COMBINING ABILITY ANALYSIS FOR VEGETABLE YIELD AND ITS COMPONENTS IN PIGEONPEA [*Cajanus cajan* (L.) Millsp.]

Thesis

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in

GENETICS AND PLANT BREEDING

by

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DECLARATION

I, Mrs Akumla Longchar, hereby declare that the subject matter of this thesis is the record of work done by me, that the contents of this thesis did not form the basis of the award of any previous degree to me or to the best of my knowledge to anybody else, and that the thesis had not been submitted by me for any research degree in any other university/institute.

This is being submitted to Nagaland University for the degree of Doctor of Philosophy in Genetics and Plant Breeding

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CERTIFICATE – I

This is to certify that the thesis entitled "**Combining Ability Analysis For Vegetable Yield And Its Components In Pigeonpea[*Cajanus Cajan* (L.)Millsp]**" submitted to Nagaland University in partial fulfillment of the requirements for the award of degree of Doctor of Philosophy in Department of Genetics and Plant Breeding is the record of research work carried out by Mrs. Akumla Longchar Registration No. 561/2014 under my personal supervision and guidance.

The result of the investigation reported in the thesis has not been submitted for any other degree or diploma. The assistance of all kinds received by the student has been duly acknowledged.

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CERTIFICATE - II

VIVA VOCE ON THESIS OF DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING

This is to certify that the thesis entitled "Combining Ability Analysis For Vegetable Yield And Its Components In Pigeonpea[Cajanus Cajan (L.)Millsp]" submitted by Akumla Longchar Admission No. Ph-138/12 Registration No. 561/2014 to the NAGALAND UNIVERSITY in partial fulfillment of the requirements for the award of degree of Doctor of Philosophy in Genetics and Plant Breeding has been examined by the Advisory Board and External examiner on ……………….............

The performance of the student has been found **Satisfactory/Unsatisfactory.**

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2. ………………………………… (External examiner)	………………………….
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Dated:

Place:

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INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp], (2n=2x=22) also known as arhar, tur and red gram, is nutritionally balanced and an exceptional source of protein in both green pea and dried grain (Faris and Singh, 1990). Along with protein, pigeonpea also renders carbohydrates and Vitamin A and C (Faris *et al*. 1987). Pigeonpea seeds are rich in proteins (generally within a range of 18 to 25% and as high as 32%), carbohydrates (57.6%), fiber (1.5%), minerals (3.5%), amino acids, methionine and cystine (Birk, 1993). Because of it rich source of protein, it is an ultimate addition to traditional cereal, banana or tuber-based diets of poor farmers that are protein deficient. Its ability to produce economic yield under limited moisture condition makes it an important crop of dryland agriculture.

Pigeonpea is used in more diverse ways among the legumes even though it ranks sixth in area and production. It is a favourite crop of marginal farmers due to its multiple uses and roles in sustainable agriculture. It is also utilized as forage, fodder, fuel and medicine besides being a primary food. It also plays an important role in controlling soil erosion in erosion prone areas that are being caused by wind and water (Saxena, 2000).

Pigeonpea, belongs to family Fabaceae. In India, it is an important pulse crop. Pigeonpea is an ideal crop for sustainable agriculture mainly for its ability to enrich soil through symbiotic nitrogen fixation and adds organic matter and other nutrients (Saxena, 2008).

In developing countries, it has been recognized as a good source of vegetarian protein where majority of the population depends on the low priced vegetarian foods. It is mainly cultivated for its dry seeds and green vegetables in dry areas of the tropics and subtropics. Pigeonpea is highly proteinaceous and the seed can be prepared into various meals and served as substitute for cowpea.

It is one of the major pulse crops of dryland agriculture because of its deep tap root system and inherent drought resistance. Its ability to produce high amount of biomass per unit area makes it useful as fodder, fuel and for thatching for the rural masses. Large quantities of foliage crop add to the organic matter of the soil. The deep and well spread root system helps in soil aeration after decomposing. Hence it is highly valued by the farmers. Local germplasm of pigeonpea in India have a broad natural genetic variability. Existences of pigeonpea wild relatives are also being reported in India. Thereby, India is considered as the native place of pigeonpea.

Pigeonpea cultivars are grown for vegetable purpose, where pods are harvested at the milking to dough stage of its development. Most of the Indian consumers prefer green podded pigeonpea among the cultivars grown for vegetable purpose. These bring in better price than stripped ones, or pods of other colours.

Pigeonpea is mostly used as a pulse crop throughout the world in which the dried seeds are used as human food. The pea can also be picked at physiological maturity and served as vegetable purpose. The green seed is considered to be more nutritious than the dry seed as it has more protein, sugar and fat. In addition, the protein in green seeds is more digestible. Green seeds have lower quantities of the sugars that produce gas (flatulence) in the green seeds whereas the mature seeds contain a bit more minerals.

Green pigeonpea seeds have more nutritional value as compared to dal. Singh *et al*. (1984, 1983) and Singh (1988) reported that polysaccharides content was high in vegetable type pigeonpea with low content of crude fiber as compared to dal, whereas pigeonpea dal is superior in starch and protein content. The vegetable type pigeonpea and garden pea [*Pisum sativum* (L.)] have almost similar crude fiber content. The vegetable pigeonpea grains have higher crude fiber, fat, and protein digestibility. Normally in vegetable type sugar levels are around 5.0% but certain varieties such as ICP7035 has been identified by researchers at ICRISAT which a sugar content as high as 8.8%. Persistent demand for vegetable pigeonpea either as canned or frozen green peas is there in Caribbean region.

Pigeonpea is not very popular across the globe. It is grown only as a backyard crop, an intercrop and sometimes for fencing purpose. Therefore there is not much agricultural statistics available in this crop. It is known as a poor man's crop grown only in very dry areas to sustain the poor farmers. However, subsequent research on this crop by plant breeders has transformed this semi- arid tropic crop into an adaptable and high yielding crop. It can be grown in high and low rainfall areas as it is resistant to diseases. This crop is a source of food, fuel, forage and enhances soil fertility due to its legumenase nature. It is now exported for its wide range of products benefiting both farmers and consumers.

Globally the area and production of pigeonpea has increased from 2.86 million ha and 1.96 million tons in 1980 to 4.36 million ha and 3.46 million tons in 2006, respectively (FAO Stat, 2008). Pigeonpea represents about 5% of world legume production and more than 70% is being produced in India.

Pigeonpea is the second most important pulse crop of India which accounts for 20 percent of the total pulse production in India. In India, pigeonpea is grown in an area around 4.04 million hectare with a production of approximately 2.65 million tons (Anonymous, 2012). It has registered a production of 4.02 million tons in the year 2017-18 (All India Coordinated Research Project on Pigeonpea, Annual Report 2017-18). As ‘dal’, pigeonpea is an important constituent of the Indian meal. Of the total pigeonpea production in the world, India alone contributes nearly 92 per cent of it.

In India average productivity of pigeonpea is lower (671 kg/ha) compared to the world average productivity (742 kg/ha) even though it leads the world in area and production (FAOSTAT, 2010). Production of pigeonpea in India is still short which cannot fulfilled the present consumption of ~19 million tonnes thereby compelling to import pulses to a range of 1.5-2.0 million tons annually (https://www.agricoop.nic.in, accessed on Feb. 28, 2013). WHO recommendation of per capita availability of protein is 80 g/day (Saroj *et al*., 2013), while it is only 28 g/day in India which does the ultimate problem of the malnutrition exist among the poor people. The chasm between per capita availability of protein in India and WHO recommendation can be bridge through pulses which is a rich source of protein.

The importance of pulses in Indian agriculture cannot be denied. Of the total pulses, red gram or pigeonpea takes an important place among rainfed resource poor farmers as it provides quality food, fertilizer, fuel wood and fodder. Despite its immense importance in sustainable agriculture its global production per hectare has remained static over last three decades. Lack of efficient management practices coupled with biotic and abiotic stresses has widened the gap between the potential yield and on-farm yield.

The conventional breeding procedures followed in pigeon pea brought improvement in seed yield and resistance to diseases and pests. However, for further boost in productivity, the possibility of producing pigeon pea hybrids and identification of superior hybrids through line x tester mating design open up new avenues.

In a breeding programme, the most important steps are the selection of suitable genotypes as parents for hybridization. Selection of parents on the basis of phenotype is not a sound procedure since phenotypically superior line may yield poor recombinants in the segregating generation. Therefore selection of parents on the basis of their genetic values is necessary. Generally, parents are chosen on the basis of gene action involved in the expression of quantitative characters.

Genetic variation among genotypes and relation between major yield contributing traits are of great vital importance in the breeding programme that aims to produce improved genotype.

Yield is a complex character, which is the product of interaction of many traits. Therefore it is necessary to have the knowledge of the contribution of different character towards yield through correlation. Basic information of the nature and extent of inter-relationships between yield and its attributes will be of great utility for the choice of characters in the selection programme.

Utilization of the cross as commercial hybrid is possible if the specific cross have high heterosis and the observations made are true for an economic character like yield, provided there exist cytoplasmic genetic male sterility and fertility restoration system. Analysis of combining ability is considered as the most potent tool for identifying the suitable parents for a hybridization programme. Selection of parents with high general combining ability (GCA) effect and cross combinations with high specific combining ability (SCA) is necessary for heterosis breeding. Therefore, the present investigation was undertaken to study the combining ability of parents and cross combinations as well as to evaluate the nature and magnitude of heterosis for green pod yield and its components.

Pigeon pea is an often cross pollinated crop and therefore, amenable to genetic improvement by following breeding methods suitable for both allogamous and autogamous crop. Understanding the nature and magnitude of genetic variance implies an appropriate breeding procedure for isolation of a suitable genotype that has maximum useful alleles.

The study of heterosis and combining ability helps plant breeders in choosing suitable parents and also helps in understanding the magnitude of gene action involved in the inheritance of quantitative traits of economic importance. Accordingly, the present investigation "Combining ability analysis for vegetable yield and its components in pigeonpea [*Cajanus cajan* (L.) Millsp.]" was undertaken to have the knowledge on nature of combining ability and heterosis for yield and yield attributes in pigeon pea.

It is an unrealistic and perhaps an impossible task for handling and analyzing of a very large number of crosses therefore, in order to avoid inconvenience for plant breeder it is necessary to select few parents with high genetic potential. In plant breeding programmes, analysis of combining ability is useful in order to have a view of the genetic worth of parents and their crosses for further exploitation.

Among analysis of combining ability, Line x tester analysis (Kempthorne, 1957) has been widely utilized. It is mostly utilized for screening of germplasm, to identify valuable donor parents and promising crosses in many crops including pigeonpea (Sarode *et al.*, 2009; Kumar *et al.*, 2009; Shoba and Balan, 2010; Gupta *et al.*, 2011; Kumar *et al.*, 2012; Yerimani *et al.* 2013). This mating design further provides information about heterosis and components of genetic variation e.g., additive and dominance components of genetic variation. Hence line x tester analysis was attempted in pigeonpea using 7 lines and 5 testers to achieve the following broad objectives:

1. To study the general and specific combining ability effects of the parents and crosses,

2. To estimate the extent of heterosis in the intervarietal crosses of pigeonpea, and
3. To estimate the components of genetic variance for green pod yield and related traits.

REVIEW OF LITERATURE

2.1 Coefficient of variability

Basavarajaiah *et al.* (2000) reported high values of PCV and GCV for days to 50 percent flowering, straw weight, pods per plant, yield per plant and length of pod bearing branches. High heritability coupled with high genetic advance was observed for days to 50 percent flowering, straw weight, yield per plant, length of pod bearing branches and 100-seed weight, indicating that additive gene effects were operating for these characters.

Venkateswarlu (2002) estimated variability in twenty-eight genotypes of pigeonpea. He reported the maximum variability for number of pods per plant followed by straw yield per plant and plant height.

Godwa *et al.* (2003) studied genetic variability for number of pods, seed yield, days to maturity, number of branches per plant and plant height in 32 early maturing varieties of pigeonpea. They reported that high phenotypic and genotypic coefficient of variability for number of branches per plant, number of pods per plant, seed yield per plant and plant height. Joshi *et al.* (2003) also evaluated fifty early maturing genotypes of pigeonpea and reported the highest genotypic coefficient of variation for number of pods per plant followed by seed yield per plant and number of branches per plant.

Baskaran and Muthaih (2007) reported highest genetic variability for number of clusters, number of pods and genotypic coefficient of variation was lowest for days to 50 percent flowering and days to maturity in their study on pigeonpea hybrid.

Sodavadiya *et al.* (2009) reported that estimates of GCV in general were higher than their corresponding PCV indicating strong inherent association among the traits. The seed yield per plant had significant and positive association with days to 50 percent flowering, days to maturity, number of branches per plant, number of pods per plant and 100 seed weight at both genotypic as well as phenotypic levels.

High PCV and GCV for number of pods, seed yield per plant, plant height and plant spread were recorded in an investigation for yield attributes in 27 genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp] by Bhadru (2010).

Khan *et al.* (2011) reported that estimate of grain yield per plant had maximum phenotypic and genotypic coefficient of variation (PCV and GCV), followed by biological yield plant per plant. Heritability estimates of all the traits were high except leaf area which shows moderate heritability. Highest heritability was recorded for days to 50 percent flowering followed by biological yield per plant, plant height, 100 seed weight, grain yield per plant, leaflets per leaf and days to maturity. Hamid *et al.* (2011) also reported on genetic variability in pigeonpea. They evaluated one hundred germplasm of pigeonpea and reported that plant height, days to flowering and pods per plant showed the discriminating variables and pods per plant was dominant in explaining maximum variance.

Singh *et al.* (2013) studied to obtain the knowledge of nature and magnitude of genetic parameters and its utilization in development of superior varieties from 21 short duration of pigeonpea. PCV was moderate for the characters like seed yield per plant, pods per plant and primary branches per plant. Maximum GCV was observed for seed yield per plant, pod per plant and primary branches per plant. Seed yield per plant was found significantly positively associated with seeds per pod, pod length and plant height at genotypic level. Genetic variability, genetic diversity and correlation on various morphological traits, yield and yield related components of pigeonpea were also studied by Kumara *et al.* (2013) and they observed that the characters of genotypes and phenotypes varied significantly for all traits under study. Number of pods per plant, number of seeds per pod, days to 50 percent flowering, 100 seed weight and yield per plant recorded high heritability. Genetic advance was high in secondary branches, pod bearing length, number of pods per plant, yield per plant. The greatest variation was observed in number of pods per plant. Rangare *et al.* (2013) also advocated that high GCV and PCV for number of pods per plant, harvest index, biological yield per plant and grain yield per plant. High heritability coupled with high genetic advance was exhibited by days to maturity, days to 50 percent flowering, days to initial flowering, plant height, number of pods per plant, biological yield per plant, grain yield per plant and harvest index so selection may be effective for these characters. A study on variability, character association and path analysis for yield and yield attributes in pigeonpea showed number of secondary branches per plant, number of pods per plant, seed yield per plant, phenol content, 100 seed weight and number of primary branches per plant showed higher estimates of phenotypic and genotypic coefficient of variation as reported by Rekha *et al.* (2013).

Ramya *et al.* (2014) in their study reported high estimates of PCV and GCV for primary branches per plant, number of clusters per plant, number of pods per plan and single plant yield. Evaluation on 23 pigeonpea genotypes to estimate genetic variability utilizing various quantitative traits for overall improvement in pigeonpea was done by Pandey *et al.* (2014). They reported that secondary branches per plant showed highest phenotypic as well as genotypic coefficient of variation followed by seed yield per plant and biological yield. High heritability coupled with high genetic advance was observed for 100 seed weight, pods per plant and seed yield per plant while, plant height, primary branches per plant, pods per plant, seeds per pod and harvest index showed high heritability with moderate genetic advance.

Saroj *et al.* (2015) studied the general mean, range, genotypic, phenotypic and environmental variance, genotypic, phenotypic and environmental coefficient of variance, heritability and genetic advance for grain yield and its components among parents, F_1's and F_2's populations of the pigeonpea. The higher values of general mean and range were observed in case of pods per plant along with moderately higher coefficient of variation. Chethana *et al.* (2015) also studied the variability in terms of genotypic and phenotypic variance, coefficient of genotypic and phenotypic variation, heritability and genetic advance. The wide range of variability was exhibited by number of pods per plant, seed yield per plant, 100 seed weight and for other yield attributing traits also.

Genetic analysis of 23 vegetable type Pigeon pea genotypes was studied by Patil *et al.* (2016). The analysis of variance revealed significant differences among all the genotypes for the traits studied. Genotypic and phenotypic coefficient of variation were of high magnitude for plant height,100 green pod weight,100 green seed weight, shelling percentage (%), TSS (%), days to 50% flowering, pod length, pod width and for number of primary branches per plant.

2.2 Heritability and genetic advance

Dahat *et al.* (1997) studied 30 genotypes of pea for 11 yield traits. They observed heritability accompanied with high genetic advance for number of secondary branches per plant, seed yield, plant height and number of pods per plant.

Patel and Patel (1999) noted data on heritability and genetic advance for 9 quantitative characters in 4 crosses of pigeonpea. High heritability coupled with high genetic advance was observed for seed yield, number of primary branches per plant and number of pods per plant.

The genetic variability and nature of character association in pigeonpea under different cropping system was studied by Deshmukh *et al.* (2000). High heritability along with genetic advance was recorded for plant height and pods per plant.

Joshi *et al.* (2003) reported high genetic advance as per cent of mean for pods per plant, yield per plant and number of branches per plant in case of 50 early maturing genotypes of pigeonpea. Yield per plant showed high genetic advance with low heritability, whereas most of the characters under study except plant height and seeds per pod showed high heritability. A study on 32 early maturing varieties of pigeonpea by Gowda *et al.* (2003) reported high heritability combined with high genetic advance for number of pods per plant, whereas, high heritability with moderate genetics advances were reported for days to maturity and seed yield. Further, a moderate genetic advance was observed for days to flower, days to maturity and harvest index.

Sarsamkar *et al.* (2008) in their study revealed that wide range of variability was exhibited by number of pods per plant, plant height and seed yield per plant. High heritability was exhibited by days to maturity, number of pods per plant, 100 seed weight, days to 50 percent flowering and seed yield per plant. However, moderate to low heritability estimates were displayed by number of secondary branches per plant and number of primary branches per plant, respectively. High genetic advance coupled with high heritability estimates were observed for number of pods per plant, seed yield per plant, plant height and days to maturity.

Ajay *et al.* (2012) estimated the genetic variability and quantitative traits of pigeonpea to the yield and revealed that high heritability with high genetic advance as percentage of mean were obtained for seed yield and number of pods per plant which indicated the presence of additive gene action influencing the inheritance of these characters.

Bhadru (2013) conducted an experiment to study genetic variability, heritability and genetic advance for pigeonpea. He found high coefficient of variation in number of pods, seed yield per plant, plant height and raceme length and high values of heritability coupled with high genetic advance as were observed in number of pods, seed yield, primary and secondary branches per plant, plant height, raceme length, and test weight, seeds per pod, pod length and plant spread. A study on variability, character association and path analysis for yield and yield attributes in pigeonpea showed high heritability with high genetic advance as percent of mean recorded for all the characters except protein content, days to 50 percent flowering and days to maturity by Rekha *et al.* (2013). Also a study on 30 genotypes of pigeonpea for grain yield and its attributing characters by Shunyu *et al.* (2013) showed high heritability and genetic advance for seed yield per plant, days to 50 percent flowering, plant height, number of pods per cluster, number of clusters per plant, pod length, 100 seed weight, number of primary branches per plant and days to maturity. Vanisree *et al.* (2013) also studied 128 germplasm lines of pigeon pea for yield and yield attributing characters. Higher amount of variation were observed in seed yield per plant, number of pods per plant and plant height.

High heritability with high genetic advance as percentage of mean was obtained in seed yield and number of pods per plant.

Santosh *et al.* (2014) studied the genetic variability and inter relationship among yield contributing character in pigeonpea. High heritability and genetic advance were observed for number of pods, plant height, test weight, days to maturity and primary and secondary branches per plant.

Saroj *et al.* (2015) studied the heritability and genetic advance for grain yield and its components among parents, F1's and F2's populations of the pigeonpea. High heritability estimates coupled with higher genetic advance were observed for plant height, primary and secondary branches per plant, pod length. Pods per plant and grain yield per plant. Chethana *et al.* (2015) also studied heritability and genetic advance in pigeonpea. High genetic advance coupled with high heritability estimates was observed in number of pods per plant, seed yield per plant, plant height and pod bearing length. A study on 24 genotypes of vegetable genotypes for yield and yield contributing traits was conducted by Swapnil *et al.* (2015) and reported high heritability accompanied with high genetic advance for 100 green pod weight and days to 50 per cent flowering.

Genetic analysis of 23 vegetable type Pigeon pea genotypes was studied by Patil *et al.* (2016). The estimate of high heritability (bs) accompanied with high expected genetic advance for 100 green pod weight and days to 50% flowering indicate the presence of additive gene action in the expression of these characters. Usharani and Kumar (2016) also revealed that high value of heritability and genetic advance were found in days to flowering, plant height, number of primary branches per plant, number of pods per plant and number of seeds per plant. A study on heritability and genetic advance in pigeonpea by

Parmar and Kathiria (2016) also reported that days to 50 percent flowering, days to maturity and 100 seed weight exhibited high heritability coupled with low genetic advance.

2.3 Correlation studies

Among quantitative characters in pigeonpea primary branches per plant exhibited positive and significant phenotypic correlation with plant height. In the same pattern, phenotypic correlation was observed between plant height and seeds per pod. . Kingshlin and subbaraman (1999) reported. Kingshlin *et al.* (1999) also studied the character association in the segregating progenies of two crosses of pigeonpea. It was observed that branches per plant, clusters per plant, pods per plant, pod length, seeds per pod and 100 seed weight were strongly associated with seed yield.

Pandey and Singh (2001) assessed the association between yield and yield attributes in pigeonpea hybrids. They reported positive and significant correlations for yield with number of primary branches/plant, pods/plant and seeds per pod at genotypic level.

An estimated correlation among yield attributes in parents, F_1 and F_2 generations of 48 crosses made in line x tester fashion in pigeonpea by Kumar *et al.* (2003) observed that genotypic correlations were slightly higher in magnitude than the phenotypic ones. Grain yield per plant had significant and positive correlation with pods per plant, pod length and 100 seed weight in all the generations, indicating that grain yield could be improved by selecting genotypes on the basis of higher number of pods per plant, pod length and 100 seed weight.

Gupta *et al.* (2003) studied correlation in seven F_3 populations generated by crossing diverse parents of chickpea. They found significant and positive association of seed yield with plant height, pods per plant and seeds per pod. They also reported that pods per plant and plant height may be selected in F_3 generation to contribute the seed yield. Padi (2003) also evaluated 10 genotypes of pigeonpea and reported that significant correlation was found between each traits and grain yield and between pairs of traits. Each trait also showed large positive direct effect on grain yield.

