (Manak) was obtained for pods plant$^{-1}$ in crosses Qms1 × TAT10 (38.1%), Qms1 × H88-22 (32.9%) and MS Prabhat (DT) × H88-43 (28.9%). For seed yield plant$^{-1}$, a good magnitude of heterosis ranging from 21.1 to 28.9 % was observed.

Khorgade *et al*. (2000) reported heterosis over mid-parent and control cultivar (BDN 2) in 24 pigeonpea hybrids. Significant heterosis was observed for seven quantitative characters studied. Significant heterosis over the mid-parent and control cultivar was recorded for seed yield plant$^{-1}$ in the hybrids AKMS 11 × AKT 9221, AKMS 11 × C11, and AKMS 21 × C11.

Chandirakala and Raveendran (2002) found heterosis for yield and yield components in 30 pigeonpea hybrids. Crosses with MS Prabhat DT showed marked heterosis for number of pods plant$^{-1}$, number of clusters plant$^{-1}$, 100-grain weight, and grain yield plant$^{-1}$. Significant negative heterosis over mid, better, and standard parents were observed in MS Prabhat DT × ICPL 88009 and MS CO 5 × ICPL 88009 for days to 50% flowering, and in MS Prabhat DT × ICPL 87104, MS Prabhat DT × ICPL 89020, MS Prabhat DT × ICPL 90012, and MS CO 5 × ICPL 87104 for plant height.

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 $plant^{-1}$ 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 heterosis of pigeonpea for yield and its related traits. In their research finding, 20 to 49.8% of standard heterosis was observed for primary branches $plant^{-1}$ in all the hybrids, except MS UPAS 120 x Pant A 134. For seed $pod^{-1}$, significant positive heterosis was observed in seven hybrids. Number of pods $plant^{-1}$ 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) crossed in a line x tester mating design. Heterosis was observed for most of the traits, except plant height. The cross AKMS 11 × AKT 9221 showed highest seed yield $plant^{-1}$ 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 that the range of heterosis for MP and BP 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 $plant^{-1}$, and -0.95 to 3.35% and -3.0

to 2.5% for secondary branches plant$^{-1}$. For number of pods plant$^{-1}$, 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 plant$^{-1}$, the range of heterosis over better parent 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) were recorded for seed yield plant$^{-1}$ in hybrid VBN 1 × ICPL 83027 (81.74%, 66.57% and 68.36%) followed by CO 5 × 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 relative heterosis and heterobeltiosis in 45 pigeonpea hybrids for days to 50% flowering, maturity, plant height, number of branches plant$^{-1}$, number of clusters plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, pod length, 100-seed weight and single plant yield. ICP 13201 × CO5 was the best with maximum heterosis for most of the yield attributing characters, followed by ICP 11961 × ICP 7118 and ICP 11961 × CO5, which showed higher heterobeltiosis and relative heterosis for most of the yield-attributing characters.

Wanjari *et al*. (2007) evaluated 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.

Hershey *et al*. (2007) from ICRISAT released the world's first pigeonpea hybrids based on the cytoplasmic male sterility system. The hybrids developed at ICRISAT have shown 30 to 150% yield advantage. The hybrids also produce

30.40% more root mass that makes them more drought resistant. The seed producers have adopted the adoption of hybrid technology and at present 22 private and 3 public seed, companies have adopted the technology. In 2007, a total of 250,000 kg of hybrid seed is being produced. This will bring about 50,000 ha land under hybrid cultivation.

Dheva *et al*. (2008a) reported heterosis in CMS based pigeonpea hybrids. The highest heterosis was observed for number of pods plant$^{-1}$ (79.43%) followed by grain yield plant$^{-1}$ (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% for heterosis over the mid parent, better parent and standard check. Among these, three hybrids showed heterosis more than 40% for number of pods and grain yield plant$^{-1}$. The range of heterosis over check for number of pods plant$^{-1}$ is 0.84 to 87.68% and 0.72 to 57.35% for grain yield.

Kumar and Krishna (2008) noted that 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 plant$^{-1}$ on the basis of their high heterosis 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 plant$^{-1}$, 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 pod$^{-1}$. 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 plant$^{-1}$, followed by pods plant$^{-1}$ and number of fruit bearing branches. Comparatively, the other yield components showed low average heterosis values. In general, early × late and medium × late combinations resulted in high heterosis for yield.

Dheva *et al*. (2009) reported heterosis in 31 hybrids. Three hybrids showed heterosis more than 40% for the number of pods and grain yield plant$^{-1}$, respectively. The highest standard heterosis was observed for the number of pods plant$^{-1}$ followed by grain yield plant$^{-1}$. The range of heterosis over check for number of pods plant$^{-1}$ was observed to be from 0.84 to 87.68% and the heterosis over check for the character grain yield plant$^{-1}$ was noticed range from 0.72 to 57.35% in desirable direction.

Kumar *et al*. (2009) reported heterosis of pigeonpea for yield and its component traits. Significant and positive heterosis over better parent and standard check for seed yield plant$^{-1}$ in four crosses was accompanied by significant and high positive heterosis for number of primary branches plant$^{-1}$, number of pods plant$^{-1}$, number of pod clusters plant$^{-1}$ and 100 seed weight. This study suggested that heterosis for yield should be through component trait heterosis. Hybrid vigour of individual yield components may have additive or synergistic effect on yield.

Phad *et al*. (2009) reported heterosis in pigeonpea by using 60 crosses in four different environments. 10 cross combinations recorded significant positive standard heterosis for number of secondary branches plant$^{-1}$, whereas nine cross combinations recorded standard heterotic effect for plant spread, number of primary branches plant$^{-1}$ and number of pods plant$^{-1}$. 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.

Sarode *et al*. (2009) estimated heterosis in long duration pigeonpea for yield and yield traits using five lines and three testers. Maximum standard heterosis was recorded in the cross Pusa 9 × Bahar (52.11%), followed by Pusa 9 × ICPL 84023 (44.17%) and DA 11 × Bahar (42.03%) for number of pods plant$^{-1}$. Hybrid Pusa 9 × Bahar exhibited maximum economic heterosis (55.32%) for 100-seed weight, number of seeds pod$^{-1}$, pods plant$^{-1}$ and number of primary and secondary branches.

Chandirakala *et al*. (2010) studied 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. 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 genic male sterile line MS Prabhat DT was greater as compared to the lines, MS Prabhat NDT and MS CO5.

Shoba and Balan (2010) studied the magnitude of heterosis in 27 early maturing hybrids. They observed that 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 plant$^{-1}$(106.0%), seed protein content (22.71%) and single plant yield (40.0%). MS CO5 x ICPL 83027 had also exhibited significant standard heterosis for plant height (98.38%), number of branches plant$^{-1}$(128.2%), number of pods plant$^{-1}$(110.0%), number of seeds pod$^{-1}$ (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% standard heterosis. Hybrid ICPH 3461 was found suitable for one environment with 42.0% standard heterosis. In on farm trials, hybrid ICPH 2671 was 11.9 to 53.1% superior in yield

over the control. The other promising hybrid ICPH 2740 also exhibited 70.0% standard heterosis in an on-farm trial.

Wanjari *et al*. (2012) stated that India is a world leader in exploitation of heterosis in $F_1$ hybrids in different crops and vegetables. pigeonpea is often cross pollinated species and with availability of male sterility and hence it is amenable for $F_1$ hybrid breeding. Initial efforts in hybrid development in pigeonpea started in the 1980's with genetic male sterility (GMS) but for more than past two decades, the thrust was on hybrids based on cytoplasmic genetic male sterility (CMS). Among five different available sources of cytoplasmic male sterility, namely, A1 to A5, only A2 and A4 have been used in hybrid pigeonpea breeding. A wide range of variation in maturity, plant type etc. is now available in the CMS lines and fertility restorers (FR). Encouraging performance of the hybrids in evaluation trials has been recorded. Heterotic hybrids like AKPH 11303 and AKPH 11324 having more than 30% yield superiority will be useful for commercial exploitation.

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 recorded highest values for mid-parent heterosis and heterobeltiosis for plant height, number of primary and secondary branches plant$^{-1}$, number of pods plant$^{-1}$ and 100-seed weight.

Patil *et al*. (2014) noticed standard heterosis in obcordate CMS based crosses over control ICPL 87119(Asha), hybrid cross ICPA 2200 x ICPL 20108 expressed significant negative heterosis for maturity. Plant height has significant increase in hybrid cross ICPA 2202 x ICPL 20108. Number of seeds/pod showed significant heterosis (11.1%) in hybrid crosses ICPA 2202 x ICPL 20093 and ICPA 2208 x ICPL 20108.In their study per se performance, high positive heterosis was revealed for crosses ICPA 2208 x ICPL 20108(60.4%), ICPA 2203 x ICPL 20116 (55.8%) and ICPA 2204 x ICPA 20093 (50.1%) with seed yield of 1649, 1604 and 1544 kg/ha respectively. Their study it was clear from yield data, which obcordate

leaf shape of A-lines has no effect on the per se performance of hybrid combinations.

Tikley *et al.* (2016) stated that the manifestation of relative heterosis indicated the over dominance for yield and yield related traits. The maximum heterotic effects for branches per plant (108,141%), pods per plant (127%), seed yield (37, 42%).The hybrid ICP 2043 x ICP 87119 expressed highest heterotic effect of 42.1%, followed by the hybrid ICP 2043 x ICP 20108(36.9%) could be utilized in heterosis breeding programmes.

Sudhir Kumar *et al*. (2016) reported that heterosis for seed yield in hybrid pigeonpea were depends upon all yield contributing characters including pollen fertility percentage. So for fully exploitation of heterosis, hybrid with good pollen fertility is needed.

# CHAPTER-III

# MATERIALS AND METHODS

The present investigation entitled **"Identification of heterotic combinations, using obcordate leaf shape CMS lines in Pigeonpea [*Cajanus cajan (*L.) Millspaugh]''** was carried out to obtain information on character associated with yield, the extent of fertility restoration and heterosis of parental lines and CMS based hybrids in Pigeonpea. The present study was conducted during *kharif* 2015 at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru ($17^o$ 53'N latitude and $78^o$ 27'E longitude, at an altitude of 545.0 m above mean sea level) which falls under the Moderate (997.59 mm) rainfall Agro-climatic zone of Telangana. The detail about environment was given in the table 3.1. 14 $F_1$ hybrids, 4 B-lines 5 R-lines and 5 standard checks.

## 3.1 Materials

The experimental material of present investigation comprised of 14 $F_1$ hybrids, 4 B-lines, 5 R-lines and 5 standard checks obtained from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru. The details of this climate, B, R lines and pedigree of hybrids were presented in tables 3.1, 3.2 and 3.3.

## 3.2 Methods

### 3.2.1 Experimental layout

The material consisting of 14 $F_1$ hybrids, 4 B-lines, 5 R-lines along with five standard checks were evaluated in a randomized complete block design with three replications in three contiguous blocks. The experimental materials were sown at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, on July 14, 2015. Popular varieties, Asha, Maruti, Rajeevlochan, ICPH 2740 and ICPH 2671 were used as standard checks. The plot size for each $F_1$ hybrid, B-lines and R-lines was two rows. Two-row plots were planted with 4 m length with inter and intra row spacing of 75 and 50 cm, respectively. Border rows were planted around the experimental plot to increase the precision of study and to reduce border

effect. All recommended agronomic practices were followed for parents and hybrids to keep the crop in good condition. Necessary and need based plant protection measures were also taken up to maintain a healthy crop.

**Table 3.1: Details of experimental site and climate**

| S. No. | Particulars | Environments |
|---|---|---|
| 1 | Location | ICRISAT, Patancheru |
| 2 | Latitude | $17^{o}$ 53'N |
| 3 | Longitude | $78^{o}$ 27'E |
| 4 | Altitude | 545.0 m |
| 5 | Soil type | Medium black |
| 6 | Climatic zone | Moderate rainfall zone |
| 7 | Temperature | |
| | Min. | 10.24 |
| 8 | Rainfall | 997.59mm |
| | Max. | 36.5 |
| 9 | Humidity | |
| | Min. | 20 |
| | Max. | 100 |
| 10 | Date of sowing | 14-07-2015 |
| 11 | Date of harvesting | 10-01-2016 |

**Table 3.2: List of pigeonpea hybrids used in present investigation:**

| Sl.no. | Hybrid | Pedigree | Type | Source |
|---|---|---|---|---|
| 1 | ICPH 4746 | ICPA 2200 X ICPL 11229 | Hybrid | ICRISAT |
| 2 | ICPH 4571 | ICPA 2200 X ICPL 20116 | Hybrid | ICRISAT |
| 3 | ICPH 4748 | ICPA 2202 X ICPL 11237 | Hybrid | ICRISAT |
| 4 | ICPH 4606 | ICPA 2202 X ICPL 20093 | Hybrid | ICRISAT |
| 5 | ICPH 4573 | ICPA 2202 X ICPL 20108 | Hybrid | ICRISAT |
| 6 | ICPH 4588 | ICPA 2202 X ICPL 20116 | Hybrid | ICRISAT |
| 7 | ICPH 4679 | ICPA 2203 X ICPL 11229 | Hybrid | ICRISAT |
| 8 | ICPH 4680 | ICPA 2203 X ICPL 11237 | Hybrid | ICRISAT |
| 9 | ICPH 4602 | ICPA 2203 X ICPL 20093 | Hybrid | ICRISAT |
| 10 | ICPH 4572 | ICPA 2203 X ICPL 20108 | Hybrid | ICRISAT |
| 11 | ICPH 4564 | ICPA 2203 X ICPL 20116 | Hybrid | ICRISAT |
| 12 | ICPH 4683 | ICPA 2204 X ICPL 11237 | Hybrid | ICRISAT |
| 13 | ICPH 4682 | ICPA 2204 X ICPL 11229 | Hybrid | ICRISAT |
| 14 | ICPH 4567 | ICPA 2204 X ICPL 20116 | Hybrid | ICRISAT |
| 15 | ICPH 2740 | ICPA 2043 X ICPL 87119 | Hybrid | ICRISAT |
| 16 | ICPH 2671 | ICPA 2047 X ICPL 87119 | Hybrid | ICRISAT |

**Table 3.3: List of B, R and checks used in present investigation:**

| Sl.no. | Name | Source |
|---|---|---|
| 1 | ICPB 2200 | ICRISAT |
| 2 | ICPB 2202 | ICRISAT |
| 3 | ICPB 2203 | ICRISAT |
| 4 | ICPB 2204 | ICRISAT |
| 5 | ICPL 11229 | ICRISAT |
| 6 | ICPL 11237 | ICRISAT |
| 7 | ICPL 20116 | ICRISAT |
| 8 | ICPL 20093 | ICRISAT |
| 9 | ICPL 20108 | ICRISAT |
| 10 | Rajeevlochan(c) | ICRISAT |
| 11 | Asha (ICPL 87119)(c) | ICRISAT |
| 12 | Maruti (ICP 8863)(c) | ICRISAT |

### 3.3 Observations recorded

Observations were recorded on randomly selected five competitive plants in each plot for all hybrids, B-lines, R-lines and the standard checks. Character wise details of observations recorded are as following pigeonpea characters.

#### 3.3.1 Characters associated with yield and yield components

##### 3.3.1.1 Days to 50 %flowering

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

##### 3.3.1.2 Days to maturity

Days required from sowing to 75% maturity were recorded.

##### 3.3.1.3 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 five plants was computed.

##### 3.3.1.4 Number of primary branches plant$^{-1}$

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

##### 3.3.1.5 Number of secondary branches plant$^{-1}$

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

##### 3.3.1.6 Number of pods plant$^{-1}$

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

##### 3.3.1.7 Number of seeds pod$^{-1}$

Seeds from randomly selected ten pods for each plant were counted and the average seeds per pod were calculated. Mean value of random sample of five plants was computed.

##### 3.3.1.8 Number of seeds plant$^{-1}$

The product of pods plant$^{-1}$ and seeds per pod from randomly selected five plants was counted and the average seeds plant$^{-1}$ was calculated. Mean value of random sample of five plants was computed.

**3.3.1.9 100-seed weight (g)**

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

**3.3.1.10 Seed yield plant$^{-1}$ (gm)**

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 five plants was computed.

**3.3.1.11 Biological yield plant $^{-1}$**

From each selected plant, weights were taken after sun drying by using electric balance. Dry weights were recorded after thorough sun drying. Mean value of random sample of five plants was computed.

**3.3.1.12 Harvest index (%)**

Harvest index was calculated by using below formula given by Donald (1962)

$$\text{Harvest index (\%)} = \frac{Economical\ \ yield}{Biological\ \ yield} \times 100$$

**3.3.1.13 Seed yield (kg ha$^{-1}$)**

Seed yield per ha was calculated by using the formula

$$Seed\ yield\ kg\ perha = \frac{10000}{factor} \times seed\ yield\ per\ plot$$

The factor was calculated by using the formula

$$Factor = Row\ length \times no.of\ rows \times row\ to\ row\ spacing$$

**3.3.2. Cyto-histological observations**

**3.3.2.1 Pollen fertility percentage**

For testing the pollen, fertility in the hybrids 2 percent aceto-carmine solutions was used to stain and differentiate the fertile and sterile pollen grains. Three 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 and sterile pollen grains in three microscopic fields was noted.

Percent pollen fertility of hybrids was calculated on mean of all the observations from a hybrid.

$$\text{Pollen fertility (\%)} = \frac{\text{Number of fertile pollens}}{\text{Total no of pollens}} \times 100$$

### 3.3.3 Qualitative observations

#### 3.3.3.1 Seed coat colour

From each selected plant, dry pods were harvested and threshed separately. Seed coat recorded by observing the seed coat.

#### 3.3.3.2 Seed protein content

Seed protein content of parents, hybrids and standard checks was estimated following Micro-Kejaldahals Method. Constant multiplier of 6.25 to obtain protein (percentage) multiplied the estimated nitrogen content in each genotype.

#### 3.3.3.3 Dal recovery (%)

Dal recovery percent of each genotype was calculated by using formula.

$$\text{Dal recovery (\%)} = \frac{Total\ weight\ of\ dehusked\ dal\ (split\ dal\ and\ broken\ dal)}{Total\ weight\ of\ seed\ used\ for\ dehusking} \times 100$$

## 3.4 Statistical analysis

The data recorded on all the traits related to yield and yield contributing characters in the season were statistically analyzed applying computer software to estimate different parameters as described below:

### 3.4.1 Analysis of variance

The mean data of each genotype was used for analysis of variance using RBD design. The model for experimental design used *i.e.* RBD can be expressed as follows:

$$Y_{ijk} = \mu + g_i + b_{ij} + e_{ijk}$$

Where,

$\mu$ = General mean

$g_i$ = Effect of $i^{th}$ genotype

$b_{ij}$ = Effect of $j^{th}$ replication on $i^{th}$ genotype

$e_{ijk}$ = Error component

The skeleton of the analysis of variance.

**Table 3.4: ANOVA for RBD**

| **Source of Variation** | **Degree of Freedom** | **Mean Sum of Squares** | **Expected Mean Sum of Squares** | **F cal.** |
|---|---|---|---|---|
| Replications | r-1 | MSR | $\sigma^2_e + g\,\sigma^2_r$ | MSR/MSE |
| Treatments | t-1 | MST | $\sigma^2_e + r\,\sigma^2_g$ | MST/MSE |
| Error | (r-1) (t-1) | MSE | $\sigma^2_e$ | |
| Total | rt-1 | | | |

Where,

r = Number of replications

t = Number of treatments

The mean data were subjected to analysis of variance and test of significance conducted as per the method of Fisher (1935).

### 3.4.2 Parameters of variation

#### 3.4.2.1 Mean

Mean is the average value of observations of genotypes of a series. It represents the standard average value over fluctuation in the environment.

Mean was calculated by the following formula:

$$X = \sum X_i / n$$

Where,

$\sum X_i$ =Summation of all the observations

n=Total number of observations

**3.4.2.2 Range**

Range is the difference between the highest and the lowest value of a series of observations and thus, provides the information about the extent of variability present in the genotypes.

Range = Highest value - Lowest value

**3.4.3 Character association studies**

**3.4.3.1 Correlation Analysis**

Phenotypic and genotypic correlations were worked out as per the procedures suggested by Johnson *et al*., (1955).

**3.4.3.1.1 Phenotypic correlation**

The Phenotypic coefficient of correlation ($r_p$) was calculated as follows

$$r(Xi\ X\ j)p = \frac{V(Xi\ )P.V(Xj\ )}{\sqrt{Cov.(X\ iXj\ )P}}$$

Where,

$(X_i\ X_j)$ p - Phenotypic correlation between $i^{th}$ and $j^{th}$ characters

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

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

Cov $(X_i\ X_j)$ p = Phenotypic covariance between $i^{th}$ and $J^{th}$ characters.

**3.4.3.1.2 Genotypic correlation**

The genotypic coefficient of correlation ($r_g$) was calculated as fallows,

$$r\ (Xi\ Xj)g = \frac{Cov.(Xi\ Xj\ )g}{\sqrt{V(Xj\ )g.\ V(Xj\ )g}}$$

Where,

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

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

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

$Cov\ (X_i\ X_j)_g$ = Genotypic covariance between $i^{th}$ and $j^{th}$ characters.

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% and 1% level, where 'n' denotes the number of paired observations used in the calculation.

**3.4.4 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).

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

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots + r_{1i}P_{iy}$$

$$r_{2y} = r_{21}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots + r_{2i}P_{iy}$$

$$\vdots$$

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

Where,

$r_{1y}$ to $r_{iy}$ = Coefficient of correlation among causal factors 40

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

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

$$A = \begin{pmatrix} r1y \\ r2y \\ r3y \\ . \\ . \\ riy \end{pmatrix} \quad C = \begin{pmatrix} 1 & r12 & r13 & . . & r1i \\ r121 & & r23 & \ldots & r3i \\ r31 & r32 & 1 & . . & r3i \\ . & . & . & & . \\ . & . & . & & . \\ ri1 & ri2 & ri3 & . . & 1 \end{pmatrix} \quad B = \begin{pmatrix} p1y \\ P2y \\ P3y \\ . \\ . \\ Piy \end{pmatrix}$$

Then B = [C]-1 A

Where,

$$[C] = \begin{bmatrix} C11 & C12 & C13 & . . & \ldots & \ldots & \ldots & . . & C1i \\ C21 & C22 & C23 & . . & \ldots & \ldots & \ldots & & C2i \\ Ci1 & Ci2 & Ci3 & . . & . & \ldots & \ldots & \ldots & . . & Cii \end{bmatrix}$$

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

$$\text{Residual effect } (P_{RY}) = \sqrt{(1 - P1yr1y + P2yr2y + \cdots + P1yry)^2}$$

Where,

$P_{RY}$ = Residual effect

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

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

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

**Table 3.5: Scales for path coefficients**

| 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 |

### 3.5 Studies on fertility restoration

For testing pollen fertility in the hybrids, 1% aceto-carmine was used as stain to differentiate between fertile and sterile pollen grains. Three plants were selected randomly from each hybrid and five buds from each plant were collected for pollen fertility studies. Anthers from the sampled flowers were removed and squashed in 1% acetocarmine solution. Three microscopic fields on each slide were examined under the light microscope. Counts for fertile and sterile pollen grains were made. Pollen grains were considered fertile if they were stained with dye (deep red color). The round and well-stained pollen grains were counted as fertile while shriveled hyaline pollen grains were scored as sterile. The mean for all the microscopic fields were worked-out and the proportion of fertile pollens was expressed in percentage on total for individual plants as follows

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

### 3.6 Studies on heterosis

The magnitude of heterosis was estimated in relation to mid parent, better parent and standard check variety.

Mid-parent heterosis or relative heterosis was calculated as the percent deviation of mean of the $F_1$ cross from its mid-parental value, between the two corresponding parents.

Heterobeltiosis was estimated as difference between the mean of the $F_1$ and that of the parent with superior expression for corresponding character in each cross combination.

Standard heterosis was expressed as percent increase (+) or decrease (-) of $F_1$ hybrid over the standard check variety.

$$\text{Relative heterosis (\%)} = \frac{\text{F1} - \text{MP}}{\text{MP}} \times 100$$

$$\text{Heterobeltiosis (\%)} = \frac{\text{F1} - \text{BP}}{\text{BP}} \times 100$$

$$\text{Standard heterosis (\%)} = \frac{\text{F1} - \text{SC}}{\text{SC}} \times 100$$

Where,

$F_1$ = Mean of the hybrid

MP = mid- parental value; i.e., the arithmetic average of two parents involved in the respective cross combination.

BP = Better parental value; i.e., the mean of the superior parent in the respective cross combination.

SC = Standard check value; the mean of the standard check varietal value.

The significance of heterosis was tested in both the situations by calculating the Critical difference (C.D) at 5% and 1% levels at error degree of freedom.