Seed yield per plant had significant and positive correlation coefficient with plant height as was reported by Jogender and Bajpai (2008). A similar correlation was noticed between numbers of chambers per pod with number of seeds per pod.

Sreelakshmi *et al.* (2010) in their study revealed that most of the yield contributing characters showed significant positive correlation except number of primary branches per plant which showed significant negative correlation with seed yield. Days to maturity had maximum direct effect on seed yield followed by number of pods per plant and plant height whereas, number of secondary branches showed negative direct effect on seed yield.

Patel *et al.* (2011) in their studies reported that, seed yield per plant were found significantly associated with seeds per pod, pod length and plant height at genotypic level, indicating that these attributes are predominant and may contribute considerably towards higher seed yield of pigeonpea.

Rama Devi *et al.* (2012) evaluated five lines, three tester and their fifteen crosses to study the genetic relationship among yield component through association and path analysis. The association studies indicated significant positive correlation of seed yield with pods per plant in parents and plant height, pods per plant and harvest index in crosses.

Dalbeer *et al.* (2013) in their study reported that the seed yield per plant showed highly significant and positive correlation with plant height, days to maturity, secondary branches per plant, pods per plant, 100 seed weight, and biological yield, whereas primary branches per plant exhibited negative correlation with number of seeds per pod.

A study on the genetic variability and correlation of various morphological traits, yield and yield related components of pigeonpea by Kumara *et al.* (2014) observed that at the phenotypic level, the seed yield showed positive correlation and significant association with the other component traits like number of primary branches per plant, secondary branches and 100 seed weight.

Chithrameenal and Jabaraj (2015) estimated the genotypic and phenotypic correlations in the parents to evaluate their performance. The association analysis indicated that grain yield was positively associated with days to 50 percent flowering, days to maturity, number of branches per plant, plant height, and number of pods per plant, hundred seed weight, and leaf area, dry weight of leaves per plant, dry weight of roots per plant and dry weight of husk per plant.

Highly significant differences for all characters under study among the genotypes of pigeonpea were observed by Pandey *et al.* (2016). Biological yield per plant, pods per plant, 100 seed weight, harvest index and secondary branches per plant showed highly significant positive correlation with seed yield. Singh and Singh (2016) also studied the phenotypic correlation coefficient of parents F_1s and F_2s of pigeonpea and reported that in F_1s, only pods per plant were positively and significantly associated with seed yield whereas in segregating populations (F_2s), plant height, pods per plant and seeds per pod revealed positively significant associations with seed yield. Yield potential of 12 medium maturity vegetable pigeonpea [*Cajanus cajan* (L.) Millsp] cultivars were evaluated by Ojwang *et al.* (2016). Significant and positive correlation coefficients were recorded between seed yield and pods per plant as well as shelling percentage.

2.4 Heterosis

Patel *et al.* (1991) observed that a large number of hybrids depicted significant and useful heterosis over better parent and standard variety. They also observed the highest heterosis for seed yield over better parent in the cross MS 3A x DL 78-1(79.9%).

Patel and Patel (1992) studied the heterosis in 30 hybrids from six lines and five testers in pigeonpea for yield and yield contributing traits. They found maximum beneficial heterotic response over better parent for number of pods per plant followed by seed per plant (136.94%).

Ajay Kumar and Srivastava (1998) evaluated heterosis, combining ability and genetic variance derived for 7 agronomic and yield-related traits in a line x tester cross of long-duration pigeon pea (*Cajanus cajan*) involving three male sterile lines as the seed parents and twelve male fertile lines as the pollen parents. Heterosis over the better parent for seed yield ranged from -77.91 to 110.07%. Pods/plant and primary branches/plant contributed substantially towards expression of heterosis for seed yield.

Khorgade *et al.* (2000) evaluated twenty-four pigeon pea hybrids, derived from crosses between 3 genetic male sterile lines and 8 diverse testers, heterosis over the mid-parent and control cultivar (BDN 2). Significant heterosis was observed in the traits viz., days to 50% flowering, plant height, number of branches per plant, number of pods per plant, 100-seed weight, protein content and seed yield per plant. Srinivas *et al.* (2000) studied heterosis for grain yield and its components in pigeonpea. Two male sterile lines ICPMS 3783 and ICPMS 288 were used in a line x tester mating design with 11 medium to late maturing genotypes. The expression of heterosis was evident for yield per plant, pods per plant and number of secondary branches.

Chandirakala and Raveendran (2002) studied heterosis for yield and yield components in 30 pigeon pea hybrids, three genic male sterile lines, and ten tester lines. Crosses with MS Prabhat DT showed marked heterosis for number of pods per plant, number of clusters per plant, 100-grain weight, and grain yield per plant. ICPL 88009, ICPL 89008, and ICPL 84023 exhibited significant heterosis for yield and yield components. Significant negative heterosis over mid, better, and standard parents were observed in MS Prabhat DT x ICPL 88009 and MS CO 5 x ICPL 88009 for days to 50% flowering, and in MS Prabhat DT x ICPL 87104, MS Prabhat DT x ICPL 89020, MS Prabhat DT x ICPL 90012, and MS CO 5 x ICPL 87104 for plant height. On the other hand, the highest positive heterosis over mid, better, and standard parents were observed in MS CO 5 x ICPL 88009 for number of branches per plant, and in MS Prabhat NDT x ICPL 88009 and MS Prabhat DT x ICPL 84023 for grain yield per plant. Heterosis in yield per plant was positively associated with heterosis for number of branches per plant, number of pods per plant, number of clusters per plant, and 100-grain weight. Also a study on heterosis over mid parent, better parent and standard check for ten characters in 45 hybrids and 10 parents by Bagade *et al.* (2002) reported high heterotic response for days to maturity and protein content, moderate for days to flowering, number of branches per plant, number of seeds per pod and plant height.

Maximum significant negative heterosis over standard variety was noticed in MS UPAS 120 x Pusa 962 for days to flower by Yadav and Singh

(2004). They also noticed maximum heterosis for yield per plant over standard variety UPAS 120 x Pant A 128. A genetic analysis of 36 pigeonpea hybrids was made by Sekhar *et al.* (2004). Evaluation for days to 50% flowering, days to maturity, plant height, plant spread, clusters per plant, pods per cluster, pods per plant, seeds per pod, 100-seed weight, seed yield per plant, biomass and harvest index, revealed the predominance of non-additive gene action. The parents QMS-1 and MS Prabhat DT among the male steriles while Sel 90309, Sel 90306, Sel 90310, Sel 90311 and Sel 90307 among the pollinators were good general combiners. The crosses QMS-1 x Sel 90307, QMS-1 x Sel 90311 and MS Prabhat NDT x Sel 90214 were the best specific combiners for yield and its components. Heterosis values of 51.3 and 171.6% were recorded for seed yield per plant, over the standard control Sel 90308 and a better parent, respectively.

Wankhade *et al.* (2005) estimated heterosis in 24 crosses of pigeonpea. The heterosis was of general occurrence for most of the characters except plant height. Significant positive heterosis was observed for number of pods per plant, followed by number of clusters per plant, seed yield per plant and number of branches per plant. Also high hybrid vigour was noticed for number of primary branches/plant, number of seeds per plant and 100 seed weight in 36 hybrids of pigeonpea by Yadav *et al.* (2005).

Banu *et al.* (2007) evaluated forty-five hybrids of pigeon pea developed through a line x tester mating design to estimate the relative heterosis and heterobeltiosis. Observations were recorded on days to 50% flowering, maturation period, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length and 100-seed weight and single plant yield. The hybrid combination ICP 13201 x CO 5 was the best with the maximum heterosis for most of the yield-attributing characters, followed by ICP 11961 x ICP 7118 and ICP 11961 x CO

5, which showed higher heretobeltiosis and relative heterosis for most of the yield-attributing characters. Twelve crosses along with their parents, viz., four lines and three testers, of the line x tester mating design were evaluated by Raju and Muthiah (2007) to study heterosis for seed yield and its components. A high degree of heterosis for seed yield per plant and other yield components over standard check (CO 5) was observed. The hybrid combination CO 5 x ICPL 87119 was considered as the best for higher seed weight and CO 6 x ICPL 87119 and CO 6 x ICPL 332 exhibited high heterosis for yield and other yield contributing characters.

Twenty hybrid pigeon pea combinations involving 5 diverse parents for yield and its components were analysed by Bhavani and Bhalla (2009) and they reported that the average heterosis was maximum for yield per plant, followed by pods per plant and number of fruit bearing branches. Comparatively, the other yield components showed low average heterosis values. In general, early x late and medium x late combinations resulted in high heterosis for yield. Dheva *et al.* (2009) studied hybrids obtained from crossing new cytoplasmic male sterile and restorer lines, to determine the heterosis over the standard control for the characters number of pods per plant and grain yield per plant. The heterosis in positive direction for number of pods per plant varied from 1.95 to 79.19% and for grain yield per plant from 0.97% to 59.68 over the control was observed. The crosses AK-120-2A x AKPR-219, GT-33A x AKPR-297 and GT-288A x AKPR-192 showed higher heterosis over the control for number of pods per plant and grain yield per plant. Phad *et al.* (2009) crossed five pigeon pea lines with 12 male parents in a line x tester fashion. All the 60 crosses along with the 17 parents were tested. One cross (BDN 2 x BDN 2010) had high heterosis, high specific combining ability (sca) and also had good stability for number of pods per plant. Same cross exhibited the highest sca effect for number of primary branches per plant, number of pods per plant and seed yield per plant. Some crosses, which were superior on the basis of sca and stability but not on heterosis or some were superior in heterosis and sca but not for stability. Sarode *et al.* (2009) also estimated the heterosis for yield and yield traits in long duration pigeon pea using 5 lines and 3 testers. The 15 crosses were made in line x tester fashion. The maximum standard heterosis was recorded in the cross Pusa 9 x Bahar, followed by Pusa 9 x ICPL 84023 and DA 11 x Bahar for number of pods per plant. Pusa 9 x Bahar also revealed significantly positive heterotic effect for most of the yield components, such as 100-seed weight, number of seeds per pod, pods per plant and number of primary and secondary branches.

The heterosis study for seed yield and its attributes was carried out in pigeonpea through line × tester mating design in four different seasons by Pagi *et al*. (2016). The variance due to hybrids, lines, testers and line × tester interactions were significant for most of the characters studied demonstrating the presence of significant variability among the material used in the study and presence of overall heterosis for all the characters. The magnitude of heterobeltiosis and standard heterosis altered for all the crosses and for all the characters were studied. In general, it is inferred that magnitudes of heterotic effects were high for seed yield per plant, pod clusters per plant, pods per plant, 100-seed weight and protein content, expressing moderate heterotic effects for days to flowering, days to maturity, seeds per pod and pod length and low for plant height. The hybrids GT 610 A× GTR 84, GT 603 A × GTR 81 and GT 610 A × GTR 82 exhibited the highest, significant and positive heterotic effect and mean performance for seed yield per plant and some of its important component traits.

2.5 Combining ability

A study carried out in pigeonpea for combining ability analysis through line x tester analysis using a genetic male sterile line for yield and yield attribute by Vanniarajan *et al.* (1999), observed preponderance of non-additive gene action over additive gene action for all the characters except days to 50% flowering, days to maturity, plant height and seeds per pod. The hybrids IMS 1 x ICPL 87, QMS 2 x ICPL 897, IMS 1 x ICPL 161, MSCO 5 x ICPL 84032, MST 21 x ICPL 161 and MST 21 x Vamban 1 were found to show good SCA effects for most of the traits including seed yield.

Sidhu *et al.* (2000) estimated the combining ability and genetic variance for nine quantitative traits in pigeonpea through line x tester analysis involving three male sterile lines, 18 pollinators and 54 F_1 hybrids. The male sterile lines and pollinators differed in their general combining ability (GCA) for almost all the traits. Additive gene effects were predominant for the inheritance of plant height, pods per plant and seed size, whereas non-additive gene effects appeared to be more important for the rest of the traits. Among the females, MS Prabhat (DT) was a good combiner for early maturity, plant height, number of primary branches, seeds per pod, seed size and grain yield. Pollinators such as AL 688 and AF 276 were observed to be high combiners for early flowering and maturity, and higher number of pods and grain yield. The three top yielding hybrids, i.e. PMS 1 x AF 276, MS Prabhat (DT) x AL 688 and PMS 1 x AL 201, also exhibited high specific combining ability (SCA) effects for seed yield.

Jayamala and Rathnaswamy (2001) studied combining ability in line x tester analysis in pigeonpea revealing non-additive gene action for the expression of days to first flowering, days to 50% flowering, number of branches per plant, plant height, number of pods per plant, days to maturity, number of seeds per pod and additive gene action for seed yield. Parents MS Prabhat DT and CORG 9060 were found to be good general combiners for days to first flowering, days to 50% flowering and days to maturity. For number of branches per plant, plant height, pods per plant and seed yield per plant, MS Co 5 and CORG 5 were the combiners. The crosses MS Co 5 x ICPL 161 and MS Co 5 x CORG 5 were the best combinations for seed yield. Pandey and Singh (2001) evaluated hybrids utilizing three genetic male sterile lines and 12 diverse genotypes of the long duration group of pigeonpea for general and specific combining ability, variance components and standard heterosis. Among the lines, DA 32, DA 34, DA 37, DA 46, DA 93-4, DA 93-2, DA 94-6 and Bahar mutant and the testers, DAMS-1 and ICPMS 3783, were found to be good general combiners for seed yield per plant and other yield contributing traits such as secondary branches per plant, clusters per plant and number of pods per plant. The tester DAMS-1 was also a good general combiner for primary branches per plant and percent pod setting. The estimates suggested partial dominance of additive genetic action for number of pods per plant, non-additive genetic variance was observed for days to flowering, days to maturity, plant height, number of primary branches per plant, percent pod setting, harvest index and seed yield per plant. Ajay Kumar *et al.* (2001) also conducted an experiment in pigeon pea and reported that non-additive genetic variance chiefly controlled the expression of yield per plant and attributes such as primary branches per plant, pods per plant, seed per pod, and 100 seed weight, whereas additive genetic variance predominantly governed the expression of days to 50% flowering and plant height. Study on combining ability variance and effects using four lines of the wild species *Cajanus sericeus* and four testers of cultivated species Line x Tester fashion were conducted by Singh and Srivastava (2001) and they reported that out of six lines one line was good general combiner for days to flowering, plant height, number of primary branches per plant, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. One tester was found to be a good general combiner for days to maturity, number of primary branches per plant, number of pods per plant, pod length, 100 seed weight and seed yield per plant.

Srinivas *et al.* (2002) conducted experiment on six medium to late duration pigeonpea lines in a 6 x 3 line x tester mating design, and analysis was done for their general and specific combining abilities with regard to seed yield, days to 50% flowering, plant height, number of primary branches, secondary branches, pods per plant, seeds per pod and 100-seed weight and reported the predominance of non-additive gene action for all traits. An experiment in pigeonpea to study combining ability conducted by Pandey and Singh (2002) also reported that five lines and two testers were found to be good general combiners for seed yield per plant and other yield contributing traits such as secondary branches per plant, clusters per plant and number of pods per plant. One tester was also a good general combiner for primary branches per plant and percent pod setting. Out of the 36 cross combinations, 10 showed higher magnitude of specific combining ability for seed yield per plant, number of secondary branches per plant, clusters per plant and pods per plant. Manivannan (2002) investigated combining ability and gene action for different quantitative characters using five genotypes as lines and two genotypes as testers. They reported non- additive gene action for plant height, number of branches/plant, number of clusters/plant, number of pods/plant and seed yield/plant. The parent KM2163 was identified as good general combiner for all the above characters except plant height.

A line x tester analysis for combining ability in pigeonpea involving 24 F_1s obtained from crosses between 3 lines and 8 testers along with their parents was conducted by Jahagirdar (2003). Significant non-additive gene action for almost all morpho-physcological traits were revealed as variance due to specific combining ability (SCA) were higher than the general combining ability (GCA) variances. The parents BDN 2, ICPL 87, BSMR 736 and ICPL 87119 were found to be the best general combiners for grain yield per plant, number of pods per plant, total biomass per plant and grain productivity per day. Ten out of 24 F_1s showed significant positive sca effects and higher per se performance for grain yield. Pawar and Tikka (2003) studied 64 hybrids in pigeon pea to understand the nature of gene action and reported higher magnitude of sca variance over gca variance for all the traits which indicated pre ponderance of non-additive gene action. The parents were good general combiners for seed yield and its two or more component traits. Also combining ability for seed yield and its components in a line x tester mating design using four male sterile lines and 14 testers of pigeonpea was studied by Krishan *et al.* (2003) and they reported that the magnitude of non-additive components of variance was much higher than that of additive components indicating the pre-dominance of non-additive gene effects for the expression of the characters studied. The female parents MS Prabhat DT, MS T-21 and tester ICPL-143 were found good general combiners for seed yield. The crosses MS Prabhat DT x H 82-135, MS Prabhat DT x 85 HP 343-1 and MS Prabhat NDT x H 82-155 showed positive specific combining ability effects for seed yield. Hybridization system such as multiple crossing or reciprocal recurrent selection which exploits both additive and non-additive gene effects simultaneously could be useful in the genetic improvement of seed yield and its component traits. An experiment in pigeonpea using line x tester model conducted by Sunilkumar *et al.* (2003) also reported non-additive gene action for all the characters except days to 50% flowering, 100-seed weight and protein content for which additive gene action was predominant. The parents were the best general combiners for grain yield and number of pods per plant. Among the crosses one cross had the highest specific combining ability (SCA) effects for grain yield, number of pods per plant, 100-seed weight, days to maturity, plant height at harvest and pod bearing length, whereas majority of the crosses showed high SCA effects for grain yield. Kumar *et al.* (2003) studied nature of gene action in pigeon pea and reported that among the parents two parents and one tester were the best general combiners for seed yield and number of pods per plant. Among the crosses two crosses were found to have highest sca effects for seed yield, pods per plant, 100-seed weight, days to maturity and plant height. A study on combining ability for yield and yield attributes by Lohithaswa and Dharmaraj (2003) reported that 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. Majority of the best specific crosses involved at least one of the parents with low general combining ability effects implying the need for heterosis breeding and recurrent selection or diallel selective mating programme in the segregating generations for substantial improvement in grain yield. Kumar *et al.* (2003) conducted an experiment in pigeonpea using seven lines and four testers and reported that magnitude of non-additive components of variance was much higher than that of additive components indicating the predominance of non-additive gene effects for the expression of the characters studied. Three female parents and one tester were good general combiners for seed yield. The crosses showed positive specific combining ability effects for seed yield. Singh and Dikshit (2003) also estimated that the SCA variance was higher than GCA variance for all the traits viz., plant height, number of clusters/plant, number of pods/plant, pod length, 100 seed weight and single plant yield, indicating the importance of non-additive gene action in the expression of the traits.

Combining ability and heterosis for eight quantitative characters through Line × Tester analysis involving five lines and four testers was studied by Anbumalarmathi *et al*. (2004) and reported high SCA variance for days to 50 per cent flowering, plant height, clusters/plant, pods/cluster, pods/plant, pod length, seeds/pod, hundred seed weight and single plant yield in greengram while high GCA variance was noticed for number of branches/plant, indicating the preponderance of non-additive gene action for these traits. Pandey (2004) studied thirty-six hybrids and their parents (12 genetically diverse lines crossed with 3 testers), and reported that partial dominance of additive genetic action was significant for number of pods per plant. For number of days to initial flowering, number of days to maturity, plant height, number of primary branches per plant, percentage of pod set, harvest index and seed yield per plant, overdominance with non-additive genetic variance was recorded. Chaudhari *et al.* (2004) conducted a study in pigeonpea to understand the nature of gene action and reported non-additive gene action for days to 50 per cent flowering, seed yield and pods per plant, pod length, reproductive period and additive gene action for days to maturity, plant height, and 100-seed weight whereas for branches per plant both additive as well as non-additive gene actions were important in pigeon pea. Predominance of non-additive gene action for days to 50% flowering, days to maturity, plant height, plant spread, pod clusters per plant, pods per cluster, pods per plant, seeds per pod, 100 seed weight, seed yield biomass and harvest index in pigeon pea hybrids was reported from the experiment in pigeon pea to estimate the variance due to sca and gca carried out by Sekhar *et al.* (2004).

Kandalkar (2006) conducted experiments on 55 crosses of pigeon pea and reported that both additive and non-additive genetic components of variance governed the expression of seed yield, pods per plant, pod clusters per plant and plant height, latter being predominant in both the generations. Stem girth and number of primary branches per plant were predominantly under the control of additive genetic components with significant role of non-additive genetic component, whereas 100 seed weight was predominantly under the control of additive genetic components.

Banu *et al.* (2006) studied the general (GCA) and specific combining abilities (SCA) in 45 pigeon pea hybrids along with their parents based on days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight and single plant yield. The components of variance due to GCA and SCA revealed pre-dominance of non-additive gene action for most of the characters studied. The parents ICP 13201 and ICP 13207 were found to be the best general combiners for the yield attributing traits. The hybrid ICP 11967 x CO 5 was identified as the best combination and could be exploited for improving seed yield in pigeonpea. Similarly evaluation of sixty crosses along with parents (5 lines and 12 testers) revealed that non-additive gene action was predominant for all the traits as variances due to specific combining ability (sca) were higher than the general combining ability (gca) variances. The parents ICPL 87119, BDN 2004, AKT 8811, BSMR 736 and BSMR 853 had good gca, whereas BDN 2 x BDN 2010, BDN 2 x BSMR 853 and BSMR 736 x AKT 8811 were the best specific cross combinations for grain yield, plant spread, and number of primary and secondary branches/plant and pods/plant Phad *et al.* (2007).

Significant role of non-additive gene action for most of the characters studied, except for number of primary branches per plant was reported from a study conducted in pigeonpea to understand nature of gene action by Raju and Muthiah (2007). One line was found to be a good general combiner for important economic traits like number of pods per plant, number of clusters per plant, 100 seed weight and seed yield per plant, while one tester was found to be good combiner for the economic traits of number of pods per plant, number of clusters per plant, 100-seed weight and seed yield per plant. Anithavasline *et al*. (2007) conducted the combining ability studies through line × tester analysis involving seven lines and three testers for seven quantitative charactersin greengram. They reported that the magnitude of SCA variances was greater than the GCA variances for all yield attributing characters indicating the preponderance of non-additive gene action. Baskaran and Muthiah (2007) revealed the preponderance of non-additive gene action over additive for all the characters studied in pigeonpea crosses. The parents, CO 5, VBN 1, and ICPL

83027 were found to be good general combiners for majority of characters. The hybrids, VBN 1 x ICPL 83027, ICPL 87 x ICPL 83024, CORG 9701 x APK 1, CORG 9904 x ICPL 83027 had good sca effects for most of the traits including seed yield and can be utilized in heterosis breeding programme. Twelve crosses along with their parents, viz., four lines and three testers, of the line x tester mating design were evaluated by Raju and Muthiah (2007) to study the combining ability for seed yield and its components. The combining ability analysis revealed a significant role of non-additive gene action for most of the characters studied, except for number of primary branches per plant and total phenolic content. For these two characters, predominant role of additive gene action was confirmed through the present study. Among the lines, CO 6 was found to be a good general combiner for important economic traits like number of pods per plant, number of clusters per plant, 100-seed weight and seed yield per plant, while the tester ICPL 87119 was good combiner for the economic traits of number of pods per plant, number of clusters per plant, 100-seed weight and seed yield per plant.

Chauhan, *et al*. (2008) studied four newly developed pigeon pea cytoplasmic male sterile (CMS) lines, crossed with 4 identified restorers, in a line x tester manner. The general combining ability (GCA)/specific combining ability (SCA) variance ratio indicated the predominance of non-additive components for all the characters, except plant height and pod length. The CMS line GT 288A was a good general combiner for seed yield, pods per plant, plant height, seeds per pod, pod length and 100-seed weight and GT 289A, GT 290A and GTR 6 were good for earliness. Crosses involving low x low GCA using parents, i.e. GT 288A x GTR 10 and GT 288A x GTR 5, exhibited high SCA effect and high per se performance for seed yield. Yadav *et al.* (2008) conducted experiment on pigeon pea to study sca and gca and they reported that mean squares due to general and specific combining ability effects were significant for all the characters except seeds per pod, exhibiting importance of both additive and non-additive gene actions in the inheritance of the studied traits. The ratio of GCA to SCA genetic variances indicated preponderance of non-additive type of gene effects in the expression of all the traits except days to 50% flowering, days to maturity and pod length. Marappa (2008) conducted Line × Tester analysis of 25 crosses obtained from five lines and five testers of greengram for 14 yield and its associated characters. Nine hybrids exhibited highest per se performance and sca effects for most of the characters studied. The variances due to specific combining ability (SCA) were found to be higher than general combining ability (GCA) variances for days to flowering, plant height, number of clusters/plant, pods/plant, seeds/pod, 100 seed weight, dry weight/plant, harvest index and seed yield/plant, indicating predominance of non-additive gene action in the inheritance of these characters studied. Also the estimates of general combining ability and specific combining ability revealed presence of non-additive gene action for days to flowering, days to maturity, branches/plant, clusters/plant, pods/cluster from a study of line × tester analysis with 19 males and four testers to assess the combining ability of the parents conducted by Priyankavyas *et al*. (2008) in greengram.

A set of 24 F_1's involving 6 lines and 4 testers of pigeonpea were estimated for variance due to gca and sca by Sameer Kumar *et al.* (2009) and they observed predominance of non-additive gene action for most of the characters under study. Among the female parents PRG 100 and LRG 30 and among the testers ICP8863 and ICPL 87119 were reported to be good combiners for most of the characters studied. They also revealed that the cross combinations viz., LRG 30 x ICP 8863, PRG 100 x ICP 8863, LRG 30 x ICP 87119, ICP L 85063 x ICP 87119 and PRG 100 x ICP 87119 exhibited significant sca effects coupled with appreciable amounts of relative heterosis, heterobeltiosis and standard heterosis for yield and its attributes suggesting these cross combination can be potentially utilized in future breeding programmes for exploitation of hybrid vigour. Sarode *et al.* (2009) studied the combining ability for yield and yield traits in long duration pigeonpea using five lines and three testers. The fifteen crosses were made in line x tester fashion. Among females, Pusa 9 and MA 98 PTH 1 and among males, ICPL 7035, ICPL 84023 and Bahar were identified as good general combiners for yield traits. The two crosses (MAL 8 x Bahar and Pusa 9 x ICPL 7035) for number of pods per plant and three crosses (MA 98 SD 74 x ICPL 84023, MAL 8 x ICPL 7035 and MA 98 PTH 1 x ICPL 7035) for seed yield per plant were found to be superior on the basis of per se performance and desirable specific combining ability. Baskaran and Muthiah (2009) studied component of genetic variance in pigeon pea using line x tester analysis and reported the predominance of non additive gene action over additive for all the characters studied.

Sunil *et al.* (2010) performed combining ability analysis involving eight parents and 28 F_1s obtained by crossing in all possible combinations excluding reciprocals in greengram. They noticed the importance of additive and non-additive components of variation in the inheritance of seed yield/plant and 100 seed weight whereas additive gene action played a role in the expression of plant height and pods/plant. To study combining ability Shoba and Balan (2010) conducted an experiment in pigeon pea and reported that combining ability analysis variances due to dominance were higher than variances due to additive for all characters indicating the preponderance of non additive gene action governing these traits.

Sathya and Jayamani (2011) studied 56 F_1 hybrids of greengram obtained by crossing four lines and fourteen exotic testers in a Line × Tester mating design. They observed that magnitude of SCA variance was greater than GCA variance for all the characters except for seed fertility, indicating preponderance of non-additive gene action. The parents were found to have superior mean performance and sca effects for number of seeds/pod, 100 seed weight, clusters/plant and single plant yield. Punam and Roopa (2011) carried out combining ability analysis in mungbean and reported that the variances due to GCA and SCA were highly significant, indicating importance of additive and non additive gene action in the inheritance of six different characters such as, plant height, number of clusters/plant, pods/cluster, pods/plant, pod length and test weight. They reported significant SCA effects for seed yield/plant and other yield contributing characters. Patil et al. (2011) employed 8 × 8 half diallel technique and revealed significant mean sum of squares of both GCA and SCA for all the characters under study indicating the presence of additive and non- additive gene actions. However, they observed preponderance of non-additive type of gene action for days to flowering, days to maturity, branches/plant, clusters/plant, 100 seed weight and seed yield/plant through the ratio of GCA to SCA variances.

An investigation on genetic analysis involving 12 parents and 20 crosses of mungbean obtained by Line × Tester mating system for 12 different characters by Sujatha and Kajjidoni (2013) revealed that days to 50% flowering, days to maturity, pods/plant, hundred seed weight, total dry matter at harvest, harvest index, seed yield/plant and seed yield/plot were governed predominantly by additive genetic variation. Since all these characters were also under significant influence of epistatic variation, it appears that additive × additive epistatic variation may be playing a decisive role in the inheritance of these characters. Arbad *et al.* (2013) carried out experiment for nine quantitative traits in pigeonpea through line x tester and reported significant differences among the parents for all characters and for hybrids except for number of seeds per pod. Non additive gene effects were predominant for all characters.

Pandey *et al*. (2014) studied hybrid pigeonpea inheritance pattern for some polygenic traits and reported that estimates of SCA variance were higher than their corresponding GCA variance for all the traits except plant height. The values of average degree of dominance was more than unity and predictability ratio was less than unity for all the traits except plant height, signifying non-additive gene action which resulted from dominance, over dominance, epistatic and various other interaction effects. Predominance of non-additive effects specifies that population is heterozygous; as such this type of genetic variance is non-fixable. A study on 32 hybrids along with their parents for combining ability analysis derived through Line × Tester mating design revealed preponderance of non additive gene action for most of the characters studied as reported by Suresh (2014) in greengram.

MATERIALS AND METHODS

3.1 Experimental site

The experiment entitled “Combining ability analysis for vegetable yield and its components in pigeonpea [*Cajanus cajan* (L.) Millsp.]” was carried out during *kharif* seasons in 2014-15 and 2015-16 at the experimental farm of Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema campus, which is located at 23° 45’ 49” N latitude, 90° 33’ 04” E longitude at an altitude of 305 m above sea level bearing sub-tropical climate.

3.2 Experimental Materials

The experimental material comprised of 7 lines and 5 testers of pigeonpea genotypes. Seeds of pigeonpea possessing different morphological and productive attributes were collected from the University of Agricultural Sciences, Bangalore and ICRISAT, Hyderabad. The different genotypes for lines and testers are listed in the table below.

	Genotype
Lines	
L1	B_1-66-1
L2	B_3-13
L3	B_2 5-2-1
L4	B_1 141-1
L5	B_1 51
L6	BRG-2
L7	B_2-10
Testers	
T1	BRG-1
T2	BRG-3
T3	B_1-169-1
T4	B_2-106-1
T5	ICP 7035

LINES

Plate No. 1: BRG 2

Plate No. 2: B2 10

Plate No. 3: B1 141-1

LINES

Plate No. 4: B1 51

Plate No. 5: B1-66-1

Plate No. 6: B2 5-2-1

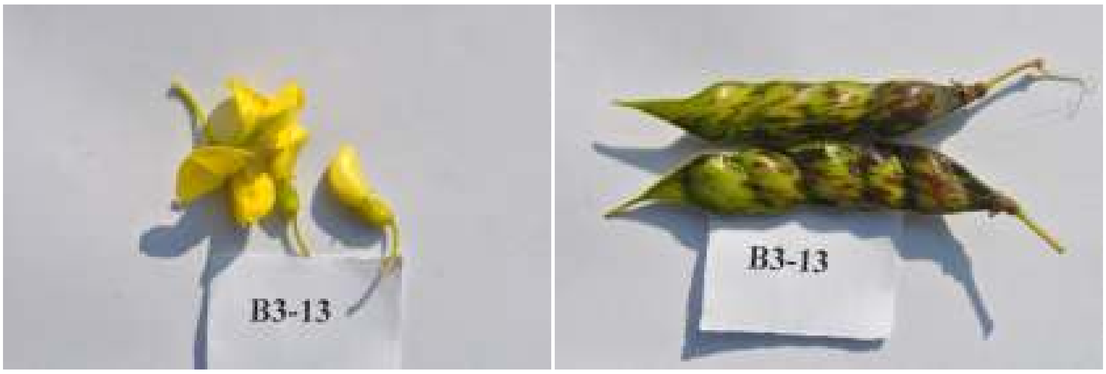

Plate No. 7: B3-13

TESTERS

Plate No. 8: B1 169-1

Plate No. 9: ICP-7035

Plate No. 10: B2-106-1

TESTERS

Plate No. 11: BRG 1

Plate No.12: BRG 3

3.3 Agro- meteorological data during the crop seasons

The climate of Medziphema, Nagaland, in general, is sub-tropical. The data on temperature, rainfall, relative humidity and sunshine hour for the periods of experimentation *viz.,* from June 2014 to February 2015 and June 2015 to February 2016 were obtained from the meteorological observatory, Indian Council of Agricultural Research, ICAR Research Complex for NEH Region, Nagaland Centre, Jharnapani. The data is presented in Table 3.1and Table 3.2.

3.4 Experimental Methods

The experiment took two crop seasons viz. *Kharif* 2014-15 and *Kharif* 2015-16. During the *kharif* season of 2014-2015, 12 parental lines i.e. 7 lines and 5 testers were sown in a Randomized Block Design (R.B.D.) with three replications to obtain data on eleven different traits for yield and yield attributes. Simultaneously, the five tester and seven parental lines were grown during *kharif* 2014-15 in a crossing plot. F_1 hybrids were produced following Line X Tester mating system involving 7 lines and 5 testers by hand emasculation and pollination technique. In the next crop season i.e., *Kharif* 2015-16, all the seeds of 35 F_1 cross combinations (7 lines x 5 testers) with the 12 parental lines (7 lines and 5 testers) totalling 47 treatments were grown in a Randomized Block Design (RBD) with three replications.

3.4.1 *Kharif* 2014-15: Production of F_1 seeds

The experimental field was thoroughly ploughed and harrowed repeatedly and brought to a good tilth. During *Kharif* 2014-15, testers were sown at three different dates

Plate No. 14: Pigeonpea Crossing

Plate No. 13: Pigeonpea Crossing

Plate No. 15: F_1 Experimental Plot

Table 3.1 Meteorological data of Jharnapani, Medziphema, Nagaland

		Temperature		Relative humidity		Rainfall (mm)	
	Week	Max	Min	Max	Min		Sunshine
2014	22	34.0	23.6	80	46	41.8	6.5
	23	34.0	24.5	80	55	13.2	5.1
	24	32.8	24.7	82	52	46.3	3.9
	25	31.5	25.2	82	61	40.4	1.8
	26	33.2	25.5	79	59	18.6	4.5
	27	31.6	25.4	85	65	33.4	2.9
	28	33.1	25.6	82	59	27.6	4.6
	29	31.6	25.4	83	65	117.0	2.9
	30	31.9	25.1	82	62	82.5	5.7
	31	31.6	25.5	83	58	124.9	4.1
	32	31.8	25.4	82	57	66.4	6.0
	33	30.3	25.3	83	69	38.8	0.7
	34	30.3	24.9	83	66	43.0	1.2
	35	31.6	24.5	83	58	43.8	3.5
	36	31.5	24.9	86	65	65.0	5.1
	37	31.8	24.8	85	56	11.8	6.7
	38	30.6	24.3	85	64	52.7	1.7
	39	28.9	23.0	86	55	20.0	5.1
	40	31.8	22.1	87	48	0.0	8.9
	41	31.1	22.9	81	48	56.2	6.2
	42	30.5	22.0	84	52	30.4	6.8
	43	28.5	18.4	83	42	2.8	5.9
	44	28.1	18.4	82	41	0.0	8.6
	45	28.3	17.9	82	36	0.0	8.6
	46	28.3	15.2	79	23	0.0	7.8
	47	27.3	14.2	78	22	0.0	7.3
	48	24.9	12.6	79	17	0.00	7.1
	49	26.2	12.8	79	22	0.0	7.6
	50	23.7	10.8	76	13	0.0	5.4
	51	24.4	10.1	74	12	4.8	6.2
	52	24.6	9.0	73	7	0.0	5.9
2015	1	23.7	14.7	81	38	24.2	4.5
	2	23.1	10.2	74	9	0.0	6.5
	3	25.0	9.7	77	7	0.0	7.8
	4	25.6	8.5	77	4	0.0	8.1
	5	25.2	8.9	75	10	0.0	7.7
	6	26.0	8.7	74	8	0.0	6.3
	7	25.0	10.0	75	9	8.2	7.0
	8	26.7	13.8	76	15	18.1	5.3
	9	30.5	15.7	79	16	0.0	3.3

Table 3.2 Meteorological data of Jharnapani, Medziphema, Nagaland

		Temperature		Relative humidity		Rainfall (mm)	Sunshine (hours)
	Week	Max	Min	Max	Min		
2015	22	30.7	23.5	80	54	8.4	4.2
	23	32.2	23.9	82	53	10.2	3.3
	24	29.9	24.2	85	61	112.3	1.7
	25	31.7	25.2	81	65	19.3	4.5
	26	32.4	25.3	81	58	47.0	4.8
	27	32.3	25.4	84	57	47.4	2.8
	28	32.4	25.2	87	59	81.8	3.6
	29	29.9	24.6	85	66	127.9	1.6
	30	32.7	24.3	83	53	53.8	6.2
	31	30.8	24.3	82	63	32.3	1.8
	32	32.1	25.0	85	65	47.1	4.7
	33	33.1	25.8	82	56	15.9	4.0
	34	30.8	24.8	84	64	60.4	2.3
	35	30.8	24.9	81	62	81.4	1.6
	36	32.0	24.6	82	58	86.2	4.8
	37	32.6	24.6	86	59	64.1	6.4
	38	31.8	24.2	85	59	30.1	4.7
	39	31.4	23.7	86	58	5.2	6.6
	40	34.0	24.4	88	64	19.7	6.1
	41	31.0	22.0	94	69	41.1	1.7
	42	30.8	20.6	91	63	0.3	8.6
	43	31.2	17.6	93	54	0.2	8.8
	44	29.2	18.6	93	66	19.8	5.5
	45	28.4	16.2	93	61	0.9	7.1
	46	28.5	15.4	94	60	0.0	7.0
	47	28.3	12.8	93	53	0.0	7.9
	48	27.9	12.7	91	54	0.0	7.3
	49	25.4	12.7	94	59	9.2	5.7
	50	24.7	13.2	92	58	0.4	4.2
	51	23.1	7.0	91	45	0.0	7.3
	52	24.4	6.4	90	47	0.0	6.7
2016	1	25.8	8.4	93	44	0.0	7.8
	2	24.1	8.6	92	46	14.1	5.9
	3	22.4	9.0	92	58	13.4	3.5
	4	23.2	9.8	93	53	2.0	5.2
	5	23.4	11.6	93	49	1.0	3.0
	6	25.2	10.2	94	52	1.4	4.8
	7	27.1	10.8	92	42	1.7	6.0
	8	30.1	15.5	89	44	5.2	4.8
	9	29.0	11.7	89	33	0.0	7.6

at an interval of 15 days and lines were also sown in two different dates so as to synchronized flowering of the various lines and testers.

The crossing between lines and testers was done during November 2014- February 2015, by adopting line x tester mating design. Enough moisture was maintained in the experimental field for which light irrigation was being done from time to time. Emasculation was done in the evening hours (between 4 and 6 pm), one day before the anthers are expected to dehisce or mature and the stigma is likely to become fully receptive. The hand emasculated flowers were covered with butter paper bags in order to prevent out- crossing. Pollination was done by collecting mature, fertile and viable pollens of male parents (testers) and placing them over emasculated flowers in the next morning. Tags containing information of date of pollination, name of tester and parental line was attached to the pollinated flowers. The crossed pods were harvested, threshed and sun dried in order to avoid any storage damage and properly labeled.

3.4.2 *Kharif* 2015-16: Growing of F_1 and parents

In *kharif* 2015-16 seeds of 5 testers, 7 parental lines and 35 F_1 seeds obtained from 35 cross combinations were sown in a well prepared experimental field in a Randomized Block Design with three replications. Each parent and cross combination were sown in five row plot of 4 meter length. Spacing was maintained at 60 cm Row to Row and 30 cm Plant to Plant.

3.5 Sampling techniques and methods of observation

3.5.1 Sampling techniques

Simple random sampling technique was followed in the present studies with data on different characters made from 10 randomly selected tagged plants from each plot in each replication.

3.5.2 Methods of observation

The observations were recorded on 10 randomly selected plants from each plot in each replication for the following 9 characters.

3.5.2.1 Plant height (cm)

The plant height was measured from the ground surface to the tip of the main shoot on ten randomly selected plants.

3.5.2.2 Days to 50% flowering

The number of days calculated from the date of sowing to the date on which 50% of the plants in a plot showed flowering.

3.5.2.3 Primary branches per plant

The branches arising from the main stem of the plant were counted and recorded as the number of primary branches.

3.5.2.4 Secondary branches per plant

All the branches arising from the primary branches were counted and recorded as secondary branches in the individual plant.

3.5.2.5 Number of pods per cluster

Number of pods on one cluster was counted for five random clusters and the mean pods per cluster were estimated.

3.5.2.6 Number of pods per plant

All the pods were counted from all the tagged plants and the mean value was taken as number of pods per plant.

3.5.2.7 Number of seeds per pod

All the seeds from five random pods were counted and the mean seed number per pod was estimated.

3.5.2.8 100-seed weight (g)

Weights of five numbers of 100 green seeds were recorded from each genotype and the average value was taken as 100-seed weight.

3.5.2.9 Green pod yield per plant (g)

Average green pod yield per plant was measured in grams from 10 random selected plants.

3.6 Statistical analysis

3.6.1 Analysis of variance

To find out the significance of mean difference between genotypes, the following statistics were computed.

(a) $\mathrm{S.Ed} = \sqrt{\frac{2 \text{ x } \mathrm{Mse}}{\mathrm{r}}}$

Where, Mse = mean square due to error

r = number of replications

Critical Difference (C.D.)

C.D. = S. Ed. x t for error degree of freedom at 5% or 1% levels of probability.

(b) Co- efficient of variation (C.V.)

In order to judge the precision of the experiment, the C.V. was calculated as under

$$\text{C.V.}(\%) = \frac{\sqrt{Mse}}{\bar{X}} \text{x } \mathbf{100}$$

Where, $\bar{X}$ = the general mean

3.6.2 Estimation of genotypic and phenotypic variance

1. Genotypic variance (σ_g^2)

$$\sigma_g^2 = \frac{MSg - MSe}{r}$$

Where,

MSg = mean square due to genotype

MSe = mean square due to error

r = number of replication.

2. Phenotypic variance σ_p^2

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

σ_g^2 = genotypic variance

σ_e^2 = environmental variance

3. Environmental variance (σ_e^2)

$$\sigma_e^2 = Mse$$

Where,

MSe = mean square due to error

3.6.3 Coefficient of Variation (CV)

The phenotypic and genotypic coefficients of variation were calculated following the method given by Burton (1952).

1. Genotypic Coefficient of Variation (GCV%)

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \text{ x } \mathbf{100}$$

2. Phenotypic Coefficient of Variation (PCV%)

$$\text{PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \text{ x } \mathbf{100}$$

3. Environmental Coefficient of Variation (ECV%)

$$\text{ECV} = \frac{\sqrt{\sigma_e^2}}{\bar{X}} \text{ x } \mathbf{100}$$

Where,

$\boldsymbol{\sigma_g^2}$= genotypic variance

$\boldsymbol{\sigma_p^2}$ = phenotypic variance

$\boldsymbol{\sigma_e^2}$ = environmental variance

$\bar{X}$ = mean for the character

3.6.4 Heritability

Heritability in broad sense (h^2_b) was calculated according to the formula suggested by Allard (1960). It was computed as the ratio of genotypic variance $\boldsymbol{\sigma_g^2}$ to the phenotypic variance $\boldsymbol{\sigma_p^2}$ and expressed in percentage.

$$h^2_b = \boldsymbol{\sigma_g^2 / \sigma_p^2 + \sigma_e^2}$$

Where,

$\boldsymbol{\sigma_g^2}$= genotypic variance

$\boldsymbol{\sigma_e^2}$= environmental variance

3.6.5 Genetic Advance (GA)

The expected genetic advance was calculated by using the formula suggested by Johnson *et al.* (1955).

$$GA = K\boldsymbol{\sigma_p}\, \boldsymbol{h_b^2}$$

Where,

K = selection differential at 5% selection intensity, the value is 2.06

$\boldsymbol{\sigma_p}$ = phenotypic standard deviation

h^2_b = heritability in broad sense

The genetic advance was expressed as percent of the mean to facilitate the comparison between different characters under study.

3.6.6 Correlation studies

The correlation coefficient at phenotypic, genotypic and environmental levels was determined according to the formula given by Searle (1961).

Genotypic correlation coefficient between character x and y

$$rg_{xy} = \frac{Cov.xy(\mathrm{g})}{\sqrt{\mathrm{Var.x(g)X\ var.y(g)}}}$$

Phenotypic correlation coefficient between character x and y

$$rp_{xy} = \frac{Cov.xy(\mathrm{p})}{\sqrt{\mathrm{Var.x(p)X\ var.y(p)}}}$$

Environmental correlation coefficient between character x and y

$$re_{xy} = \frac{Cov.xy(\mathrm{e})}{\sqrt{\mathrm{Var.x(e)X\ var.y(e)}}}$$

Where,

cov.xy(g), *cov.xy*(p),and *cov.xy*(e) denote genotypic , phenotypic and environmental co-variance for characters x and y, respectively

Var.x (g), Var.x (p) and Var.x (e), denotes genotypic, phenotypic and environmental variance for character x

Var.y (g), Var.y (p) and Var.y (e), denotes genotypic, phenotypic and environmental variance for character y

The calculated genotypic and phenotypic correlation coefficients were tested for significance by applying t-test as follows:

$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$ at (n-2) degree of freedom

Where,

n = number of genotypes

The calculated t value was compared with t-value at 5% or 1% probability level with (n-2) degree of freedom for its significance.