C.D = S.E X t α (error d.f)

S.E for relative heterosis = $\sqrt{\frac{3}{2} \times \frac{\text{M'e}}{\text{r}}}$

S.E for heterobeltiosis = $\sqrt{2 \times \frac{M'e}{r}}$

Where,

S. E = Standard error.

M'e = Error mean sum of square.

r = Number of replications.

### 3.7 Determination of seed protein content

This was done by Kjeidhal method. The total $N_2$ was determined and multiplied with factor 6.25 to obtain the protein content. 1 gram of sample was mixed with 10mls of concentrated $H_2SO_4$ in a digestion flask. A tablet of selenium catalyst was added to tit before it was heated under a fume cupboard until a clear solution was obtained (i.e. the digest).The digest was diluted to 100mls in a volumetric flask and used for analysis. Then 10mls of the digest was mixed with equal volume of 40% NaOH solution in a Kjeldahl distillation apparatus. The mixture was distilled into 10ml of 4% boric acid containing 3 drops of mixed indicator 9 bromocressol green and methyl red). A total of 50mls of distillate was collected and titrated against 0.01N EDTA from green to a deep red end point. A reagent lank was also digested, distilled and titrated. The N2 content and the protein content were calculated using the formula below.

$$\% \text{ Protein} = \%N_2 \times 6.25$$

$$N_2 \text{ content} = \frac{(sample\ \ TV - Blank\ \ TV) \times Normality of\ \ \ HCl \times 14 \times 100}{Weight\ of\ sample\ \times 1000}$$

Where,

TV - titer value in ml

6.25 - Protein factor.

# CHAPTER-IV

# RESULTS AND DISCUSSION

The present investigation entitled **"Identification of heterotic combinations, using obcordate leaf shape CMS lines in Pigeonpea [*Cajanus cajan (*L.) Millspaugh]''** was carried out using 14 hybrids, 4 B-line, 5 R-lines and 5 checks. A set of 14 hybrids were developed by crossing the parents during *kharif* 2014-15. This study was conducted at Patancheru during *kharif* 2015-16 to study their character association with yield, fertility restoration and heterosis in hybrids. Observations were recorded on yield and yield contributing characters such as days to 50% flowering, pollen fertility%, days to maturity, plant height (cm), number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, number of seeds plant$^{-1}$,100-seed weight (g), seed yield plant$^{-1}$(g), biological yield plant$^{-1}$,seed yield (kg ha$^{-1}$) and harvest index(%). In addition, some quality parameters like dal recovery %, seed protein content and seed coat colour were also recorded.

The results obtained from the statistical analyses of the data from 14 hybrids, 4 B-line, 5 R-lines and 5 checks of pigeonpea for yield, yield component characters, mean pollen fertility% and heterosis are presented here under the following heads:

4.1 Analysis of variance

4.2 Per se performance

4.3 Character association

4.4 Path coefficient analysis

4.5 Fertility restoration studies in CMS based hybrids

4.6 Heterosis

## 4.1 Analysis of variance

The raw data recorded from the experiment was subjected to analysis of variance and data was presented in the Table 4.1. The analysis of variance (ANOVA) showed that the mean sum of squares due to genotypes were significant for all most all characters. These results indicated that significant genotypic differences in all the $F_1$ hybrids, parents and standard checks. Thus, the experimental material chosen for the present study was highly variable in nature and suitable for analyzing various parameters.

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

| Name of the character | Mean sum square | | |
|---|---|---|---|
| | **Replications** DF=2 | **Genotypes** DF=27 | **Error** DF=54 |
| Days to 50% flowering | 2.821 | 109.787** | 1.61 |
| Days to Maturity | 27.512 | 59.617** | 8.228 |
| Pollen fertility% | 13.861 | 32.99** | 1.452 |
| Number of primary branches plant$^{-1}$ | 311.003 | 19.291* | 11.368 |
| Number of secondary branches plant$^{-1}$ | 104.749 | 175.309* | 87.007 |
| Plant height | 1985.97 | 404.341** | 68.313 |
| Number of pods plant$^{-1}$ | 31351.122 | 37853.23** | 9,371.31 |
| Number of seeds pod$^{-1}$ | 0.002 | 0.015** | 0.008 |
| Number of seeds plant$^{-1}$ | 32222.796 | 276949.038** | 38,791.75 |
| 100seed wt. | 0.181 | 1.269** | 0.219 |
| Biological yield plant$^{-1}$ | 3426.333 | 14688.151** | 2,345.65 |
| Seed yield(kg/ha) | 31570.825 | 103083.944 | 70,583.70 |
| Harvest index | 4.047 | 53.958** | 14.041 |
| Dal Recovery % | 187.606 | 22.884** | 5.683 |
| Seed Protein Content | 0.516 | 1.528** | 0.58 |
| Seed yield plant$^{-1}$ | 1664.695 | 3400.78** | 467.29 |

Where, *, ** = significant at 5% level and 1% level of probability, respectively

## 4.2 Per se performance

The performance of all the tested materials was good for plant growth. However, there was variation in temperature and rainfall during *kharif* 2015-16 leading to differences in the flowering response of the genotypes. 14 hybrids were evaluated in *kharif* 2015-16 along with their parents (4 B lines and 5 R lines) and five standard check varieties, Asha, Rajeevlochan, Maruti, ICPH 2740 and ICPH 2671.

The results on per se performance of the 28 genotypes (14 hybrids, 4 B lines, 5 R lines and 5 checks) for seed yield and yield components, *viz*., days to 50% flowering, pollen fertility %, days to maturity, plant height (cm), number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, number of seeds plant$^{-1}$, 100seed weight(g), seed yield plant$^{-1}$(g), biological yield plant$^{-1}$, seed yield (kg ha$^{-1}$) , harvest index(%), dal recovery %, seed protein content and seed coat colour are presented in Tables 4.2a,4.2b and 4.2c.

### 4.2.1 Days to 50 per cent flowering and days to maturity

Among the twenty eight genotypes, in hybrids ICPH 4682 (98 days) was the earliest to days 50% flowering followed by ICPH 4573(99 days), ICPH 4567 (99.33 days) and ICPH 4571(99.33 days) these four hybrids were significantly earlier for days 50% flowering than check Asha. In B lines, ICPB 2200 (99 days) was earliest to days 50% flowering and ICPB 2202 (116 days) was late for days 50% flowering. In R lines, ICPL 20116 (99 days) was earliest and ICPL 20093 was late for days 50% flowering. The check Asha and Maruti took 107 days and 98 days to 50% flowering respectively. The range of days to 50% flowering was from 98 days (ICPH 4682) to 119 days (ICPL 20093), out of 28 genotypes, while general mean was 104 days.

### 4.2.2 Days to maturity

Out of twenty eight genotypes, among hybrids, ICPH 4746 and ICPH 4572 (148 days) were noted the earliest for days to maturity and ICPH 4564 (151 days) was the late for days to maturity. All hybrids showed significantly earlier to mature than

check Asha (160 days) and check Maruti (158 days). Among B lines ICPB 2200 (152 days) was earliest and ICPB 2202 (163 days) was late for days to maturity. Whereas, among R lines ICPL 20116 (149 days) was earliest and ICPL 11237 (167 days) was the late for days to maturity. The range of days to maturity varied from 147 (ICPH 4746) to 167 days (ICPL 11237), out of 28 genotypes, while general mean was 152 days.

**4.2.3 Plant height**

Among twenty eight genotypes, out of 14 hybrids, ICPH 4564 (211cm) was the tallest followed by ICPH 4572 (210.33cm) and all hybrids are significantly taller than checks Asha (184.67cm) and Maruti (180cm). In B lines ICPB 2202(235cm) was the tallest and ICPB 2200 (185.67cm) was the shortest and Among R lines, ICPL 20108 (196.67 cm) was tallest and ICPL 20093 (175.33 cm) was the shortest. Except ICPL 20093, all genotypes showed positive significance difference over Asha (180.0cm). The range of plant height was from 175.33 (ICPL 20093) to 235.0cm (ICPB 2202), out of 28 genotypes; while general mean was 196.50 cm.

**4.2.4 Number of primary branches plant$^{-1}$**

Number of primary branches plant$^{-1}$ was the important quantitative trait for yield it was recorded among the 28 genotypes, in out off 14 hybrids number of primary branches plant$^{-1}$ was maximum in ICPH 4572 (26.33) followed by ICPH 4564 (25), ICPH 4679 (24.67) ICPH 4746 (22.67). Except ICPH 4682 (20.67) all hybrids shows significantly higher in number of primary branches plant$^{-1}$ than check Asha and Maruti (21.33 and 17.33), B lines and R lines. Among 4 B lines ICPB 2200 (20.67) was the highest and ICPB 2202 (16.67) was the lowest in number of primary branches plant$^{-1}$ . B lines significantly lower than R lines. In 5 R lines, ICPL 20108 (23.33) was the highest and ICPL 20093 (19.33) was the lowest for number of primary branches plant$^{-1}$. Range of number of primary branches plant$^{-1}$ from 16.67 (ICPB 2202) to 27.67 (ICPH 2671), out of 28 genotypes, while general mean was 21.94.

**4.2.5 Number of secondary branches per plant$^{-1}$**

In the present study, among 14 hybrids ICPH 4573 and ICPH 4571 (68.67) were highest followed by ICPH 4567 (65.67) and ICPH 4606 (63.67). Five hybrids, ICPH

4682 (56), ICPH 4746 (54.67), ICPH 4588 (53) and ICPH 4680 (52.33) were significantly lower than check Asha (57.67). All hybrids significantly higher then check Maruti (45.33) in number of secondary branches per plant$^{-1}$. In B lines ICPB 2200 (50.33) was the highest and ICPB 2202 (41.00) was the lowest. All B lines were significantly lower than check Asha (57.67) and ICPB 2200 (50.33) and ICPB 2204 (49.67) were significantly higher then check Maruti (45). In R line, ICPL 20116 (59.33) was the highest and ICPL 11237 (48.33) was the lowest. B lines significantly lower than R lines for number of secondary branches per plant$^{-1}$. The range of number of secondary branches per plant$^{-1}$ from 41 (ICPB 2202) to 71 (ICPH 2671), among 28 genotypes, while general mean 56.60.

**4.2.6 Number of pods per plant$^{-1}$**

In 14 hybrids ICPH 4567 (858) was the highest followed by ICPH 4571(811), ICPH 4748 (705.67) and ICPH 4683 (655.67) for number of pods per plant$^{-1}$. Seven hybrids, ICPH 4571(811), ICPH 4748 (705), ICPH 4573 (607.3), ICPH 4564 (596), ICPH 4683(655), ICPH 4682 (642.33) and ICPH 4567(655.67) were significantly higher than check Maruti (587.67) and all hybrids were significantly higher than check Asha (402.67) for number of pods per plant$^{-1}$. In B lines, ICPB 2204 (667.33) was highest and ICPB 2203 (362.33) was the lowest in number of pods per plant$^{-1}$. In R lines, ICPL 20116 (689.67) was highest and ICPL 11237 (402.33) was recorded lowest number of pods per plant$^{-1}$. The range of number of pods per plant$^{-1}$ from 362.33 (ICPB 2203) to 858 (ICPH 4567), among 28 genotypes, while general mean 575.13.

**4.2.7 Number of seeds pod$^{-1}$**

Among 28 genotypes, in 14 hybrids, ICPH 4679 (3.70) was the highest followed by ICPH 4746 (3.65), ICPH 4571 (3.65) and ICPH 4606 (3.64) for seeds pod$^{-1}$.Two hybrids, ICPH 4748 (3.48) and ICPH 4680 (3.47) significantly lower than check Asha (3.49). Five hybrids, ICPH 4746 (3.65), ICPH 4571 (3.65), ICPH 4606 (3.64), ICPH 4679 (3.70) and ICPH 4572 (3.62) were significantly higher seeds pod$^{-1}$ than check Maruti. In B lines, ICPB 2202 (3.67) was the highest and ICPB 2200 (3.56) was the lowest for seeds pod$^{-1}$. In R lines, ICPL 20108 (3.61) was the highest and ICPL 11237

(3.42) was the lowest for seeds pod$^{-1}$. The number of seeds pod$^{-1}$ ranged from 3.42 (ICPL 11237) to 3.70 (ICPH 4679) with general mean of 3.57.

**4.2.8 Number of seeds plant$^{-1}$**

Out of 28 genotypes, in 14 hybrids, ICPH 4567 (3047.86) was the highest followed by ICPH 4748 (2275.45), ICPH 4683 (2358.53) and ICPH 4682 (2261.70). All hybrids were observed with significantly higher number of seeds plant$^{-1}$ than Asha (1519.60). Six hybrids, ICPH 4746 (186.83), ICPH 4606 (1773.93), ICPH 4573 (1962.19), ICPH 4680 (1856.99), ICPH 4602 (1990.98) and ICPH 4572 (1953.01) were significantly lower number of seeds plant$^{-1}$ than Maruti (2018.88). In B lines, ICPB 2204 (1950.90) was the highest and ICPB 2200 (1437.80) was the lowest in number of seeds plant$^{-1}$. In R lines, ICPL 20116 (2278.45) was the highest and ICPL 11237 (1907.96) was lowest in number of seeds plant$^{-1}$. The number of seeds plant$^{-1}$ ranged from 1437.80 (ICPB 2200) to 3047.86 (ICPH 4567) with general mean of 2027.46.

**4.2.9 100-seed weight**

Among 28 genotypes, out of 14 hybrids, ICPH 4573 (10.49g) was the highest and ICPH 4567 (8.81g) was the lowest for 100seed weight. All hybrids significantly lower than check Asha (10.69) for 100seed weight. Whereas, Six hybrids *viz.*, ICPH4648 (10.26g), ICPH 4606 (10.05g), ICPH 4573 (10.49g), ICPH 4679 (10.04g), ICPH 4602 (9.88g) and ICPH 4572 (9.89g) gave significantly higher 100-seed weight than check variety (9.87g). In B lines, ICPB 2202 (11.17g) was highest and ICPB 2200 (8.95g) was lowest for 100-seed weight. In R lines, ICPL 20108 (10.54g) was highest and ICPL 20116 (8.87g) was lowest for 100-seed weight. The 100-seed weight ranged from 8.81g (ICPH 4567) to 11.17g (ICPB 202) with general mean of 9.80g.

**4.2.10 Biological yield plant$^{-1}$(g)**

Out of 14 hybrids, ICPH 4567 (524.47g) was the highest and ICPH 4746 (342.33g) was the lowest for biological yield plant$^{-1}$. All hybrids were significantly higher in biological yield plant$^{-1}$ than check Maruti (273.40g). Three hybrids, ICPH 4746 (342.33g), ICPH 4606 (376.60g) and ICPH 4682 (372g) were significantly lower in biological yield plant$^{-1}$ than check Asha (381.27g). In B lines, ICPB 2203 (407.47g)

was the highest and ICPB 2202 (245.00g) was the lowest for biological yield plant$^{-1}$. In R lines, ICPL 20108 (421.33g) was the highest and ICPL 11237 (340.07g) was the lowest for biological yield plant$^{-1}$. The biological yield plant$^{-1}$ ranged from 245.00g (ICPB 2202) to 552.33g (ICPH 2671) with general mean of 405.78g.

**4.2.11Seed yield plant$^{-1}$(g)**

Over all the hybrids recorded highest in seed yield plant$^{-1}$ than B lines and R lines. Among 28 genotypes, in 14 hybrids, ICPH 4567 (194.95g) was the highest for yield plant$^{-1}$ and ICPH 4680 (114.29g) was the lowest for seed yield plant$^{-1}$. Except ICPH 4680 (114.29g) all hybrids significantly higher seed yield plant$^{-1}$ than check Maruti (123.44g). Four hybrids, *viz*., ICPH 4746 (126.86), ICPH 4748 (128.95g), ICPH 4679 (131.52g) and ICPH 4680 (114.29g) were lower seed yield plant$^{-1}$ than check Asha (123.44g). In B lines, ICPB 2204 (146.02g) was the highest and ICPB 2202 (60.00) was the lowest for seed yield plant$^{-1}$. In R lines, ICPL 20116 (186.05g) was the highest and ICPL 20108 (121.85g) was the lowest for seed yield plant$^{-1}$. The seed yield plant$^{-1}$ ranged from 60.00g (ICPB 2202) to 194.95g (ICPH 4567) with general mean of 141.35g.

**4.2.12 Pollen fertility%**

Among 28 genotypes, in 14 hybrids, ICPH 4602 was the highest and ICPH 4572 was the lowest with 87.33% and 83% for pollen fertility% with respectively. All hybrids were significantly lower in pollen fertility% than check Asha (98.53%) except the hybrid ICPH 4602 (87.33%). Except ICPH 4572 (83%), all hybrids were significantly higher than check Maruti (97.85%) for the trait. Among B lines, ICPB 2202 (93.67%) was the highest and ICPB 2200 (84.00%) was the lowest for pollen fertility%. In R lines, ICPL 11237 (96.33%) was the highest and ICPL 20116 (83.67%) was the lowest for pollen fertility%. The pollen fertility% ranged from 83% (ICPH 4572) to 96.33% (ICPL 11237) with general mean of 86.36%.

**4.2.13 Seed yield (kg/ha)**

Among 28 genotypes, including 14 hybrids, ICPH 4564 (3312.30kg) was the highest followed by ICPH 4746 (2950.42kg), ICPH 4682 (2949.55kg), ICPH 4573 (2922.43kg) and ICPH 4588 (2761.50kg) in seed yield (kg/ha). All the 14 hybrids

were recorded significantly higher in seed yield (kg/ha) as compared to check Maruti (1964.34kg). Two hybrids, ICPH 4602 (1976.90kg) and ICPH 4567 (1985.20kg) were lower seed yield (kg/ha) than Asha (2001.47kg). In B lines, ICPB 2204 (1577.44kg) was the highest and ICPB 2202 (857.08kg) was the lowest for seed yield (kg/ha). In R lines, ICPL 11229 (2590.37kg) was the highest and ICPL 20093 (1598.07kg) was the lowest for seed yield (kg/ha). Except ICPL 11229 (2590.37kg) all were significantly lower in seed yield (kg/ha) than check varieties Asha (2001.47kg) and Maruti (1964.34kg). The seed yield (kg/ha) ranged from 857.08kg (ICPB 2202) to 3312.30kg (ICPH 4564) with general mean of 2167.32kg.

**4.2.14 Harvest index**

Among 28 genotypes, in 14 hybrids, ICPH 4564 (37.19%) was noticed with the highest and ICPH 4572 (23.83%) was the lowest for harvest index. Five hybrids, *viz*., ICPH 4606 (35.57%), ICPH 4588 (34.61%), ICPH 4564 (37.19%), ICPH 4682 (34.98%) and ICPH 4573 (30.64%) were significantly higher harvest index than check Maruti (30.38%). Five hybrids, ICPH 4571 (23.94%), ICPH 4748 (24.66%), ICPH 4602 (24.60%), ICPH 4572 (23.83%) and ICPH 4567 (24.60%) were significantly lower harvest index than check Asha (28.25%). Among B lines, ICPB 2202 (31.40%) was the highest and ICPB 2200 (22.85%) was the lowest. Except ICPB 2202 all were significantly lower in harvest index as compared to check varieties Asha and Maruti. Whereas, among R lines, ICPL 11229 (35.08%) was having the highest and ICPL 20093 (25.11%) was the lowest for harvest index. Except ICPL 11229 all were significantly lower harvest index than check Maruti. Two R lines, ICPL 11229 (35.08%) and ICPL 20116 (29.82%) were having higher harvest index than check Asha. The harvest index ranged from 22.85% (ICPB 2200) to 37.19% (ICPH 4564) with general mean of 28.17%.

**4.2.15 Dal recovery %**

Among 28 genotypes, out of 14 hybrids, ICPH 4564 (71.07%) was the highest and ICPH 4679 (63.03%) was the lowest in dal recovery %. Two hybrids, ICPH 4564 (71.07%) and ICPH 4567 (70.40%) were significantly higher in dal recovery % than check variety Asha (70.33%). Three hybrids, *viz.*, ICPH 4564 (71.07%), ICPH 4567

(70.40%) and ICPH 4748 (69.60%) were significantly higher in dal recovery % compared to check Maruti (69.07%). In B lines, ICPB 2202 (68.17%) was the highest and ICPH 2200 (62.17%) was the lowest for dal recovery %. All B lines were significantly lower in dal recovery % than both the check varieties Asha and Maruti. In R lines, ICPL 20116 (69.00%) was the highest and ICPH 20108 (62.37%) was the lowest for dal recovery %. All R lines were significantly lower dal recovery % than check variety Asha and Maruti. The dal recovery % ranged from 62.17% (ICPB 2200) to 71.17% (ICPH 2740) with general mean of 66.80%.

**4.2.16 Seed protein content**

Among 28 genotypes, in 14 hybrids, ICPH 4683 (22.09%) was the highest in seed protein content followed by ICPH 4573 (22.02%), ICPH 4682 (21.77%), ICPH 4748 (21.69%) and ICPH 4567 (21.48%). All hybrids were significantly lower in seed protein content than check variety Asha (22.13%) and Maruti (22.35%). In B lines, ICPB 2202 (22.18%) was the highest and ICPB 2203 (20.61%) was the lowest for seed protein content. Except ICPB 2202 (22.18%), all B lines were significantly lower seed protein content than check variety Asha (22.13%) and Maruti (22.35%). In R lines, ICPL 11229 (21.44%) was the highest and ICPL 20116 (21.19%) was the lowest for seed protein content. All R lines were significantly lower seed protein content than check variety Asha (22.13%) and Maruti (22.35%). The seed protein content ranged from 19.81% (ICPH 4588) to 22.28% (ICPH 2740) with general mean of 21.31%.

**4.2.16 Seed coat colour**

In seed colour, little variation was found in 14 hybrids. Out of 14 hybrids, six hybrids viz., ICPH 4746, ICPH 4571, ICPH 4588, ICPH 4679, ICPH 44682 and ICPH 4567 were purple seed coat colour. Five hybrids viz., ICPH 4748, ICPH 4606, ICPH 4680, ICPH 4602 and ICPH 4683 were dark brown in colour. Two hybrids were purple seed coat colour with cream dots and ICPH 4564 only the hybrid found for brown seed colour. B lines used in this study all were white seed coat colour and all R lines were brown seed coat colour except ICPL 20108, which was white in seed coat colour. All checks used in this study were brown seed coat colour.