3.6.7 Heterosis

The estimation of heterosis in terms of increase or decrease in the performance of F_1 over the respective better parent or mid parent was calculated by the following formula.

a) Heterosis over mid parent

Average heterosis (%) = $\frac{\overline{F1} - \overline{MP}}{\overline{MP}} x100$

Where,

$\overline{F1}$ = mean value of F_1 hybrid

$\overline{MP}$ = mean value of two parents of a particular cross

b) Heterosis over better parent.

Heterobeltiosis = $\frac{\overline{F1} - \overline{BP}}{\overline{BP}} x100$

Where,

$\overline{\mathrm{F1}}$ = mean value of F_1 hybrid

$\overline{\mathrm{BP}}$ = mean value of better parent of a particular cross

Significance of estimates of heterosis was tested by computing ‘t’ as given below:

$$\text{‘t’(MP)} = \frac{\overline{\mathrm{F1}} - \overline{\mathrm{MP}}}{\text{SE of heterosis over } \overline{\mathrm{MP}}}$$

$$\text{‘t’(BP)} = \frac{\overline{\mathrm{F1}} - \overline{\mathrm{BP}}}{\text{SE of heterosis over } \overline{\mathrm{BP}}}$$

Where,

SE of heterosis over mid parent = $\sqrt{\mathrm{V}\,\overline{\mathrm{F1}} + \mathrm{V}\,\overline{\mathrm{MP}}}$

SE of heterosis over better parent = $\sqrt{\mathrm{V}\,\overline{\mathrm{F1}} + \mathrm{V}\,\overline{\mathrm{BP}}}$

$\mathrm{V}\,\overline{\mathrm{F1}}$ = Variance of $\overline{\mathrm{F1}}$
$\mathrm{V}\,\overline{\mathrm{MP}}$ = Variance of $\overline{\mathrm{MP}}$
$\mathrm{V}\,\overline{\mathrm{BP}}$ = Variance of $\overline{\mathrm{BP}}$

The calculated‘t’ values were compared with the table of‘t’ at error degree of freedom for test of significance.

$$\text{C. D. for midparent heterosis} = \sqrt{\frac{3 \text{ x Me}}{2\text{r}}} X' t' value$$

$$\text{C. D. for better parent heterosis} = \sqrt{\frac{2 \text{ x Me}}{2\text{r}}} X' t' value$$

Where’
Me = error mean square of R.B.D analysis
r = number of replication.

t = table value of‘t’ at error degrees of freedom corresponding to 5% and 1% level of significance.

3.6.8 Combining ability analysis

The experimental data obtained on each character were subjected to the analysis of variance (Gomez and Gomez, 1984). After testing the significance of treatment i.e. genotypes including parents and crosses, line x tester analysis for estimation of combining ability was done.

(i) Line x tester analysis

For estimation of general and specific combining ability effects and variance, the line x tester analysis as outlined by Kempthrone (1957) and worked out example of Singh and Choudhary (1977) were followed. The form of analysis of variance is as below.

Source	**d.f.**	**S.S.**	**M.S.**
Replication	(r-1)	S.S. $_{(R)}$	
Treatments	(T-1)	S.S. $_{(T)}$	M_T
Parents	(P-1)	S.S. $_{(P)}$	M_P
Crosses	(C-1)	S.S. $_{(C)}$	M_C
Parents Vs Crosses	1	S.S. $_{(PC)}$	M_{PC}
Line	(l-1)	S.S. $_{(l)}$	M_l
Testers	(t-1)	S.S. $_{(t)}$	M_t
Line x Testers	(l-1) (t-1)	S.S. $_{(l \times t)}$	$M_{l \times t}$
Error	(r-1) (T-1)	S.S. $_{(e)}$	M_e

Where, r = number of replications, l = number of lines, t = number of testers, T = number of treatments, P = number of parents, C = number of crosses, PC = parents Vs crosses and Me = mean squares due to error.

The estimates of the mean square for lines, testers and line x testers were calculated to assess the general combining ability of lines and testers and also to assess the specific combining ability of line x testers.

(ii) Estimation of combining ability effects

The model used to estimate the combining ability effects of the ijk^th^ observation are as follows:

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

Where, μ = general mean

g_i =gca effects of the i^{th} line

g_j =gca effects of the j^{th} tester

S_{ij} = sca effect of the the ij^{th} combination

e_{ijk} = error associated with ij observation at K^{th} plots.

i = 1, 2, 3, … … … … … … … … … … … … … … l

j = 1, 2, 3, … … … … … … … … … … … … … … t

k = number of replications (1, 2, 3 … … … … r)

The individual effect is estimated as below:

$$\mu = \frac{x....}{rlt}$$

Where x... is the total of all the hybrid combinations.

gca effect (lines):

$$\hat{gi} = \frac{Xi..}{rt} - \frac{x...}{rlt}$$

Where, $X_i..$ is the total of i^{th} lines over all testers and replications.

r = number of lines

t = number of testers

gca effects (testers):

$$\hat{g}j = \frac{x._j.}{rl} - \frac{x....}{rlt}$$

Where, $X._j.$ is the total of jth tester over lines and replications

sca effects:

$$S_{ij} = \frac{x_{ij}.}{r} - \frac{x_{i}..}{rt} - \frac{x._j.}{lr} + \frac{x_{...}}{rlt}$$

Where, X_{ij} is the total of ij^{th} combinations over all replications.

3.6.9 Standard error for combining ability effects

$$\mathrm{S.E.(gca\ line)} = \sqrt{\frac{\mathrm{Me}}{\mathrm{rt}}}$$

$$\mathrm{S.E.(gca\ tester)} = \sqrt{\frac{\mathrm{Me}}{\mathrm{r}l}}$$

$$\mathrm{S.E.(gca\ effects)} = \sqrt{\frac{\mathrm{Me}}{\mathrm{r}}}$$

$$\mathrm{S.E.}(g_i - g_j)\mathrm{lines} = \sqrt{\frac{2\mathrm{Me}}{\mathrm{rt}}}$$

$$\mathrm{S.E.}(g_i - g_j)\mathrm{tester} = \sqrt{\frac{2\mathrm{Me}}{\mathrm{r}l}}$$

$$\mathrm{S.E.}(S_{ij} - S_{kl}) = \sqrt{\frac{2\mathrm{Me}}{\mathrm{r}}}$$

Critical difference (C.D.) was calculated as:

C.D. = S.E. x t 5% or 1% at error d.f.

The significance of the gca line, gca testers and sca effects were tested by comparing with the respective C.D. value.

3.6.10 Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines (\%)} = \frac{\text{SS }(l)}{\text{SS (crosses)}}\text{x}100$$

$$\text{Contribution of testers (\%)} = \frac{\text{SS (t)}}{\text{SS (crosses)}}\text{x}100$$

$$\text{Contribution of line x testers (\%)} = \frac{\text{SS }(lxt)}{\text{SS (crosses)}}\text{x}100$$

3.6.11 Genetic components of variance

$$\text{Cov H. S. (line)} = \frac{(\text{M}_l - \text{M}_{lxt})}{\text{rt}}$$

$$\text{Cov H. S. (tester)} = \frac{(\text{M}_\text{t} - \text{M}_{lxt})}{\text{r}l}$$

$$\text{Cov H. S. (average)} = \frac{l}{\text{r}(2l\text{t} - l - \text{t})}\left[\frac{(l-1)(\text{M}_l) + (\text{t}-1)(\text{M}_t)}{l + \text{t} - 2} - \text{M}_{l\text{xt}}\right]$$

$$\text{Cov F. S.} = \frac{(\text{M}_l - \text{M}_\text{e}) + (\text{M}_\text{t} - \text{M}_\text{e}) + (M_{lxt} - \text{M}_\text{e})}{3\text{r}} + \frac{6\text{r Cov H. S (average)} - \text{ r }(l + \text{t})\text{Cov H. S. (average)}}{3\text{r}}$$

$$\text{gca variance } (\sigma^2\text{g}) = \text{Cov H. S. (average)} = \left[\frac{1+\text{F}}{4}\right]\sigma^2\text{A}$$

sca variance (σ^2s) was calculated following Dabholkar (1992)

$$\text{sca variance } (\sigma^2\text{s}) = \text{Cov F. S.} - 2\text{ Cov H. S. (average)} = \left[\frac{1+\text{F}}{2}\right]^2\sigma^2\text{D}$$

Where, ‘F’ is the coefficient of inbreeding.

In the present study, F was assumed as zero.

RESULTS AND DISCUSSION

The experimental results obtained from the present study are presented under the following heads.

4.1 Analysis of variance

The analysis of variance for yield and its component characters based on experiment conducted during *kharif* 2014-15 is presented in Table 4.1. All the genotypes differed significantly for 4 out of 9 characters indicating the presence of considerable amount of genetic variation among the genotypes.

The general mean performance of twelve genotypes and the range of variation for yield and yield related traits are presented in Table 4.2. The experimental findings for general mean and range of variation for nine characters of pigeonpea are as follows.

4.1.1 Plant height

Difference in plant height was observed among the genotypes. The plant height varied from158.40 cm (BRG3) to 250.80 cm (B1-66-1) with a general mean of 211.95 cm.

4.1.2 Days to 50% flowering

The general mean for days to 50% flowering was 166.19 with a range varying from 156.00 days to 168.67 days. The genotype ICP7035 was the earliest to flower (156.00) followed by B2-106-1 (166.00), whereas maximum period for flowering was taken by B1-66-1 (168.67).

4.1.3 Primary branches per plant

The number of primary branches ranged from 14.77 to 34.37 with a mean of 27.92 primary branches. Variations among the genotypes

Table 4.1 Analysis of variance for nine characters of pigeonpea.

		Mean squares								
		Plant height (cm)	Days to 50% flowering	Primary branches	Secondary branches	Number of pods /cluster	Number of pods/plant	Number of seeds/pod	100 seed (green) weight (g)	Green pod yield /plant (g)
Source	**d.f.**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
Replication	2	35087.38	0.53	764.43	10887.08	0.08	2503.83	0.19	75.81	3470.88
Treatment	11	2429.15	32.39**	136.57**	4844.12**	0.31	1286.15**	0.59*	8.93	31541.99
Error	22	1277.66	3.19	12.74	213.31	0.33	57.71	0.26	6.61	36882.93
CV %		16.86	1.08	12.79	14.45	36.05	16.18	10.95	10.87	66.57

*, ** Significant at 5% and 1% levels of probability

Table 4.2 Mean performance of pigeonpea genotypes for yield and yield related traits

Characters Genotypes	Plant height	Days 50% to Flowering	Primary branches	Sec. branches	Pods /cluster	Pods/ plant	Seeds/ pods	100 seed (green) weight	Green pod yield/ plant
B1-66-1	250.80	168.67	27.80	109.00	1.33	39.70	4.67	24.86	313.20
B3-13	231.74	167.00	34.37	124.00	2.00	85.90	4.33	21.31	231.63
B2-5-2-1	246.40	167.33	32.20	94.60	1.67	64.17	5.00	22.77	249.48
B1-141-1	207.60	166.67	27.57	108.63	1.67	50.80	4.67	22.60	327.37
B1-51	192.60	167.33	30.60	91.80	1.67	44.73	4.33	20.74	156.26
BRG-2	217.81	166.67	34.00	106.60	1.33	48.47	5.00	23.87	225.30
B2-10	200.73	167.00	28.60	93.20	1.67	30.87	4.33	23.57	280.36
BRG1	173.97	166.33	16.40	44.80	1.33	17.27	4.67	24.31	440.99
BRG3	158.40	167.67	14.77	33.00	1.33	30.43	5.33	24.11	483.80
B1-169-1	242.77	167.67	33.00	166.60	1.33	54.70	4.33	25.01	133.72
B2-106-1	210.60	166.00	33.57	165.43	2.33	74.20	3.67	27.24	288.25
ICP-7035	210.00	156.00	22.20	75.40	1.33	22.20	5.00	23.50	331.78
G- Mean	**211.95**	**166.19**	**27.92**	**101.09**	**1.58**	**46.95**	**4.61**	**23.66**	**288.51**
C.D-5%	-	3.03	6.05	24.73	-	12.86	0.86	-	-
C.D-1%	-	4.11	8.22	33.61	-	17.48	1.16	-	-
S.E	20.64	1.03	2.06	8.42	0.33	4.39	0.29	1.48	110.88

were observed for primary branches. The highest primary branches per plant were observed in B3-13 and the lowest in BRG3.

4.1.4 Secondary branches per plant

The number of secondary branches ranged from 33.00 to 166.60 with a mean of 101.09 secondary branches. Variations among the genotypes were observed for secondary branches. The highest secondary branches per plant were observed in B1-169-1 and the lowest in BRG3.

4.1.5 Number of pods per cluster

The number of pods/cluster ranged from 1.33 to 2.33 with a mean of 1.58. Variations among the genotypes were not much for number of pods/cluster.

4.1.6 Number of pods per plant

The number of pods/plant ranged from 17.27 to 85.90 with a mean of 46.95. Variations among the genotypes were observed for number of pods/plant. The highest number of pods/plant was observed in B3-13 and the lowest in BRG1.

4.1.7 Number of seeds per pod

The number of seeds/pod ranged from 3.67 to 5.33 with a mean of 4.61. Variations among the genotypes were not much for number of seeds/pod.

4.1.8 100 seed weight

The 100 seed weight ranged from 20.74 to 27.24 with a mean of 23.66. Variations among the genotypes were for 100 seed weight. The highest 100 grain weight was observed in B2-106-1 and the lowest in B1-51.

4.1.9 Green pod yield per plant

The green pod yield/plant ranged from 133.72 to 483.80 with a mean of 288.51 g. Variations among the genotypes was observed for green pod yield/plant. The highest yield / plant were observed in BRG3 and the lowest in B1-169-1.

4.2 Coefficient of variation, heritability and genetic advance for yield and yield related traits

The estimate of coefficient of variation, heritability and genetic advance for yield and yield related traits are given in Table 4.3.

The highest genotypic coefficient of variation (GCV) was observed for number of pods/plant (43.10%) followed by secondary branches (38.87%). However, days to flowering (1.88%), 100 grain weight (3.71%) and number of pods/ cluster (4.49%) exhibited the lowest genotypic coefficient of variation.

The highest phenotypic coefficient of variation (PCV) was observed for green pod yield (64.94%) followed by number of pods/ plant (46.03%) and secondary branches (41.46%). However, days to 50% flowering (2.16%), 100 grain weight (11.49%) and number of seeds/pod (13.17%) exhibited the lowest phenotypic coefficient of variation.

High heritability estimates were observed for number of pods/plant (88.00%), secondary branches (87.86%), primary branches (76.41%) and days to 50% flowering (75.29%) whereas lowest heritability estimates was exhibited by number of pods/cluster (2.00%). The genetic advance as percentage of mean was highest for number of pods/plant (83.12%) followed by secondary branches (75.04%).

Table 4.3 Variability and other genetic parameters for 9 characters in parents of pigeonpea

Characters	Mean	Range	GCV%	PCV%	Heritability (%)	GA as % of mean
Plant height (cm)	211.95	158.40-250.80	9.24	19.23	23.10	9.15
Days to 50% flowering	166.19	156.00-168.67	1.88	2.16	75.29	3.36
Primary branches	27.92	14.77-34.37	23.01	26.32	76.41	41.43
Secondary branches	101.09	33.00-166.60	38.87	41.46	87.86	75.05
Number of pods /cluster	1.58	1.33-2.33	4.49	35.77	2.00	1.16
Number of pods /plant	46.95	17.27-85.90	43.10	46.03	88.00	83.12
Number of seeds / pod	4.61	3.67-5.33	7.31	13.17	30.82	8.36
100 seed (green) weight (g)	23.66	20.74-27.24	3.71	11.49	10.44	2.47
Green pod yield / plant (g)	288.51	133.72-483.80	14.62	64.94	5.00	6.78

4.3 Correlation coefficients for yield and yield related traits

The phenotypic and genotypic correlation coefficient for yield and its components are presented in Table 4.4. Primary branches and plant height had a positive phenotypic correlation coefficient (0.62) with each other. Also secondary branches and primary branches had a positive association (0.75) with each other. Significant and positive phenotypic correlation coefficient association was observed between pods/ plant and primary branches (0.72). Pods/plant exhibited positive and significant phenotypic correlation coefficient with secondary branches (0.70).

4.4 Heterosis

Studies on heterosis in F_1 generation revealed the following.

4.4.1 Plant height.

Heterosis over the mid parent and better parent for plant height, along with their means and ranges are presented in Table 4.5.1. The extent of heterosis over mid parent ranged from -63.69 (BRG-2 X B2-106-1) to 19.08 (B1-51 X ICP7035). The extent of heterosis over better parent ranged from -63.69 (BRG-2 X B2-106-1) to 9.70 (B1-51 X ICP7035). Significant negative heterosis over the mid parent and better parent was observed for crosses B1-66-1 X BRG3, B1-141-1 X BRG3, B1-51 X BRG1, B1-51 X BRG3, BRG2 X BRG1, BRG2 X B1-169-1, BRG2 X B2-106-1 and BRG2 X ICP7035.

Table 4.4 Phenotypic (r_p) and genotypic correlation (r_g) correlation coefficient of yield and its contributing characters in pigeonpea

Characters	DT 50% F	Primary branches	Sec. branches	Pods /cluster	Pods/ plant	Seeds/ pods	100 seed weight	Green pod yield/ plant	
Plant height	0.08	0.62*	0.48	-0.17	0.41	0.11	-0.07	-0.38	P
	(0.01)	(0.25)	(0.23)	(0.19)	(0.18)	(-0.20)	(-0.01)	(-0.30)	G
DT 50%F	-	0.19	0.15	0.14	0.26	-0.11	-0.02	-0.07	P
	-	(0.08)	(0.06)	(0.02)	(0.12)	(-0.07)	(0.02	(-0.05)	G
Pri. branches	-	-	0.75**	0.15	0.72**	-0.34	0.07	-0.46	P
	-	-	(0.28)	(0.28)	(0.26)	(-0.22)	(-0.13)	(-0.40)	G
Sec. branches	-	-	-	0.30	0.70*	-0.57	0.15	-0.35	P
	-	-	-	(0.21)	(0.23)	(-0.26)	(0.11)	(-0.36)	G
Pods/cluster	-	-	-	-	0.39	-0.45	-0.08	-0.21	P
	-	-	-	-	(0.32)	(-0.22)	(0.21)	(0.09)	G
Pods/plant	-	-	-	-	-	-0.44	-0.04	-0.30	P
	-	-	-	-	-	(-0.16)	(-0.03)	(-0.25)	G
Seeds/pods	-	-	-	-	-	-	-0.25	0.14	P
	-	-	-	-	-	-	(-0.17)	(0.09)	G
100 seed weight	-	-	-	-	-	-	-	0.05	P
	-	-	-	-	-	-	-	(-0.03)	G

Note: Values in the column are phenotypic correlation coefficients (r_p) and those in parenthesis are genotypic correlation coefficients (r_g)

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

Table 4.5.1 Heterosis (%) of plant height in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-15.63	-11.49
2	B1-66-1 X .BRG-3	-23.93*	-21.92*
3	B1-66-1 X B1-169-1	-12.19	-10.75
4	B1-66-1 X 106-1	-17.35	-15.30
5	B1-66-1 X ICP-7035	-13.43	-2.31
6	B3-13 X BRG-1	-5.32	-4.60
7	B3-13 X BRG-3	-5.41	-2.55
8	B3-13 X B1-169-1	-9.72	-6.08
9	B3-13 X B2-106-1	-4.12	-1.06
10	B3-13 X ICP-7035	3.93	11.44
11	B2-5-2-1 X BRG-1	-5.59	-3.46
12	B2-5-2-1 X BRG-3	-3.53	-3.52
13	B2-5-2-1 X B1-169-1	0.69	1.70
14	B2-5-2-1 X B2-106-1	-0.65	-0.48
15	B2-5-2-1 X ICP-7035	-16.79	-8.28
16	B1-141-1 X BRG-1	-5.99	-2.65
17	B1-141-1 X BRG-3	-37.60**	-36.80**
18	B1-141-1 X B1-169-1	-10.17	-9.91
19	B1-141-1 X B2-106-1	-12.01	-11.03
20	B1-141-1 X ICP-7035	-0.19	11.30
21	B1-51 X BRG-1	-42.26**	-41.94**
22	B1-51 X BRG-3	-60.61**	-59.94**
23	B1-51 X B1-169-1	-18.17	-15.96
24	B1-51 X B2-106-1	-10.11	-8.42
25	B1-51 X ICP-7035	9.70	19.08
26	BRG-2 X BRG-1	-63.24**	-62.73**
27	BRG-2 X BRG-3	3.72	4.66
28	BRG-2 X B1-169-1	-42.08**	-40.98**
29	BRG-2 X B2-106-1	-63.69**	-63.30**
30	BRG-2 X ICP-7035	-58.56**	-54.68**
31	B2-10 X BRG-1	-14.99	-9.62
32	B2-10 X BRG-3	-11.97	-8.40
33	B2-10 X B1-169-1	4.64	7.84
34	B2-10 X B2-106-1		-5.46
35	B2-10 X ICP-7035	-9.85	2.98
SE		35.96	31.14
Range		-63.69-9.70	-63.30-19.08
Mean		-6.94	-3.05

*, ** Significant at 5% and 1% levels, respectively

4.4.2 Days to 50% flowering.

Heterosis over the mid parent and better parent for days to 50% flowering, along with their means and ranges were presented in Table 4.5.2. The cross B1-141-1 X ICP7035 showed significant negative heterosis over better parent. The maximum negative mid parent heterosis of 1.45 percent were recorded from the cross B1-141-1 X ICP7035.

4.4.3 Primary branches per plant.

Heterosis over the mid parent and better parent for primary branches, along with their means and ranges is presented in Table 4.5.3. Among the 35 crosses, the cross B1-141-1 X BRG-1 exhibited maximum significant positive heterosis of 199.12 and 225.09 over better parent and mid parent respectively. The maximum negative mid parent and better parent heterosis of -80.88 and -81.78 were recorded from the cross BRG-2 X BRG-1.

4.4.4 Secondary branches per plant.

Heterosis over the mid parent and better parent for secondary branches, along with their means and ranges are presented in Table 4.5.4. The maximum significant mid parent heterosis of 140.92 and better parent heterosis of 126.06 were observed in the cross B1-51 X ICP7035 followed by BRG2 X BRG3 . Maximum significant negative mid parent heterosis of -92.28 and better parent of -92.39 were recorded in the cross BRG-2 X B2-106-1.

4.4.5 Number of pods per cluster.

Heterosis for number of pods/cluster over better parent and mid parent along with their respective means and ranges are presented in Table 4.5.5. The extent of heterosis for number of pods/cluster over mid parent ranged from -53.85 (B1-51 X BRG-1and BRG-2 X ICP7035) to 50.00 (B2-5-2-1 X B1-169-1). The extent of heterosis over better parent ranged from -70.00

Table 4.5.2 Heterosis (%) of Days to 50% flowering in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-0.60	-0.30
2	B1-66-1 X .BRG-3	1.80	1.90
3	B1-66-1 X B1-169-1	1.00	1.61
4	B1-66-1 X 106-1	1.79	2.19
5	B1-66-1 X ICP-7035	-1.20	2.38
6	B3-13 X BRG-1	0.40	0.60
7	B3-13 X BRG-3	0.00	0.40
8	B3-13 X B1-169-1	0.61	0.71
9	B3-13 X B2-106-1	-0.20	0.70
10	B3-13 X ICP-7035	-0.61	2.50
11	B2-5-2-1 X BRG-1	-1.01	-0.91
12	B2-5-2-1 X BRG-3	0.00	0.30
13	B2-5-2-1 X B1-169-1	0.40	0.61
14	B2-5-2-1 X B2-106-1	-0.40	0.40
15	B2-5-2-1 X ICP-7035	0.00	3.23*
16	B1-141-1 X BRG-1	5.17**	5.80**
17	B1-141-1 X BRG-3	0.40	0.80
18	B1-141-1 X B1-169-1	0.20	1.10
19	B1-141-1 X B2-106-1	0.79	0.89
20	B1-141-1 X ICP-7035	-5.17**	-1.45
21	B1-51 X BRG-1	10.25**	12.43**
22	B1-51 X BRG-3	14.89**	16.93**
23	B1-51 X B1-169-1	-1.35	0.89
24	B1-51 X B2-106-1	-1.93	-0.69
25	B1-51 X ICP-7035	-2.51	2.65
26	BRG-2 X BRG-1	7.14**	7.89**
27	BRG-2 X BRG-3	-0.60	-0.10
28	BRG-2 X B1-169-1	10.12**	11.22**
29	BRG-2 X B2-106-1	9.52**	9.52**
30	BRG-2 X ICP-7035	6.55**	10.84**
31	B2-10 X BRG-1	1.00	1.40
32	B2-10 X BRG-3	0.40	0.60
33	B2-10 X B1-169-1	-1.40	-0.70
34	B2-10 X B2-106-1	-0.60	-0.30
35	B2-10 X ICP-7035	0.40	4.14**
SE		2.58	2.24
Range		-5.17-14.89	-1.45-16.93
mean		-0.12	0.70

*, ** Significant at 5% and 1% levels, respectively

Table 4.5.3 Heterosis (%) of primary branches in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-38.65	-35.30
2	B1-66-1 X .BRG-3	-61.95	-59.40
3	B1-66-1 X B1-169-1	-36.45	-33.89
4	B1-66-1 X 106-1	-35.11	-31.60
5	B1-66-1 X ICP-7035	-47.23	-42.84
6	B3-13 X BRG-1	-26.37	-22.45
7	B3-13 X BRG-3	-10.58	-4.71
8	B3-13 X B1-169-1	-17.84	-14.64
9	B3-13 X B2-106-1	-21.69	-17.55
10	B3-13 X ICP-7035	-15.82	-8.70
11	B2-5-2-1 X BRG-1	-11.29	-10.07
12	B2-5-2-1 X BRG-3	-18.70	-16.58
13	B2-5-2-1 X B1-169-1	-17.95	-17.89
14	B2-5-2-1 X B2-106-1	-14.64	-13.51
15	B2-5-2-1 X ICP-7035	-41.24	-33.97
16	B1-141-1 X BRG-1	199.12**	225.09**
17	B1-141-1 X BRG-3	-31.41	-24.62
18	B1-141-1 X B1-169-1	-37.80	-33.29
19	B1-141-1 X B2-106-1	-29.22	-23.11
20	B1-141-1 X ICP-7035	-30.51	-26.96
21	B1-51 X BRG-1	-71.51*	-70.18*
22	B1-51 X BRG-3	-75.58*	-74.14*
23	B1-51 X B1-169-1	-36.91	-34.87
24	B1-51 X B2-106-1	-20.40	-16.73
25	B1-51 X ICP-7035	-6.78	1.73
26	BRG-2 X BRG-1	-81.78*	-80.88*
27	BRG-2 X BRG-3	17.41	24.64
28	BRG-2 X B1-169-1	-65.59	-64.39*
29	BRG-2 X B2-106-1	-77.73*	-76.65*
30	BRG-2 X ICP-7035	-72.88*	-70.48*
31	B2-10 X BRG-1	-35.85	-28.96
32	B2-10 X BRG-3	-25.57	-16.67
33	B2-10 X B1-169-1	-13.93	-5.91
34	B2-10 X B2-106-1	-15.73	-6.71
35	B2-10 X ICP-7035	-21.23	-18.84
SE		16.94	14.67
Range		-81.78-199.12	-80.88-225.09
mean		-26.52	-20.48

*, ** Significant at 5% and 1% levels, respectively

Table 4.5.4 Heterosis (%) of secondary branches in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	40.77	94.67*
2	B1-66-1 X .BRG-3	-71.40*	-69.57*
3	B1-66-1 X B1-169-1	-55.44	-48.91
4	B1-66-1 X 106-1	-55.16	-53.76
5	B1-66-1 X ICP-7035	-42.23	-35.33
6	B3-13 X BRG-1	2.28	45.52
7	B3-13 X BRG-3	-17.54	-8.37
8	B3-13 X B1-169-1	-19.60	-4.11
9	B3-13 X B2-106-1	-34.85	-29.73
10	B3-13 X ICP-7035	48.51	73.18*
11	B2-5-2-1 X BRG-1	20.63	58.33
12	B2-5-2-1 X BRG-3	-14.13	-12.75
13	B2-5-2-1 X B1-169-1	-11.71	-5.77
14	B2-5-2-1 X B2-106-1	-12.25	-7.97
15	B2-5-2-1 X ICP-7035	-40.81	-38.44
16	B1-141-1 X BRG-1	-32.36	-4.53
17	B1-141-1 X BRG-3	-12.88	-4.36
18	B1-141-1 X B1-169-1	-38.33	-27.26
19	B1-141-1 X B2-106-1	-24.83	-19.93
20	B1-141-1 X ICP-7035	14.01	31.44
21	B1-51 X BRG-1	-86.17	-83.21
22	B1-51 X BRG-3	-90.25*	89.06*
23	B1-51 X B1-169-1	-40.89	-38.62
24	B1-51 X B2-106-1	1.52	17.09
25	B1-51 X ICP-7035	126.06**	140.92**
26	BRG-2 X BRG-1	-92.17**	-89.48*
27	BRG-2 X BRG-3	121.45**	125.53**
28	BRG-2 X B1-169-1	-86.42*	-85.04*
29	BRG-2 X B2-106-1	-92.39**	-92.28**
30	BRG-2 X ICP-7035	-89.55**	-88.78**
31	B2-10 X BRG-1	-45.36*	-17.71
32	B2-10 X BRG-3	-44.30	-32.35
33	B2-10 X B1-169-1	-44.13	-27.78
34	B2-10 X B2-106-1	-47.91*	-38.37
35	B2-10 X ICP-7035	-29.63	-10.82
SE		64.59	55.93
Range		-92.39-126.06	-92.28-140.92
mean		-21.18	-15.91

*, ** Significant at 5% and 1% levels, respectively

Table 4.5.5 Heterosis (%) of pods per cluster in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-37.50*	-16.67
2	B1-66-1 X .BRG-3	-57.14**	-45.45*
3	B1-66-1 X B1-169-1	-42.86*	-27.27
4	B1-66-1 X 106-1	-33.33	-20.00
5	B1-66-1 X ICP-7035	-10.00	28.57
6	B3-13 X BRG-1	-12.50	0.00
7	B3-13 X BRG-3	-14.29	-7.69
8	B3-13 X B1-169-1	28.57	38.46*
9	B3-13 X B2-106-1	16.67	16.67
10	B3-13 X ICP-7035	-10.00	12.50
11	B2-5-2-1 X BRG-1	-25.00	-7.69
12	B2-5-2-1 X BRG-3	14.29	33.33
13	B2-5-2-1 X B1-169-1	28.57	50.00**
14	B2-5-2-1 X B2-106-1	33.33	45.45*
15	B2-5-2-1 X ICP-7035	-40.00**	-20.00
16	B1-141-1 X BRG-1	-62.50**	-53.85**
17	B1-141-1 X BRG-3	-28.57	-16.67
18	B1-141-1 X B1-169-1	-42.86*	-33.33
19	B1-141-1 X B2-106-1	16.67	27.27
20	B1-141-1 X ICP-7035	-10.00	20.00
21	B1-51 X BRG-1	-62.50**	-53.85**
22	B1-51 X BRG-3	-57.14**	-50.00**
23	B1-51 X B1-169-1	-57.14**	-50.00**
24	B1-51 X B2-106-1	16.67	27.27
25	B1-51 X ICP-7035	-40.00**	-20.00
26	BRG-2 X BRG-1	-62.50**	-45.45*
27	BRG-2 X BRG-3	-14.29	20.00
28	BRG-2 X B1-169-1	-57.14**	-40.00
29	BRG-2 X B2-106-1	-50.00*	-33.33
30	BRG-2 X ICP-7035	-70.00**	-53.85**
31	B2-10 X BRG-1	-25.00	-20.00
32	B2-10 X BRG-3	14.29	14.29
33	B2-10 X B1-169-1	0.00	0.00
34	B2-10 X B2-106-1	0.00	7.69
35	B2-10 X ICP-7035	-50.00**	-41.18**
SE		0.42	0.36
Range		-70.00-33.33	-53.85-50.00
mean		-0.69	-2.29

*, ** Significant at 5% and 1% levels, respectively

(BRG-2 X ICP7035) to 33.33 (B2-5-2-1 X B1-106-1). Most crosses exhibited significant negative heterosis while significant positive mid parent values were observed for the crosses B3-13 X BRG, B2-5-2-1 X B1-169-1 and B2-5-2-1 X B2-106-1.

4.4.6 Number of pods per plant.

Heterosis for number of pods/plant over better parent and mid parent along with their respective means and ranges are presented in Table 4.5.6. The maximum significant mid parent (196.15) and better parent (179.32) heterosis were recorded from the cross B1-141-1 X ICP7035.

4.4.7 Number of seeds per pod.

Heterosis for number of seeds/pod over better parent and mid parent along with their respective means and ranges are presented in Table 4.5.7. The maximum significant mid parent (20.00) and better parent (20.00) heterosis were recorded from the crosses B1-141-1 X ICP7035 and B1-51 X ICP7035, respectively.

4.4.8 100 Seed weight.

Heterosis for 100 grain weight over better parent and mid parent along with their respective means and ranges are presented in Table 4.5.8. The extent of heterosis for 100 grain weight over mid parent ranged from -31.21(B3-13 X B1-169-1) to 17.35 (B1-51 X ICP7035). The extent of heterosis over better parent ranged from -17.38 (B1-51 X BRG-3) to 21.76 (B1-51 X ICP7035).

4.4.9 Green pod yield per plant.

Heterosis for green pod yield/plant over better parent and mid parent along with their respective means and ranges are presented in Table 4.5.9. The

Table 4.5.6 Heterosis (%) of pods per plant in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-59.78	-55.04
2	B1-66-1 X .BRG-3	-91.68**	-90.48**
3	B1-66-1 X B1-169-1	-62.50	-54.28
4	B1-66-1 X 106-1	-78.61	-77.21
5	B1-66-1 X ICP-7035	32.56	37.66
6	B3-13 X BRG-1	75.36*	83.02*
7	B3-13 X BRG-3	-34.63	-30.08
8	B3-13 X B1-169-1	-11.89	13.58
9	B3-13 X B2-106-1	-38.06	-29.42
10	B3-13 X ICP-7035	28.23	32.87
11	B2-5-2-1 X BRG-1	-5.74	33.29
12	B2-5-2-1 X BRG-3	-40.81	-15.04
13	B2-5-2-1 X B1-169-1	94.58	113.85
14	B2-5-2-1 X B2-106-1	17.11	46.49
15	B2-5-2-1 X ICP-7035	-55.71	-40.39
16	B1-141-1 X BRG-1	-68.30	-63.89
17	B1-141-1 X BRG-3	-31.69	-20.43
18	B1-141-1 X B1-169-1	-22.52	-7.15
19	B1-141-1 X B2-106-1	-13.49	-9.69
20	B1-141-1 X ICP-7035	179.32**	196.15**
21	B1-51 X BRG-1	-92.11*	-88.69*
22	B1-51 X BRG-3	-90.64**	-86.38*
23	B1-51 X B1-169-1	-85.90	-84.18
24	B1-51 X B2-106-1	-16.99	5.65
25	B1-51 X ICP-7035	35.03	84.50
26	BRG-2 X BRG-1	-95.40**	-94.16*
27	BRG-2 X BRG-3	78.11*	130.23**
28	BRG-2 X B1-169-1	-79.47	-78.12
29	BRG-2 X B2-106-1	-93.66	-93.09
30	BRG-2 X ICP-7035	-92.54*	-91.10*
31	B2-10 X BRG-1	-53.65	-45.24
32	B2-10 X BRG-3	-13.83	3.95
33	B2-10 X B1-169-1	43.57	66.06
34	B2-10 X B2-106-1	-24.79	-24.72
35	B2-10 X ICP-7035	-12.94	-3.97
SE		53.91	46.69
Range		-95.40-179.32	-94.16-196.15
Mean		-24.22	-10.89

*, ** Significant at 5% and 1% levels, respectively

Table4.5.7 Heterosis (%) of seeds per pod in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-6.67	-6.67
2	B1-66-1 X .BRG-3	0.00	0.00
3	B1-66-1 X B1-169-1	-6.25	-3.23
4	B1-66-1 X 106-1	0.00	0.00
5	B1-66-1 X ICP-7035	13.33	13.33*
6	B3-13 X BRG-1	-13.33	-7.14
7	B3-13 X BRG-3	0.00	7.14
8	B3-13 X B1-169-1	0.00	10.34
9	B3-13 X B2-106-1	0.00	7.14
10	B3-13 X ICP-7035	0.00	7.14
11	B2-5-2-1 X BRG-1	-6.67	-6.67
12	B2-5-2-1 X BRG-3	-6.67	-6.67
13	B2-5-2-1 X B1-169-1	0.00	3.23
14	B2-5-2-1 X B2-106-1	0.00	0.00
15	B2-5-2-1 X ICP-7035	-6.67	-6.67
16	B1-141-1 X BRG-1	0.00	0.00
17	B1-141-1 X BRG-3	0.00	0.00
18	B1-141-1 X B1-169-1	-6.25	-3.23
19	B1-141-1 X B2-106-1	6.67	6.67
20	B1-141-1 X ICP-7035	20.00**	20.00**
21	B1-51 X BRG-1	-20.00**	-20.00**
22	B1-51 X BRG-3	-20.00**	-20.00**
23	B1-51 X B1-169-1	-12.50	-9.68
24	B1-51 X B2-106-1	0.00	0.00
25	B1-51 X ICP-7035	20.00**	20.00**
26	BRG-2 X BRG-1	-20.00**	-20.00**
27	BRG-2 X BRG-3	0.00	0.00
28	BRG-2 X B1-169-1	-25.00**	-22.58**
29	BRG-2 X B2-106-1	-20.00**	-20.00**
30	BRG-2 X ICP-7035	-20.00**	-20.00**
31	B2-10 X BRG-1	-6.67	-6.67
32	B2-10 X BRG-3	0.00	0.00
33	B2-10 X B1-169-1	6.25	9.68
34	B2-10 X B2-106-1	0.00	0.00
35	B2-10 X ICP-7035	6.67	6.67
SE		0.33	0.29
Range		-25.00-20.00	-22.58-20.00
Mean		-1.44	0.05

*, ** Significant at 5% and 1% levels, respectively

Table 4.5.8 Heterosis (%) of 100 seed (green) weight in the crosses of Pigeonpea

	Crosses	Better parent	Mid parent
1	B1-66-1X BRG-1	-5.92	-0.77
2	B1-66-1 X .BRG-3	-5.12	0.68
3	B1-66-1 X B1-169-1	0.51	2.67
4	B1-66-1 X 106-1	-5.02	-0.35
5	B1-66-1 X ICP-7035	-8.63	-3.95
6	B3-13 X BRG-1	-5.31	-0.70
7	B3-13 X BRG-3	-7.73	-2.66
8	B3-13 X B1-169-1	-14.53**	-13.21**
9	B3-13 X B2-106-1	-2.14	2.07
10	B3-13 X ICP-7035	-7.35	-2.04
11	B2-5-2-1 X BRG-1	-8.90	-2.81
12	B2-5-2-1 X BRG-3	-16.07**	-9.92*
13	B2-5-2-1 X B1-169-1	-4.19	-0.96
14	B2-5-2-1 X B2-106-1	-4.41	1.44
15	B2-5-2-1 X ICP-7035	-3.65	0.11
16	B1-141-1 X BRG-1	-11.58*	-6.52
17	B1-141-1 X BRG-3	-5.56	0.44
18	B1-141-1 X B1-169-1	-8.72	-6.53
19	B1-141-1 X B2-106-1	-8.48	-3.76
20	B1-141-1 X ICP-7035	2.79	7.80
21	B1-51 X BRG-1	-8.52	-2.55
22	B1-51 X BRG-3	-17.38**	-11.47*
23	B1-51 X B1-169-1	-2.58	0.54
24	B1-51 X B2-106-1	-5.57	0.06
25	B1-51 X ICP-7035	12.76*	17.35**
26	BRG-2 X BRG-1	-10.83*	-3.43
27	BRG-2 X BRG-3	-9.94*	-1.90
28	BRG-2 X B1-169-1	-11.63*	-7.23
29	BRG-2 X B2-106-1	-12.24*	-5.45
30	BRG-2 X ICP-7035	-5.62	-3.46
31	B2-10 X BRG-1	-14.43*	-8.91
32	B2-10 X BRG-3	-14.73**	-8.69
33	B2-10 X B1-169-1	0.27	3.40
34	B2-10 X B2-106-1	-11.80	-6.61
35	B2-10 X ICP-7035	-4.50	-0.54
SE		1.30	1.13
Range		-17.38-12.76	-13.21-17.35
Mean		-5.26	-1.96

*, ** Significant at 5% and 1% levels, respectively

Table 4.5.9 Heterosis (%) of green pod yield per plant in the crosses of Pigeonpea

	Crosses	**Better parent**	**Mid parent**
1	B1-66-1X BRG-1	58.20	113.32
2	B1-66-1 X .BRG-3	-63.78	-61.61
3	B1-66-1 X B1-169-1	5.53	10.01
4	B1-66-1 X 106-1	-65.54	-54.34
5	B1-66-1 X ICP-7035	327.76**	452.49**
6	B3-13 X BRG-1	367.53**	592.05**
7	B3-13 X BRG-3	105.64	150.08
8	B3-13 X B1-169-1	46.36	75.55
9	B3-13 X B2-106-1	-6.62	9.78
10	B3-13 X ICP-7035	151.85	260.15*
11	B2-5-2-1 X BRG-1	66.27	177.81*
12	B2-5-2-1 X BRG-3	15.67	69.89
13	B2-5-2-1 X B1-169-1	22.40	78.10
14	B2-5-2-1 X B2-106-1	41.09	56.76
15	B2-5-2-1 X ICP-7035	-35.62	5.23
16	B1-141-1 X BRG-1	-4.12	42.49
17	B1-141-1 X BRG-3	116.18	164.46
18	B1-141-1 X B1-169-1	30.32	57.26
19	B1-141-1 X B2-106-1	34.41	57.01
20	B1-141-1 X ICP-7035	577.59**	873.17**
21	B1-51 X BRG-1	-74.32	-64.10
22	B1-51 X BRG-3	-68.93	-65.29
23	B1-51 X B1-169-1	-78.39	-76.23
24	B1-51 X B2-106-1	12.96	43.71
25	B1-51 X ICP-7035	291.21**	425.59**
26	BRG-2 X BRG-1	88.97	-84.27
27	BRG-2 X BRG-3	534.53**	630.24**
28	BRG-2 X B1-169-1	-73.75	-70.24
29	BRG-2 X B2-106-1	-91.38	-89.30
30	BRG-2 X ICP-7035	-81.01	-73.92
31	B2-10 X BRG-1	130.08	185.85
32	B2-10 X BRG-3	308.53*	331.54**
33	B2-10 X B1-169-1	240.27	265.35*
34	B2-10 X B2-106-1	5.27	49.97
35	B2-10 X ICP-7035	257.30	322.29*
SE		118.29	102.44
Range		-91.38-577.59	-89.30—873.17
Mean		27.08	21.21

*, ** Significant at 5% and 1% levels, respectively

maximum significant mid parent (873.17) and better parent (577.59) heterosis were recorded from the cross B1-141-1 X ICP7035.

4.5 Analysis of Variance for line x tester analysis including parents.

Analysis of variance for line x tester including parents for nine traits are presented in Table 4.6. An indebth study of the table reveals that the variance ratios due to different sources of variance were highly significant for maximum characters. Out of the total characters studied the source of variance due to testers was found significant for all the characters except for primary branches per plant.

Significant differences of variance ratio due to treatment, crosses and line x testers were observed in the present study.

Variances for testers were significant for almost all the characters except for primary branches per plant. Variances for lines were significant for almost all the characters except for 100 seed (green) weight.

4.6 Combining ability analysis

4.6.1 Combining ability effects

Combining ability effects of line, testers and line x tester from the present study are presented below.

Table 4.6 Analysis of variance for combining ability

		Mean sum of squares								
		Plant height (cm)	Days to 50% flowering	Primary branches	Secondary branches	Number of pods /cluster	Number of pods/ plant	Number of seeds /pod	100 seed (green) weight (g)	Green Pod yield / plant (g)
Source	**d.f.**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
Replication	2	8348.41	7.04	468.65	28509.07	2.56	7387.53	0.26	1.94	48383.64
Treatment	46	9864.07 **	169.34**	554.37**	23068.49**	1.42**	16365.61**	0.69**	6.31**	121378.42**
Parents	11	1281.65	48.21**	66.36	6992.35	1.18**	3271.67	0.15	8.54**	10368.65
Parents Vs Crosses	1	40633.46**	534.67**	4981.94**	41200.33**	0.35	1941.34	0.20	4.64	496149.69**
Crosses	34	11735.75**	197.78**	582.03**	27736.30**	1.54**	21026.13**	0.88**	5.63**	146270.66**
Lines	6	34372.62**	524.44**	1105.45**	22158.72**	3.86**	22397.73**	1.84**	5.28	127828.46**
Testers	4	3684.44*	118.18**	86.09	29287.91**	1.29**	20830.86**	1.63**	7.21*	166182.27**
Linex Testers	24	7418.42**	129.38**	533.83**	28872.10**	0.99**	20715.77**	0.52**	5.46**	147562.60**
Error	92	1430.84	10.04	196.96	4223.57	0.27	4430.19	0.17	2.55	20988.80

*, ** Significant at 5% and 1% levels of probability.