**Table 4.2a: Per se performance of hybrids, parents and checks for yield and yield components in pigeonpea**

| Entry name | Days to50% flowering | Days to maturity | No.of primary branches plant$^{-1}$ | No.of secondary branches plant$^{-1}$ | Plant height(cm) |
|---|---|---|---|---|---|
| ICPH 4746 | 107.33 | 147.67 | 22.67 | 54.67 | 201.00 |
| ICPH 4571 | 99.33 | 150.00 | 21.33 | 68.67 | 199.67 |
| ICPH 4748 | 106.33 | 150.33 | 22.33 | 63.00 | 197.67 |
| ICPH 4606 | 106.67 | 150.33 | 24.33 | 63.67 | 189.00 |
| ICPH 4573 | 99.00 | 150.33 | 24.67 | 68.67 | 204.33 |
| ICPH 4588 | 104.33 | 150.67 | 23.33 | 53.00 | 207.00 |
| ICPH 4679 | 106.33 | 150.33 | 24.67 | 53.00 | 206.00 |
| ICPH 4680 | 105.67 | 153.00 | 21.00 | 52.33 | 196.33 |
| ICPH 4602 | 108.33 | 150.67 | 22.67 | 61.67 | 189.67 |
| ICPH 4572 | 99.33 | 148.00 | 26.33 | 59.00 | 210.33 |
| ICPH 4564 | 104.67 | 151.33 | 25.00 | 63.33 | 211.00 |
| ICPH 4683 | 106.67 | 151.00 | 24.67 | 61.00 | 198.67 |
| ICPH 4682 | 98.00 | 150.00 | 20.67 | 56.00 | 185.00 |
| ICPH 4567 | 99.33 | 148.33 | 22.00 | 65.67 | 194.33 |
| ICPB 2200 | 99.00 | 151.67 | 20.67 | 50.33 | 185.67 |
| ICPB 2202 | 115.67 | 163.00 | 16.67 | 41.00 | 235.00 |
| ICPB 2203 | 106.33 | 152.33 | 19.67 | 44.67 | 193.67 |
| ICPB 2204 | 106.67 | 154.00 | 18.00 | 49.67 | 189.33 |
| ICPL 11229 | 105.67 | 151.00 | 20.33 | 55.33 | 190.67 |
| ICPL 11237 | 119.67 | 167.67 | 21.00 | 48.33 | 193.33 |
| ICPL 20116 | 98.67 | 149.33 | 21.33 | 59.33 | 190.00 |
| ICPL 20093 | 119.67 | 160.33 | 19.33 | 52.00 | 175.33 |
| ICPL 20108 | 107.00 | 151.00 | 23.33 | 58.67 | 196.67 |
| Rajeevlochan(c) | 98.00 | 150.33 | 21.00 | 48.00 | 202.33 |
| Asha (c) | 117.33 | 168.00 | 21.33 | 57.67 | 184.67 |
| Maruti (c) | 97.67 | 162.00 | 17.33 | 45.33 | 180.00 |
| ICPH 2671(hy.c) | 98.67 | 149.33 | 21.00 | 71.00 | 192.33 |
| ICPH 2740 (hy.c) | 106.67 | 151.67 | 27.67 | 59.67 | 203.00 |
| **Mean** | **104.93** | **151.99** | **21.94** | **56.60** | **196.50** |
| **Range:** | | | | | |
| **Min.** | **97.67** | **147.67** | **16.67** | **41.00** | **175.33** |
| **Max.** | **119.67** | **167.67** | **27.67** | **71.00** | **235.00** |
| **C.D.** | **2.12** | **4.71** | **5.54** | **15.37** | **13.57** |
| **SE(m)** | **0.74** | **1.66** | **1.95** | **5.41** | **4.77** |
| **C.V.** | **1.23** | **1.89** | **15.38** | **16.54** | **4.21** |

**Table 4.2b: Per se performance of hybrids, parents and checks for yield and yield components in pigeonpea**

| Entry name | Pods plant$^{-1}$ | Seeds pod$^{-1}$ | Seeds plant$^{-1}$ | 100Seed wt. | Biological Yield Plant$^{-1}$(g) | Seed yield plant$^{-1}$(g) |
|---|---|---|---|---|---|---|
| ICPH 4746 | 576.00 | 3.65 | 1861.83 | 9.80 | 342.33 | 126.86 |
| ICPH 4571 | 811.00 | 3.65 | 2117.99 | 9.35 | 451.53 | 171.32 |
| ICPH 4748 | 705.67 | 3.48 | 2275.45 | 10.26 | 457.53 | 128.95 |
| ICPH 4606 | 564.00 | 3.64 | 1773.93 | 10.05 | 376.60 | 157.17 |
| ICPH 4573 | 607.33 | 3.57 | 1962.19 | 10.49 | 455.93 | 169.19 |
| ICPH 4588 | 561.33 | 3.49 | 2133.35 | 9.46 | 401.67 | 147.23 |
| ICPH 4679 | 538.67 | 3.70 | 2061.21 | 10.04 | 428.67 | 131.52 |
| ICPH 4680 | 494.33 | 3.47 | 1856.99 | 9.58 | 477.33 | 114.29 |
| ICPH 4602 | 541.67 | 3.49 | 1990.98 | 9.88 | 401.67 | 150.93 |
| ICPH 4572 | 513.33 | 3.62 | 1953.01 | 9.89 | 413.60 | 147.67 |
| ICPH 4564 | 596.00 | 3.55 | 2219.40 | 9.16 | 428.33 | 175.25 |
| ICPH 4683 | 655.67 | 3.55 | 2358.53 | 9.27 | 492.33 | 192.93 |
| ICPH 4682 | 642.33 | 3.51 | 2261.70 | 9.05 | 372.00 | 146.08 |
| ICPH 4567 | 858.00 | 3.57 | 3047.86 | 8.81 | 524.47 | 194.95 |
| ICPB 2200 | 400.67 | 3.56 | 1437.80 | 8.95 | 332.67 | 74.81 |
| ICPB 2202 | 569.33 | 3.67 | 1696.40 | 11.17 | 245.00 | 60.00 |
| ICPB 2203 | 362.33 | 3.57 | 1617.10 | 9.41 | 407.47 | 68.48 |
| ICPB 2204 | 667.33 | 3.59 | 1950.90 | 9.04 | 326.20 | 146.02 |
| ICPL 11229 | 577.67 | 3.55 | 2089.59 | 10.17 | 355.13 | 168.54 |
| ICPL 11237 | 402.33 | 3.42 | 1907.96 | 9.39 | 340.07 | 127.42 |
| ICPL 20116 | 689.67 | 3.56 | 2278.45 | 8.87 | 388.33 | 186.05 |
| ICPL 20093 | 602.00 | 3.53 | 2096.01 | 9.93 | 402.67 | 147.19 |
| ICPL 20108 | 546.00 | 3.61 | 1952.22 | 10.54 | 421.33 | 121.85 |
| Rajeevlochan (c) | 562.33 | 3.66 | 1966.45 | 9.54 | 428.93 | 129.22 |
| Asha (c) | 402.67 | 3.49 | 1519.60 | 10.69 | 381.27 | 140.80 |
| Maruti (c) | 587.67 | 3.58 | 2018.88 | 9.87 | 273.40 | 123.44 |
| ICPH 2671(hy.c) | 542.67 | 3.61 | 2225.03 | 10.59 | 552.33 | 160.53 |
| ICPH 2740 (hy.c) | 525.67 | 3.67 | 2138.18 | 11.01 | 482.93 | 149.19 |
| **Mean** | **575.13** | **3.57** | **2027.46** | **9.80** | **405.78** | **141.35** |
| **Range:** | | | | | | |
| **Min.** | **362.33** | **3.42** | **1437.80** | **8.81** | **245.00** | **60.00** |
| **Max.** | **858.00** | **3.70** | **3047.86** | **11.17** | **552.33** | **194.95** |
| **C.D.** | **158.94** | **0.15** | **323.29** | **0.77** | **79.50** | **35.49** |
| **SE(m)** | **55.90** | **0.05** | **113.71** | **0.27** | **27.96** | **12.48** |
| **C.V.** | **16.84** | **2.51** | **9.71** | **4.77** | **11.94** | **15.29** |

**Table 4.2c: Per se performance of hybrids, parents and checks for yield and yield components in pigeonpea**

| Entry name | Pollen fertility% | Seed Yield(kg/ha) | Harvest index | Dal recovery% | Seed protein content |
|---|---|---|---|---|---|
| ICPH 4746 | 85.67 | 2,950.42 | 28.73 | 68.00 | 21.28 |
| ICPH 4571 | 84.00 | 2,752.95 | 23.94 | 68.93 | 21.33 |
| ICPH 4748 | 86.33 | 2,247.72 | 24.66 | 69.60 | 21.69 |
| ICPH 4606 | 86.33 | 2,208.72 | 35.57 | 68.73 | 20.32 |
| ICPH 4573 | 83.67 | 2,922.43 | 30.64 | 63.17 | 22.02 |
| ICPH 4588 | 85.67 | 2,761.50 | 34.61 | 68.27 | 19.81 |
| ICPH 4679 | 86.33 | 2,723.02 | 28.31 | 63.07 | 21.17 |
| ICPH 4680 | 87.00 | 2,294.46 | 29.33 | 68.33 | 21.06 |
| ICPH 4602 | 87.33 | 1,976.90 | 24.76 | 64.40 | 20.48 |
| ICPH 4572 | 83.00 | 2,255.44 | 23.83 | 65.60 | 20.10 |
| ICPH 4564 | 86.00 | 3,312.30 | 37.19 | 71.07 | 21.54 |
| ICPH 4683 | 86.67 | 2,137.30 | 27.74 | 68.07 | 22.09 |
| ICPH 4682 | 83.33 | 2,949.55 | 34.98 | 63.87 | 21.77 |
| ICPH 4567 | 83.33 | 1,985.20 | 24.60 | 70.40 | 21.48 |
| ICPB 2200 | 84.00 | 1,222.95 | 22.85 | 62.17 | 21.20 |
| ICPB 2202 | 93.67 | 857.08 | 31.40 | 68.17 | 22.18 |
| ICPB 2203 | 87.00 | 1,014.35 | 23.07 | 65.33 | 20.61 |
| ICPB 2204 | 87.33 | 1,577.44 | 25.71 | 64.47 | 20.74 |
| ICPL 11229 | 86.00 | 2,590.37 | 35.08 | 64.27 | 21.44 |
| ICPL 11237 | 96.33 | 1,947.05 | 28.03 | 67.33 | 20.85 |
| ICPL 20116 | 83.67 | 1,956.40 | 29.82 | 69.00 | 21.19 |
| ICPL 20093 | 94.00 | 1,598.07 | 25.11 | 65.30 | 20.95 |
| ICPL 20108 | 86.67 | 1,852.20 | 25.50 | 62.37 | 20.38 |
| Rajeevlochan(c) | 84.00 | 2,211.91 | 23.05 | 65.00 | 22.24 |
| Asha (c) | 98.53 | 2,001.47 | 28.25 | 70.33 | 22.13 |
| Maruti (c) | 97.85 | 1,964.34 | 30.38 | 69.07 | 22.35 |
| ICPH 2671(hy.c) | 83.33 | 2,273.52 | 25.23 | 64.83 | 21.91 |
| ICPH 2740(hy.c) | 86.67 | 2,139.86 | 26.53 | 71.17 | 22.28 |
| **Mean** | **86.36** | **2167.32** | **28.17** | **66.80** | **21.31** |
| **Range:** | | | | | |
| **Min.** | **83.00** | **857.08** | **22.85** | **62.17** | **19.81** |
| **Max.** | **96.33** | **3312.30** | **37.19** | **71.17** | **22.28** |
| **C.D.** | **1.98** | **436.11** | **6.15** | **3.91** | **1.25** |
| **SE(m)** | **0.70** | **153.39** | **2.16** | **1.38** | **0.44** |
| **C.V.** | **1.39** | **12.26** | **13.30** | **3.57** | **3.57** |

## 4.3 Character association

### 4.3.1 Correlation coefficient analysis

Yield is a complex 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 coefficient (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 narrowed 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 non-significant, it means that, these two characters are independent. However, if the values of genotypic and phenotypic correlation coefficients are also non-significant, it further indicates the independent nature of two characters.

The results obtained on correlation coefficient analysis for yield and yield components are presented in Table 4.3 (Phenotypic correlations ($r_p$) and Genotypic correlations($r_g$)), 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).

Seed yield plant$^{-1}$ was observed to be significantly and positively associated with number of primary branches plant$^{-1}$ ($r_p$=0.260*, $r_g$=0.735***), number of secondary branches plant$^{-1}$($r_p$=0.579***, $r_g$=0.971***), number of pods plant$^{-1}$ ($r_p$=0.579***, $r_g$=0.663***), number of seeds plant$^{-1}$($r_p$=0.59***, $r_g$=0.808***), biological yield plant$^{-1}$ ($r_p$=0.497***, $r_g$=0.542***) and seed yield (kg/ha) ($r_p$=0.527***, $r_g$=0.636***) at both phenotypic and genotypic levels indicating their importance as selection criteria in pigeonpea yield improvement programmes. However, seed yield plant$^{-1}$ was also observed to be significantly and negatively associated with days to 50% flowering ($r_p$=-0.254*, $r_g$=-0.297**), days to maturity ($r_p$=-0.298**, $r_g$=-0.453***) and pollen fertility % ($r_p$=-0.284**, $r_g$=-0.379***). Association of Seed yield plant$^{-1}$ with other characters, *viz.*, plant height ($r_p$=-0.154, $r_g$=-0.221), number of seeds pod$^{-1}$ ($r_p$=-0.093, $r_g$=-0.022), 100-seed weight ($r_p$=-0.136, $r_g$=-0.323**) and harvest index ($r_p$=0.170, $r_g$=0.273) at both phenotypic and genotypic levels was found but non-significant. The significant and positive association of seed yield with its component characters indicated that selection for these traits will be rewarded.

Similar findings also reported by Rao *et a.l* (2013) for number of primary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$ and harvest index in pigeonpea.

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 ($r_p$=0.733***, $r_g$=0.861***), pollen fertility % ($r_p$=0.941***, $r_g$=0.977***) and 100-seed weight ($r_p$=0.243*, $r_g$=0.339**); days to maturity with pollen fertility ($r_p$=0.910***, $r_g$=0.951***) and seed yield (kg/ha) ($r_p$=0.405***, $r_g$=0.503***); number of primary branches plant$^{-1}$ with number of secondary branches plant$^{-1}$ ($r_p$=0.353**, $r_g$=1.074***), plant height ($r_p$=0.257*, $r_g$=0.261*), biological yield plant$^{-1}$($r_p$=0.394***, $r_g$=0.836***) and seed yield (kg/ha) ($r_p$=0.319**, $r_g$=0.861***).

Number of secondary branches per plant with number of pods plant$^{-1}$ ($r_p$=0.395***, $r_g$=0.594***); number of seeds plant$^{-1}$ ($r_p$=0.404***, $r_g$=0.619***), biological yield plant$^{-1}$ ($r_p$=0.504***, $r_g$=1.013***) and seed yield (kg/ha) ($r_p$=0.376***, $r_g$=0.761***); plant height with 100-seed weight ($r_p$=0.296**, $r_g$=0.335**); number of pods plant$^{-1}$ with number of seeds plant$^{-1}$ ($r_p$=0.641***, $r_g$=0.909***), biological yield plant$^{-1}$ ($r_p$=0.271**, $r_g$=0.291**) and seed yield (kg/ha) ($r_p$=0.302**, $r_g$=0.323**) all positive and significant at both phenotypic and genotypic level.

Number of seeds plant$^{-1}$ exhibited significant and positive association with biological yield plant$^{-1}$ ($r_p$=0.432***, $r_g$=0.64***) and seed yield (kg/ha) ($r_p$=0.33**, $r_g$=0.386***); biological yield plant$^{-1}$ with seed yield (kg/ha) ($r_p$=0.330**, $r_g$=0.349**) similarly, seed yield (kg/ha) with harvest index ($r_p$=0.459***, $r_g$=0.52***) positive and significant at both the phenotypic and genotypic level indicating the possibility of simultaneous improvement of these characters through selection. However significant and negative inter character association was observed for days to 50% flowering with number of primary branches plant$^{-1}$ ($r_p$=-0.257*, $r_g$=-0.530***), number of pods plant$^{-1}$ ($r_p$=-0.242*, $r_g$=-0.350**), number of seeds plant$^{-1}$ ($r_p$=-0.223*, $r_g$=-0.263*), biological yield plant$^{-1}$ ($r_p$=-0.264*, $r_g$=-0.310**) and seed yield (kg/ha) ($r_p$=-0.317**, $r_g$=-0.503***); days to maturity with number of primary branches plant$^{-1}$ ($r_p$=-0.315**, $r_g$=-0.59***), number of pods plant$^{-1}$ ($r_p$=-0.241*, $r_g$=-0.38***) and biological yield plant$^{-1}$ ($r_p$=-0.328**, $r_g$=-0.474***); biological yield plant$^{-1}$ with harvest index ($r_p$=-0.245*, $r_g$=-0.318**) at phenotypic and genotypic levels, indicating 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 traits.

Based on association studies, improvement in pigeonpea can be attained by isolating individuals possessing high values for the characters like primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds plant$^{-1}$and biological yield plant$^{-1}$.

**Table 4.3: Phenotypic and Genotypic correlations for yield and yield components in pigeonpea genotypes**

| Character | Corre. Coeffi. | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **G** | 1 | 0.861*** | 0.977*** | -0.201 | -0.53*** | 0.11 | -0.350** | -0.38*** | -0.263* | 0.243* | -0.31** | -0.357*** | 0.060 | -0.244* | 0.102 | **-0.297**** |
| | **P** | 1 | 0.733*** | 0.941*** | -0.134 | -0.257* | 0.046 | -0.242* | -0.143 | -0.223* | 0.339** | -0.264* | -0.317** | 0.021 | -0.164 | 0.051 | **-0.254*** |
| **2** | **G** | | 1 | 0.951*** | -0.59*** | -0.785*** | 0.182 | -0.38*** | -0.47*** | -0.33** | 0.185 | -0.474*** | -0.503*** | 0.057 | 0.057 | 0.011 | **-0.453***** |
| | **P** | | 1 | 0.910*** | -0.315** | -0.312*** | 0.019 | -0.241* | -0.175 | -0.208 | 0.101 | -0.328** | 0.405*** | -0.022 | -0.082 | -0.001 | **-0.298**** |
| **3** | **G** | | | 1 | -0.39*** | -0.670*** | 0.142 | -0.37*** | -0.43*** | -0.299** | 0.28** | -0.390*** | -0.438*** | 0.049 | -0.101 | 0.079 | **-0.379***** |
| | **P** | | | 1 | -0.236* | -0.297** | 0.049 | -0.256* | -0.169 | -0.224* | 0.195 | -0.299** | -0.385*** | -0.009 | -0.140 | 0.044 | **-0.284**** |
| **4** | **G** | | | | 1 | 1.074*** | 0.26* | -0.099 | 0.52*** | 0.351** | 0.133 | 0.836*** | 0.861*** | 0.183 | -0.259* | 0.293** | **0.735***** |
| | **P** | | | | 1 | 0.353*** | 0.257* | 0.064 | 0.021 | 0.132 | 0.125 | 0.394*** | 0.319** | 0.006 | -0.109 | 0.041 | **0.260**** |
| **5** | **G** | | | | | 1 | -0.073 | 0.594*** | 0.212* | 0.619*** | 0.018 | 1.013*** | 0.761*** | 0.176 | 0.181 | 0.271* | **0.971***** |
| | **P** | | | | | 1 | -0.057 | 0.395*** | -0.053 | 0.404*** | 0.080 | 0.504*** | 0.376*** | -0.102 | -0.046 | 0.076 | **0.579***** |
| **6** | **G** | | | | | | 1 | 0.015 | 0.73*** | -0.029 | 0.334** | -0.062 | 0.0938 | 0.201 | 0.042 | 0.197 | **-0.221*** |
| | **P** | | | | | | 1 | 0.081 | 0.184 | 0.002 | 0.296** | 0.060 | 0.089 | 0.098 | 0.105 | 0.129 | **-0.154** |
| **7** | **G** | | | | | | | 1 | 0.49*** | 0.909*** | -0.37*** | 0.291** | 0.323** | 0.045 | 0.271* | 0.40*** | **0.663***** |
| | **P** | | | | | | | 1 | -0.019 | 0.641*** | -0.173 | 0.271* | 0.302** | 0.045 | 0.087 | 0.152 | **0.579***** |
| **8** | **G** | | | | | | | | 1 | 0.0286 | 0.47*** | -0.016 | -0.024 | -0.187 | 0.306** | -0.192 | **-0.022** |
| | **P** | | | | | | | | 1 | -0.061 | 0.156 | 0.0347 | 0.010 | -0.116 | 0.107 | -0.032 | **-0.093** |
| **9** | **G** | | | | | | | | | 1 | -0.38*** | 0.641*** | 0.386*** | 0.117 | 0.245* | 0.353*** | **0.809***** |
| | **P** | | | | | | | | | 1 | -0.20 | 0.432*** | 0.330** | -0.024 | 0.039 | 0.223* | **0.59****** |
| **10** | **G** | | | | | | | | | | 1 | -0.054 | -0.122 | 0.017 | 0.441*** | 0.021 | **-0.323**** |
| | **P** | | | | | | | | | | 1 | 0.029 | -0.065 | 0.047 | 0.13 | -0.002 | **-0.136** |
| **11** | **G** | | | | | | | | | | | 1 | 0.349** | -0.318** | 0.099 | 0.097 | **0.542***** |
| | **P** | | | | | | | | | | | 1 | 0.330 ** | -0.245* | 0.044 | 0.132 | **0.497***** |
| **12** | **G** | | | | | | | | | | | | 1 | 0.520 | 0.039 | 0.154 | **0.636***** |
| | **P** | | | | | | | | | | | | 1 | 0.459*** | 0.083 | 0.106 | **0.527***** |
| **13** | **G** | | | | | | | | | | | | | 1 | 0.009 | 0.362 | **0.273*** |
| | **P** | | | | | | | | | | | | | 1 | 0.047 | 0.109 | **0.170** |
| **14** | **G** | | | | | | | | | | | | | | 1 | 0.421*** | **0.124** |
| | **P** | | | | | | | | | | | | | | 1 | 0.118 | **-0.004** |
| **15** | **G** | | | | | | | | | | | | | | | 1 | **0.326**** |
| | **P** | | | | | | | | | | | | | | | 1 | **0.201** |

**Note: Significant at 5% level, 1% and 0.1% level of significance**

Note: 1-Days to 50% flowering, 2-Days to maturity, 3- Pollen fertility, 4- No.of primary branches plant$^{-1}$,5-No.of secondary branches plant$^{-1}$, 6-Plant height, 7-Pods plant$^{-1}$, 8-Seeds pod$^{-1}$,9-Seeds plant$^{-1}$, 10-100Seed weight, 11-Biological yield plant$^{-1}$, 12-Yield(kg/ha), 13-Harvest index, 14-seed protein content, 15-Dal recovery% and 16-Yield plant$^{-1}$.

### 4.3.2 Path coefficient analysis

The path coefficient analysis provides a more realistic evidence of the interrelationship, as it considers direct and indirect effects of the variables by partitioning the correlation coefficients. Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation into measures its 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 based on correlated response may not be fruitful. Hence, critical evaluation, the correlation coefficient need to be split into its 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.

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.

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 was estimated considering seed yield plant$^{-1}$ as a dependent

character. In the present investigation all the 28 genotypes were subjected to path analysis for all the traits. The results obtained were presented in Table 4.4.

A perusal of these results revealed genotypic and phenotypic path co-efficients to be of similar direction and magnitude in general. Further, the genotypic path coefficients were observed to be of higher magnitude, compared to phenotypic path coefficients indicating the masking effect of environment. The results also indicated moderately higher residual effect for both the phenotypic (0.5680) and genotypic (0.4788) path co-efficients respectively indicating that variables studied in the present investigation explained only about 43 (phenotypic) and 52 (genotypic) percent of the variability in yield and therefore, other attributes besides the characters studied are contributing for seed yield plant$^{-1}$ and needs to be considering in further studies. The detailed path coefficient analysis showed that pollen fertility% had maximum positive direct effect ($P_p$=0.547 and $P_g$=23.942) fallowed by biological yield plant$^{-1}$ ($P_p$=0.289 and $P_g$=1.858), harvest index ($P_p$ =0.196 and $P_g$ =1.184), number of secondary branches plant$^{-1}$ ($P_p$=0.297 and $P_g$=0.117) and dal recovery% ($P_p$=0.059 and $P_g$=0.004).

Whereas, the characters *viz.*, days to 50% flowering ($P_p$=–0.362 and $P_g$=-13.137), days to maturity ($P_p$=-0.223 and $P_g$=-11.752), and seed protein content ($P_p$=-0.019 and $P_g$=-0.141) showed negative and high direct effects on grain yield at both genotypic and phenotypic levels. Whereas, number of seeds plant$^{-1}$($P_p$=0.195 and $P_g$=-1.238), number of primary branches ($P_p$=0.122 and $P_g$=-1.014), 100-seed weight ($P_p$=0.288 and $P_g$=-0.242) and number of seeds pod$^{-1}$ ($P_p$=0.007 and $P_g$=-0.191) in these cases genotypic had showed negative direct effect but phenotypic had showed positive and direct effects on the seed yield plant$^{-1}$.

Plant height ($P_p$=-0.270 and $P_g$=0.212), number of pods plant$^{-1}$($P_p$=-0.390 and $P_g$=1.008), at genotypic level had showed positive direct effect but negative direct effect on the grain yield phenotypic level. The highly significant and positive correlation of pollen fertility% had found with grain yield due to their maximum direct and indirect effect via days to 50% flowering and days to maturity respectively.

Number of seeds pod$^{-1}$ showed medium positive direct effect and their genotypic correlation with grain yield was significant.

Characters *viz.*, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, pods plant$^{-1}$, seeds pod$^{-1}$, seeds plant$^{-1}$, biological yield plant$^{-1}$, seed protein content had high positive indirect effect *via* days to 50% flowering ($P_g$=2.38, 7.072, 4.593, 4.951, 3.457, 4.074 and 3.205) at genotypic levels, respectively. *Via* days to maturity characters *viz.*, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, pods plant$^{-1}$, seeds pod$^{-1}$, seeds plant$^{-1}$and biological yield plant$^{-1}$ had high positive indirect effect at genotypic levels ($P_g$=7.132, 9.333, 4.472, 5.524, 3.885 and 5.574). Characters *viz.*, days to 50% flowering, days to maturity and pollen fertility% had showed positive indirect effect *via* number of primary branches plant$^{-1}$at genotypic levels ($P_g$=0.182, 0.609 and 0.381). Also, characters *viz.*, number of secondary branches plant$^{-1}$, seeds pod$^{-1}$, seeds plant$^{-1}$and biological yield plant$^{-1}$had showed positive indirect effects at genotypic levels *via* pods plant$^{-1}$($P_g$=, 0.599, 0.505, 0.918 and 0.294). Similarly, *via* seeds plant$^{-1}$ characters *viz.*, days to maturity, pollen fertility% and 100-seed weight were showed positive indirect effects at genotypic levels ($P_g$=0.408, 0.377 and 0.474). Characters *viz.*, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, pods plant$^{-1}$and seeds plant$^{-1}$ were showed positive indirect effects at genotypic levels ($P_g$=1.566, 1.894, 0.542 and 1.193). And characters *viz.*, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$ and plant height had showed positive indirect effects at genotypic levels *via* harvest index ($P_g$=, 0.215, 0.209 and 0.239).