4.6.1.1 Plant height

The combining ability effects for plant height are presented in Table 4.7.1. The sca effects ranged from -107.94 to 148.28. The maximum sca effects was observed in the cross BRG-2 X BRG-3.

The gca values of lines and testers ranged from -93.66 to 41.33 and -20.58 to 14.77 respectively. The maximum value of gca in lines and testers were observed in B2-10 and B1-169-1.

4.6.1.2 Days to 50% flowering.

The combining ability effect for Days to 50% flowering is presented in Table 4.7.2. The sca effects ranged from -13.47 to 17.53. The maximum sca effects was observed in the cross BRG2 X BRG3.

The gca for lines and testers ranged from -4.64 to 8.56 and -3.63 to 2.56, respectively. The maximum value of gca lines and testers were observed in B2-5-2-1 and ICP7035.

4.6.1.3 Primary branches per plant.

The combining ability effects for primary branches is presented in Table 4.7.3. The sca effects ranged from -18.12 to 35.39. The maximum sca effects was observed in the cross BRG2 X BRG3.

The gca lines and testers ranged from -13.45 to 8.73 and -1.45 to 3.49 respectively. The maximum value of gca lines and testers were observed in B1-414-1 and ICP7035, respectively.

Table 4.7.1 Combining ability effects for plant height

	Lines	Testers					
		BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	23.40	-23.37	-0.91	-1.38	2.26	6.32
2	B3-13	9.14	1.55	-21.27	7.30	3.28	25.24*
3	B2-5-2-1	17.85	4.07	7.85	14.69	-44.46*	28.45**
4	B1-141-1	26.82	-10.75	-21.59	-11.24	16.76	25.76
5	B1-51	-37.84	-107.94**	11.14	47.69*	86.96**	-33.44**
6	BRG-2	-37.62	148.28**	-2.97	-55.87*	-51.82*	-93.66**
7	B2-10	-1.75	-11.85	27.77	-1.19	-12.97	41.33**
	gca (testers)	-20.58*	-0.48	14.77	-1.33	7.62	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	9.77	8.25	21.84	13.81	11.67	30.89
C.D. (5%)	19.49	16.47	43.58	27.56	23.29	61.63
C.D. (1%)	25.88	21.87	57.88	36.60	30.94	81.84

Table 4.7.2 Combining ability effects for days to 50% flowering

	Lines	Testers					
		BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	-4.76*	0.33	1.19	2.81	0.43	-2.57**
2	B3-13	-2.29	-1.20	0.66	1.28	1.56	-4.37**
3	B2-5-2-1	-4.36*	-0.93	0.92	1.21	3.16	-4.64**
4	B1-141-1	5.57**	-1.33	0.52	0.81	-5.57**	-2.24**
5	B1-51	8.44**	17.53**	-8.28**	-10.32**	-7.37**	8.56**
6	BRG-2	-1.56	-13.47**	6.72**	4.68*	3.63	8.56**
7	B2-10	-1.03	0.93	-1.74	-0.46	4.16*	-3.31**
	gca (testers)	2.56**	1.47*	-0.72	0.32	-3.63**	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	0.82	0.69	1.83	1.16	0.98	2.59
C.D. (5%)	1.63	1.38	3.65	2.31	1.95	5.16
C.D. (1%)	2.17	1.83	4.85	3.06	2.59	6.86

NB: Since earliness is desirable –ve sign is desirable

Table 4.7.3 Combining ability effects for primary branches per plant

	Lines	BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	2.98	-9.88	4.20	4.03	-1.33	-6.67
2	B3-13	-4.17	2.48	0.21	-2.55	4.02	6.51
3	B2-5-2-1	4.14	-0.48	1.26	1.89	-6.81	2.34
4	B1-141-1	30.49**	-7.74	-9.79	-6.07	-6.87	8.73*
5	B1-51	-14.89	-18.12*	2.23	9.49	21.29*	-5.43
6	BRG-2	-11.88	35.91**	-3.75	-10.59	-9.69	-13.45**
7	B2-10	-6.66	-2.17	5.64	3.80	-0.62	7.96*
	gca (testers)	-1.32	-0.11	-1.45	-0.61	3.49	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	3.62	3.06	8.10	5.12	4.33	11.46
C.D. (5%)	7.23	6.11	16.17	10.23	8.64	22.87
C.D. (1%)	9.60	8.12	21.47	13.58	11.48	30.37

4.6.1.4 Secondary branches per plant.

The combining ability effect for secondary branches is presented in Table 4.7.4. The sca effects ranged from –145.59 to 301.09. The maximum sca effects was observed in the cross BRG2 X BRG3.

The gca lines and testers ranged from -51.02 to 47.68 and –35.42 to 53.51, respectively. The maximum value of gca lines and testers was observed in B3-13 and ICP7035.

4.6.1.5 Number of pods per cluster

The combining ability effects for Pods/cluster are presented in Table 4.7.5. The sca effects ranged from -0.86 to 1.01.

The maximum positive significant sca effects was recorded in the cross between B1-66-1 X ICP7035. The gca (lines) and gca (testers) ranged from -0.71 to 0.62 and -0.34 to 0.32, respectively and maximum value was recorded in B3-13 and ICP7035.

4.6.1.6 Number of pods per plant

The combining ability effects for pods/plant are presented in Table 4.7.6. The sca effects ranged from -107.72 to 212.82

The maximum positive significant sca effects was recorded in the cross between BRG 2 X BRG 3. The gca (lines) and gca (testers) ranged from -41.92 to 50.81 and -28.47 to 51.47, respectively and maximum was recorded in B3-13 and ICP7035.

Table 4.7.4 Combining ability effects for secondary branches per plant

	Lines	Testers					
		BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	59.70	-61.17	22.64	9.40	-30.57	-51.02**
2	B3-13	-45.53	-29.61	15.97	-33.05	92.21*	47.68**
3	B2-5-2-1	88.91*	-26.57	23.09	24.40	-109.83**	12.85
4	B1-141-1	5.15	-9.45	-16.27	0.23	20.35	32.87
5	B1-51	-85.26*	-145.59**	-20.94	72.97	178.81**	-8.60
6	BRG-2	-49.58	301.09**	-46.59	-71.41	-133.51**	-49.28**
7	B2-10	26.60	-28.72	22.10	-2.52	-17.46	15.50
	gca (testers)	-35.42*	22.91	-27.41	-13.59	53.51**	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	16.78	14.18	37.52	23.73	20.06	53.06
C.D. (5%)	33.48	28.29	74.87	47.35	40.02	105.89
C.D. (1%)	44.47	37.58	99.44	62.89	53.15	140.62

Table 4.7.5 Combining ability effects for number of pods per cluster

	Lines	Testers					
		BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	0.34	-0.61*	-0.28	-0.47	1.01**	-0.25
2	B3-13	0.14	-0.48	0.52	-0.33	0.14	0.62**
3	B2-5-2-1	-0.12	0.26	0.59	0.07	-0.79*	0.55**
4	B1-141-1	-0.52	-0.14	-0.48	0.33	0.81**	-0.05
5	B1-51	-0.12	-0.41	-0.41	0.73*	0.21	-0.45
6	BRG-2	0.14	0.86**	-0.14	-0.33	-0.52	-0.71**
7	B2-10	0.14	0.52	0.19	0.00	-0.86**	0.29*
	gca (testers)	-0.34**	-0.06	-0.06	0.13	0.32**	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	0.13	0.11	0.30	0.19	0.16	0.42
C.D. (5%)	0.27	0.23	0.59	0.38	0.32	0.85
C.D. (1%)	0.36	0.30	0.79	0.50	0.43	1.13

Table 4.7.6 Combining ability effects for number of pods per plant

	Lines	BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	11.99	-57.24	-2.45	-9.25	56.94	-37.62*
2	B3-13	129.07**	-54.28	-13.11	-37.05	-24.63	50.81**
3	B2-5-2-1	43.90	-26.02	51.83	38.02	-107.72**	12.64
4	B1-141-1	-79.18*	-39.35	-36.65	-13.76	168.93**	40.59*
5	B1-51	-34.21	-54.61	-32.32	56.69	64.44	-41.92*
6	BRG-2	-44.11	212.82**	-31.39	-30.19	-107.13**	-35.68*
7	B2-10	-27.48	18.67	64.08	-4.45	-50.83	11.18
	gca (testers)	-14.23	7.18	-15.95	-28.47	51.47**	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	17.19	14.52	38.43	24.30	20.54	54.35
C.D. (5%)	34.29	28.98	76.68	48.49	40.99	108.45
C.D. (1%)	45.54	38.49	101.84	64.41	54.43	144.02

4.6.1.7 Number of seeds per pod

The combining ability effects for seeds/pod are presented in Table 4.7.7. The sca effects ranged from -0.66 to 0.91.

The maximum positive significant sca effects was recorded in the cross between B1-51 X ICP7035. The gca (lines) and gca (testers) ranged from -0.69 to 0.38 and -0.41 to 0.35, respectively and maximum was recorded in B1-141-1 and ICP7035.

4.6.1.8 100 seed weight

The combining ability effects for 100 seed weight are presented in Table 4.7.8. The sca effects ranged from -2.36 to 2.76.

The maximum positive significant sca effects was recorded in the cross between B1-51 X ICP7035. The gca (lines) and gca (testers) ranged from -0.94 to 0.69 and -0.82 to 0.65, respectively and maximum was recorded in B1-66-1 and B2-106-1.

4.6.1.9 Green pod yield per plant

The combining ability effects for green pod yield/ plant are presented in Table 4.7.9. The sca effects ranged from -282.22 to 567.27.

The maximum positive significant sca effects were recorded in the cross between BRG2 X BRG3. The gca (lines) and gca (testers) ranged from -102.99 to 120.79 and -86.81 to 130.27, respectively and maximum were recorded in B1-141-1 and ICP7035.

4.7. Contribution of lines, testers and their interactions

The contribution of lines, testers and line x testers towards total variance are presented in Table 4.8. Out of the nine characters studied, considerably

Table 4.7.7 Combining ability effects for number of seeds per pod

	Lines	Testers					
		BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	0.01	0.01	-0.18	-0.09	0.25	0.18
2	B3-13	-0.19	0.14	0.29	0.05	-0.29	0.05
3	B2-5-2-1	0.21	-0.12	0.35	0.11	-0.55*	-0.02
4	B1-141-1	0.14	-0.19	-0.38	0.05	0.38	0.38**
5	B1-51	-0.32	-0.66**	-0.18	0.25	0.91**	-0.15
6	BRG-2	0.21	0.88**	-0.13	-0.22	-0.55*	-0.69**
7	B2-10	-0.06	-0.06	0.42	-0.15	-0.15	0.25*
	gca (testers)	-0.41**	-0.08	0.11	0.02	0.35**	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	0.11	0.09	0.24	0.15	0.13	0.34
C.D. (5%)	0.21	0.18	0.47	0.29	0.25	0.67
C.D. (1%)	0.28	0.24	0.63	0.39	0.34	0.89

Table 4.7.8 Combining ability effects for 100 seed (green) weight

	Lines	Testers					
		BRG1	**BRG3**	**B1-169-1**	**B2-106-1**	**ICP-7035**	**gca (lines)**
1	B1-66-1	0.23	0.89	0.91	-0.14	-1.89*	0.69
2	B3-13	0.99	0.78	-2.27*	1.22	-0.72	0.09
3	B2-5-2-1	0.26	-1.25	0.56	0.85	-0.42	-0.14
4	B1-141-1	-0.83	1.22	-0.96	-0.61	1.18	0.23
5	B1-51	-0.39	-2.36*	0.21	-0.21	2.76**	0.61
6	BRG-2	0.54	1.20	-0.52	-0.43	-0.79	-0.94*
7	B2-10	-0.81	-0.48	2.09*	-0.69	-0.10	-0.55
	gca (testers)	0.32	0.21	-0.36	0.65	-0.82*	

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

	gca (L)	**gca (T)**	**sca**	**$g_i - g_j$ (L)**	**$g_i - g_j$ (T)**	**$S_{ij} - S_{kl}$**
S.E.	0.41	0.35	0.92	0.58	0.49	1.30
C.D. (5%)	0.82	0.69	1.84	1.16	0.98	2.60
C.D. (1%)	1.09	0.92	2.45	1.55	1.31	3.46

Table 4.7.9 Combining ability effects for green pod yield per plant

	Lines	Testers					
		BRG1	BRG3	B1-169-1	B2-106-1	ICP-7035	gca (lines)
1	B1-66-1	25.19	-174.80*	31.33	-29.87	148.15	-93.33*
2	B3-13	349.35**	-97.79	-48.01	-88.77	-114.67	85.36*
3	B2-5-2-1	138.69	-63.49	87.92	113.48	-276.59**	51.76
4	B1-141-1	-214.04*	-113.48	-103.47	-40.81	471.79**	120.79**
5	B1-51	-99.19	-166.54	-43.22	139.38	169.57*	-102.99**
6	BRG-2	-135.77	567.27**	-56.09	-93.18	-282.22**	-82.56*
7	B2-10	-64.12	48.84	131.53	-0.22	-116.03	20.97
	gca (testers)	-26.09	47.51	-86.81**	-64.88*	130.27**	

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

	gca (L)	gca (T)	sca	$g_i - g_j$ (L)	$g_i - g_j$ (T)	$S_{ij} - S_{kl}$
S.E.	37.41	31.61	83.64	52.90	44.71	118.29
C.D. (5%)	74.64	63.09	166.91	105.56	89.22	236.04
C.D. (1%)	99.13	83.78	221.66	140.19	118.48	313.48

Table 4.8 Proportionate contribution of lines, testers and their interactions

Characters	Percentage		
	Lines	**Testers**	**Line x Testers**
Plant hieght	51.69	3.69	44.62
Days to 50% flowering	46.79	7.03	46.18
Primary branches	33.52	1.74	64.74
Secondary branches	14.10	12.42	73.48
Number of pods / cluster	44.35	9.92	45.73
Number of pods /plant	18.80	11.66	69.55
Number of seeds / pod	36.81	21.81	41.39
100 seed weight	16.54	15.05	68.41
Green pod yield / plant	15.42	13.37	71.21

contributions were recorded from the lines ranging from a minimum of 14.10 per cent for secondary branches per plant to a maximum of 51.69 per cent in case of plant height which is closely followed by 46.79 per cent for days to 50 % flowering and 44.35 per cent for number of pods per cluster.

Lower contribution towards total variance was recorded in case of testers with minimum and maximum values of 1.74 per cent in primary branches and 21.81 per cent in case of number of seeds per pod.

Higher to medium contributions were recorded from line x testers ranging from 41.39 per cent in number of seeds per pod to 73.48 per cent in secondary branches per plant.

4.8. Genetic components of variance

Genetic components of variance in intervarietal crosses of pigeonpea are presented in Table 4.9. Among the characters studied, sca variance (σ^2s) and non –additive (σ^2D) variance components were higher than genetic variance (σ^2g) and additive (σ^2A) variance for all the characters under study except for pods per cluster and seeds per pod where additive component of gene action (σ^2A) was higher than non additive variance (σ^2D).

Table 4.9 Genetic components of variance in intervarietal crosses of pigeonpea

Characters	σ^2g	σ^2s	σ^2g/σ^2s	σ^2A	σ^2D
Plant height	977.65	1995.86	0.49	3910.60	7983.44
Days to 50% flowering	17.29	39.78	0.43	69.17	159.12
Primary branches	22.16	112.29	0.20	88.62	449.16
Secondary branches	1194.43	8216.18	0.15	4777.72	32864.71
Number of pods/ cluster	0.13	0.24	0.53	0.51	0.97
Number of pods/ plant	954.67	5428.53	0.18	3818.69	21714.10
Number of seeds / pod	0.09	0.12	0.75	0.35	0.46
100 seed weight	0.21	0.97	0.21	0.82	3.88
Green pod yield /plant	7000.92	42191.27	0.17	28003.68	168765.07

4.9. Discussion

Genetic variation among genotypes and relation between major yield contributing traits are of great vital importance in the breeding programme that aims to produce improved genotype. Knowledge on genotypic and phenotypic coefficient of variation is a prerequisite in order to get an idea of relative extent of heritable and non-heritable variation. A wide range of variability may exist in any population, which hinder in making effective selection. Estimation of heritability and genetic advance serves as important parameters by permitting greater effectiveness of selection by separating out the desired genotypes, which are of great value for the plant breeding programme.

Yield is a complex character, which is the product of interaction of many traits. Therefore it is necessary to have the knowledge of the contribution of different character towards yield through correlation. Basic information of the nature and extent of inter-relationships between yield and its attributes will be of great utility for the choice of characters in the selection programme.

The improvement in pigeonpea is directed towards development of new varieties/hybrids possessing desirable traits. One of the major achievements is the exploitation of heterosis through the development of commercial hybrid varieties. In order to develop superior F_1 hybrids, it is essential to choose desirable parents with better cross combination. Therefore, selection on high heterosis of more than one yield components will be more practicable for significant achievement in crop improvement.

In any crop improvement programme the ultimate goal for any plant breeder is higher yield. Seed yield is a very complex character which is the ultimate result of the added contributions made by different individual characters. This complex situation has to be simplified by the plant breeder in order to achieve higher yield through character compensation mechanism. The knowledge of the genetic makeup of the characters is a pre- requisite in rational choosing of the parents for a hybridization programme for genetic improvement of crop plants either through conventional breeding or heterosis breeding approaches looking into the taste and preferences of the farmers as well as the consumer.

4.9.1 Phenotypic and genotypic coefficient of variation

Coefficient of variation can be defined as the relative measure of variation among the characters under study. The magnitude of variability in a population will be due to genetic and environmental factors. The estimate of variability is of primary importance to get an idea of relative extent of heritable and non-heritable variations.

In the present experiment, phenotypic coefficient of variation was higher than genotypic coefficient of variation indicating the influence of environmental factors. The difference between GCV and PCV, were high for number of pods/cluster, 100 seed weight, plant height and green pod yield indicating the significant role of environment.

High genotypic and phenotypic coefficient of variation were obtained for number of pods /plant (43.10 and 46.03) and secondary branches (38.87 and 41.46), whereas it was lowest for days to 50% flowering (1.88 and 2.16). Similar findings were also reported by Gowda *et al*. (2003); Joshi *et al*. (2003); Baskaran and Muthaih (2007); Bhadru (2010) and Chethana *et al*. (2015). The present findings revealed that there was a great scope for further improvement of the traits having high genotypic and phenotypic coefficient of variation through selection in the desirable direction, whereas low values of phenotypic and genotypic coefficient of variation for days to 50% flowering suggested limited scope for the improvement.

4.9.2 Heritability and genetic advance

It is inevitable to have an understanding of the expected heritability and genetic advance of various characters in order to select superior lines. These two parameters help the plant breeder in making effective selection. Estimates of heritability in broad sense indicate the extent of genetic control of a given trait and thus it reflects the efficiency of selection of that trait. High heritability naturally indicates the correspondence between genotype and phenotype. However, high heritability with high genetic advance is more beneficial for effective selection (Johnson *et al*., 1955).

The present experimental study revealed that secondary branches, number of pods/plant and primary branches showed high heritability along with high genetic advance as percent of mean manifesting that the selection for these traits are likely to accumulate more additive genes leading to further improvement of their performance. Dahat *et al*. (1997); Patel and Patel (1999); Deshmukh *et al*. (2000); Ajay *et al*., (2012) and Vanishree *et al*. (2013) also reported the similar findings.

The character with moderate to low heritability with moderate to low genetic advance indicates involvement of non-additive gene action and simple selection for these traits would not be much effective (Nath and Talukdar, 1997). In the present investigation, such characters were shown by number of pods per cluster and 100 grain weight. Parmer and Kathiria (2016) also reported the similar findings. This indicates that these characters are under the control of non additive gene action. Hence, these traits do not offer much scope for improvement through selection.

4.9.3 Correlation

Grain yield is a dependent trait, which is influenced by many independent traits. The correlation among the yield and yield contributing characters provides definitive information on nature and direction of selection. In order to select desirable plant type association of yield and its components is an effective tool. Correlation coefficient study helps to identify certain characters or combination of characters, which helps in finding of high yield by way of evaluating the relative influence of various characters on grain yield and among themselves as well. It provides definitive information of desirable yield component characters.

In the present investigation, primary branches and plant height had a positive phenotypic correlation coefficient with each other. Also secondary branches and primary branches had a positive association with each other. Significant and positive phenotypic correlation coefficient was observed between pods/plant and primary branches. Pod/plant exhibited positive and significant phenotypic correlation coefficient with secondary branches.

The results were in confirmity with the results of Kingshlin and Subbaraman (1999); Kingshlin *et al.* (1999); Kumara *et al.* (2014); and Singh and Singh (2016). Green pod yield /plant show lack of association with days to 50% flowering which provides an opportunity to the breeder for simultaneous selection of high yielding and early maturing genotypes.

4.9.4 Heterosis

Heterosis refers to the superiority of F_1 hybrid in one or more characters over its parents. Based on the relative performance of the F_1 with the parental lines, heterosis may be expressed as mid parent heterosis or relative heterosis and better parent heterosis or heterobeltiosis. Exploitation of heterosis in pigeonpea is one of the important potential avenues for breaking yield barriers. It provides great opportunities in crop improvement and is only effective conventional means of combining desirable characters of two or more varieties.

In the present study, mid- parent heterosis may not be of much value as the modern plant breeders are always looking for higher yield only. So, for the better parent heterosis, the better parent depending upon the traits, may fall either in the two directions- positive or negative. For example, in the case of days to first flowering and days to maturity (i.e., earliness), the emphasis may shift towards the negative side as desirable heterosis whereas for the traits like plant height, primary branches, secondary branches, number of pods / cluster, number of pods / pod, number of pods / plant, 100 grain weight and green pod yield / plant positive heterosis may be desirable.

The estimates of significant heterosis over better parent indicated the true superiority of F_1 over better parent.

The results of the present heterosis studies among the crosses indicated from high to medium mid- parent and better parent heterosis. The range of heterosis and the cross combinations which manifested the best and second best heterotic effects of the 11 morphological traits are summarised and presented in Table 4.10.