Whereas, characters *viz.*, days to maturity, pollen fertility%, 100-seed weight, harvest index and dal recovery% had high negative indirect effect *via* days to 50% flowering ($P_g$=-11.309, -12.804, -4.448, -0.791 and -1.342) at genotypic levels, respectively. *Via* days to maturity characters *viz.*, days to 50% flowering and pollen fertility% had high negative indirect effect at genotypic levels ($P_g$=-10.121, -11.206). *Via* pollen fertility% characters *viz.*, number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, seeds plant$^{-1}$, biological yield plant$^{-1}$ and seed protein

content were showed negative indirect effects at genotypic levels ($P_g$=-9.083, -16.277, -7.306, -9.362 and -2.623). Characters *viz.,* plant height, seeds pod$^{-1,}$ seeds plant$^{-1}$, biological yield plant$^{-1}$and dal recovery% had showed negative indirect effects at genotypic levels ($P_g$=-0.234, -0.537, -0.368, -0.845 and -0.308). Moderately high negative indirect effects showed *via* pods plant$^{-1}$were *viz.,* days to 50% flowering, days to maturity, pollen fertility% and 100-seed weight at genotypic levels($P_g$=-0.333, -0.384, -0.379 and -0.374). In addition, characters *viz.,* number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, biological yield plant$^{-1}$, dal recovery% and seed protein content were showed negative indirect effects at genotypic levels ($P_g$=-0.452, -0.774, -0.791, -0.436 and -0.303) *via* seeds plant$^{-1}$. And *via* biological yield plant$^{-1}$ characters *viz.,* days to maturity, pollen fertility% and harvest index were showed negative indirect effects at genotypic levels ($P_g$=-0.883, -0.728 and -0.592).

Considering overall observation of path analysis the traits *viz.,* pollen fertility%, biological yield plant$^{-1}$, harvest index, pods plant$^{-1}$and number of primary branches plant$^{-1}$ showed considerable positive direct influence on seed yield plant$^{-1}$. However, the character pollen fertility% did not exhibit positive correlation on yield due to its high negative indirect effect *via* days to 50% flowering, days to maturity, pods plant$^{-1}$ and biological yield plant$^{-1}$. Hence, improving seed yield of pigeonpea may be possible through selection for these traits.

The character seed yield plant$^{-1}$ had high to moderate positive indirect effects *via* characters *viz.,* pods plant$^{-1}$, seeds plant$^{-1}$, number of secondary branches plant$^{-1}$ and biological yield plant$^{-1}$ also exhibited the significant and positive association with seed yield.

Similar results are also reported by Rao *et.al.* (2013) for number of primary branches, pods plant$^{-1,}$ seeds pod$^{-1}$, days to 50% flowering and harvest index.

**4.4: Genotypic and Phenotypic path co-efficient for yield and yield components in pigeonpea**

| Character | Path coeff. | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | $r_g$ and $r_p$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **G** | **-13.13** | -10.121 | 23.331 | 0.182 | -0.068 | 0.023 | -0.353 | 0.072 | 0.325 | -0.083 | -0.577 | 0.071 | 0.000 | 0.034 | **-0.297**** |
| | **P** | **-0.362** | -0.388 | -0.499 | 0.071 | 0.136 | -0.024 | 0.128 | 0.076 | 0.118 | -0.129 | 0.139 | -0.011 | -0.027 | 0.087 | **-0.254*** |
| **2** | **G** | -11.309 | **-11.752** | 22.814 | 0.609 | -0.099 | 0.038 | -0.384 | 0.089 | 0.408 | -0.045 | -0.883 | 0.068 | 0.000 | -0.008 | **-0.453***** |
| | **P** | -0.275 | **-0.223** | -0.341 | 0.118 | 0.117 | -0.007 | 0.090 | 0.066 | 0.078 | -0.038 | 0.123 | 0.008 | 0.001 | 0.031 | **-0.298**** |
| **3** | **G** | -12.804 | -11.206 | **23.942** | 0.381 | -0.085 | 0.030 | -0.379 | 0.080 | 0.377 | -0.069 | -0.728 | 0.066 | 0.000 | 0.015 | **-0.379***** |
| | **P** | 0.837 | 0.809 | **0.547** | -0.210 | -0.265 | 0.043 | -0.228 | -0.151 | -0.199 | 0.173 | -0.266 | -0.008 | 0.039 | -0.125 | **-0.284**** |
| **4** | **G** | 2.380 | 7.132 | -9.083 | **-1.014** | 0.138 | 0.049 | -0.064 | -0.102 | -0.452 | -0.032 | 1.565 | 0.215 | 0.001 | 0.044 | **0.735***** |
| | **P** | -0.012 | -0.029 | -0.022 | **0.122** | 0.033 | 0.024 | 0.006 | 0.002 | 0.012 | 0.012 | 0.037 | 0.001 | 0.004 | -0.010 | **0.260**** |
| **5** | **G** | 7.072 | 9.333 | -16.277 | -1.108 | **0.117** | -0.017 | 0.599 | -0.042 | -0.774 | -0.005 | 1.894 | 0.209 | 0.001 | -0.026 | **0.971***** |
| | **P** | -0.056 | -0.067 | -0.064 | 0.076 | **0.297** | -0.013 | 0.085 | -0.011 | 0.087 | 0.017 | 0.108 | -0.022 | 0.016 | -0.010 | **0.579***** |
| **6** | **G** | -1.433 | -2.126 | 3.419 | -0.234 | -0.01 | **0.212** | 0.014 | -0.138 | 0.037 | -0.081 | -0.115 | 0.239 | 0.001 | -0.006 | **-0.221*** |
| | **P** | -0.011 | -0.005 | -0.012 | -0.063 | 0.014 | **-0.270** | -0.020 | -0.046 | -0.000 | -0.074 | -0.015 | -0.024 | -0.032 | -0.026 | **-0.154** |
| **7** | **G** | 4.593 | 4.472 | -8.984 | 0.064 | 0.074 | 0.003 | 1.008 | -0.095 | -1.122 | 0.090 | 0.542 | 0.054 | 0.002 | -0.038 | **0.663***** |
| | **P** | -0.073 | -0.072 | -0.077 | 0.019 | 0.118 | 0.024 | -0.390 | -0.006 | 0.192 | -0.051 | 0.081 | 0.014 | 0.046 | 0.026 | **0.579***** |
| **8** | **G** | 4.951 | 5.524 | -10.008 | -0.537 | 0.027 | 0.154 | 0.505 | **-0.191** | -0.035 | -0.114 | -0.031 | -0.222 | -0.001 | -0.043 | **-0.022** |
| | **P** | -0.001 | -0.001 | -0.001 | 0.000 | -0.000 | 0.001 | -0.000 | **0.007** | -0.001 | 0.001 | 0.000 | -0.001 | -0.000 | 0.001 | **-0.093** |
| **9** | **G** | 3.457 | 3.885 | -7.306 | -0.368 | 0.079 | -0.006 | 0.918 | -0.006 | **-1.238** | 0.092 | 1.193 | 0.139 | 0.001 | -0.034 | **0.809***** |
| | **P** | -0.032 | -0.03 | -0.033 | 0.019 | 0.059 | 0.000 | 0.093 | -0.009 | **0.195** | -0.029 | 0.063 | -0.004 | 0.033 | 0.006 | **0.59****** |
| **10** | **G** | -4.448 | -2.179 | 6.74 | -0.134 | 0.002 | 0.071 | -0.374 | -0.089 | 0.474 | **-0.242** | -0.101 | 0.019 | 0.000 | -0.062 | **-0.323**** |
| | **P** | -0.005 | -0.002 | -0.004 | -0.003 | -0.002 | -0.006 | 0.004 | -0.003 | 0.004 | **0.288** | -0.001 | -0.001 | 0.000 | -0.003 | **-0.136** |
| **11** | **G** | 4.074 | 5.574 | -9.362 | -0.845 | 0.129 | -0.013 | 0.294 | 0.003 | -0.791 | 0.013 | **1.858** | -0.377 | 0.000 | -0.015 | **0.542***** |
| | **P** | -0.057 | -0.071 | -0.065 | 0.085 | 0.109 | 0.013 | 0.059 | 0.008 | 0.094 | 0.006 | **0.289** | -0.053 | 0.029 | 0.009 | **0.497***** |
| **12** | **G** | -0.791 | -0.673 | 1.334 | -0.182 | 0.022 | 0.043 | 0.046 | 0.036 | -0.145 | -0.004 | -0.592 | **1.184** | 0.001 | -0.001 | **0.273*** |
| | **P** | 0.004 | -0.004 | -0.001 | 0.001 | -0.019 | 0.019 | 0.009 | -0.023 | -0.005 | 0.009 | -0.048 | **0.196** | 0.021 | 0.01 | **0.170** |
| **13** | **G** | -1.342 | -0.125 | 1.471 | -0.308 | 0.035 | 0.042 | 0.406 | 0.037 | -0.436 | -0.005 | 0.181 | 0.428 | **0.004** | -0.059 | **0.326**** |
| | **P** | 0.003 | 0.0001 | 0.003 | 0.002 | 0.004 | 0.008 | 0.009 | -0.000 | 0.013 | -0.000 | 0.001 | 0.006 | **0.059** | 0.007 | **0.201** |
| **14** | **G** | 3.205 | -0.669 | -2.623 | 0.318 | 0.023 | 0.009 | 0.273 | -0.058 | -0.303 | -0.107 | 0.186 | 0.011 | 0.002 | **-0.141** | **0.124** |
| | **P** | 0.003 | 0.002 | 0.003 | 0.002 | 0.000 | -0.002 | -0.001 | -0.002 | -0.001 | -0.003 | -0.001 | 0.001 | 0.001 | **-0.019** | **-0.004** |

* **Residual effect=0.4788 for Genotypic path and Residual effect=0.5680 for Phenotypic path coefficients. Diagonal values = direct effects Off-diagonal values = indirect effects.**

* Note: 1-Days to 50% flowering, 2-Days to maturity, 3-Pollen fertility%, 4- No.of primary branches plant$^{-1}$,5-No.of secondary branches plant$^{-1}$, 6-Plant height, 7-Pods plant$^{-1}$, 8-Seeds pod$^{-1}$,9-Seeds plant$^{-1}$, 10-100Seed weight, 11-Biological yield plant$^{-1}$, 12-Harvest index, 13-Dal recovery% and 14-seed protein content.

* $r_g$ and $r_p$ – Gnotypic correlation and Phenotypic correlation

### 4.4 Fertility restoration in CMS based hybrids

Pollen fertility percentage 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 mandatory for successful production of high yielding CMS-based hybrids of pigeonpea. In present investigation, the pollen fertility percentage was studied and presented in table 4.5 and 4.6. Based on data obtained the pollen fertility percentage range varied from 83.00 to 87.33 % among all genotypes.

**Table 4.5: Pollen fertility% in CMS based pigeonpea hybrids**

| Sl.no. | Hybrids | Pollen fertility% |
|---|---|---|
| 1 | ICPA 2200 X ICPL 11229 | 85.67 |
| 2 | ICPA 2200 X ICPL 20116 | 84.00 |
| 3 | ICPA 2202 X ICPL 11237 | 86.33 |
| 4 | ICPA 2202 X ICPL 20093 | 86.33 |
| 5 | ICPA 2202 X ICPL 20108 | 83.67 |
| 6 | ICPA 2202 X ICPL 20116 | 85.67 |
| 7 | ICPA 2203 X ICPL 11229 | 86.33 |
| 8 | ICPA 2203 X ICPL 11237 | 87.00 |
| 9 | ICPA 2203 X ICPL 20093 | 87.33 |
| 10 | ICPA 2203 X ICPL 20108 | 83.00 |
| 11 | ICPA 2203 X ICPL 20116 | 86.00 |
| 12 | ICPA 2204 X ICPL 11237 | 86.67 |
| 13 | ICPA 2204 X ICPL 11229 | 83.33 |
| 14 | ICPA 2204 X ICPL 20116 | 83.33 |
| 15 | Asha (check) | 98.53 |
| 16 | Maruti(check) | 97.85 |

Among 14 hybrids, ICPH 4602 recorded maximum pollen fertility (87.33%) followed by ICPH 4680 (87.00%) and ICPH 4679 (86.33%).Whereas minimum pollen fertility was recorded in ICPH 4682 (83.33%) followed by ICPH 4542 (83.33%) and ICPH 4573 (83.67%). Out of 14 CMS based hybrids 14 (ICPH 4746 (85.67%), ICPH 4571 (84%), ICPH 4748 (86.33%), ICPH 4606 (86.33%), ICPH 4573 (83.67%), ICPH 4588 (85.67%), ICPH 4679 (86.33%), ICPH 4680 (87%), ICPH 4602 (87.33%), ICPH 4572 (83%), ICPH 4564 (86%), ICPH 4683 (86.67%), ICPH 4682 (83.33%) and ICPH 4567 (83.33%)) showed high fertility restoration with more than 80% pollen

fertility. It means that the R lines used in these crosses were good restorers. Because of high pollen fertility% in their hybrids.

Sawargaonkar et al. (2012), Saxena *et al.* (2014), Reddy *et al.* (2015), Saroj *et al*. (2015) and Kumar *et al.* (2015) also reported similar results for fertility restoration in pigeonpea CMS lines.

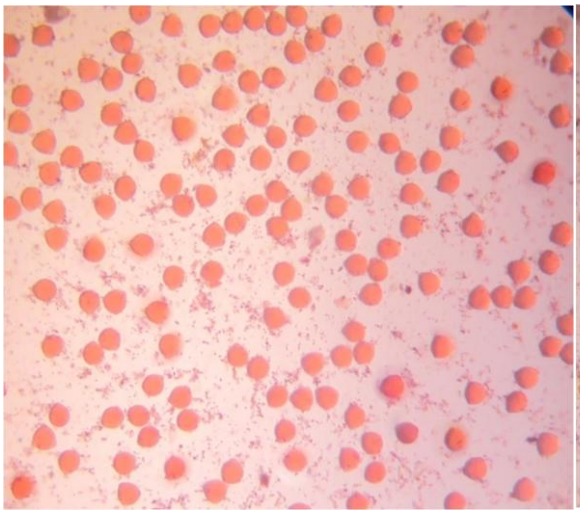


**Fig. No.4.1: Microscopic view of pollen grains produced by male fertile plant.**

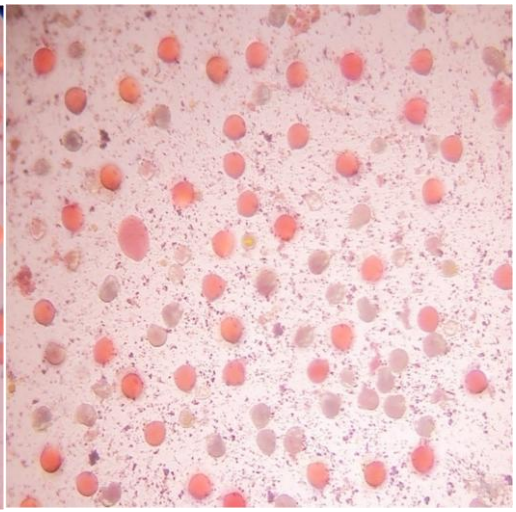


**Fig. No.4.2: Microscopic view of pollen grains produced by partial male fertile plant**

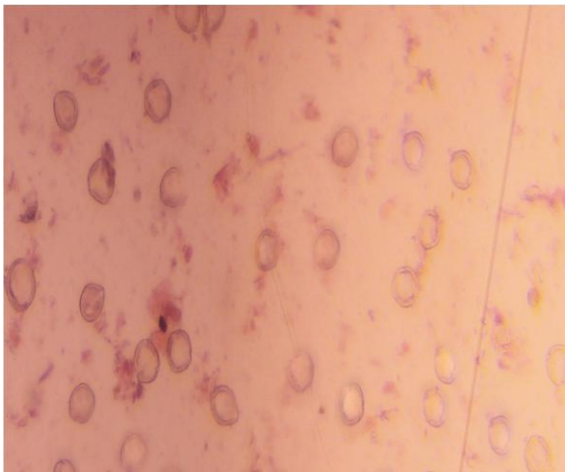


**Fig. No.4.3: Microscopic view of pollen grains produced by partial male sterile plant.**

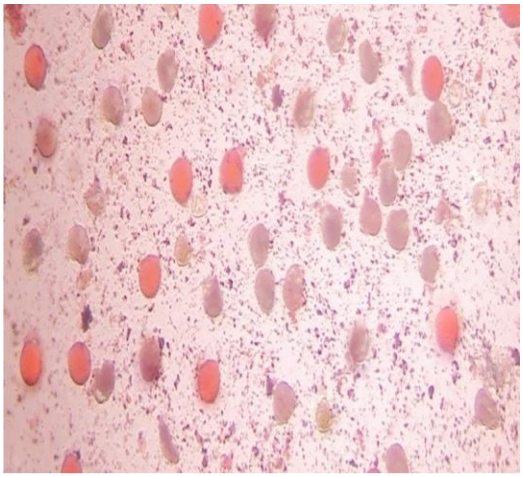


**Fig. No.4.4: Microscopic view of pollen grains produced by fully male sterile plant.**

**Table 4.6: Fertility restoration studies in pigeonpea hybrids**

| R lines | No.of crosses attempted | Pollen fertility status of the hybrids | Extent of fertility restoration (%) | Hybrids produced |
|---|---|---|---|---|
| ICPL 11229 | 3 | Fully fertile– 3 | 83.33 – 86.33 | ICPH4746,ICPH4679& ICPH4682 |
| ICPL 20116 | 4 | Fully fertile – 4 | 83.33 - 86 | ICPH4567,ICPH4564, ICPH4588 & ICPH4571 |
| ICPL 11237 | 3 | Fully fertile – 3 | 86.33 – 87 | ICPH 4748, ICPH4680 & ICPH 4683 |
| ICPL 20093 | 2 | Fully fertile – 2 | 87.33 - 86.33 | ICPH4602 & ICPH4606 |
| ICPL 20108 | 2 | Fully fertile – 2 | 83 – 83.67 | ICPH4573 & ICPH4572 |
| Asha | Check | Fully fertile | 87.88 | Check |

## 4.5 Heterosis

Commercial exploitation of heterosis in crop plants is regarded as a major breakthrough in the realm of plant breeding. Heterosis breeding had led to considerable yield improvement of several cereal and other crops (Rai, 1979). Saxena and Sharma, (1990), reported a considerable additive and non-additive gene action that can be exploited in heterosis breeding of pigeonpea. 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 vigour 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 filial generation. 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 also revealed significant levels of heterosis for yield and yield component characters. The results on heterosis of 14 pigeonpea hybrids in the present study, different levels of heterosis were measured as percent increase or decrease of hybrids over mid-parent (relative heterosis), better parent (heterobeltiosis) and the standard heterosis for different characters. For standard heterosis, two check varieties were taken. The research findings for different traits are presented in Tables 4.7a, 4.7b, 4.7c and 4.7d and are discussed hereunder.

### 4.6.1 Days to 50% flowering

Among 14 hybrids, ICPH 4748 (-7.536%), ICPH 4606 (-7.826%), ICPH 4573 (-15.384%), ICPH 4680 (-0.314%), ICPH 4572 (-6.289%), ICPH 4683 (-3.773%), ICPH 4682 (-7.547%) and ICPH 4567 (-10.105%) showed negative desirable heterosis for days to 50% flowering over better parent. The range of heterobeltiosis for days to 50% flowering was from -15.384% (ICPH 4573) to -0.314% (ICPH 4680). For relative heterosis, out of 14 hybrids, 10 hybrids showed desirable negative heterosis of which, ICPH 4573 (-14.655%) recorded with the highest negative heterosis followed by ICPH 4572 (-10.911%). However, ICPH 4746 (4.715%), ICPH 4564 (1.960%), ICPH 4571(0.846%) and ICPH 4679 (0.314%) exhibited positive heterosis. The relative heterosis for days to 50% flowering ranged from -14.655% (ICPH 4573) to 4.715% (ICPH 4746).

All the hybrids showed negative heterosis for days to 50% flowering over standard check variety, Asha. Among these, five hybrids ICPH 4682 (-16.239%), ICPH 4567 (-15.099%), ICPH 4571 (-15.099%), ICPH 4602 (-15.099%) and ICPH 4683 (-12.821%) were significantly earlier than the standard check and the rests were on par. The range of standard heterosis varied from -16.239% (ICPH 4682) to 7.407% (ICPH 4602).

All the hybrids had desirable negative heterosis for days to 50% flowering. Among these, hybrids ICPH 4682, ICPH 4573, ICPH 4567, ICPH 4571, and ICPH 4683 were the top five hybrids with significant negative heterosis. Early to flower and mature is a desirable trait in hybrid pigeonpea in escaping drought and ensuring high yield. Based on the present research findings, the hybrid ICPH 4682 ranked first in higher negative heterosis indicating the presence of exploitable hybrid vigour for early flowering.

Wankhade *et al*. (2005) also reported significant negative heterosis for days to 50% flower in the hybrids based on genetic male-sterility system where as Sarode *et al*. (2009) investigated significant negative heterosis in long duration pigeonpea.

Kandalkar (2007) and Shoba and Balan (2010) reported significant negative heterosis in CMS based hybrids showing preference for the early flowering hybrids.

**4.6.2 Days to maturity**

Negative heterosis in days to maturity over different levels of heterosis is a desirable heterosis for early maturity. Among all the 14 hybrids, the significant negative heterosis over better parent was observed in eleven hybrids. Among these, hybrid ICPH 4748 (-9.980%) showed the highest negative value followed by ICPH 4602 (-8.889%), ICPH 4606 (-6.042%) and ICPH 4567 (-3.68%). Almost all the hybrids showed negative heterosis except three hybrids *viz.*, ICPH 4571, ICPH 4588 and ICPH 4680 for positive heterosis for days to maturity was observed. The negative heterosis over mid parent was observed in 13 out of 14 hybrids. One hybrid ICPH 4680 (0.658%) showed positive heterosis with mid parent. The range of relative heterosis varied from -7.771% (ICPH 4748) to -0.662% (ICPH 4571). All the hybrids manifested significant negative heterosis for days to maturity over the check variety Asha and Maruti. ICPH 4746 (-12.103%) was the earliest to mature followed by ICPH 4572 (-11.905), ICPH 4567 (-11.706), ICPH 4571 (-10.714%), ICPH 4606 (-10.516%) and ICPH 4683 (-10.119%), respectively.

Heterosis for days to maturity ranged from -9.980 to 1.119%, -7.771 to -0.439% and 12.103 to -8.929% over better, mid and standard parent respectively.

Extent of negative heterosis for days to maturity was reported by Chaudhari (1979) and Pandey and Singh (2002). The crosses maturing early involved at least one early maturing parent. Phad (2003) and Kandalkar (2007), Sarode et al. (2009), and Shoba and Balan (2010) also reported similar results on heterosis in pigeonpea.

**4.6.3 Plant height**

For the character plant height the hybrids *viz.*, ICPH 4606 (19.574), ICPH 4748 (15.887), ICPH 4573 (-13.050), ICPH 4588 (-11.915), ICPH 4682 (-2.974%) and ICPH 4602 (-1.727%) recorded with the negative heterobeltiosis. Moreover, eight hybrids ICPH 4564 (9.326%), ICPH 4572 (6.947%), ICPH 4679 (6.736%), ICPH 4746 (5.348%), ICPH 4571 (5.088%), ICPH 4683 (2.760%), ICPH 4567 (2.281%), and ICPH 4680 (1.796%) showed positive heterosis for plant height. Out of 14 hybrids nine hybrids, ICPH 4564 (10.183%), ICPH 4572 (7.955), ICPH 4679 (7.384), ICPH 4746 (6.747), ICPH 4571 (6.299), ICPH 4683 (3.835), ICPH 4567 (2.461), ICPH 4602 (2.987) and ICPH 4680 (1.709%) showed positive heterosis over mid parent for plant height. Five hybrids *viz.*, ICPH 4748, ICPH 4606, ICPH 4573, ICPH 4588 and ICPH 4682 exhibited negative heterosis for plant height over mid parent in plant height (Table 4.12). The range of relative heterosis for plant height varied from 10.183% (ICPH 4564) to -7.879% (ICPH 4606). All hybrids manifested significant positive heterosis over standard check Asha. In these ICPH 4564 (14.258%) showed highest positive value followed by ICPH 4572 (13.897), ICPH 4588 (12.092%), ICPH 4679 (11.550) and ICPH 4746 (8.771%) for plant height, respectively.

Heterosis for plant height ranged from -19.574% to 9.326% for heterobeltiosis, -7.879% to 10.183% for relative heterosis and 0.179% to 14.258% for standard heterosis, respectively.

Several workers including Solomon *et al*. (1957), Singh (1971), Sharma et al. (1973), Veeraswamy *et al*. (1973), Chaudhari (1979), Jain, and Saxena (1990) reported significant positive heterosis for plant height. Pandey and Singh (2002) reported negative standard heterosis for plant height in pigeonpea. The negative heterosis in the context of breeding dwarf genotype will be desirable. However, later

Wankhade *et al*. (2005), Sarode *et al*. (2009), and Shoba and Balan (2010) also reported significant positive heterosis for plant height.

**4.6.4 Number of primary branches plant$^{-1}$**

The 14 hybrids under study showed positive heterosis for number of primary branches plant$^{-1}$ over better parent. In these ICPH 4606 (26.184%) exhibited the high positive heterosis for number of primary branches plant$^{-1}$ over better parent followed by ICPH 4679 (20.675%), ICPH 4683 (17.460%) and ICPH 4564 (16.580%). The range of heterobeltiosis for number of primary branches plant$^{-1}$ varied from 26.675% (ICPH 26.184%) to 0.000% (ICPH 4680). Fourteen out of 14 hybrids recorded positive heterosis for number of primary branches plant$^{-1}$ over mid parent. Among these, ICPH 4606 (36.296%) was the high positive heterosis over mid parent and ICPH 4571 (1.905%) showed the lowest positive heterosis over mid parent for number of primary branches plant$^{-1}$. The range of relative heterosis for number of primary branches plant$^{-1}$ varied from 36.296% (ICPH 4606) to 1.905% (ICPH 4571). Out of 14 hybrids, two hybrids were had negative heterosis over standard check and the rest 12 hybrids manifested positive heterosis for number of primary branches plant$^{-1}$. Among these, ICPH 4572 (22.832%) was the high positive heterosis over standard check and followed by ICPH 4564 (16.581%), ICPH 4683 (15.643%) and ICPH 4679 (15.018%) showed significant positive heterosis for number of primary branches plant$^{-1}$ over standard variety Asha. Two hybrids ICPH 4682 (-3.422%) and ICPH 4680 (-1.547%) recorded negative heterosis for number of primary branches plant$^{-1}$ over Asha.

Among the 14 hybrids, all are manifested positive heterosis over mid, better parents and standard variety, respectively. Except ICPH 4682 (-3.422%) and ICPH 4680 (-1.547%) where these two hybrids showed negative heterosis for number of primary branches plant$^{-1}$ over standard check variety Asha. For the number of primary branches plant$^{-1}$, the range of heterosis over better parent, mid parent and standard check was from 26.676% to 0.000%, 36.296% to 1.905% and 22.832% to -3.422%, respectively.

Solomon et al. (1957) also reported significant negative heterosis for branches, likewise Chaudhary (1979), Narladkar and Khapre (1996), Pandey and Singh (2002),

Wankhade *et al*. (2005), and Sarode *et al*. (2009) also in agreement with the present findings. However, Shoba and Balan (2010) reported significant positive and negative heterosis in CMS/GMS based pigeonpea hybrids.

**4.6.5 Number of secondary branches plant$^{-1}$**

Out of 14 hybrids, twelve showed significant positive heterosis for number of secondary branches plant$^{-1}$ over better parent. In these, ICPH 4748 (30.492%) was noted with the highest positive heterosis for number of secondary branches plant$^{-1}$ and followed by ICPH 4564 (26.101%), ICPH 4683 (22.676%), ICPH 4606 (22.308%) and ICPH 4602 (18.333%). The range of heterobeltiosis for number of secondary branches plant$^{-1}$ varied from 30.492% (ICPH 4748) to -10.444% (ICPH 4588). All the 14 hybrids were significantly positive over mid parent. The range of relative heterosis for number of secondary branches plant$^{-1}$ was from 41.199% (ICPH 4748) to 3.224% (ICPH 4746).

Standard heterosis revealed that nine hybrids showed significant positive heterosis for number of secondary branches plant$^{-1}$ over Asha. Among these ICPH 4571(18.837%) was manifested the highest positive heterosis over Asha followed by ICPH 4573(18.606%), ICPH 4567 (13.982%) and ICPH 4606 (10.283%). Five hybrids ICPH 4680 (-9.254%), ICPH 4588 (-7.866), ICPH 4679 (-7.751%), ICPH 4746 (-5.439%), and ICPH 4682 (-3.127%) showed negative heterosis for number of secondary branches plant$^{-1}$ over the standard variety. The range of heterosis for number of secondary branches plant$^{-1}$ over better, mid and standard check was from 30.492 to -10.444%, 41.199 to 3.224% and 18.837 to -7.867% respectively.

**4.6.6 Number of pod plant$^{-1}$**

Among 14 hybrids, five hybrids ICPH 4567 (24.369%), ICPH 4748 (23.982%), ICPH 4680 (22.917%), ICPH 4571 (17.321%) and ICPH 4573 (6.675%) showed positive heterosis for number of pods plant$^{-1}$ over better parent. All the hybrids were showed positive heterosis for number of pods plant$^{-1}$ over mid parent. The range of relative heterosis for number of pods plant$^{-1}$ was from 48.798 (ICPH 4571) to -10.850% (ICPH 4588). All the hybrids showed significant positive heterosis for number of pods plant$^{-1}$ over Asha. Among these hybrids, ICPH 4567 (113.011%)

was the highest positive heterosis over standard check Asha and followed by ICPH 4571 (101.455%), ICPH 4748 (75.297%), ICPH 4683 (62.830%) and ICPH 4682 (59.502%). The range of standard heterosis for number of pods plant$^{-1}$ was from 113.011 to 22.814%. The range of heterosis for number of pods plant$^{-1}$ was from 24.369 to -10.011% for heterobeltiosis, 48.798 to -10.850% for relative heterosis, and 113.011 to 22.814% for standard heterosis.

These observations are in agreement with findings of Singh (1971), Veeraswamy *et al*. (1973), Chaudhari (1979), Patel and Patel (1992), Pandey and Singh (2002) and Kandalakar (2007). Narladkar and Khapre (1996) reported that heterosis for grain yield was due to total number of pods plant$^{-1.}$

**4.6.7 Number of seeds pod$^{-1}$**

Out of 14 hybrids, ten hybrids showed negative heterosis for number of seeds pod$^{-1}$ over better parent. Among these, ICPH 4748 (-5.177%) was the highest over better parent followed by ICPH 4588 (-4.814%), ICPH 4680 (-2.894%), ICPH 4588 (-2.816%) and ICPH 4602 (-2.148%) recorded negative heterosis for number of seeds pod$^{-1}$ over better parent. Hybrids ICPH 4679 (3.641%), ICPH 4571 (2.622%) and ICPH 4746 (2.434%) showed significant heterobeltiosis in positive direction. Six hybrids showed positive heterosis for number of seeds pod$^{-1}$ over mid-parent. Among these, ICPH 4679 (3.933%) was showed the highest positive heterosis for number of seeds pod$^{-1}$ over mid-parent followed by ICPH 4571 (2.622%), ICPH 4746 (2.579%) and ICPH 4606 (1.111%) showed positive heterosis for number of seeds pod$^{-1}$ over mid-parent while eight hybrids manifested negative in relative heterosis for number of seeds pod$^{-1}$. Among these, ICPH 4588 (-3.366%) was the highest negative heterosis over mid parent followed by ICPH 4573 (-2.015%), ICPH 4748 (-1.834%) and ICPH 4602 (1.596%). ICPH 4679 (6.017%) was showed the highest heterosis over standard check Asha followed by ICPH 4571 (4.680%), ICPH 4746 (4.489%), ICPH 4606 (4.298%), ICPH 4572 (3.725%) and ICPH 4567 (2.388%) exhibited standard heterosis in positive direction for number of seeds pod$^{-1}$. Two hybrids, ICPH 4680 (-0.669%) and ICPH 4748 (-0.287%) had showed negative heterosis for number of seeds pod$^{-1}$ but it was on par with Asha.

The *per se* range of heterosis over better, mid and standard parent varied from 3.641% to -5.177%, 3.933% to -3.366% and 6.017 to -0.669%, respectively. The number of seeds pod$^{-1}$ is also an important character, which contributes to the higher yield.

On contrary to the above findings, Phad (2003) reported seeds pod$^{-1}$ as an important character, which is positively correlated with grain yield. Wankhade *et al*. (2005) also reported significant positive heterosis for seeds pod$^{-1}$.

**4.6.8 Number of Seeds plant$^{-1}$**

Six hybrids ICPH 4567 (33.769%), ICPH 4683 (23.615%), ICPH 4748 (19.261%), ICPH 4682 (8.237%), ICPH 4573 (0.511%) and ICPH 4572 (0.040%) showed positive heterosis for number of seeds plant$^{-1}$ over better parent. Eight hybrids ICPH 4746, ICPH 4571, ICPH 4606, ICPH 4588, ICPH 4679, ICPH 4680, ICPH 4602 and ICPH 4564 were showed negative heterosis for number of seeds plant$^{-1}$ over better parent. Similarly, significant positive heterosis for number of seeds plant$^{-1}$ over mid-parent was observed in all hybrids except one hybrid (ICPH 4606). Among these hybrids, ICPH 4567 (44.129%) was recorded the highest positive heterosis over mid parent followed by ICPH 4748 (26.261%), ICPH 4683 (22.240%), ICPH 4571 (13.985%), ICPH 4564 (13.945%) and ICPH 4679 (11.215%) for number of seeds plant$^{-1}$. One hybrid ICPH 4606 showed negative relative heterosis for number of seeds plant$^{-1}$. All hybrids manifested positive heterosis for number of seeds plant$^{-1}$ over Asha. Among these, ICPH 4567 (100.570%) was showed highest positive heterosis over Asha followed by ICPH 4683 (55.207%), ICPH 4748 (49.740%), ICPH 4682 (48.835%), ICPH 4564 (46.052%), ICPH 4588 (40.389%) and ICPH 4571 (39.378%) exhibited standard heterosis for number of seeds plant$^{-1}$ in desirable direction. Heterosis for number of seeds plant$^{-1}$ ranged from 33.769 to -15.366%, 44.129 to -6.448% and 100.570 to 16.737% over better, mid and standard parent, respectively.

**4.6.9 100-seed weight**

ICPH 4571 (4.51%) and ICPH 4680 (1.81%) were exhibited positive heterosis over better parent. The rest of all the hybrids exhibited negative heterosis over better parent. Out of 14 hybrids, 12 showed negative heterosis for 100-seed weight over

better parent. The range of heterobeltiosis was from 4.51 (ICPH 4571) to -11.05% (ICPH 4682). For relative heterosis, ICPH 4746, ICPH 4571, ICPH 4679, ICPH 4680, ICPH 4602, ICPH 4564 and ICPH 4683 manifested significant positive heterosis for 100seed weight. The other tested hybrids were on par with mid-parent and showed negative heterosis for 100-seed weight. All the hybrids were exhibited negative heterosis for 100-seed weight over standard check Asha. The range of heterosis for 100-seed weight in the present findings was from 4.51 to -11.05%, 4.98 to -5.81% and -1.90 to -17.62% over better, mid and standard parent respectively.

The above findings are in agreement with the findings of Chaudhari (1979), Reddy *et al*. (1979), Manivel *et al*. (1999), Deshmukh *et al*. (2001), Wankhade *et al*. (2005) and Kandalkar (2007) who also reported positive standard heterosis in pigeonpea for 100seed weight.

**4.6.10 Biological yield plant$^{-1}$**

Out of fourteen hybrids, 10 were recorded positive heterosis over better parent. Among these, ICPH 4683 (44.77%) showed the highest positive heterosis for biological yield plant$^{-1}$ over better parent followed by ICPH 4567 (35.06%), ICPH 4748 (34.54%), ICPH 4680 (17.15%), ICPH 4571(16.28%) and ICPH 4573 (8.21%) showed positive heterosis and four hybrids, ICPH 4746 (-3.60%), ICPH 4606 (-6.47%), ICPH 4602 (-1.42%) and ICPH 4572 (-1.83%) had showed negative heterosis for biological yield plant$^{-1}$ over better parent. The range of heterobeltiosis was from 44.77% (ICPH 4683) to -6.47% (ICPH 4606). Out of 14 hybrids, 11 hybrids were recorded significant positive heterosis over mid parent. Among these, ICPH 4748 (56.40%) showed highest positive heterosis over mid parent followed by ICPH 4683 (47.79%), ICPH 4567 (46.80%), ICPH 4573 (36.85%) and ICPH 4680 (27.71%) recorded positive heterosis for biological yield plant$^{-1}$ over mid parent. Only three hybrids, ICPH 4602 (-0.84%), ICPH 4746 (0.46%) and ICPH 4572 (-0.19%) showed negative heterosis for biological yield plant$^{-1}$ over mid parental value. Among fourteen hybrids, 11 were showed positive heterosis for biological yield plant$^{-1}$ over Asha. In these, ICPH 4567 (37.58%) was recorded the highest followed by ICPH 4683 (29.15%), ICPH 4680 (25.22%), ICPH 4748 (20.02%), and ICPH 4573 (19.60%)

showed positive heterosis for biological yield plant$^{-1}$ over Asha. Three hybrids showed negative heterosis over the standard variety, Asha. The range of standard heterosis for biological yield plant$^{-1}$ was from 37.58% (ICPH 4567) to -10.20% (ICPH 4746). The range of heterobeltiosis for biological yield plant$^{-1}$ varied from 44.77 to -6.47%, 56.40 to -0.84% for relative heterosis, and 37.58 to -10.20% for standard heterosis.

**4.6.11 Seed yield plant$^{-1}$ (g)**

The range of heterobeltiosis varied from 38.85% (ICPH 4573) to -55.88% (ICPH 4571). Out of fourteen hybrids, six hybrids showed significant positive heterosis over better parent. Among these ICPH 4573 (38.85%) was recorded the highest heterosis over better parent followed by ICPH 4683 (32.12%), ICPH 4572 (21.19%), ICPH 4606 (6.78%), ICPH 4602 (2.54%) and ICPH 4748 (1.20%) showed significant and positive heterosis for seed yield plant$^{-1}$ over better parent and eight hybrids, ICPH 4746, ICPH 4571, ICPH 4588, ICPH 4679, ICPH 4680, ICPH 4564, ICPH 4682 and ICPH 4567 were recorded negative heterosis for seed yield plant$^{-1}$ over better parent.

The relative heterosis revealed that, out of fourteen hybrids, ten hybrids, ICPH 4573 (86.08%), ICPH 4572 (55.17%), ICPH 4606 (51.71%), ICPH 4683 (41.11%), ICPH 4602 (39.96%), ICPH 4748 (37.61%), ICPH 4588 (19.67%), ICPH 4680 (16.68%), ICPH 4679 (10.98%) and ICPH 4746 (4.26%) exhibited relative heterosis for seed yield plant$^{-1}$ in positive direction. ICPH 4567 (-27.03%), ICPH 4571 (-23.02%), ICPH 4564 (-23.27%) and ICPH 4682 (-7.12%) had showed the negative heterosis for seed yield plant$^{-1}$ over mid-parent. ICPH 4567 (38.456%), ICPH 4683 (37.022%), ICPH 4564 (24.465%), ICPH 4571 (21.676%), ICPH 4573 (20.166%), ICPH 4606 (11.6241%), ICPH 4602 (7.1922%), ICPH 4572 (4.877%), ICPH 4588 (4.56439%) and ICPH 4682 (3.75%) showed significant positive heterosis for seed yield plant$^{-1}$ over Asha. Four hybrids ICPH 4680 (-18.83%), ICPH 4746 (-9.901%), ICPH 4748 (-8.414%) and ICPH 4679 (-6.591%) manifested negative heterosis for seed yield plant$^{-1}$ over Asha. The range of standard heterosis was from 38.456 (ICPH 4567) to 18.83% (ICPH 4680). Based on the present investigation, a wide range of positive and negative heterosis was observed in seed yield plant$^{-1}$.

The estimated range of heterosis over better, mid, and standard parents for seed yield plant$^{-1}$ varied from 38.85 to -55.88%, 86.08 to -27.03%, and 38.456 to -18.83%, respectively.

Yadav and Singh (2004), Sekhar *et al*. (2004) and Wankhade *et al*. (2005) also reported positive standard heterosis for seed yield plant$^{-1}$ in pigeonpea. The positive heterosis could be useful for further exploitation (Wanjari *et al*., 2007).

**4.6.12 Pollen fertility %**

All hybrids were exhibited negative heterosis for pollen fertility % over better parent. Among these, ICPH 4573 (10.561%) was recorded the highest negative heterosis for pollen fertility % over better parent followed by ICPH 4748 (-10.493%), ICPH 4683 (-10.147%), ICPH 4680 (-9.801%), ICPH 4588 (-8.544%), ICPH 4606 (8.156%) and ICPH 4602 (-7.447%) showed significant negative heterosis for pollen fertility % over better parent. The range of heterobeltiosis for pollen fertility % was from -10.561% (ICPH 4573) to -0.265% (ICPH 4571).

Relative heterosis, twelve hybrids ICPH 4748 (-9.239%), ICPH 4606 (-7.995%), ICPH 4573 (-7.009%), ICPH 4683 (-5.743%), ICPH 4680 (-5.21%), ICPH 4572 (-4.289%), ICPH 4602 (-3.867%), ICPH 4682 (-3.844%), ICPH 4588 (-3.387%), ICPH 4567 (-2.664%), ICPH 4679 (-0.321%) and ICPH 4571(-0.068%) manifested negative heterosis for pollen fertility %. Two hybrids showed positive heterosis recorded in ICPH 4746 (0.784%) and ICPH 4564 (0.779%) over mid-parent for pollen fertility %. Out of 14 hybrids, all were exhibited negative standard heterosis for pollen fertility % over standard check Asha. Among these, ICPH 4572 (-4.831%) was recorded highest negative heterosis over mid parent followed by ICPH 4567 (-4.704%), ICPH 4682 (-4.577%), ICPH 4571 (-4.068%), ICPH 4746 (1.905%) and ICPH 4748 (-1.269%) exhibited negative standard heterosis for pollen fertility % over standard check.

**4.6.13 Seed yield (kg /ha)**

All the 14 hybrids recorded positive heterosis in desirable direction over better parent. Among these ICPH 4564 (69.31%) was exhibited highest positive heterosis over better parent followed by ICPH 4573 (57.78%), ICPH 4588 (41.15%), ICPH

4571 (40.72%), ICPH 4606 (38.21%) and ICPH 4602 (23.71%) were noted with positive heterosis for seed yield (kg/ha) over better parent. The range of heterobeltiosis for seed yield (kg/ha) was from 69.31% (ICPH 4564) to 1.47% (ICPH 4567). For relative heterosis, all hybrids manifested significant positive heterosis for seed yield (kg/ha). Among these ICPH 4564 (122.99%) was recorded the highest positive heterosis for seed yield (kg/ha) over mid parent followed by ICPH 4573 (115.73%), ICPH 4588 (96.31%), ICPH 4606 (79.93%), ICPH 4571 (73.18%), ICPH 4748 (60.32%) and ICPH 4680 (54.96%) manifested positive heterosis for seed yield (kg/ha). Out of 22 hybrids, nine ICPH 2671 (208.44%), ICPH 2740 (121.45%), ICPH 3477 (119.45%), ICPH 3491 (134.17%), ICPH 3497 (88.93%), ICPH 3761 (102.17%), ICPH 3933 (80.47%), ICPH 4017 (184.9%), ICPH 4022 (155.64%) exhibited significant standard heterosis for seed yield (kg/ha). Two hybrids ICPH 4602 (-1.23%) and ICPH 4567 (-0.81%) showed negative heterosis for seed yield (kg/ha) over standard check.

Hybrids ICPH 4746(47.41%), ICPH 4571(37.55%), ICPH 4748(12.3%), ICPH 4606(10.36%), ICPH 4573(46.01%), ICPH 4588(37.97%), ICPH 4679(36.05%), ICPH 4680(14.64%), ICPH 4572(12.69%), ICPH 4564(65.65.49%), ICPH 4683(6.79%), and ICPH 4682(47.37%) exhibited positive heterosis for seed yield (kg/ha) over standard check indicating the presence of exploitable heterosis in this material of pigeonpea. In the present study, ICPH 4564 showed 69.31% heterobeltiosis, 122.99% relative heterosis, and 65.49% standard heterosis for seed yield (kg/ha) respectively.

Sekhar *et al*. (2004) also reported supportive standard heterosis over 40% in pigeonpea. Kandalkar (2007) reported significant positive heterosis (upto – 155.7%) for grain yield in CMS based hybrids of pigeonpea. In general, positive and high magnitude of heterosis for grain yield was noticed and this may be due to the heterosis contributed by one or more yield contributing characters (Chandirakala *et al*., 2010). Similar findings has also been recorded in the present study.

### 4.6.14 Harvest index

Out of 14 hybrids, nine hybrids *viz.*, ICPH 4564 (47.68%), ICPH 4682 (44.88%), ICPH 4606 (22.87%), ICPH 4588 (18.41%), ICPH 4680 (4.07%), ICPH 4573 (3.93%), ICPH 4683 (1.93%), ICPH 4602 (1.84%) and ICPH 4748 (1.10%) exhibited positive heterosis for harvest index over standard check Asha. Five hybrids ICPH 4571 (-22.58%), ICPH 4567 (-18.09%), ICPH 4572 (-17.59%), ICPH 4679 (-13.59%) and ICPH 4746 (-0.88%) showed negative heterosis for harvest index over standard check Asha. Hybrids ICPH 4606, ICPH 4588, ICPH 4680, ICPH 4602, ICPH 4564, ICPH 4582 and ICPH 4683 exhibited positive heterosis for harvest index over mid parent, better parent and standard check indicating the presence of exploitable heterosis in pigeonpea.

Out of 14 hybrids, eight hybrids *viz.*, ICPH 4679 (-30.42%), ICPH 4571 (-26.66%), ICPH 4567 (-22.40%), ICPH 4746 (-20.18%), ICPH 4748 (-9.04%), ICPH 4573 (-6.50%), ICPH 4572 (-7.07%) showed negative heterosis for harvest index over better parent. Seven hybrids *viz*., ICPH 4606(10.54%), ICPH 4588(6.53%), ICPH 4680(1.89%), ICPH 4602(14.58%), ICPH 4564(39.91%), ICPH 4683(2.75%) and ICPH 4682(16.68%) were recorded with the positive heterosis for harvest index over better parent. Among these ICPH 4564 (39.91%) and ICPH 4683 (2.75%) showed highest and lowest positive heterosis for harvest index over better parent. The range of heterobeltiosis for harvest index varied from -30.42% (ICPH 4679) to 39.91% (ICPH 4564). For relative heterosis, eight hybrids *viz.*, ICPH 4564 (57.76%), ICPH 4682 (34.66%), ICPH 4606 (22.85%), ICPH 4602 (19.43%), ICPH 4680 (15.07%), ICPH 4588 (9.28%), ICPH 4683 (7.18%) and ICPH 4573 (4.02%) manifested positive heterosis for harvest index over mid parent. Although six hybrids showed negative heterosis over mid-parent.

### 4.6.15 Dal recovery %

Eight hybrids *viz*., ICPH 4746 (5.80%), ICPH 4564 (3.00%), ICPH 4748 (2.10%), ICPH 4567 (2.03%), ICPH 4680 (1.49%), ICPH 4683 (1.09%), ICPH 4606 (0.83%) and ICPH 4572 (0.41%) showed positive heterosis for dal recovery % over

better parent. ICPH 4573 (-7.34%), ICPH 4679 (-3.46%), ICPH 4602 (-1.42%), ICPH 4682 (-0.94%) and ICPH 4748 (-0.10%) showed negative heterosis for dal recovery % over better parent. The range of heterobeltiosis for dal recovery % was from -7.34% (ICPH 4573) to 5.80% (ICPH 4746).

For relative heterosis, nine hybrids ICPH 4746 (7.561%), ICPH 4567 (5.492%), ICPH 4564 (5.809%), ICPH 4571 (5.105%), ICPH 4683 (3.288%) and ICPH 4680 (3.020%) manifested significant positive heterosis for dal recovery %. Although five hybrids showed negative heterosis for dal recovery %, they were on par to mid-parent. Out of 14 hybrids, twelve hybrids *viz.*, ICPH 4679 (-10.23%), ICPH 4573 (-10.19%), ICPH 4682 (-9.19%), ICPH 4602 (-8.43%), ICPH 4572 (-6.73%), ICPH 4746 (-3.31%), ICPH 4683 (-3.22%), ICPH 4588 (-2.93%), ICPH 4606 (-2.27%) exhibited negative standard heterosis for dal recovery % over check Asha. Two hybrids ICPH 4564 (1.05%) and ICPH 4567 (0.10%) showed positive heterosis for dal recovery % over standard check. Hybrids ICPH 4567 and ICPH 4564 exhibited positive heterosis for dal recovery % over mid parent, better parent and standard check indicating the presence of exploitable heterosis in pigeonpea.