Character	Relative Heterosis (%)	Heterobeltiosis (%)
Plant height	19.08 to -63.30 i.BRG2 x B2-106-1 (-63.30) ii.BRG2 x BRG1 (-62.73)	9.70 o -63.69 i.BRG2 x B2-106-1 (-63.69) ii.B2-10 X B1-169-1 (-63.24)
Days to 50% flowering	16.93 to -1.45 i. B1-141-1 x ICP7035 (-1.45) ii. B2-5-2-1 x BRG1(-0.91)	14.89 to -5.17 i. B1-141-1 x ICP7035 (-5.17) ii. B1-51 x ICP7035 (-2.51)
Primary branches	225.09 to -80.88 i. B1-141-1 x BRG1 (225.09) ii. BRG2 x BRG3 (24.64)	199.12 to -81.78 i. B1-141-1 x BRG1 (199.12) ii. BRG2 x BRG3 (17.41)
Secondary branches	140.92 to -92.28 i. B1-51 x ICP7035 (140.92) ii. BRG2 x BRG3 (125.53)	126.06 to -92.39 i. B1-51 x ICP7035 (126.06) ii. BRG2 x BRG3 (121.45)
Number of pods / cluster	50.00 to -53.85 i. B2-5-2-1 x B1-169-1 (50.00) ii. B2-5-2-1 x B2-106-1 (45.45)	33.33 to -70.00 i. B2-5-2-1 x B2-106-1 (33.33) ii. B2-5-2-1 x B1-169-1 (28.57) & B3-13 x B1-169-1 (28.5)
Number of pods / plant	196.15 o -94.16 i.B1-141-1 x ICP7035 (196.15) ii.BRG2 x BRG3 (130.23)	179.32 to -95.40 i. B1-141-1 x ICP7035 (179.32) ii. B2-5-2-1 x B1-169-1 (94.58)
Number of seeds / pod	20.00 to -22.58 i. B1-51 x ICP7035 (20.00) & B1-141-1 x ICP7035 (20.00) ii. B1-66-1 x ICP7035 (13.33)	20.00 to -25.00 i. B1-51 x ICP7035 (20.00) & B1-141-1 x ICP7035 (20.00) ii. . B1-66-1 x ICP70351 (13.33)
100 seed (green)weight	17.35 to -13.21 i. B1-51 x ICP7035 (17.35) ii. B1-141-1 x ICP7035 (7.80)	12.76 to -17.38 i. B1-51 x ICPL87091 (12.76) ii. B1-141-1 x ICP7035 (2.79)
Green pod yield / plant	873.17 to -89.30 i. B1-141-1 x ICP7035(873.17) ii. BRG2 x BRG3 (630.24)	577.59 to -91.38 i. B1-141-1 x ICP7035(577.59) ii. BRG2 x BRG3 (534.53)

Out of the nine characters studied in 35 crosses, the lowest maximum values of relative heterosis and heterobeltiosis were recorded from the characters 100 seed weight for relative heterosis and plant height for heterobeltiosis in the cross B1-51 x ICP7035 while the maximum values of heterobeltiosis and relative heterosis were recorded from the character green pod yield per plant in the crosses B1-141-1 x ICP7035, followed by the character primary branches , pods / plant and secondary branches. Similar results were recorded by Patel *et al.,* (1991); Patel and Patel (1992); Kumar and Srivastava (1998); Srinivas *et al.* (2000); Khorgade *et al.* (2000); Sekhar *et al.* (2004); Wankhade *et al.* (2005); Yadav *et al.* (2005) and Sarode *et al.* (2009).

The cross B1-141-1 x ICP7035 (-5.17) expressed significant negative heterobeltiosis for days to 50% flowering showing scope for earliness.

None of the 35 crosses expressed positive significant heterobeltiosis and relative heterosis for plant height. Maximum negative significant heterobeltiosis and relative heterosis was expressed by the cross BRG2 X B2-106-1 which may be conducive for short plant height.

For number of primary branches, positive significant heterobeltiosis and relative heterosis were observed in the cross B1-141-1 x BRG1. The crosses B1-51 x ICP7035 and BRG2 x BRG3 exhibited positive significant heterobeltiosis for secondary branches.

The crosses B1-141-1 x ICP7035 and BRG2 x BRG3 expressed positive significant heterobeltiosis and relative heterosis for pods/plant while the crosses B1-141-1 x ICP7035 and B1-51 x ICP7035 expressed positive significant heterobeltiosis and relative heterosis for seeds/ pod.

Positive significant heterobeltiosis and relative heterosis was observed in the cross B1-51 x ICP7035 for 100 seed weight.

Among the 35 crosses, six of the hybrids exhibited significant positive heterobeltiosis for green pod yield per plant. The maximum significant positive heterobeltiosis was recorded in the cross B1-141-1 x ICP7035 followed by the cross BRG2 x BRG3. It also manifested high significant heterobeltiosis and relative heterosis for the characters 100 seed weight, number of seeds/pod, number of pods/ plant, secondary branches and primary branches suggesting the possibility of utilizing F_1 and further segregating generations in pigeonpea improvement programme.

4.9.5 Combining ability

The knowledge of combining ability is of prime importance in selecting potential parents in crop improvement programme. The general combining ability (gca) effects represent the fixable component of genetic variance, in contrast, specific combining ability (sca) effects represent dominance and epistatic components of variation which are non fixable and related to hybrid vigour. Hence, sca effects could contribute towards the improvement of crops only when commercial exploitation of heterosis is feasible.

Highly significant difference among line x tester for almost all the characters studied was exhibited in analysis of variance, indicating that the materials chosen were desirable for initiating a crop improvement programme.

The lines showed significant differences for all the characters under study except for 100 seed (green) weight thereby suggesting that the lines were genetically different from one another for characters under study.

The testers under study revealed significant differences for almost all the characters under study except for primary branches per plant which suggested little genetic differences among the testers.

4.9.5.1General combining ability

From the present study, the best two genotypes with highest gca effects for lines and testers for each character are summarised and presented in Table 4.11

Table 4.11 Best two genotypes with highest gca effects for lines and testers for each character

Character	gca effects	
	Lines	Tester
Plant height	i. B2-10 (41.33)	B1-169-1 (14.77)
	ii. B2-5-2-1 (28.45)	ICP7035 (7.62)
Days to 50% flowering	i. B2-5-2-1 (-4.64)	ICP 7035(-3.63)
	ii. B3-13 (-4.37)	B1-169-1 (-0.72)
Primary branches	i. B1-141-1 (8.73)	ICP 7035 (3.49)
	ii. B2-10 (7.96)	BRG3 (-0.11)
Secondary branches	i.B3-13 (47.68)	ICP7035 (53.51)
	ii.B1-141-1 (32.87)	BRG3 (22.91)
Number of pods /cluster	i.B3-13 (0.62)	ICP7035 (0.32)
	ii. B2-5-2-1 (0.55)	B2-106-1 (0.13)
Number of pods /plant	i. B3-13 (50.81)	ICP7035 (51.47)
	ii.B1-141-1 (40.59)	BRG3 (7.18)
Number of seeds /pod	i.B1-141-1 (0.38)	ICP7035 (0.35)
	ii B2-10 (0.25)	B1-169-1 (0.11)
100 grain weight	i.B1-66-1 (0.69)	B2-106-1 (0.65)
	ii. B1-51 (0.61)	BRG1 (0.32)
Green pod yield / plant	i. B1-141-1 (120.79)	ICP7035 (130.27)
	ii.B3-13 (85.36)	BRG3 (47.51)

The parents B1-141-1, B3-13 among lines and ICP7035and BRG3 among testers proved to be good combiners for green pod yield / plant. Also the line B3-13 and B1-141-1 proved to be the best combiner for secondary, number of pods / plant and number of pods /cluster. B1-141-1 proved to be the best combiner for primary branches, secondary branches, number of pods /plant and green pod yield / plant.

The present outcome implies that the genotypes with high *per se* performance for a character are good general combiner of the particular character. The present findings are in concurrence with that of Srinivas *et al.* (2000); Sindhu *et al.* (2000); Jayamala and Rathnaswamy (2000); Pandey and Singh (2002); Kumar *et al.* (2003); Banu *et al.* (2006); Raju and Muthiah (2007); Phad *et al.* (2007); Marppa (2008) and Sarode *et al.* (2009).

4.9.5.2 Specific combining ability

High specific combining ability (sca) among the hybridizing parents is due to existence of dominance and interaction effects. Sprague and Tatum defined sca as those cases in which certain hybrid combinations perform better or poorer than would be expected on the basis of the average performance of the parental inbred lines. The best two crosses with the highest values of sca effects for eleven characters are summarized and presented in Table 4.12.

Table 4.12 best two crosses with the highest values of sca effects for nine characters

Character	sca (crosses)
Plant height	i. BRG2 x BRG3 (148.28)
	ii. B1-51 x ICP7035 (86.96)
Days to 50% flowering	i. BRG2 x BRG3 (-13.47)
	ii. B1-51 x B2-106-1 (-10.32)
Primary branches	i. BRG2 x BRG3 (35.91)
	ii. B1-141-1 x BRG1 (30.49)
Secondary branches	i. BRG2 x BRG3 (301.09)
	ii. B1-51 x ICP7035 (178.81)
Number of pods / cluster	i. B1-66-1 x ICP7035 (1.01)
	ii. BRG2 x BRG3 (0.86)
Number of pods / plant	i. BRG2 x BRG3 (212.82)
	ii. B1-141-1 x ICP7035 (168.93)
Number of seeds/ pod	i. B1-51 x ICP7035 (0.91)
	ii. BRG2 x BRG3(0.88)
100 grain weight	i. B1-51 x ICP7035 (2.76)
	ii. B2-10 x B1-169-1 (2.09)
Green pod yield / plant	i. BRG2 x BRG3 (576.27)
	ii. B1-141-1 x ICP7035 (471.79)

In the present studies, the cross BRG2 x BRG3 exhibited the highest sca effects for plant height, days to 50% flowering, primary branches, secondary branches, number of pods / plant, green pod yield / plant and second highest sca effects for number of pods /cluster and number of seeds / pod. It also exhibited second highest value of heterobeltiosis and relative heterosis for primary branches, secondary branches, number of pods /plant and green pod yield / plant.

Similarly, B1-141-1 x ICPL7035 exhibited second highest sca effects for number of pods /plant and green pod yield /plant also exhibited highest value of relative heterosis, heterobeltiosis for days to 50% flowering, primary branches, number of pods /plant, green pod yield /plant and second highest for relative and heterobeltiosis in the character number of seeds / pod and 100 grain weight. Similarly many of the characters also showed the same result in relation to sca effect and heterotic effects.

This substantiate the agreement that "the larger the sca effect, the greater is the heterotic effect in the cross", independence of heterotic effect from the sca effect could not be ruled out for the specific character of specific cross combinations according to the number of genes governing the traits, their linkage relationship, the gene frequency in the parental lines, unpredictability of environment conditions etc.

The results are in concurence with Srinivas *et al*. (2000); Sidhu *et al.* (2000); Kumar *et al.* (2001); Sunilkumar *et al*. (2003); Sekhar *et al*. (2004); Baskaran and Muthiah (2007); Sameer Kumar *et al*. (2009); Sathya and Jayamani (2011) and Punam and Roopa (2011).

4.9.6 Genetic components of variance

The gca variance (σ^2g) arises from differences in the gca effects of parents while the sca variance (σ^2s) arise from difference in sca effects of crosses. The gca variance corresponds to the variance of the breeding values i.e. additive genetic variance (σ^2A) and sca variance corresponds to mainly dominance variance i.e. non- additive genetic variance (σ^2D). The ratio of (σ^2g) to (σ^2s) provides information regarding the relative importance of additive or non- additive genetic variance. If the value is equal to unity, it suggests the importance of additive and non- additive genetic variances.

In the present study, notable role of both the additive and non- additive genes gives the impression in controlling the expression of the characters. The major role of non- additive component was evident for plant height, days to 50% flowering, primary branches, secondary branches, number of pods / plant, 100 seed weight and green pod yield / plant; as the magnitude estimated dominance (σ^2D) component of variance was higher than that of the additive (σ^2A) component of variance. For the character number of pods per cluster and number of seeds per pod, equal importance of additive and non- additive components were observed.

The results are in general agreement with that of Chaudhari *et al* (2004); Sekhar *et al.* (2004); Kandalkar (2005); Banu *et al.* (2006); Raju and Muthiah (2007); Raju *et al*. (2007); Anithavasline et al. (2007); Yadav et al. (2008); Barad *et al*. (2008); Marrappa (2008); Priyankavyas *et al*. (2008); Kumar *et al*. (2009); Patel *et al*. (2009); Shoba and Balan (2010); Baskaran, K. and Muthiah (2009); Sunil *et al*. (2010); Bhavani and Bhalla*,* (2010); Patil *et al.* (2011); Arbad *et al*. (2013) and Suresh (2014).

SUMMARY AND CONCLUSION

The present investigation entitled “Combining ability analysis for vegetable yield and its components in pigeonpea (*Cajanus Cajan* (L.) millsp.)”, was undertaken to ascertain the extent of genetic variability, association among yield and its related characters, the magnitude of exploitable heterosis, combining ability effects of the genotypes and components of genetic variance for yield and its components in some of the pigeonpea genotypes.

During the *kharif* season of 2013-2014, 12 parental lines i.e. 7 lines and 4 testers were sown in a Randomized Block Design with three replications to obtain data on eleven different traits for yield and yield attributes. Simultaneously, 35 F_1 hybrids of pigeonpea were produced following line x tester mating system involving 7 lines and 5 testers. All the 35 F_1s with 12 parental lines i.e. 7 lines and 4 testers were sown during *kharif* season of 2014-2015 in a Randomized Block Design with three replications to obtain data on eleven different traits for yield and yield attributes. The results of the present study are summarized as follows:

In the present investigation, analysis of variance indicates significance for most of the characters which indicates the existence of genetic variation among the genotypes.

The high estimate of genotypic coefficient of variation was obtained for number of pods /plant and secondary branches highlighting the presence of wider genetic variability for these characters.

High heritability with high genetic advance as percent of mean was expressed by secondary branches, number of pods /plant and primary branches.

Significant and positive correlation was observed between pods / plant with primary branches and secondary branches at phenotypic level. These traits could be considered for improving the yield per plant considerably.

The estimates of significant heterosis over better parent indicated the true superiority of F_1s over better parent. Heterobeltiosis for green pod yield /plant of 577.59% and relative heterosis of 873.17% were recorded from the cross B1-141-1 x ICP7035 followed by 534.53 in the cross BRG2 x BRG3 for heterobeltiosis and 630.24 in BRG2 x BRG3 for relative heterosis suggesting the possibility of utilizing F_1 and further segregating generations in pigeonpea improvement programmes. Highly significant better parent heterosis as expressed by a number of crosses for various traits in the present study further suggested the possibilities of operating dominance mechanism of heterosis in these crosses of pigeonpea.

Highly significant difference among line x tester for almost all the characters studied was exhibited in analysis of variance, indicating that the materials chosen were desirable for initiating a crop improvement programme. The lines showed significant differences for almost all the traits except for 100 seed (green) weight. The above findings suggested that there were diversity among the lines.

B3-13, B1-141-1 among lines and ICP7035 and BRG3 among testers were proved to be good general combiners for green pod yield / plant and early flowering. The genotypes with high gca effects may provide a base for developing the desired lines for the concerned trait.

High specific combining ability (sca) among the hybridizing parents is due to existence of dominance and interaction effects. Thirteen crosses of the total 35 crosses signify positive sca effects for green pod yield /plant. The best sca effects was observed in the cross, BRG2 x BRG3 for green pod yield /plant which also showed best sca effect for plant height, days to 50% flowering, primary branches, secondary branches, number of pods /plant and green pod yield /plant.

In the present study, notable role of both the additive and non-additive genes gives the impression in controlling the expression of the characters. The major role of non- additive component was evident for; plant height, days to flowering, primary branches, secondary branches, number of pods /plant, 100 grain weight and green pod yield /plant; as the magnitude estimated dominance (σ^2D) component of variance was higher than that of the additive (σ^2A) component of variance. For the character namely number of pods/ cluster and number of seeds / pod, equal importance of additive and non-additive components were observed.

Based on the above observations, the following may be concluded:

i. Among the parents, genotypes ICP7035, BRG2 and BRG3 may be considered as the potential genotypes for incorporation in pigeonpea breeding programme.

ii. Genetic improvement in the green pod yield can be achieved by applying strong selection for the characters like secondary branches and number of pods /plant.

iii. On the basis of high mean performance for green pod yield per plant, high heterosis for days to flowering and green pod yield /plant, good combiner for yield and yield related traits, the crosses B1-141-1 x ICP7035 and BRG2 x BRG3 were observed to be promising.

Selected lines from crosses i.e. B1-141-1 x ICP7035 and BRG2 x BRG3 deserves further evaluation to screen the best lines, which after multilocational testing at different agro-climatic zones may be proposed for zone specific recommendations.

REFERENCES

Ajay, B.C., Ganesh, B.N., Gowda, M.B., Prasad, P.S., Veerakumar, G.N., Venkatesh, S.C., Fiyaz, R.A. and Raamya. 2012 Genetic analysis of yield and quantitative traits in pigeonpea (*Cajanus cajan* (L.) Millsp.). *International Journal of Plant Breeding*. **186** (3): 705.

Akram, S., Hussian, B. M. N., Bari, Md, A., Burrit. D. J and Hossain, M.A. 2016. Genetic variability and association analysis of soybean (*Glycine max* (L.) Merrill) for yield and yield attributing traits. *Plant Gene and Trait*. **7**(13):1-11.

Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and Sons Inc.
New York.

Annual report. 2017-18. All India coordinated research project on pigeonpea.
IIPR, Kanpur.

Anonymous. 2010. Agriculture statistics at a glance, Department of Agriculture and cooperation, Ministry of Agriculture, Govt. of India, New Delhi, 108-109.

Anonymous. 2012. Directorate of Economics and Statistics, Ministry of Agriculture, Govt of India, New Delhi.

Anbumalarmathi, J., Rangasamy, P and Yogameenakshi, P. 2004. Studies oncombining ability analysis for quality traits in mungbean (*Vigna radiata* (L.) Wilczek). *Madras Agricultural Journal*. 92(4-6): 188-192.

Anithavasline, Y., Suguna, V and Padmavathi, S. 2007. Combining ability for seed yield and its components in greengram (*Vigna radiata* (L.) Wilczek). *Crop Improvement*. 34(2): 163-165.

Arbad, S. K. Madrap, I. A. Jadhav, P. 2013. Combining ability for yield and yield contributing characters in pigeonpea. *International Journal of Agricultural Sciences*. 9(1):252-255.

Arshad, M., Bakhsh, A., Zubiar, M. And Abudul Ghafoor. 2003. Genetic variability and correlation studies in chickpea. *Pakistan Journal of Botany*. **35** (4): 605-611.

Bagade, A.B; Patel, D.U; Singh, B. and Desai, N.C. 2002. Heterosis for yield and yield components in Indian bean. *Indian Journal of Pulses Research*. **15**(1): 46-48.

Banu, M. R.; Muthaiah, A.R. and Ashok, S. 2006. Combining ability studies in pigeonpea. *Crop Research.* **31** (3): 396-398.

Banu, M. R.; Muthaiah, A. R. and Ashok, S. 2007. Heterosis studies in pigeonpea. *Advances in Plant Sciences.* **20** (1): 37-38.

Barad, H.R., Pithia, M.S and Vachhani, J.H. 2008. Heterosis and combining ability studies for economic traits in genetically diverse lines of mungbean (*Vigna radiata* (L.) Wilczek). *Legume Research*. 31(1): 68-71.

Basavarajaiah, D., Gowda, M. B., Lohithaswa, H.C. and Kulkarni, R.S. 2000. Assesment of pigeonpea germplasm and isolation of elite genotypes for Karnataka. *Crop Research*. **20** (3): 444-448.

Baskaran, K. and Muthaih, A.R. 2007. Association between yield and yield attributes in pigeonpea. *Legume Research*. **30** (1): 64-66.

Baskaran, K. and Muthian, A. R. 2007. Studies on combining ability in pigeonpea [*Cajanus cajan* (L.) Millsp.] *Legume Research*. **30** (1): 67-69.

Baskaran, K. and Muthiah, A.R. 2009. Influence of parents and their habit on genetic diversity among hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Madras Agricultural Journal*. 95(6): 32-37.

Bhadru, D. 2010. Studies on genetic parameters and interrelationships among yield and yield contributing traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. **33** (1): 23-27.

Bhadru, D. 2013. Studied Genetic variability of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Electronic Journal of Plant Breeding.* **2** (1): 132-134.

Bhavani, N. L. and Bhalla, J .K 2009 Heterosis of yield components in pigeonpea (*Cajanus cajan* (L) Mill sp.). *Advances in Plant Sciences*. **22**(1): 257-259.

Bhavani, N.L. and Bhalla, J.K. 2010. Combining ability analysis for yield and yield components in pigeonpea [*Cajanus cajan* L.]. *Advances in Plant Science.* 23(1): 257-259.

Birk Y. 1993. Anti-nutritional factors (ANFs) in lupin and other legume seeds: Pros and cons. Pages 424–429 *in* Advances in lupin research (Martins and da Costa, eds.). Advances in lupin research. Proceedings of the 7th Lupin Conference held at Evora, Portugal, 18-23 April 1993. www.hort.purdue.edu.

Briggle, L.W. 1963. Heterosis in wheat. A review. *Crop science*. **3**: 407-412.

Burton, G.W. 1952. Quantitative genetics in grasses. *Proc. 6th International Grassland Cong*. **1**: 277-288.

Chandrakala, R and Raveendran, T.S. 2002. Heterosis in pigeonpea (*Cajanus cajan* L.) *Annals of Agricultural Research*. **23**(2): 304-308.

Chandrakala, R. And Subbaraman, N. 2010. Character association and path analysis in pigeonpea. *Indian Journal of Agricultural Research*. **32** (3): 211-216.

Chaudhari, K.N., Chauhan, R.M. and Prajapati, B.H. 2004. Combing ability analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Journal of Bioscience Reporter*. 2(2): 304-308.

Chauhan, R.M; Parmar,.L.D; Patel, P.T and Tikka, S.B.S. 2008. Identification of heterotic combinations of CMS lines and restorers of pigeonpea. *Journal of Food Legumes*. **21**(1)**:** 25-27.

Chethana, C. K. D., Harmaraj, P. S., Muniswamy, S., Yamanura, Gangadhara, K. and Nagaraju, C. H. 2015. All India Co-ordinated Research Project on Pigeonpea, Agricultural Research. *Trends in Biosciences*. **8** (1).

Chithrameenal, K. and Jebaraj, S. 2015. Association studies in pigeonpea [*Cajanus cajan* (L.) Millsp.]. For yield and yield attributes including physiological traits. *International Journal of Science and Nature*. **6** (3): 372-375.

Dahat, D.V; Deshmukh, R.B and Patil, J.V. 1997. Genetic variability and character association in pigeonpea grown as sole and inter crop in Pearl millet. *Indian Journal of Agriculture Research*. **31**(2): 82-86.

Dalbeer, Nath, S., Verma, O.P., Kavita and Kumar, K. 2013. Correlation and path coefficient analysis for yield attributes in lentil (*Lence culinaris* L.). *International Journal of Science and Research.* **4**:8.

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

Dheva,N.G; Patil,A.N and Wanjari,K.B 2009 Heterosis in cytoplasmic male sterility based hybrids of pigeonpea. Muzaffarnagar, India: Hind Agri-Horticultural Society. *International Journal of Plant Sciences Muzaffarnagar* . **4**(1): 270-273.

FAO 2008. http://faostat.fao.org/ .
FAO 2009. http://faostat.fao.org.

FAOStat. 2010. Online agricultural statistics. http//www.faostat.org.