**4.6.16 Seed protein content**

Six hybrids *viz*., ICPH 4683 (5.95%), ICPH 4682 (1.55%), ICPH 4567 (1.35%), ICPH 4680 (1.66%), ICPH 4680 (1.01%) and ICPH 4571 (0.61%) showed positive heterosis for seed protein content over better parent. Eight hybrids showed negative heterosis *viz.*, ICPH 4588 (-10.66%), ICPH 4606 (-8.39%) and ICPH 4572 (-2.48%) showed negative heterosis for seed protein content. The range of heterobeltiosis for seed protein content varied from -10.66% (ICPH 4588) to 5.95% (ICPH 4683).

For relative heterosis, nine hybrids ICPH 4683 (6.230%), ICPH 4573 (3.493%), ICPH 4682 (3.234%), ICPH 4564 (3.068%), ICPH 4567 (2.434%) and ICPH 4680 (1.595%) manifested positive heterosis for seed protein content. Although five hybrids showed negative heterosis for seed protein content, they were on par to mid-parent. Out of 14 hybrids, all hybrids showed negative heterosis for seed protein content over standard check Asha. ICPH 4746 (-3.85%), ICPH 4571 (-3.62%), ICPH

4748 (-1.99%), ICPH 4606 (-8.18%), ICPH 4573 (-0.48%), ICPH 4588 (-10.46%), ICPH 4679 (-4.35%), ICPH 4680 (-4.83%), ICPH 4602 (-7.47%) exhibited negative heterosis for seed protein content over standard check Asha.

For seed protein content, none of the hybrid had expressed positive heterosis over better parent, mid parent and standard check Asha. It indicated that no definite heterotic relation of seed protein content was existed to the line of heterosis for seed yield. It appears from the data that hybrids showing positive heterosis for seed yield but are negative in heterosis for seed protein content. Indicated that parents with moderate to low in seed protein may result high heterotic hybrids for seed yield.

**Table 4.7a: Mid parent (MPH), better parent (BPH) and standard heterosis (SH) for yield and yield components in pigeonpea hybrids**

| | | DFF | | | DM | | | NPBr | | | NScBr | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sl.No.** | **Hybrid** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** |
| 1 | ICPH 4746 | 4.715* | 1.258 | -8.262* | -2.208 | -2.208 | -12.10* | 11.545* | 10.627* | 7.204* | 3.224* | -1.439 | -5.439* |
| 2 | ICPH 4571 | 0.846 | 1.258 | -15.19* | -0.662 | 0.671 | -10.71* | 1.905 | 0.328 | 0.328 | 24.992** | 15.512** | 18.837** |
| 3 | ICPH 4748 | -9.117* | -7.54* | -9.117* | -7.771* | -9.98* | -10.55* | 19.989** | 7.619* | 5.954* | 41.199** | 30.492** | 9.358* |
| 4 | ICPH 4606 | -9.402* | -7.826* | -9.402* | -7.771* | -6.042* | -10.55* | 36.296** | 26.918** | 15.02* | 36.774** | 22.308* | 10.283* |
| 5 | ICPH 4573 | -14.655* | -15.39** | -15.385* | -7.771* | -0.442 | -10.55* | 22.333** | 4.872* | 14.71* | 37.253** | 16.584* | 18.606** |
| 6 | ICPH 4588 | -2.034 | 6.463* | -10.826* | -7.567* | 1.119 | -10.32* | 22.105** | 8.767* | 8.767* | 5.917* | -10.444* | -7.867* |
| 7 | ICPH 4679 | 0.315 | 0.315 | -9.117* | -1.097 | -0.442 | -10.55* | 22.667** | 20.676** | 15.02* | 6.40* | -3.849* | -7.751* |
| 8 | ICPH 4680 | -6.074* | -0.315 | -9.687* | 0.658 | 0.6579 | -8.929* | 3.270* | 0.000 | -1.547 | 12.545* | 8.283* | -9.254* |
| 9 | ICPH 4602 | -3.704* | 2.201 | -7.407* | -0.877 | -8.889* | -10.32* | 17.265** | 16.252** | 7.204* | 27.306** | 18.333* | 6.699* |
| 10 | ICPH 4572 | -10.91* | -6.289* | -15.19** | -2.632* | -2.632* | -11.91* | 21.861** | 12.302** | 22.832** | 14.315* | 0.676 | 2.422 |
| 11 | ICPH 4564 | 1.961 | 5.66* | -11.11* | -0.439 | -0.439 | -9.921* | 21.301** | 16.581** | 16.581** | 33.614** | 26.101** | 10.051* |
| 12 | ICPH 4683 | -9.333* | -3.774* | -12.82* | -1.948 | -1.948 | -10.12* | 26.496** | 17.46** | 15.643** | 24.354** | 22.676** | 5.659* |
| 13 | ICPH 4682 | -7.547* | -7.547* | -16.24** | -2.597 | -2.597* | -10.71* | 7.488* | 1.328 | -3.422* | 6.413* | 0.969 | -3.127* |
| 14 | ICPH 4567 | -10.11* | -6.289* | -15.099* | -2.09* | -3.679* | -11.71* | 11.196* | 2.516* | 2.516 | 20.612** | 10.793* | 13.982* |

Where, *, ** = significant at 5% and 1% level, respectively.

Note: MPH-mid parent heterosis, BPH-better parent heterosis, SCH-Standard heterosis (Asha).

Note: DF-Days to 50% flowering, DM-Days to maturity, NPBr- No.of primary branches plant$^{-1}$ and NScBr-No.of secondary branches plant$^{-1}$.

**Table 4.7b: Mid parent (MPH), better parent (BPH) and standard heterosis (SH) for yield and yield components in pigeonpea hybrids (conti..)**

| | | Pht | | | P/Pl | | | S/P | | | S/Pl | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sl.No.** | **Hybrid** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** |
| 1 | ICPH 4746 | 6.747* | 5.348* | 8.771* | 17.764** | -0.278 | 43.062** | 2.579 | 2.434 | 4.489* | 5.564* | -10.90* | 22.521** |
| 2 | ICPH 4571 | 6.299* | 5.088* | 8.121* | 48.798** | 17.621** | 101.455** | 2.622* | 2.622* | 4.68* | 13.985** | -7.043* | 39.378** |
| 3 | ICPH 4748 | -7.704* | -15.887** | 7.038* | 45.291** | 23.982** | 75.297** | -1.834 | -5.177* | -0.287 | 26.261** | 19.261** | 49.74** |
| 4 | ICPH 4606 | -7.879* | -19.574** | 2.345 | -3.676* | -6.290* | 40.098** | 1.111 | -0.817 | 4.298* | -6.448* | -15.366** | 16.737** |
| 5 | ICPH 4573 | -5.329* | -13.05* | 10.648* | 8.906* | 6.675* | 50.827** | -2.015 | -2.816* | 2.197 | 7.558* | 0.511 | 29.125** |
| 6 | ICPH 4588 | -2.588 | -11.915* | 12.092** | -10.85* | -18.628** | 39.37** | -3.366* | -4.814* | 0.096 | 7.342* | -6.369* | 40.389** |
| 7 | ICPH 4679 | 7.384* | 6.736* | 11.55* | 14.624** | -6.740* | 33.79** | 3.933* | 3.641* | 6.017* | 11.215* | -1.358 | 35.641** |
| 8 | ICPH 4680 | 1.709 | 1.796 | 6.388* | 29.347** | 22.917** | 22.814** | -0.811 | -2.894* | -0.669 | 5.36* | -2.671* | 22.203** |
| 9 | ICPH 4602 | 2.987* | -1.727 | 2.706 | 12.354** | -10.011* | 34.535** | -1.596 | -2.148 | 0.096 | 7.241* | -5.011* | 31.02** |
| 10 | ICPH 4572 | 7.955* | 6.947* | 13.897** | 13.043** | -5.971* | 27.499** | 0.836 | 0.277 | 3.725* | 9.433* | 0.040 | 28.521** |
| 11 | ICPH 4564 | 10.183* | 9.326* | 14.258** | 13.346** | -13.553** | 48.062** | -0.327 | -0.467 | 1.815 | 13.945** | -2.592 | 46.052** |
| 12 | ICPH 4683 | 3.835* | 2.760* | 7.579* | 22.593** | -1.748 | 62.83** | 1.379 | -1.021 | 1.815 | 22.24** | 23.615** | 55.207** |
| 13 | ICPH 4682 | -2.632* | -2.974* | 0.179 | 3.175* | -3.756* | 59.502** | -1.587 | -2.136 | 0.669 | 11.952* | 8.237* | 48.835** |
| 14 | ICPH 4567 | 2.461 | 2.281 | 5.233* | 26.416** | 24.369** | 113.011** | -0.047 | -0.464 | 2.388* | 44.129** | 33.769** | 100.57** |

Where, *, ** = significant at 5% and 1% level, respectively.

Note: MPH-mid parent heterosis, BPH-better parent heterosis, SCH-Standard heterosis (Asha).

Note: Pht-Plant height, P/Pl-Pods plant$^{-1}$, S/P-Seeds pod$^{-1}$ and S/Pl-Seeds plant$^{-1}$.

**Table 4.7c: Mid parent (MPH), better parent (BPH) and standard heterosis (SH) for yield and yield components in pigeonpea hybrids (conti..)**

| | | 100swt. | | | BY/Pl | | | Y/Pl | | | PF% | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sl.No.** | **Hybrid** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** |
| 1 | ICPH 4746 | 2.51* | -3.64* | -8.33* | -0.46 | -3.60* | -10.20* | 4.26* | -24.73** | -9.901* | 0.784 | -0.388 | -1.905 |
| 2 | ICPH 4571 | 4.98* | 4.51* | -12.50** | 25.25** | 16.28** | 18.45** | -26.02** | -55.88** | 21.676** | -0.068 | -0.265 | -4.068* |
| 3 | ICPH 4748 | -0.19 | -8.15* | -4.02* | 56.40** | 34.54** | 20.02** | 37.61** | 1.20 | -8.414* | -9.239* | -10.493* | -1.269 |
| 4 | ICPH 4606 | -4.71* | -10.00* | -5.96* | 16.29** | -6.47* | -1.21 | 51.71** | 6.78* | 11.624* | -7.995* | -8.156* | -1.141 |
| 5 | ICPH 4573 | -3.39* | -6.12* | -1.90 | 36.85** | 8.21* | 19.60** | 86.08** | 38.85** | 20.166** | -7.089* | -10.561* | -4.068* |
| 6 | ICPH 4588 | -5.59* | -15.31** | -11.51** | 26.84** | 3.43* | 5.37* | 19.67** | -20.87** | 4.564* | -3.387* | -8.544* | -1.905 |
| 7 | ICPH 4679 | 2.55* | -1.28 | -6.08* | 12.42** | 5.20* | 12.45** | 10.98* | -21.97** | -6.591* | -0.321 | -0.894 | -1.269 |
| 8 | ICPH 4680 | 1.91 | 1.81 | -10.38* | 27.71** | 17.15** | 25.22** | 16.68** | -10.31* | -18.83** | -5.210* | -9.801* | -0.505 |
| 9 | ICPH 4602 | 2.17 | -0.50 | -7.58* | -0.84 | -1.42 | 5.37* | 39.96** | 2.54 | 7.1922* | -3.867* | -7.447* | -0.378 |
| 10 | ICPH 4572 | -0.82 | -6.14* | -7.45* | -0.19 | -1.83 | 8.50* | 55.17** | 21.19** | 4.877* | -4.289* | -4.47* | -4.831* |
| 11 | ICPH 4564 | 0.22 | -2.66* | -14.31** | 7.65* | 5.12* | 12.36** | -23.27** | -54.87** | 24.47** | 0.779 | -1.149 | -1.523 |
| 12 | ICPH 4683 | 0.63 | -1.24 | -13.25** | 47.79** | 44.77** | 29.15** | 41.11** | 32.12** | 37.022** | -5.744* | -10.147* | -0.887 |
| 13 | ICPH 4682 | -5.81* | -11.05* | -15.37** | 9.20* | 4.75* | -2.42 | -7.12* | -13.33** | 3.75* | -3.844* | -4.577* | -4.577* |
| 14 | ICPH 4567 | -1.66 | -2.58 | -17.62** | 46.80** | 35.06** | 37.58** | -27.03** | -49.80** | 38.456** | -2.664* | -4.704* | -4.704* |

Where, *, ** = significant at 5% and 1% level, respectively.

Note: MPH-mid parent heterosis, BPH-better parent heterosis, SCH-Standard heterosis (Asha)

Note: PF%-Pollen fertility, 100Swt-100-Seed weight, BY/Pl-Biological yield plant$^{-1}$ and Y/Pl-Yield plant$^{-1}$

**Table 4.7d: Mid parent (MPH), better parent (BPH) and standard heterosis (SH) for yield and yield components in pigeonpea hybrids (cont.)**

| | | Y(kg/ha) | | | HI | | | DR% | | | SPC | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sl.No.** | **Hybrid** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** | **MPH** | **BPH** | **SCH** |
| 1 | ICPH 4746 | 54.74** | 13.90* | 47.41** | -3.33 | -20.18** | -0.88 | 7.561* | 5.80* | -3.31* | -0.198 | -0.76 | -3.85* |
| 2 | ICPH 4571 | 73.18** | 40.72** | 37.55** | -16.95* | -26.66** | -22.58** | 5.105* | -0.10 | -1.99 | 0.633 | 0.61 | -3.62 |
| 3 | ICPH 4748 | 60.32** | 15.44* | 12.30* | -3.89 | -9.04* | 1.10 | 2.731* | 2.10* | -1.04 | 0.807 | -2.22 | -1.99 |
| 4 | ICPH 4606 | 79.93** | 38.21** | 10.36* | 22.85* | 10.54* | 22.87** | 2.994* | 0.83 | -2.27* | -5.778* | -8.39* | -8.18* |
| 5 | ICPH 4573 | 115.73** | 57.78** | 46.01** | 4.02 | -6.50* | 3.93* | -3.223* | -7.34* | -10.2* | 3.493* | -0.71 | -0.48 |
| 6 | ICPH 4588 | 96.31** | 41.15** | 37.97** | 9.28* | 6.53* | 18.41* | -0.464 | -1.06 | -2.93* | -8.624* | -10.66* | -10.46* |
| 7 | ICPH 4679 | 51.08** | 5.12* | 36.05** | -16.04* | -30.42** | -13.59* | -2.675* | -3.46* | -10.33* | 0.679 | -1.27 | -4.35* |
| 8 | ICPH 4680 | 54.96** | 17.84* | 14.64* | 15.07* | 4.89* | 4.07* | 3.020* | 1.49 | -2.84 | 1.595 | 1.01 | -4.83* |
| 9 | ICPH 4602 | 51.35** | 23.71* | -1.23 | 19.43** | 14.58* | 1.84 | -1.401* | -1.42 | -8.43* | -1.456 | -2.26 | -7.47* |
| 10 | ICPH 4572 | 57.36** | 21.77* | 12.69* | -3.24 | -7.07* | -17.59* | 2.741* | 0.41 | -6.73* | -1.937 | -2.48 | -9.18* |
| 11 | ICPH 4564 | 122.99** | 69.31** | 65.49** | 57.76** | 39.91** | 47.68** | 5.809* | 3.00* | 1.05 | 3.068* | 1.66 | -2.66* |
| 12 | ICPH 4683 | 21.28* | 9.77* | 6.79* | 7.18* | 2.75* | 1.95 | 3.288* | 1.09 | -3.22 | 6.230* | 5.95* | -0.18 |
| 13 | ICPH 4682 | 41.54*** | 13.87* | 47.37** | 34.66** | 16.68* | 44.88** | -0.782 | -0.94 | -9.19* | 3.234* | 1.55 | -1.62 |
| 14 | ICPH 4567 | 12.35* | 1.47 | -0.81 | -16.66* | -22.40** | -18.09* | 5.492* | 2.03* | 0.10 | 2.434 | 1.35 | -2.96* |

Where, *, ** = significant at 5% and 1% level, respectively.

Note: MPH-mid parent heterosis, BPH-better parent heterosis, SCH-Standard heterosis (Asha)

Note: Y (kg/ha)-Yield (kg/ha), HI-Harvest index, SPC-seed protein content and DR%-Dal recovery% .

# CHAPTER-V

# SUMMARY AND CONCLUSION

The analysis of variance (ANOVA) for 28 genotypes revealed significant differences among the genotypes for all the characters studied, indicating the presence of sufficient amount of variability for carrying out various analyses. Studies on *per se* performance of the 28 genotypes were revealed that the lower means for days to 50 per cent flowering, days to maturity. Higher means for pollen fertility, plant height, number of primary and secondary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, number of seeds plant$^{-1}$, 100 seed weight, biological yield plant$^{-1}$, seed yield (kg/ha), harvest index, dal recovery, seed protein content, seed coat colour and seed yield plant$^{-1}$ for hybrids compared with B and R lines. Further, seed yield plant$^{-1}$ for hybrids was observed to range from 194.95g (ICPH 4567) to 114.29g (ICPH 4680) with a mean of 153.88g, B lines was observed to range from 146.02g (ICPB 2204) to 60.00g (ICPB 2202) with a mean of 87.32g, while for R lines, it was noticed to range from 186.05g (ICPL 20116) to 121.85g (ICPL 20108) with a mean of 151.68g. All hybrids, ICPH 4571, ICPH 4606, ICPH 4573, ICPH 4588, ICPH 4602, ICPH 4564, ICPH 4683 and ICPH 4682 recorded higher seed yield plant$^{-1}$ over the maximum value of R and B lines seed yield plant$^{-1}$. The B lines, ICPB 2200 and ICPB 2203 had also recorded seed yield plant$^{-1}$ on par with the maximum B line value, while the genotypes, ICPL 11229, ICPL 11237 and ICPL 20093 were also observed to possess seed yield plant$^{-1}$ on par with the maximum R line value. High seed yield plant$^{-1}$ of these genotypes was noticed to be due to more number of pods plant$^{-1}$ and number of seeds pod$^{-1}$.

The results on correlation coefficients for yield and yield components revealed that phenotypic and genotypic correlations obtained were in the similar direction and significance. In addition, 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, seed yield plant$^{-1}$ was observed to be significantly and positively associated with number of primary branches plant$^{-1}$, number of secondary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds pod$^{-1}$, biological yield plant$^{-1}$, seed yield (kg/ha) and harvest index indicating their importance as selection criteria in pigeonpea yield improvement programmes. 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, pollen fertility % and 100seed weight; days to maturity with pollen fertility and seed yield (kg/ha); number of primary branches plant$^{-1}$ with number of secondary branches plant$^{-1}$, plant height, biological yield plant$^{-1}$ and seed yield (kg/ha). Number of secondary branches plant$^{-1}$ with number of pods plant$^{-1}$; number of seeds plant$^{-1}$, biological yield plant$^{-1}$ and seed yield (kg/ha); plant height with 100seed weight; number of pods plant$^{-1}$ with number of seeds plant$^{-1}$, biological yield plant$^{-1}$ and seed yield (kg/ha); number of seeds plant$^{-1}$ with biological yield plant$^{-1}$ and seed yield (kg/ha); biological yield plant$^{-1}$ with seed yield (kg/ha); seed yield (kg/ha) with harvest index phenotypic and genotypic levels, indicating the possibility of simultaneous improvement of these characters through selection. However negative and significant inter character association was observed for days to 50% flowering with number of primary branches plant$^{-1}$, number of pods plant$^{-1}$, number of seeds plant$^{-1}$, biological yield plant$^{-1}$ and seed yield (kg/ha); days to maturity with number of primary branches plant$^{-1}$, number of pods plant$^{-1}$ and biological yield plant$^{-1}$; biological yield plant$^{-1}$ with harvest index at phenotypic and genotypic levels, indicating 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 traits.

A perusal of the results on path coefficients revealed that genotypic and phenotypic path coefficients noted in the similar in the direction and magnitude in general. Further, the genotypic path coefficients were observed to be of higher in magnitude as compared to phenotypic path co-efficients indicating the masking effect of environment. The results also revealed high residual effect for both phenotypic

(0.5680) and genotypic (0.4788) path co-efficients, respectively indicating that variables studied in the present investigation explained only about 44 (phenotypic) and 53 (genotypic) percent of the variability in yield and therefore, other attributes besides the characters studied are contributing for seed yield plant$^{-1}$. The detailed path co-efficient analysis showed that pollen fertility% had maximum direct effect fallowed by biological yield plant$^{-1}$, harvest index, number of pods plant$^{-1}$, number of secondary branches plant$^{-1}$ and dal recovery. In these traits, except pollen fertility% had also exhibited highly significant and positive association with seed yield plant$^{-1}$. High direct effects of these traits therefore appeared to be the main factor for their strong association with seed yield plant$^{-1}$. Hence, these traits should be considered as important selection criteria in all yield improvement programmes and direct selection for these traits are recommended. Further, studies on fertility restoration indicated that pollen fertility percent for the hybrids ranged from 83.00 to 87.33% with an average of 85.11%. Based on pollen fertility percent of the hybrids can classified into fully fertile, partial fertile and fully sterile but present study all hybrids were recorded more than 80% pollen fertility so all were categorized as fully fertile. In addition, R lines of 14 hybrids studied in the present investigation explained about their extent of fertility restoration percent based on their hybrids pollen fertility percent. Results showed that R lines, ICPL 11229, ICPL 11237, ICPL 20116, ICPL 20093 and ICPL 20108 were good restorers with more than 80% fertility restoration in their hybrids.

The present investigation also revealed significant levels of heterosis for yield and yield component characters. The results on heterosis of 14 pigeonpea hybrids over mid-parent, better parent, and the standard check for seed yield and yield components revealed maximum heterosis over mid parent followed by better parent and standard check. Among these, for seed yield (kg/ha) was recorded higher heterosis followed by number of secondary branches plant$^{-1}$ and number of pods plant$^{-1}$. Heterosis for seed yield (kg/ha) was observed to range from 12.35 (ICPH 4567) to 122.99% (ICPH 4564) over mid parent, while it ranged from 1.47 (ICPH 4567) to 69.31% per cent (ICPH 4564) over better parent; and from -0.81 (ICPH 4567) to 65.49% (ICPH 4564) over

the check, Asha. Further, ICPH 4679, ICPH 4571 and ICPH 4746 hybrids had uniformly recorded significant and desirable heterosis over mid and better parents, in addition to the check, Asha. However, high heterosis, more than 100%, over the mid-parent; more than 50% over the check Asha ; and more than 30% over better parent, was noticed in the hybrids, ICPH 4564 and ICPH 4588. High heterosis for seed yield (kg/ha) in these two hybrids was also in general reflected for the yield attributes. ICPL 20116, ICPL 20093 R lines, ICPB 2204, and ICPB 2200 B lines were observed to be superior for seed yield and other important yield attributes in the present study and are recommended for use in hybrid pigeonpea breeding programmes.

**Conclusion**

Based on overall observation on present investigation the following salient conclusion can drawn:

- ✓ The per se performance of all the tested material was good for plant growth.It can be used in yield improvement in pigeonpea
- ✓ The results obtained from present investigations concluded that correlation analysis revealed that secondary branches plant$^{-1}$, primary branches plant$^{-1}$, pods plant$^{-1}$, seeds plant$^{-1}$, biological yield plant$^{-1}$ and harvest index showing positive and significant association with seed yield plant$^{-1}$ may given priority for improving yield in pigeonpea.
- ✓ Path coefficient analysis revealed that of yield contributing traits *viz.*, pollen fertility%, secondary branches plant$^{-1}$, primary branches plant$^{-1}$, pods plant$^{-1}$, seeds plant$^{-1}$, biological yield plant$^{-1}$ and harvest index showing positive and significant direct effect on seed yield plant$^{-1}$ may given priority for improving yield in pigeonpea.
- ✓ CMS lines used for synthesis of 14 hybrids showed high level of male sterility and highly effective. In present study all the five male pollinators genotypes performed good fertility restoration. Hence, five male lines may be used as fertility restorers in future.

- ✓ Significant variability for pollen fertility was present among the hybrids. Yield point of view, most of the hybrids showed positive standard heterosis for yield.

Therefore, overall most of the hybrids and its component showed good impact in terms of production of hybrid seeds and yield potential of pigeonpea hybrid.