Faris DG, Saxena KB, Mazumdar S and Singh U. 1987. Vegetable Pigeonpea: A promising Crop for India. ICRISAT, Patancheru, A.P., India. P. 3.

Faris DG and Singh U. 1990. Pigeonpea: Nutrition and Products. In: Nene YL, Hall SD, Shiela VK (Eds.) The Pigeonpea. ICRISAT, Patancheru 502 324, A.P. India. CAB International, U.K. pp. 401-433.

Fisher, R.A. 1918. The correlation among relatives on the supposition of Mendelian Inheritance. *Trans. Royal Soc. Edinberg.*, **52**: 399-433.

Gomez, K. A. and Gomez, A. A. 1984. Statistical procedures for agricultural research. John Wiley and Sons. Inc., New York.

Goswami, A., Yadava, H.S. and Pawar, K.S. 2003. Genetic variability among advanced generation lines of chickpea developed from desi x kabuli recombination. In: *Abstract of the National symposium on pulses for crop diversification and natural resource management*, 20 – 22 December 2003. I.I.P.R. Kanpur,U.P. pp. 42.

Gowda, M.B; Mahadevu, P; Lakshmidevamma, T.N. and Saifull, M. 2003. Genetic variability and association studies in early maturing pigeon pea genotypes. In : *Abstracts of the National Symposium on pulses for crop* *diversification and Natural Resource Management,* 20 – 22 December 2003. I.I.P.R. Kanpur,U.P. pp. 70.

Gupta DK, Acharya S and Patel JB 2011 Combining ability and heterosis studies in pigeonpea using A2 cytoplasm from *Cajanus scarabaeoides* as source of male sterility. *Food Legumes*. 24: 58-64.

Gupta, S.K; Kaur, A.; Singh, Kuldip and Singh, D. 2003. Correlation among yield and yield attributed in F_3 population of chickpea. In : *Abstracts of the National Symposium on pulses for crop diversification and Natural Resource Management,* 20 – 22 December 2003. I.I.P.R. Kanpur,U.P. pp. 46.

Hamid, A., Husna, A., Haque, M.M. and Islam, M.R. 2011. Genetic variability in pigeonpea [*Cajanus cajan* (L.) Millsp *Electronic Journal of Plant Breeding.* **2** (1): 117-123.

Harshal E. Patil, Nilamani Dikshit, S.A. Aklade and Paresh A. Vavdiya 2016. Evaluation of vegetable type pigeonpea (*Cajanus cajan* (L.) genotypes for yield and yield contributing traits. *International Journal of envirobiotech* . Vol **22**:247-254.

Hayes. H.K.; Immer, F.F. and Smith, D.C. 1955. *Methods of plant breeding*, Mc Graw- Hill, publishing Co. Ltd., New Delhi, 52-65.

Jahagirdar, J. E. 2003. Line x tester analysis for combining ability in pigeonpea. *Indian Journal of Pulse Research*. **16** (1): 17-19.

Jayamala, P and Rathnaswamy, R 2001. Combining ability in pigeonpea. *Madras Agricultural Journal*. **87**(7/9): 418-422.

Jogender, S.B. and Bajpai, V.P. 2008. Genetic variability and character association in interspecific crosses of pigeonpea. *Environment and Ecology*. **26** (3): 1138-1140.

Johnson, H.W.; Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic variability and environmental variability in soybean. *Agron Journal.* **47**: 314-3128.

Joseph, J and Santhoshkumar, A.V. 2000. Genetic analysis of quantitative characters through biparental matings in greengram [*Vigna radiata* (L.) Wilczek]. *Crops Research*. 2: 221-225.

Joshi, V.C; Patel, P.T; Parmar, L.D; Solanki, S.D and Chauhan, R.M. 2003. Variability and association analysis in pigeonpea. In : *Abstracts of the National Symposium on pulses for crop diversification and Natural Resource Management,* 20 – 22 December 2003. I.I.P.R. Kanpur,U.P. pp. 76.

Kandalkar, V. S. 2006 Gene effects for grain yield and its attributes in varietal crosses of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Crop Research*.32(1):97-100.

Kempthorne, O. 1957. An introduction to genetic statistics. John Wiley and Sons. Inc., New York; Chapman and Hali. London.

Khan, R., Farhatullah and Khan, H. 2011. Dissection of genetic variability and heritability estimates of chickpea germplasm for various morphological markers and quantitative traits. *Sarhad Journal Agriculture*. **27**(1).

Khorgade,.P.W; Wankhade,.R.R and Satange,.I.V 2000. Heterosis studies in pigeonpea hybrids based on male sterile lines. PB: Karnal, India: Agricultural Research Communication Centre. *Indian Journal of Agricultural Research.* **34**(3): 168-171.

Kingshlin, M. and Subbaraman, N. 1999. Correlation and path coefficient analysis among quantitative characters in pigeonpea. *Annals agriculture journal*. 20 (2): 154.

Kingshlin, M., Subbaraman, N, and Vanniarajan, C. 1999. Estimation of heritability and genetic advance in the full-sib progenies of pigeonpea. *Crop Research*. **14** (2): 303 – 306.

Krishan Kumar; Ram.Dhari and Tomer,.Y.S. 2003. Combining ability analysis for seed yield and its attributes in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *National Journal of Plant Improvement*. **5**(2): 124-126.

Kumar, A. and Srivastava, D.P. 1998. Heterosis in relation to combining ability in long duration pigeonpea. *Indian Journal of Pulses Research***.** **11** (2): 1-5.

Kumar, Ajay and Srivastava,.D.P 1998. Heterosis in relation to combining ability in long duration pigeonpea. *Indian Journal of Pulses Research*. **11** (2): 1-5.

Kumar, Ajay., Srivastava, D. P, Singh, I. P and Dixit, G. P. 2001. Combining ability analysis of male sterile lines and hybrids in pigeonpea. *Legume Research*. **24** (3): 178-181

Kumar, B. and Krishna, R. 2003. Character association studies in segregating population derived through line x tester in pigeonpea. In : *Abstracts of the National Symposium on pulses for crop diversification and Natural Resource Management,* 20 – 22 December 2003. I.I.P.R Kanpur,U.P. pp. 64.

Kumar, C.V.S., Sreelakshami, C.H. and Verma, P.K. 2009. Studies on combining ability and heterosis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. **32**(2): 92-97.

Kumar, K., Ram, D. and Tomer, Y.S. (2003). Combining ability analysis for seed yield and its attributes in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *National Journal of Plant improvement*. 5(2): 124-126.

Kumar CVS, Sreelakshmi CH, Shivani D 2012. Gene effects, heterosis and inbreeding depression in pigeonpea (*Cajanus cajan* L.). *Electronic Journal of Plant Breeding*. 3: 682-685.

Kumara, B.N., Santoshagowda, G.B., Nishanth, G.K. and Dharmaraj, P.S. 2013. Genetic diversity variability and correlation studies in advanced genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Research Article, Acta Biologica Indica*. **2** (2): 406-411.

Kumara, S., Singh, S.S., Shivani, E.R. 2014. Studies on genetic variability and interrelationship among yield contributing characters in pigeonpea grown under rain fed lowland of eastern region of India. *Journal of legumes*. **27** (21): 104.

Lohithaswa, H.C. and Dharmaraj P.S. 2003. Implication of heterosis combining ability and per se performance in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Karnataka Journal of Agricultural Sciences.* 16(3): 403-407.

Malik, F.M.A., Shahid, I.A. and Niaz. S. 2008. Comparative study of quantitative traits and association of yield and its components in black gram (*Vigna mungo*) genotypes. *Assian Journal of Plant Science*. **7** (1): 26-29.

Manivannan, N. 2002. Line × Tester analysis in kharif greengram. *Legume research*. 25(2): 127-130.

Marappa, N. 2008. Line × Tester analysis in mungbean [*Vigna radiata* (L.)Wilczek]. *Asian Journal of Bio Science*. 3(2): 289-294.

Meena, B.L., Das, S.P., Meena, S.K., Kumari, R., Devi, A.G. and Devi., H.L. 2017. Assesment of GCV, PCV, heritability and genetic advance for yield and its components in field pea (*Pisum sativum* L.). *International Journal of Current Microbiology and Applied Sciences*. **6** (5): 1025-1033.

Nath, N. and Talukdar, P. 1997. Genetic variability and correlation studies in segregating population of indigenous scented x high yielding non- scented crosses of rice. *Oryza*. **34** (2): 91-93.

Ojwang, J.D., Nyankanga, R.O., Ukuku, D.U. and Imungi, J. 2016. Yield components of vegetable pigeonpea cultivars. *Subtropical Agriculture and Environments*. **67**: 1-12.

Padi, F.K. 2003. Correlation and path coefficient analysis of yield and yield components in pigeonpea. *Pakistan Journal of Biological Sciences*. **6**: 1689-1694.

Pagi N.K., Ravindrababu, Y., Dharajiya, D. T., Patel, J. M., and Patel, M. P. 2016. Heterosis for Seed Yield and Its Component Characters in Pigeonpea [*Cajanus cajan* L. Millsp.]. *International Journal of Agriculture Sciences*, 8(60): 3391-3395.

Pal, S.S; Sandhu, J.S and Singh, I. 2005. Exploitation of genetic variability in interspecific cross between *Vigna mungo x V. Umbellata*. *Indian Journal of Pulses Research*. **18** (1): 9-11.

Pandey, N. 1999. Heterosis and combining ability in pigeonpea. *Legume Research*. **22**(3): 147-151.

Pandey, N. 2004. Line x tester analysis in long-duration hybrid pigeonpea. *Legume Research*; 27(2):79-87.

Pandey, N. and Singh, N.B. 1998. Correlation studies in pre-rabi pigeonpea hybrids. *Indian Journal of Pulses Research*. **11** (2): 133-136.

Pandey, N. and Singh, N.B. 2001. Association between yield and yield attributes in pigeonpea hybrids. *Madras Agricultural Journal*.**88** (12): 640-643.

Pandey, N and Singh,.N.B.2001. Hybrid vigour and combining ability in long duration pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids involving male sterile lines. *Indian Journal of Genetics and Plant Breeding.* **62**(3):221-225.

Pandey, Praveen and Rajesh Kumar Pandey, V. R. 2014. Genetic studies for quantitative traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Crops Research*; 16(1):154-161.

Pandey, P., Kumar, R and Pandey, V.R. 2016. Genetic association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. **39**(2): 189-193.

Parmar, M.B. and Kathiria, K.B. 2016. Genetic analysis for heritability and genetic advance in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Ecology, Environment and Conservation Paper*.**22**:41-45.

Patel, G.V. Zaveri, P.P. and Pathak A.R. 1991. Heterosis for morphophysiological attributed in pigeonpea. *Indian Journal of Pulses Research***. 4** (1): 35-41.

Patel, J.A. and Patel, D.B. 1992. Heterosis for yield and yield components in pigeonpea. *Indian Journal of Pulses Research***. 5** (1): 15-20.

Patel, J.B., Acharya, S., Joshi, V.C. and Vaghela, K.O. 2011. Genetic divergence and character association in Indo-African derivatives of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Journal of Food Legumes*.**24** (3): 198-201.

Patel, K.N and Patel, D.R. 1998. Studies on genetic variability in pigeonpea. *International Chickpea and pigeonpea Newsletter*, No. 5: 28-30.

Patel, P.T., Chauhan, R.M., Parmar, L.D. and Tikka, S.B.S. 2009. Phenotypic stability of yield and related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*., 32(4): 235-239.

Patil, H. E., Dikshit, N., Aklade, S. A. and Vavdiya, P. A. 2016. Evaluation of vegetable type pigeonpea (*Cajanus cajan* (L.) genotypes for yield and yield contributing traits. *Ecology, environment and conservation paper.* 22: 247-254.

Pawar, R. M. and Tikka, S. B. S. 2003. Combining ability analysis in Pigeonpea. GAU Research Journal. **28** (1-2):5-8.

Phad, D. S. Madrap, I. A. Dalvi, V. A. 2007. Study of combining ability analysis in pigeonpea under different environments for yield contributing characters. *Legume Research*; 30(2):123-127.

Phad, D.S; Madrap, I.A and Dalvi, V.A 2007. Study of combining ability analysis in pigeonpea under different environments for yield contributing characters. *Legume Research.*; **30**(2): 123-127.

Phad, D.S.; Madrap, I.A. and Dalvi, V.A 2009. Heterosis in relation to combining ability effects and phenotypic stability in pigeonpea. *Journal of Food Legumes*. **22**(1): 59-61.

Priyankavyas., Vishwakarma, D.N and Singh, P.K. 2008. Heterosis and combining ability for grain yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *Progressive Research*. 3(2): 123-125.

Punam, S.Y and Roopa, L.G. 2011. Estimation of combining ability effects in mungbean (*Vigna radiata* (L.) Wilczek) crosses. *Madras Agricultural Journal.* 98(7-9): 213-215.

Raju, P.A and Muthiah, A.R 2007. Heterosis and combining ability for quantitative and qualitative traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Crops Research*. **8**(3): 625-631.

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 Research*. **35** (3): 207-213.

Ramya, B., Nallathamb, G and Ram, S.G. 2014. Genetic variability, heritability and genetic advance in induced mutagenesis black fram (*Vigna mungo* L. Hepper). *Plant Archives*.**14** (1):139-141.

Rangare, N.R., Reddy, G.E. and Kumar, S.R. 2013. Study of heritability, genetic advance and variability for yield contributing characters in pigeonpea (*Cajanus cajan* L.). *Trends in biosciences.* **6** (5): 660-662.

Rekha, R., Prasanthi, L., Sekhar, M.R. and Priya, M.S. 2013. Variability, character association and path analysis for yield and yield attributes in pigeonpea. *Electronic Journal of Plant Breeding*.**4** (4): 1331-1335.

Rout, K., Mishra, T.K., Pradhan, B and Bastia, D. 2009. Studies on combining ability for yield and yield components in mungbean. *Journal of Food Legumes*. 22(4): 248-250.

Saleem, M., Shahzad, K., Javid, M. And Abdul, S. 2002. Heritability estimates for grain yield and quality characters in chickpea (*Cicer arietinum*). *International Journal of Agricultural and Biology*.**4** (2).

Sameer Kumar, C.V.; Sreelakshmi, C.H. and Kishor Varma, P. 2009. Studies on combining ability and heterosis in pigeonpea (*Cajanus cajan* L.). *Legume Research*. **32** (2): 92-97.

Santosh, K., Sanjeev. K., Singh, S.S., Elanchezhian, R. And Shivani. 2014. Studies on genetic variability and inter-relationship among yield contributing characters in pigeonpea grown under rain fed lowland of eastern region of India. *Journal of Food Legumes*.**27** (2):104-107.

Sarode,.S.B; Singh,.M.N and Singh,. U.P 2009. Combining ability analysis in long duration pigeonpea [*Cajanus cajsan* (L.) Millsp.]. *International Journal of Agricultural Sciences*. **5**(1): 165-167.

Saroj, S. K., Singh, M. N., Kumar, R., Singh, T. and Singh, M. K., 2013. Genetic variability, correlation and path analysis for yield attributes in pigeonpea. *The Bioscan* 8: 941-944.

Saroj, S.K., Singh, R.S., Singh, M. and Pathak, N. 2015. Studies on genetic variability of parents, F1,'S and F2,'S populations in pigeonpea. *Agricultural for Sustainable Development*.**3**(1): 32-36.

Sarsamkar, S.S., Borgaonkar, S.B., Kalyankar, S, V., Kadam, B. PandKadam, G.R. 2008. *International Journal of Plalnt Sciences*.**3** (2):502-503.

Sathya, M and Jayamani, P. 2011. Heterosis and combining ability studies in greengram. *Journal of Food Legumes*. 24(4): 282-287.

Saxena KB, Singh L and Gupta MD**.** 1990. Variation for natural out-crossing in pigeonpea. *Euphytica* 46:143-148.

Saxena, K.B. 2000 Pigeonpea theory and techniques, In: Gupta, S.K. Ed., Agroloios (India), Jodhpur, 82-112.

Saxena KB. 2000. Pigeonpea in China. International Crops Research Institute for the Semi Arid Tropics, Patancheru 502 324, A.P. India. p. 29.

Saxena, K.B. 2008 Genetic improvement of pigeonpea - A review. *Tropical Plant Biology*, **1**, 159-178.

Searles, S.R. 1961. Phenotypic, genotypic and environmental correlations. *Biometrics*, **17**: 474-480.

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 Journal of Genetics and Plant Breeding*. **64**(3): 212-216.

Shoba, D. and Balan, A. 2010. Combining ability in CMS/GMS based pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids. *Madras Agricultural Journal*. **97**(3): 25-28.290.

Shunyu, V., Chaturvedi, H.P., Changkija, S. And Singh, J. 2013. Genetic Diversity in Pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes of Nagaland. *International Journal of Agricultural Innovations and Research.***2** (1): 2319-1473.

Sidhu,.P.S; Devinder Sandhu; Sekhon,.R.S and Sarlach,.R.S 2000. Combining ability studies involving male sterile lines in pigeonpea. *Journal of Research*, Punjab Agricultural University. **37**(1/2): 1-8.

Singh, A.P., Singh, U.P. Singh, R.M. and Raina, R. 2003. Relative efficiencies of four population improvement schemes in pigeonpea [*Cajanus cajan* (L.)Millsp.]. *Crop Research.* **25**(2): 305-311.

Singh, B. B. and Dikshit, H. K. (2003). Combining ability studies for yield and architectural traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Indian Journal of Genetics*. **63**(4): 351-352.

Singh, I.P. and Singh J.D. 2003. Heritability and genetic advance in urd bean.74.

Singh, I.P. and Srivastava, D.P. 2001. Combining ability analysis in inter specific hybrids of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Indian Journal of Pulses Research.* **14**(1): 27-30.

Singh, J., Fiyaz, R. A., Sudhir Kumar, M. A., Anasari and Sanjay Gupta. 2013. Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in pigeonpea grown under rainfed conditions of Manipur. *Indian Journal of Agricultural Sciences*. **83** (8): 858.

Singh, R.K. and Choudhary, B.D. 1977. Biometrical mehods in quantitative genetic analysis. Kalyani publisher. New Delhi.

Singh, R.S. and Singh, M.N. 2016. Character association trend among yield attributing traits in pigeonpea pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Indian Journal of Science and Technology*. **9** (6): 10.

Singh U. 1988. Anti-nutritional factors of chickpea and pigeonpea and their removal by processing. *Plant and Foods Human Nutrition.* **38**: 251-261.

Singh, U; Jain, K. C.; Jambinathan, R. and Faris D. G. 1983. Nutritional quality of vegetable pigeonpea (*Cajanus cajan*). Dry matter accumulation, carbohydrates and protein.. *Journal of Food Science*. **49**: 799-802.

Singh, U; Jain, K. C.; Jambinathan, R. and Faris D. G. 1984. Nutritional quality of vegetable pigeonpea (*Cajanus cajan*). Mineral and trace elements. *Journal of Food Science*. **49**: 645-646.

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 Research.***32** (3): 203-205.

Sprague, G. F. and Tatum, L.A. 1942. General versus specific combining ability in single crosses of corn. *Journal of the American society of agronomy*. 34: 923-932.

Sreelakshmi, C., Kumar, C.V.S. and Shivani, D. 2010. Genetic analysis of yield and its component traits in drought tolerant genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Electronic Journal of Plant Breeding*.**1** (6): 1488-1491.

Srinivas, T., Jain, K.C. and Reddy, M.S.S. 2002. Combining ability studies of medium and long duration pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Crops Reserach*, **1**(3): 297-301.

Srinivas, T., Jain, K.C., Reddy, M.V. and Reddy, M.S.S. 2000. Genetic relationships among yield components in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Indian Journal of Pulse Research*. **12**(2): 180-186.

Srinivas, T; Jain, K.C; Reddy, M.V and Reddy, M.S.S. 2000. Heterosis for grain yield and its component characters in pigeonpea. . *Crops Research*, **1** (3): 302-306.

Sujatha, K and Kajjidoni, S.T. 2013. Genetic analysis involving selected powdery mildew resistant lines in mungbean (*Vigna radiata* (L.) Wilczek). *Molecular plant breeding*. **4**(5): 38-43.

Sunil, K.B., Prakash, M and Gokul Krishna, J. 2010. Combining ability analysis in mungbean (*Vigna radiata* (L.) Wilczek). *Crop Improvement*. **37**(2): 165-167.

Sunilkumar; Lohithaswa, H.C.; and Dharmaraj, P.S. 2003. Combining ability analysis for grain yield, protein content and other qwuantitative traits in pigeonpea. *Journal of Maharashtra Agricultural Univesity*. **28** (2): 141-144.

Suresh, 2014. Combining ability analysis for yield and yield component traits in mungbean [*Vigna radiata* (L.) Wilczek]. 2nd International Conference on Agricultural and Horticultural Sciences February. 03-05.

Swapnil. 2015. Genetic analysis for yield and yield contributing traits in vegetable type genotypes in pigeonpea (*Cajanus cajan* (L.). *International Journal of Tropical Agriculture*. **33** (2).

Toker Cengiz. 2004. Estimates of broad-sense heritability for seed yield and yield criteria in faba bean (*Vicia faba* L.). *Hereditas*. **140**: 222-225.

Usharani, K.S and Kumar, C.R.A. 2016. Estimation of variability, heritability and genetic advance in mutant populations of black gram (*Vigna mungo* L. Hepper). *Journal of Breeding and Genetics*.**48** (3): 258-265.

Vanisree, S., Sreedhar, M. And Surender, R.C.H. 2013. Studies on genetic characteristics of pigeonpea and determination of selection criteria with path co-efficient analysis. *International Journal of Applied Biology and Pharmaceutical*.**4** (2).

Vanniarajan, V., Rangasamy, P., Nadarajan, N. and Ramalingam, J. 1999. Assessment of stability performance in pigeonpea. *Madras Agriculture Journal*. 86: 438-440

Venkateswarlu, O. 2002. Genetic variability in pigeonpea. *Legume Research*. **24** (30): 205-206.

Wankhade, Rajesh. 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 Journal of Pulses Research*. **18** (2): 141 – 143.

Yadav, A.S., Tank, C.J., Acharya, S. and Patel, J.B. 2008. Combining ability analysis involving indo-African genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Journal on Food legumes*, **21** (2): 95-98.

Yadav, R.K., Dixit, R.K. and Singh, H.L. 2005. Hybrid vigour strides in pigeonpea. In : Abstract of 4th International Food Legumes Research Conferance on Food Legumes for Nutrional Security and Sustainable Agriculture held at I.A.R.I, New Delhi Oct. 18 -22 : 2005 pp. 139.

Yadav, S.S. and Singh, D.P. 2004. Heterosis in Pigeonpea. *Indian Journal of Pulses Research*. **17** (2): 179 – 180.

Yerimani AS, Mehetre S. and Kharde MN, 2013 Genetic variability for yield and yield component traits in advanced F3 and F4 generations of pigeonpea [*Cajanus cajan* (L.)]. *Molecular Plant Breeding*. 4(16): 136-140.