**Suggestions for future studies**

Based on achievements of the present study, the following guidelines are being made for future pigeonpea improvement programme:

- Further genetic progress demands more information on the inheritance of the key yield contributing traits and their association with other plant traits according to the prevailing weather conditions of the target environment.
- Seed yield plant$^{-1}$, arguably the most important trait, a polygenic in nature, difficult to improve, and highly influenced by the environment , may be improved through indirect selection of yield contributing traits with the restriction that other characters may not suffer and the phenology of plants may suit to the growing environment.
- Crosses should be evaluated in order to judge the stability of gene effects over multi-locations.
- Parents R lines ICPL 20116, ICPL 20093 and B lines ICPB 2204 and ICPB 2200 found to be good for seed yield plant$^{-1}$ may be involved in the future breeding programmes of pigeonpea.
- Pollen fertility %, number of pods plant$^{-1}$ and number of seeds pod$^{-1}$ directly influenced the seed yield plant$^{-1}$ and therefore, these traits could be used as selection criteria for yield improvement programme in pigeonpea.

# REFERENCES


Adams, M. W. and Grafius, J. E. 1971. Yield-components compensation: alternative interpretations. Crop Sci., 11: 33-35.

Aher, R. P, Dahat, D.V. and Thombre, B.B. 1998. Path analysis in pigeonpea. J. Maharashtra Agricultural Universities, 23 (3): 318 – 319.

Aher, G.U., Madrap, I.A., Tike, M.A. and Gore, D.R. 2006. Heterosis and inbreeding depression in pigeonpea. J. Maharashtra Agricultural Universities, 31 (1): 33 – 37.

Angadi, S.P., Kulkarni, R.S. and Rao, M.R.G. 1988. Note on character association and path analysis in pigeonpea (*Cajanus cajan* (L.) Millsp). Legume Research, 11:2, 99-100.

Anuradha, B., Koteswara Rao, Y. Rama Kumar, P.V. and Srinivasa Rao, V. 2007. Correlation and path analysis for seed yield and yield contributing characters in pigeonpea. The Andhra Agriculture J., 54(1&2): 9-12

Asawa, B.M., Chandra, R.K and Pandey, R.L. 1981. Character correlations and divergence in pigeonpea. Indian J. Agric. Sci., 51:12-17.

Bainiwal, C.R and Jatasra, D. S. 1980. Genetic divergence in pigeonpea. Indian J. Genet., 40: 153-156.

Balakrishnan and Natarajaratnam. 1989. Association of yield attributes in pigeonpea. MASU J., l76 (6): 348-350.

Balyan, H.S. and Sudhakar, M.V. 1985. Variability, character association and path coefficient studies on genotypes of early maturity group in pigeonpea (*Cajanus cajan* (L.) Millsp.). MASU J., 72: 168-12.

Banu, M.R., Muthaiah, A.R. and Ashok, S. 2007. Heterosis studies in pigeonpea. Adv. Plant Sci., 20 (1): 37 – 38.

Basavarajaiah, D., Byre Gowda, M., Kulakarni, R.S. and Ramesh, S. 1999. Character association and path coefficient analysis in pigeonpea. Crop Res., 17: 386-389.

Baskaran, K. and Muthiah, A.R. 2006. Interpretation of hybrid vigour in different cross combinations of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Res. Crops, 7(1):243-248.

Baskaran, K. and Muthiah, A.R. 2007. Associations between yield and yield attributes in pigeonpea (*Cajanus cajan* (L.) Millsp). Legume Res., 30(1): 64-66. 7 (1): 243 –248.

Bhadru, D. 2011. Studies on genetic parameters and interrelationships among yield and yield contributing traits in pigeonpea (*Cajanus cajan* (L.) Millsp). Legume Res., 33(1):23-27.

Bhavani, N.L. and Bhalla, J.K. 2009. Heterosis of yield components in pigeonpea (*Cajanus cajan* (L) Millsp.). Adv. Plant Sci., 22 (1): 257 – 259.

Bharadwaj, D.N. and Gupta, P. 2004. Associations of yield and quality contributing parameters in pigeonpea. Farm Sci. J., 13(2): 133-135.

Bhongale, A.T. and Raut, R.S. 1987. Genetic variability, correlation among different lines of pigeonpea. PKV Res. J., 11(2): 123-126.

Birhan, 2013. correlation and path analysis in pigeonpea (*Cajanus cajan* (L.) Millsp.). Indian J. Agril. Res., 47(5): 441-444. 14 ref.

Chandirakala, R and Raveendran, T.S. 1998. Studies on association and path analysis in pigeonpea. Indian J. Agril. Res., 32(3): 211-216.

Chandirakala, R. and Raveendran, T.S. 2002. Heterosis in pigeonpea (*Cajanus cajan* (L.) Millsp.). Ann. Agril. Res., 23 (2): 304 – 308.

Chandirakala, R., Subbaraman, N. and Hameed, A. 2010. Heterosis for yield in pigeon pea (*Cajanus cajan* (L.) Millsp.). Electron. J. Plant Breed., 1 (2) : 205 – 208.

Chattopadhyay, K. and Dhiman, K.R. 2005. Characterization, variability, diversity and path coefficient analysis of pigeonpea germplasm from north-east India under rainfed upland condition in Tripura. Legume Res., 28(2): 140-142.

Chaudhary, S.B., Kachole, L.U., Shinde, M.S. and Tambe, A.R. (2006). Characterization of diverse cytosteriles of sorghum through fertility restoration. Ann. Pl. Physiol., 20 (2):260-262.

Chaudhari, V.P. 1979. Heterosis and combining ability in pigeonpea (*Cajanus cajan* (L.) Millsp.). Ph.D. thesis submitted to MAU, Parbhani, Maharashtra, India.

Chauhan, R.M., Parmar, L.D., Patel, P.T and Tikka, S.B.S. 2004. Fertility restoration in cytoplasmic genetic male sterile lines of pigeonpea (*Cajanus cajan* (L.) Millsp.) derived from *Cajanus scarbaeoides*. Indian J. Genetics, 64 (2): 112 – 114.

Chauhan .2008. Hybrid Pigeonpea. In: Masood Ali and Shiv Kumar (Eds.), Advances in Pigeonpea Research, pp. 96-133. Indian Institute of Pulses Research, Kanpur, India.

Dahiya, B.S., Brar, J.S. 1976. The relationship between seed size and protein content in pigeonpea (*Cajanus cajan* (L.) Millsp.). Trop. Grain Legume Bull, 3:18-19

Dalvi, V.A., Saxena, K.B., Madrap, I.A and Ravikoti, V.K. 2008. Cytogenetic studies in A4 cytoplasmic-nuclear male-sterility system of pigeonpea. J. Hered., 99 (6): 667– 670.

Dalvi, V. A., Saxena, K. B. and Madrap, I. A., 2008a. Fertility restoration in cytoplasmic nuclear male-sterile lines derived from 3 wild relatives of pigeonpea. J. Hered., 99(6):671-673.

Dalvi, V. A., Saxena, K. B., Madrap, I. A. and Ravikoti, V. K., 2008b. Cytogenetic studies in A4 cytoplasmic-nuclear male-sterility system of pigeonpea. J. Hered., 99 (6):667-670.

Das .(1988). Identification of component traits contributing to seed yield in pigeonpea. J. Arid Legumes, 3(2):66-67.

Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India, 2013-14.

Deshmukh, R.B., Rodge, R.G., Patil, J.V and Sahane, D.V. 2000. Genetic variability and character association in pigeonpea under different cropping systems. Journal of Maharashtra Agricultural Universities, 25(2): 176-178.

Dewey, D.R. and Lu, K.H. 1959. A correlation path coefficient analysis of components of crested wheat grass. A. J., 51: 515-518.

Dhameliya, H.R., Pathak, A.R. and Zaveri, P.P. 1994. Genetic analysis of heterogeneous population in pigeonpea (*Cajanus cajan* (L.) Millsp). Gujarat Agricultural University Research Journal, 20: 1,46-51.

Dheva, N.G., Patil, A.N. and Wanjari, K.B. 2008a. Heterosis for economic characters in CGMS based hybrids of pigeonpea. Ann. Plant Physiol., 22 (2): 231-234.

Dheva, N.G., Patil, A.N and Wanjari, K.B. 2008b. Heterosis evaluation in CGMS based hybrids of pigeonpea. A. Plant Physiol., 22 (2): 228 – 230.

Dheva, N.G., Patil, A.N. and Wanjari, K.B. 2009. Heterosis in cytoplasmic male sterility based hybrids of pigeonpea. Int. J. Plant Sci., 4 (1): 270 –273.

Dodake, S.S., Patil, B.B., Gare, B.N. and Burli, A.V. 2009. Genetic variability and correlation studies in pigeonpea under sub-montane zone of Maharashtra. Journal of Maharashtra Agricultural Universities, 34: 2, 144-146.

Dumbre, A.D., Deshmukh, R.B and Patil, J.V. 1985. Path analysis in pigeonpea. Legume Res., 8(1): 37-38.

Dundas, I. S., Saxena, K. B., and Byth, D. E., 1981. Microsporogenesis and anther wall development in male sterile and fertile lines of pigeonpea (*Cajanus cajan* (L.) Millsp.). Euphytica, 30:431-435.

FAOSTAT. (2012). Online Agriculture Statistics. http://www.faostat.org

Firoz Mahamad, Gowda, M. B. and Girish, G. 2006 Assessment of genetic divergence in vegetable pigeonpea germplasm. Environ. and ecology, 24S (Special 4):1135-1139.

Fisher, R. A. and Yates, F. 1963. Statistical tables for biological, agricultural and medical research. Oliver and Boyd London, pp.46-63.

Ganesh Murthy, K. and Stephen Dorairaj, M .1990. Genetic divergence in pigeonpea (*Cajanus cajan* (L.) Millsp). Indian J. Genet., 50(3) : 279-282.

Gangwar, L. K. and Bajpai, G. C. 2005. Studies on pollen fertility in interspecific crosses of pigeonpea. J. Crop Improv., 32 (1):60-62

Gangwar, L.K. and Bajpai, G.C. 2006 .Seed protein relationship in interspecific populations in genus *Cajanus*. Indian J. Pulses Res., 19: 2, 250.

Garten, S.L, Tomer, Y. S. and Singh, V. P. 1989. Genetic divergence in early maturing pigeonpea. Indian J. Pulse Res., 2(1): 25-31

Gite, U.K. Madrap, I.A. Patil, D.K. and Kamble, K.R. 2014. Exploitation of heterosis in CMS based hybrids in pigeonpea (*Cajanus cajan* L.) J. Agr. Sci. Tech., 39(1);138-140.7 ref

Gohil, R.H. 2006. Genetic divergence and variability in pigeonpea. Res. on crops, 7(3):748-750

Grafius, J.E. 1956 Components of yield in oats. A geometrical interpretation. Agron. J., 48:419-423

Gumber, R.K., Sarvjeet Singh. and Sandhu, T.S. 1996. Association of seed yield with different phases of the reproductive period in pigeonpea. Indian J. Genet., 56: 3, 318-322.

Gumber, R.K. and Singh, S. 1996. Heterosis and inbreeding depression in pigeonpea (*Cajanus cajan* (L.) Millsp.) crosses involving genotypes of different growth habit. International Chickpea and Pigeonpea Newsletter, 3: 67 – 68.

Hamid, A., Husana, A. haque, M. M. and Islam, M.R. 2011. Genetic Variability in Pigeon pea (*Cajanus cajan* L. Millspaugh). Electron. J. Plant Breed., 2(1): 117-123.

Henry, A. and Krishna, G .V. S. R. 1992. Genetic divergence in pigeonpea. MASU. J., 79(1):41-43.

Hooda, J.S., Tomer, Y. S., Singh, V.P. and Singh, S. 1999. Heterosis and inbreeding depression in pigeonpea (*Cajanus cajan* (L.) Millsp.). Legume Res., 22 (1): 62 – 64.

Jain, K.C. and Saxena, K.B. 1990. Performance of medium-duration hybrid pigeonpea at ICRISAT Center. International Pigeonpea Newsletter, 12: 9 – 11.

Jogendra singh, Badana, V. P. and Shiv Datt. 2008. Correlation and path coefficient analysis among yield and its contributing traits in pigeonpea. Environ. and ecology, 26(3A):1396-1399.

Johnson, H.W., Robinson, H.O and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. Agron. J., 47: 314-318.

Kalaimagal, T, Amala Balu, P. and Sumathi, P. 2008. Genetic studies in segregating populations of pigeonpea. J. Crop improv., 35(1):31-34.

Kandhola, and Panwar, 1999. Genetic divergence in pigeonpea (*Cajanus cajan* (L.) Millsp). Indian J. Genet., 50(3): 279-282.

Kandalkar, V.S. 2007. Evaluation of standard heterosis in advanced CMS based hybrids for grain yield, harvest index and their attributes in pigeonpea. In: Proceeding of 7$^{th}$ International Conference on Sustainable Agriculture for Food, Bio-energy and Livelihood Security. 14-16 February 2007, Jabalpur, Madhya Pradesh, India. 195.

Katiyar, P. K, Dua, R. P, Singh, I. P, Singh, B. B. and Singh, F. 2004. Multivariate analysis for genetic diversity in early pigeonpea accessions. Legume Res., 27(3) : 164-170.

Khin lay kyu and Saxena, K. B. 2011. Inheritence of fertility restoration in pigeon pea J. food legumes, 24(4):273-276.

Khorgade, P.W., Wankhade, R. R. and Satange, I.V. 2000. Heterosis studies in pigeonpea hybrids based on male sterile lines. J. Agril. Res., 34 (3):168 – 171.

Kolreuter, D. J. G. (1763). Vorlaufige Nachricht von Einigen das Geschlecht der Pflanzen Betreffendon Versuchen und Beobachtungen. Fortsetzung1. Ostwaldsklassiker der Exakten Wissenschaften Nr. 41, Engelmann, Leipzig.

Kingshlin, M. and Subbaraman, N. 1997. Character association and path analysis in pigeonpea (*Cajanus cajan* (L). Millsp). Legume Res., 20(3/4): 175-178.

Krishna Chaithanya Kumar, A. and Srivastava, D.P. 1998. Heterosis in relation to combining ability in long duration pigeopea. Indian J. Pulses Res., 11 (2):1– 5.

Kumar, B. and Krishna, R. 2008. Heterosis and inbreeding depression in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Intern. J. Plant Sci., (Muzaffarnagar). 3 (1): 181–183.

Kumar and Srivastava, 2009. Heterosis in relation to combining ability in long duration pigeopea. Indian J. Pulses Res., 11 (2):1 – 5.

Kumar, S. R. Reddy, G. E. Rangare, N. R. 2013. Path analysis in pigeonpea. J. Agril. Res, 31(4A):1993-1995. 6 ref.

Lad, P. and Wanjari, K. B., 2005. Fertility traits in pigeonpea: segregation pattern and Mendelian inheritance in selfed plant to row progenies. Ann. Plant Physiol., 19 (1):88-91.

Lay, K. K. and Saxena, K. B., 2011. Inheritance of fertility restoration in pigeonpea. J. Food Legumes, 24 (4):273-276.

Lay, K.K., Saxena, K.B., Kumar, R.V. and Rathore, A. 2011. Prospects of hybrids in enhancing production and productivity of pigeonpea in Myanmar. J. Food Legumes, 24 (1): 1 – 7.

Lenka, D. and Misra, B., 1973 Path coefficient analysis of yield in rice varieties. Indian J. Agril. Sci., 43: 376-379.

Lohithaswa, H.C. and Dharmaraj, P.S. 2003. Implications of heterosis, combining ability and per se performance in pigeonpea. Karnataka J. Agril. Sci., 16 (3): 403 –407.

Magar, M.N. 2003. Genetic variability, path analysis and genetic diversity in pigeonpea ( *Cajanus cajan* (L) Millsp.). M.Sc (Ag) Thesis, MPKV Rahuri.

Magar, N.M., Mane, L.L, Gavit, A,F. and Patil, S.S. 2008 Genetic diversity in pigeonpea. Adv. Plant Sci., 21(2):679-681.

Mahajan, V., Shukla, S.K., Tiwari, V., Prasad, S.V.S. and Gupta, H.S. 2007. Path analysis in pigeonpea (*Cajanus cajan* (L.) Millsp) in midaltitudes of north-western Himalayas. J. Crop Improv., 34: 1, 56- 58.

Mahalanobis, P.C. 1936. On the generalised distance in statistics. Proceedings of National Institute of Sciences (Indiana),2: 49-55.

Manivel, P. and Rangasamy P. 1999. Heterosis studies involving genetic male sterile lines of pigeonpea. School of Genetics, Tamil Nadu Agricultural University, Coimbatore, 641 003, India. Crop Res., Hisar. September. 18 (2): 240 – 242.

Mallikarjuna, N. and Saxena, K. B. 2002. Production of hybrids between Cajanus acutifolius and C. cajan. Euphytica, 124 (1):107-110.

Marekar, R.V. and Nerker, Y.S. 1987. Correlation and path analysis in F1 generation of pigeonpea. PKV Res. J., 11(1):1-6.

Maurya, and singh. 1977. The nature of genetic divergence in relation to breeding system in crop plants. Indian J. Genet., 26: 188-198.

Mittal, V.P., Brar, K.S and Paramjit Singh. 2006. Identification of component traits contributing to seed yield in pigeonpea (*Cajanus cajan* (L.) Millsp). J. Arid Legumes, 3(2): 66-67.

Mittal, V.P., Paramjit Singh, and Brar, K.S. 2010. Character Association and Path Coefficient Analysis for Yield Components in Pigeon pea (*Cajanus cajan* L). MASU. J., 97(10-12): 319-320.

Murugan E, Manivannan N, Viswanathan .P.L. and Dhanakodi .C.V. 2000 Genetic divergence in redgram (*Cajanus cajan* (L.) Millsp). MASU. J., 87:174-176.

Musaana, M.S. and Nahdy, M.S. 1998. Path coefficient analysis of yield andits components in pigeonpea. African Crop Sci. J., 6 (2): 143-148.

Muthiah, A. R., Kalaimagal, T. and Sassikumar, D. (1998). Cost of seed production: redgram hybrid COPH 2. Legume. Res., 21:65–66.

Nadarajan, N., Ram, S. G. and Petchiammal, K. I., 2008. Fertility restoration studies in short duration red gram (*Cajanus cajan* (L.) Millsp.) hybrids involving CGMS system. MASU. J., 95 (7/12):320-327.

Nandan R, Paul, P. R, Singh R. K. and Sarkar, P. 1996 Genetic divergence for yield and yield contributing characters in pigeonpea. J. Appl. Bio., 6: 6-8.

Narladkar, V.W. and Khapre, P.R. 1996. Heterosis for yield and yield components in pigeonpea. Ann. Agric. Res., 8 (2): 184 – 186.

Natarajan, C, Thyagarajan, K. and Ayymperumal, A. 1990. Genetic variability, correlation and path analysis in pigeonpea. MASU. J., 77: 378-381.

Pandey, N and Singh, N.B. 2001. Association between yield and yield attributes in pigeonpea hybrids. MASU. J., 88(10-12): 640-643.

Pandey, N. and Singh, N.B. 2002. Hybrid vigour and combining ability in long duration pigeonpea (*Cajanus cajan* (L.) Millsp.) hybrids involving male sterile lines. Indian J. Genet., 62 (3): 221 – 225.

Panse, V.G and Sukhatme, P.V. 1961. Statistical methods for agricultural workers, ICAR, New Delhi, Inida.

Patel, G.V., Zaveri, P.P. and Pathak, A.R. 1991. Heterosis for morphological attributes in pigeonpea. Indian J. Pulses Res., 4 (1): 35 – 41.

Patel, J.A and Patel, D.B. 1992. Heterosis for yield and yield components in pigeonpea. Indian J. Pulses Res., 5 (1): 15 – 20.

Patel, M.P. and Tikka, S.B.S. 2008. Heterosis for yield and yield components in pigeonpea. J. Food Legumes, 21 (1): 65 – 66.

Patel J.N, Vashi, P. S Desai, R. T. and Vashi, R. D. 1988. Genetic divergence in pigeonpea. International Pigeonpea News letter, 8: 2-4.

Patil, S.B., Hingane, A.J., Sameer kumar, C.V., Mula, M.G., Kumar, R.V and Saxena, K.B. 2014. Combining ability studies of pigeonpea cytoplasmic male sterile (CMS) lines with obcordate leaf marker. J. Plant Breed. Crop Sci., 6(7); 84-90.

Paul, S.K. and Upadhaya, L.P. 1991. Interrelationship between yield and yield contributing characters in pigeonpea (*Cajanus cajan* (L.) Millsp). Intern. J. Trop. Agric., IX (2):135- 140.

Paul, P.R., Singh, R.M., Nandan, R and Raina, R. 1996. Character association and path coefficient analysis in hybrid pigeonpea. MASU. J., 83 (1): 34-37.

Phad, D.S. 2003. Heterosis, Combining ability and stability analysis in pigeonpea *Cajanus cajan* (L.) Millsp. Ph.D thesis, Marathwada Agricultural University, Parbhani.

Praveen Pandey, Rajesh Kumar, Vankat Raman Pandey, Mritunjay Tripathi, 2013. Genetic Divergence Studies in Pigeonpea [*Cajanus cajan* (L.) Millsp.] American J. Plant Sci., 2013. 4; 2126-2130

Rai, B. 1979. Heterosis breeding. Agro-biological publications, New Delhi.

Rai, N. and Rai, M. (2006). Heterosis Breeding in Vegetable Crops. G. Kalloo (ed.), 531. New India Publishing Agency, New Delhi, India.

Rama Devi, S. 2011. Heterosis and Combining ability analysis in pigeonpea (*Cajanus cajan* (L.) Millsp.). M. Sc.(Ag) Thesis, S.V. Agricultural College, Tirupati, Andhra Pradesh.

Rama Devi, S., Prasanthi, L., Hari Prasad Reddy, K. and Baskara Reddy, B.V. 2012. Studies on interrelationships of yield and its attributes and path analysis in pigeonpea (*Cajanus cajan* (L.) Millsp.). Legume Res., 35 (3):207-213.

Rao, P. J. M, Malathi, S, Reddy, D.V.V, Upender, M. 2013. Genetic Studies of Association and Path Coefficient Analysis of Yield and its Component Traits in Pigeon Pea (*Cajanus Cajan* (L.) Millsp.). International Journal of Scientific and Research Publications, 3(8):1–5.

Rao, C.R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York pp: 357-363.

Reddy, R.P. and Rao, N.G.P. 1979. Heterosis and combining ability in pigeonpea. Indian J. Genet., 39: 240 – 246.

Reddy, L.J., Rao, K.N. and Saxena, K.B., 2000. Production and characterization of hybrids between *Cajanus cajan* x *C. reticulates* var. *grandifolius*. Euphytica, 121:93-98.

Rekha, R. 2009. Studies on genetic divergence and character association in pigeonpea [*Cajanus cajan* (L.) Millsp]. M. Sc.(Ag) Thesis, S.V. Agricultural College, Tirupati, Andhra Pradesh.

Salunke, J.S., Aher, R.P., Shinde, G.C and Kute, N.S. 1995. Correlation and path coefficient analysis in early pigeonpea. Legume Res., 18(3/4): 162-166.

Samal., K. M, Senapathi., N, Patnaik, H. P and Nandi, A. 2001. Genetic divergence in mutant lines of pigeonpea (*Cajanus cajan* (L.) Millsp). Legume Res., 24(3) : 186-189.

Sameer Kumar, C.V, Saxena, K.B, Patil, S.B, Vijaykumar, R, Mula, M.G, Hingane, A.J, Ganga Rao, N.V.P.R, Saxena, R.K, Singh, V.K and Varshney, R.K. 2014. A unique hybrid parental line identification system using obcordate leaf shape marker in pigeonpea. *In VII International Conference on Legume Genetics and Genomics (ICLGG)*, Saskatchewan, Canada. July 3-8, 2014.

Sandhu, T. S, Reddy, K. R. and Gumber, R. K. 1993 Assessment of genetic divergence in pigeonpea germplasm. International Pigeonpea Newsletter, 17 : 8-10.

Sarma, R.N. and Roy, A. 1994. Genetic divergence in early maturing pigeonpea. Indian J. Genet., 54(2) : 184-187.

Sarode, S.B., Singh, M.N. and Singh, U.P. 2009. Heterosis in long duration pigeonpea [*Cajanus cajan* (L.) Millsp.]. Intern. J. Plant Sci., 4 (1): 106 –108.

Satpute, R.G. 1994. Plant population effects on the interrelationship of seed yield and its components in pigeonpea (*Cajanus*.) genotypes. Legume Res., 17 (2): 96-100.

Sawant, M.N. 2001. Character association, path analysis and genetic diversity in pigeonpea (*Cajanus cajan* (L.) Millsp.). M.Sc. (Agri.) thesis, MPKV, Rahuri.

Sawant, M.N., Sonone, A.H. and Anarase, S.A. 2009. Character association, path coefficient analysis and genetic diversity in pigeonpea. MASU. J. Universities, 34 (2): 134-137.

Sawargaonkar, S. L., Saxena, K. B. and Madrap, I. A., 2011. Stability analysis of yield and related traits in pigeonpea hybrids. J. food legumes, 24 (3): 184-193.

Sawargaonkar, S. L., Madrap, I. A., and Saxena, K. B., 2012. Stability of cytoplasmic malesterile lines in pigeonpea under different month temperature. Green farming, 3 (5):515-517.

Saxena, K.B., Faris, D.G., Singh, U. and Kumar, R.V.1986. Relationship between seed size and protein content in newly developed high protein lines of pigeonpea. Plant Foods for Human Nutrition, 36:335-340

Saxena, K.B., Ariyanayagam, R.P. and Reddy, L.J. 1992a. Genetics of a high-selfing trait in pigeonpea. Euphytica, 59 : 125 – 127.

Saxena, K. B. and Kumar, R.V. 2001. Genetics of a new male-sterility locus in pigeonpea (*Cajanus cajan* [L.] Millsp.). J. Hered., 92 (5):437-439.

Saxena, K. B. and Kumar. R.V. 2003. Development of a cytoplasmic-nuclear male-sterility system in pigeonpea using [*Cajanus scarabaeoides* (L.) Thours.]. Indian J. Genet. 63 (3): 225-229.

Saxena, K. B. and Sharma, D. 1990. Pigeonpea genetics. In: The Pigeonpea, (Nene, Y. L., Hall, S. D. and Sheila, V. K.) CAB International, Wallingford, U. K. Pp 137-158.

Saxena, K. B. 2005. Opportunities for exploiting hybrid vigour in grain legumes for increasing yield and adaptation – a success story of pigeonpea. Paper presented in *7th Annual Symposium of the Department of Agriculture*, 29 – 30, September 2005, Gannoruwa, Sri Lanka, 59-76.

Saxena, K.B. 2006a. Seed Production systems in pigeonpea. Patancheru-502-324 Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics, 76.

Saxena, K.B., Kumar R.V., Madhavi Latha, K. and Dalvi, V.A. 2006b. Commercial pigeonpea hybrids are just a few steps away. Indian J. Pulses Res., 19 (1): 7 – 16.

Saxena, K. B. 2008. Genetic improvement of pigeonpea- A Review. Trop. Plant Biol., 1:159-178.

Saxena, K.B., Sultana, R., Mallikarjuna, N., Saxena, R.K., Kumar, R.V., Sawargaonkar, S. L. and Varshney, R. K., 2010. Male sterility systems in pigeonpea and their role in enhancing yield. Plant Breed., 129 (2):125-134.

Saxena, K. B. and Nadarajan, N., 2010. Prospects of pigeonpea hybrids in Indian agriculture. Electron. J. Plant Breed., 1 (4):1107-1117.

Saxena, K.B., Vales, M.I., Kumar, R.V., Sultana, R. and Srivastava, R.K. 2011a.Towards ensuring genetic purity of pigeonpea hybrids by incorporating 'obcordate leaf' morphological marker in A and B lines. J. Crop Sci., 51 (4):1564-1570.

Saxena, K.B., Sultana, R., Saxena, R.K., Kumar, R.V., Sandhu, J.S., Rathore, A., Kishor, P.B.K. and Varshney, R. K., 2011b. Genetics of fertility restoration in A4- based, diverse maturing hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.]. J. Crop Sci., 51 (2):574-587.

Saxena, K. B., 2013 (unpublished). A novel CMS system in pigeonpea derived from Cajanus reticulatus. J. Crop Sci. (Communicated).

Saxena, K. B. 2005. Opportunities for exploiting hybrid vigour in grain legumes for increasing yield and adaptation – a success story of pigeonpea. Paper presented in 7th Annual Symposium of the Department of Agriculture, 29 – 30, September 2005, Gannoruwa, Sri Lanka. 59-76.

Saxena, K. B. and Nadarajan, N. 2010. Prospects of pigeonpea hybrids in Indian agriculture. Electron. J. Plant Breed., 1 (4):1107-1117.

Saxena, K. B., Ariyanayagam, R. P. and Kumar R. V. 1992. Development of hybrids and their production technology. ICRISAT, pigeonpea breeding progress report, (32): 38-56.

Saxena, K. B., Singh, L. and Gupta, M. D. (1990). Variation for natural out-crossing in pigeonpea. Euphytica, 39:143–148.

Sekhar, M.R., Singh, S.P., Mehra, R.B and Govil, J.N. 2004. Combining ability and heterosis in early maturing pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids. Indian J. Genetics Plant Breed., 64 (3): 212 – 216.

Sharma, H.K., Singh, L and Sharma, D. 1973. Combining ability in diallel crosses in pigeonpea. Indian J. Agric. Sci., 43 (1): 25 – 29.

Sharma, R. N. and Roy, A. 1999. Genetic divergence in early maturing pigeonpea Indian J. Genetics Plant Breed., 54(2): 184-187.

Shoba, D. and Balan, A. 2010. Heterosis in CMS/GMS based pigeonpea (*Cajanus cajan* (L.) Millisp.) hybrids. Agric. Sci. Digest., 30 (1): 32 – 36.

Shrivastava, M. P, Singh, L and Singh, R.P. 1976. Heterosis in pigeonpea. Indian J. Genet., 36 (2): 197:200.

Sidhu, P.S., Verma, M.M., Cheema, H.S and Sra, S.S. 1985. Genetic relationships among yield components in pigeonpea. Indian J. Agric. Sci., 55(4): 232-235.

Singh, K.B. 1971. Heterosis breeding in pulse crops. *Proceeding V. All Inida Kharif Pulse workshop*, 18-20 March, Hissar. 33 – 37.

Singh, R. K. and Chaudhary, B. D. 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi; pp.215-218.

Singh, R.K. and Kakar, S .N. 1977. control on indiv'idual trait means during index selection. *Proceedings of Third Congress*, SABRAO (Canberra), 3:22-25.

Singh, S. and Gumbar, R. K. 1996. Assessment of genetic diversity in basic generations of pigeonpea. International Chickpea and Pigeonpea Newsletter, 3 : 62-64.

Singh, J. and Bajpai, G. C. 2005. Studies on pollen fertility and morphology of interspecific hybrids and their parents in *Cajanus* sp. Indian J. Pulses Res., 18 (2): 122– 123.

Singh, R. S., Singh, M. N. and Singh, U. P. 2006. Nature of pollen sterility in two cytoplasmic genetic male sterile lines in pigeonpea (*Cajanus cajan* (L.) Millsp.). *Proceedings of the National Academy of Sciences India*. Section B, Biological Sciences, 76 (4):377-379.

Singh, R.S. and Singh, M. N. 2016. Character association trend among yield attributing traits in Pigeon pea (*Cajanus cajan* (L.) Millsp.). Indian J. Sci. Tech., 9 (6).

Sodavadiya, P.R., Pithia, M.S., Savaliya, J.J., Pansuriya, A.G. and Korat, V.P. 2009. Studies on characters association and path analysis for seed yield and its components in pigeonpea (*Cajanus cajan* (L.) Millsp). Legume Res., 32 (3): 203-205.

Solomon, S., Argikar, G.P., Salanki, M.S and Morbad, I.R. 1957. A study of heterosis in *Cajanus cajan* (L.) Millsp. Indian J. Genet., 17 (1): 90 – 95.

Sreelakshmi, C. Shivani, D. Kumar, C.V.S. 2010. Genetic divergence and stabilityanalysis in Pigeonpea (*Cajanus cajan* (L.)). Electron. J. Plant Breed., 1(4):530-535.

Sreelakshmi, Ch., Sameer Kumar, C.V. and Shivani. D. 2011. Genetic analysis of yield and its component traits in drought tolerant genotypes of Pigeonpea (*Cajanus cajan (L.)* Millsp). Electron. J. Plant Breed., 1(6): 1488-1491.

Srinivas, T., Reddy, M.V., Jain, K.C. and Reddy M.S.S. 1997. Inheritance of resistance to two isolates of sterility mosaic pathogen in pigeonpea (*Cajanus cajan* (L.) Millsp.). Euphytica, 97 (1): 45 – 52.

Srinivas. T. 1996. Genetics of resistance to sterility mosaic disease of pigeonpea (*Cajanus cajan* (L.) Millsp.). Ph.D thesis, Andhra Pradesh Agricultural University, Hyderabad.

Srinivas, T., Jain, K.C., Reddy , M.V. and Reddy, M.S.S. 1999. Genetic relationships among yield components in pigeonpea. Indian J. Pulses Res., 12(2) : 180-186.

Srivastava, J.P., Singh, H.N. and Singh, S.P. 1972. Genetic Studies on yield components in pea (*Pisum sativum* (L.) var. *arvence Pior*). Indian J. Agric. Sci., 42:1001-1004.

Srivastava, M.P., Singh, L. and Singh, R.P. 1976. Heterosis in pigeonpea. Indian J. Genet., 36 : 197 – 200.

Sunil Chaudhari, Tiklea, A.N., Uttamchand, Saxena, K. B. and Rathore, A. 2015. Stability of Cytoplasmic Genetic Male Sterility and Fertility Restoration in Pigeon pea. J. Crop Improv., 29:3, 269-280.

Sudhir kumar, Debnath, M. K., Sameer kumar, C.V., Singh, P.K., and Sultana, R. 2015. Study of heterosis and pollen fertility in CGMS based pigeonpea ( *Cajanus cajan* (L.) Millsphaugh) hybrids. Res. Environ. Life Sci., 9(1) 107-110.

Thombre., B. B, Aher, R. R. and Dahat, D. V. 2000. Genetic divergence in pigeonpea. Indian J. Agric. Res., 34: 126-129

Udensi, O. Ikpeme, E. V. 2012. Correlation and path analysis in pigeonpea. American J. Experimental Agric., 2(3):351-358. 23 ref.

Vander Maesen, L. J. G. 1980. India is the native home of the pigeonpea. Pages 257-262 in Libergratulalatorius in honorem HCD de Wit (Arenda JC, Boelema G, de Groot CT and Leeuwenberg AJM, eds.). Lnadbouwhoge school Miscellaneous Paper no. 19. Netherlands: Wageningen.

Vander Maesen, L. J. G. 1986. Cajanus D C and Atylosia W & A. (Leguminosae). Page 225 in Agriculture University wageningen Paper 85-4 (1985), wageningen, the Netherlands Agriculture University.

Veeraswamy, R., Rathnaswamy, R., Ragupathy, A. and Palaniswamy, G.A. 1973.Genotypic and phenotypic correlations in *Cajanus cajan* (L.) Millsp. MASU. J., 60; 1823 – 1825.

Vencovsky, R and Barriga, P. 1992. Genética Biométrica no Fitomelhoramento. Sociedade Brasileira de Genética, Ribeirão Preto. pp 496.

Vikas and Singh, S.P. 1998. Variability And Character Assocaiation In Early And Extra Early Genotypes Of Pigeonpea (*Cajanus cajan* (L.) Millsp.) Legume Res., 21(3/4): 229-232.

Viramgama, A. V. and Goyal, S. N. 1994 Genetic divergence in pigeonpea. Gujarat Agricultural University Res. J., 19(2) : 65-71.

Visakho Shunyu, Chaturvedi, H. P. Sapu Changkija, Jogendra Singh. 2013. Genetic diversity in pigeonpea. Intern. J. Agric. Innovations Res., 2(1):89-90. 11ref.

Wanjari, K.B., Bhongle, S.A and Sable, N.H. 2007. Evaluation of heterosis in CMS based hybrids in pigeonpea. J. Food Legumes, 20 (1): 107 – 108.

Wanjari, K.B, Rathod, S.T.(2012) Exploitation of heterosis through F1 hybrid in pigeon pea (*Cajanus cajan* L.) Indian J. Genet.., 72(3);257-263.53 ref.

Wankhade, R.R., Wanjari, K.B., Kadam, G.M. and Jadhav, B.P. 2005. Heterosis for yield and yield components in pigeonpea involving male sterile lines. Indian J. Pulses Res., 18 (2): 141 – 143.

Wilks, S. S. 1932. Certain generalizations in the analysis of variance. Biometrika, 1932. 24 (3-4): 471-494.

Wright, S. 1921. Correlation and causation. J. Agric. Sci., 20: 557-585.Biometrics 24: 471.

Yadav, S.S. and Singh, D.P. 2004. Heterosis in pigeonpea. Indian J. Pulses Res., 17 (2): 179 – 180.

Yogendra Prasad, 2013, Role of genetic divergence in relation to heterosis in pigeonpea. An international quarterly journal of sciences. 8(2): 409-416, Department of Plant Breeding and Genetic, RAU, Pusa, Samastipur - 848 125, Tirhut College of Agriculture, Dholi - 843 121.

Yogesh Kumar Nag and Sharma, R.N. 2012. Genetic diversity and path coefficient analysis in Pigeonpea (*Cajanus cajan* (L.) Millsp.) germplasm accessions of Bastar origin. Electron J. Plant Breed., 3(2): 818-824.

## APPENDIX – A

### Statistical analysis

**Table A1 : ANOVA for Days to 50% flowering**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 5.643 | | | |
| Treatment | 27 | 2,964.24 | 109.787 | 66.099** | 0 |
| Error | 54 | 89.69 | 1.661 | | |
| Total | 83 | 3,059.57 | | | |

**Table A2 : ANOVA for Days to maturity**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 55.024 | | | |
| Treatment | 27 | 1,609.66 | 59.617 | 7.246** | 0 |
| Error | 54 | 444.31 | 8.228 | | |
| Total | 83 | 2,108.99 | | | |

**Table A3: ANOVA for Pollen fertility %**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Signficance |
|---|---|---|---|---|---|
| Replication | 2 | 24.5 | | | |
| Treatment | 27 | 886.619 | 32.838 | 22.685** | 0 |
| Error | 54 | 78.167 | 1.448 | | |
| Total | 83 | 989.286 | | | |

**Table A4: ANOVA for No. of Primary branches plant$^{-1}$**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 641.024 | | | |
| Treatment | 27 | 544.702 | 20.174 | 1.771* | 0.03706 |
| Error | 54 | 614.976 | 11.388 | | |
| Total | 83 | 1,800.70 | | | |

**Table A5: ANOVA for No. of secondary branches plant$^{-1}$**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 224.595 | | | |
| Treatment | 27 | 4,810.24 | 178.157 | 2.032* | 0.01337 |
| Error | 54 | 4,733.41 | 87.656 | | |
| Total | 83 | 9,768.24 | | | |

**Table A6: ANOVA for Plant height (cm)**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 3,966.07 | | | |
| Treatment | 27 | 10,917.00 | 404.333 | 5.914** | 0 |
| Error | 54 | 3,691.93 | 68.369 | | |
| Total | 83 | 18,575.00 | | | |

**Table A7: ANOVA for Pods plant$^{-1}$**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 62,878.02 | | | |
| Treatment | 27 | 1,021,951.56 | 37,850.06 | 4.037** | 0.00001 |
| Error | 54 | 506,243.98 | 9,374.89 | | |
| Total | 83 | 1,591,073.56 | | | |

**Table A8: ANOVA for Seeds pod$^{-1}$**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Signficance |
|---|---|---|---|---|---|
| Replication | 2 | 0.004 | | | |
| Treatment | 27 | 0.406 | 0.015 | 1.875** | 0.02483 |
| Error | 54 | 0.433 | 0.008 | | |
| Total | 83 | 0.843 | | | |

**Table A9: ANOVA for seeds plant$^{-1}$**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 64,572.92 | | | |
| Treatment | 27 | 7,477,780.53 | 276,954.83 | 7.14** | 0 |
| Error | 54 | 2,094,625.77 | 38,789.37 | | |
| Total | 83 | 9,636,979.21 | | | |

**Table A10: ANOVA for 100seed wt.**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 0.366 | | | |
| Treatment | 27 | 34.254 | 1.269 | 5.803** | 0 |
| Error | 54 | 11.805 | 0.219 | | |
| Total | 83 | 46.425 | | | |

**Table A11: ANOVA for Biological yield plant$^{-1}$**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 6,853.44 | | | |
| Treatment | 27 | 396,580.99 | 14,688.19 | 6.262** | 0 |
| Error | 54 | 126,664.15 | 2,345.63 | | |
| Total | 83 | 530,098.57 | | | |

**Table A12: ANOVA for Yield plant$^{-1}$(g)**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 3,328.85 | | | |
| Treatment | 27 | 91,820.61 | 3,400.76 | 7.277** | 0 |
| Error | 54 | 25,234.20 | 467.3 | | |
| Total | 83 | 120,383.66 | | | |

**Table A13: ANOVA for Seed yield (kg/ha)**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 63,192.98 | | | |
| Treatment | 27 | 27,832,453.74 | 1,030,831.62 | 14.605 | 0 |
| Error | 54 | 3,811,463.47 | 70,582.66 | | |
| Total | 83 | 31,707,110.19 | | | |

**Table A14: ANOVA for Harvest index (%)**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 8.094 | | | |
| Treatment | 27 | 1,456.87 | 53.958 | 3.843** | 0.00001 |
| Error | 54 | 758.215 | 14.041 | | |
| Total | 83 | 2,223.18 | | | |

**Table A15: ANOVA for Dal recovery %**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 375.163 | | | |
| Treatment | 27 | 617.823 | 22.882 | 4.026** | 0.00001 |
| Error | 54 | 306.95 | 5.684 | | |
| Total | 83 | 1,299.94 | | | |

**Table A16: ANOVA for seed protein content**

| Source of Variation | DF | Sum of Squares | Mean Squares | F-Calculated | Significance |
|---|---|---|---|---|---|
| Replication | 2 | 1.037 | | | |
| Treatment | 27 | 41.279 | 1.529 | 2.638** | 0.00121 |
| Error | 54 | 31.296 | 0.58 | | |
| Total | 83 | 73.611 | | | |

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

## APPENDIX – B

**Table B1: State wise share of Pigeonpea production in India**

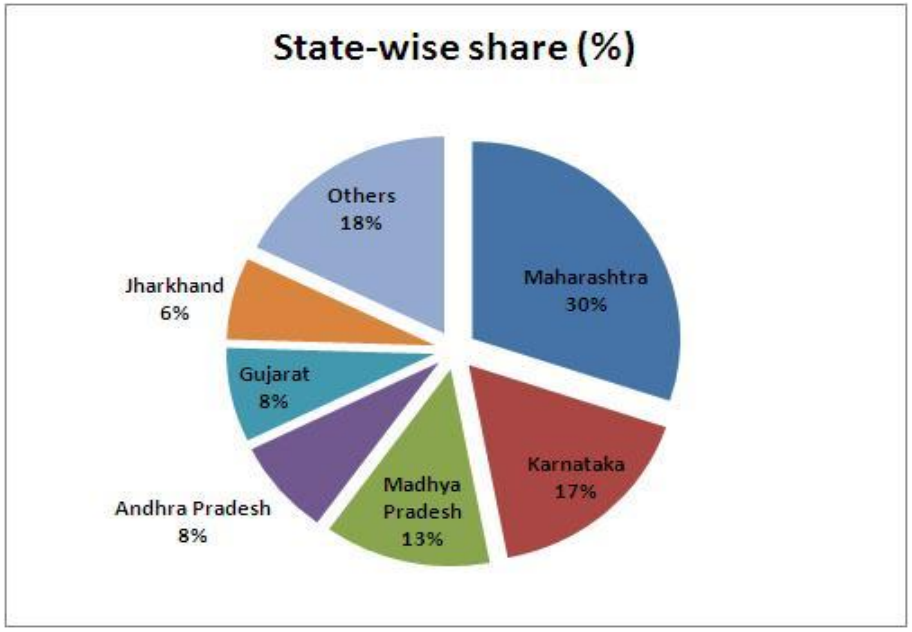
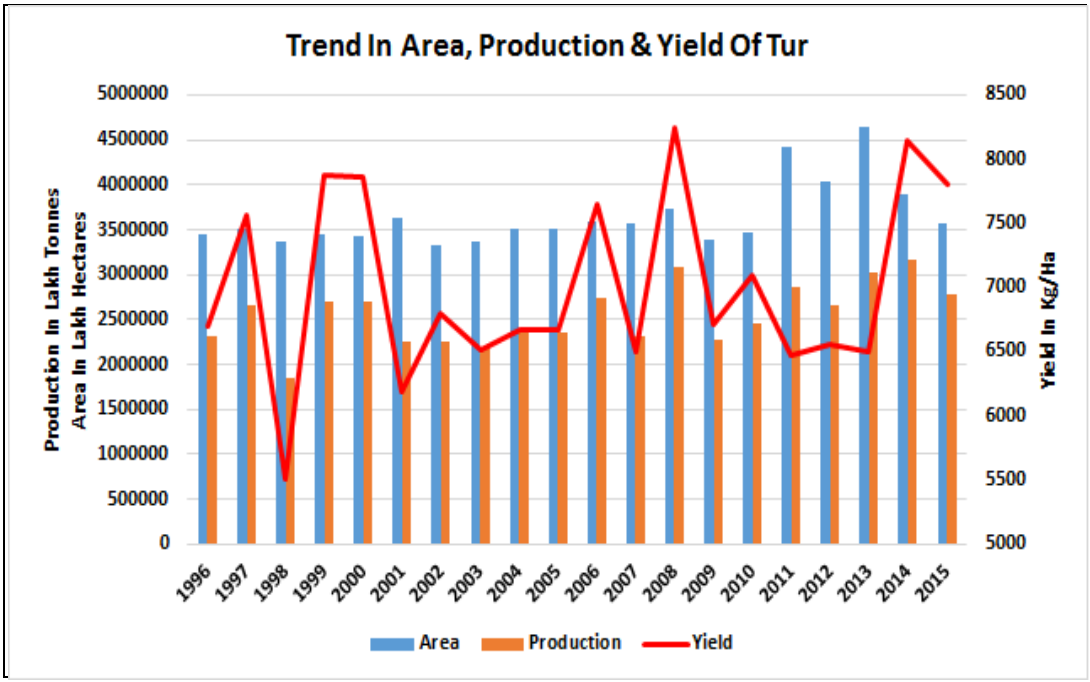



**Table B2: Area and production of Pigeonpea (Tur) (IIPR, Kanpur, 2016)**



## APPENDIX – C

**Table C1: List of CMS sources derived from different wild relatives of pigeonpea**

| S. No. | Wild relative | CMS System |
|---|---|---|
| 1 | *Cajanus sericeus* (Ariyanayagam *et al*., 1995) | A1 |
| 2 | *Cajanus scarabaeoides* (Saxena and Kumar, 2003) | A2 |
| 3 | *Cajanus volubilis* (Wanjari *et al*., 2001) | A3 |
| 4 | *Cajanus cajanifolius* (Saxena *et al*., 2005) | A4 |
| 5 | *Cajanus cajan* (Mallikarjuna & Saxena, 2005) | A5 |
| 6 | *Cajanus lineatus* | A6 |
| 7 | *Cajanus platycarpus* (Mallikarjuna *et al*., 2011) | A7 |
| 8 | *Cajanus reticulates* (Saxena *et al*., unpublished) | A8 |

Source: Saxena *et al*. 2010 and Mallikarjuna N. 2012.

**Table C2: $F_1$ plants classified as follows: (Khin lay kyu and K.B.Saxena 2011)**

| Progeny type | Extent of pollen fertility |
|---|---|
| Fertile | >80% pollen fertility |
| Partial fertile | 11 - 80% pollen fertility |
| Sterile | 0 - 10% pollen fertility |

## APPENDIX – D

**Table D1: Meteorological data recorded from June 2015 to January 2016 at ICRISAT**

| Months | Temperature (°C) | | Relative Humidity% | | Rainfall Amount (mm) | Sunshine Duration (Hrs.) |
|---|---|---|---|---|---|---|
| | Max. | Min. | 7am | 2pm | | |
| June | 33.84 | 23.5 | 84.03 | 51.85 | 109.4 | 4.46 |
| July | 33.6 | 23.39 | 79.93 | 50.03 | 45.79 | 6.46 |
| August | 30.69 | 22.32 | 89.57 | 65.48 | 139.4 | 4.46 |
| September | 31.07 | 21.78 | 91.76 | 63.89 | 173.0 | 5.29 |
| October | 32.32 | 19.67 | 89.54 | 45.21 | 63.6 | 7.99 |
| November | 30.91 | 17.03 | 87.65 | 45.22 | 0.3 | 7.67 |
| December | 31.28 | 14.53 | 89.4 | 36.7 | 2.2 | 8.00 |
| January | 30.42 | 13.25 | 83.93 | 37.96 | 2.2 | 8.11 |

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# Paper Acknowledgment.

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