COMBINING ABILITY AND GENE EFFECTS IN VEGETABLE-TYPE PIGEONPEA [(*Cajanus cajan* (L.) Millsp.)] UNDER FOOTHILLS OF NAGALAND

Thesis

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of

DOCTOR OF PHILOSOPHY

in

GENETICS AND PLANT BREEDING

by

N. MOSES
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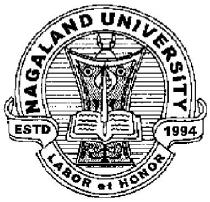

Department of Genetics and Plant Breeding,
School of Agricultural Sciences and Rural Development,
Nagaland University, Medziphema Campus – 797 106
Nagaland
2019

Affectionately

Dedicated

To My

Parents

DECLARATION

I, N. Moses 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.

Date:
Place: **(N. MOSES)**

……
Dr. Malini B Sharma
Supervisor

NAGALAND UNIVERSITY
Medziphema Campus
School of Agricultural Sciences and Rural Development
Medziphema – 797 106, Nagaland

Dr. Malini B. Sharma
Assoc. Professor
Department of Genetics and Plant Breeding

CERTIFICATE – I

This is to certify that the thesis entitled **"Combining ability and gene effects in vegetable type pigeonpea [(*Cajanus cajan* (L.) Millsp.)] under foothill of Nagaland"** submitted to Nagaland University in partial fulfillment of the requirements for the award of degree of Doctor of Philosophy (Agriculture) in Genetics and Plant Breeding is the record of research work carried out by N. Moses Registration No. 817/2018 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.

Date :
Place :

…….
DR. MALINI B. SHARMA
Supervisor

NAGALAND UNIVERSITY
Medziphema Campus
School of Agricultural Sciences and Rural Development
Medziphema – 797 106, Nagaland

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 and gene effects in vegetable type pigeonpea [(*Cajanus cajan* (L.) Millsp.)] under foothill of Nagaland"** submitted by N. Moses Admission No. Ph-167/14 Registration No. 817/2018 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.**

Member	Signature
1. Dr. Malini B. Sharma (Supervisor & Chairman)	…….
2. Dr. Jogendra Singh (External examiner)	…….
3. Dr. Pankaj Shah	…….
4. Dr. Kigwe Seyie	…….
5. Dr. Susanta Banik	…….
6. Dr. A.K. Sahu	…….

Head
Department of Genetics &
Plant Breeding

Dean
School of Agricultural Sciences
and Rural Development

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Date:

Place: Medziphema *(N. MOSES)*

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ABBREVIATIONS

Analysis of Variance	ANOVA
As such mean	*per se*
Centimetre	cm
Combining ability	CA
Degree Celsius	□C
Et alibi and others	*et al.*
East	E
Figure	Fig
General combining ability	GCA/gca
Gram	g
Hectare	ha
Height	ht.
Journal	J
Kilogram	kg
Metre	m
Nitrogen	N
North	N
Number	No.
Per	/
Primary	Pri.

Per cent	%
Phosphorus	P
Potassium	K
Species	spp.
South	S
Secondary	Sec.
Specific combining ability	SCA/sca
Standard Error	S.E
Tonnes	T
Namely	*viz.*
Weight	wt.

CHAPTER I

INTRODUCTION

INTRODUCTION

Pigeonpea (*Cajanus cajan* (L.) Mills) is among the major grain legume crops of the world in the tropical and subtropical regions. Primary centre of origin and diversification of pigeonpea is considered as India (Van der Maesen, 1990). The species is diploid (2n=2x=22). Pigeonpea is a hardy, widely adapted and drought tolerant crop with a high temporal variation (97-299 days) for grain maturity. It can be cultivated in a wide range of environments and different cropping systems because of these traits. Pigeonpea belong to perennial member of the family Leguminosae (Fabaceae), *Sub family:* Papilionaceae, *Tribe:* Phaseoleae, *Sub ribe:* Cajanae, *Genus: Cajanus, Species: cajan.* Hooker (1879) classified the genus *Cajanus* into a single species, *Cajanus indicus*, whereas, Duthie and Fuller (1883) reported two species, *Cajanus flavous* and *Cajanus bicolor* under the genus *Cajanus* and were called as 'tur' and 'arhar' respectively.

The cultivation of pigeonpea was reported ~ 4000 years back (Joshi *et al.,* 2001). Based on the abundance of natural genetic variability in local germplasm in vast number and presence of numerous wild relatives, Asia is most likely considered centre of origin, and then from Asia it travelled to East Africa by means of the slave trade to the American continent. The genus *Cajanus* comprises 32 species, of which 18 species are distributed in Asia; Australia has 15 and one in West Africa. Of these, *Cajanus cajan* is the only domesticated species and *Cajanus cajanifolius* is supposed to be the most probable progenitor of pigeonpea. Besides, these eleven related genera including *Rhynchosia, Eriosema*, *Dunbaria, Flemingia*, and *Paracalyx* have been described in the subtribe, *Cajaninae* (Van der Maesen, 1990).

Globally, pigeonpea is cultivated on 5.32 m ha with an annual production of 4.24 mt. The largest pigeonpea growing country in the world is

India, followed by Myanmar (0.90 m ha), Malawi (0.23 m ha), Tanzania (0.20 m ha) and Kenya (0.08 m ha). In India, pigeon pea is grown in an area of 44.59 lac hectares with a production of 41.80 lac tons (GOI 2019). Nearly 92 per cent of the total pigeonpea production in the world is contributed by Indian sub-continent alone. India leads both in area and production of pigeonpea in the world. Its productivity is lower (673 kg/ha) than the world average (762.4 kg/ha) (FAOSTAT 2015). In India, pigeonpea is widely grown in the states of Maharashtra (1.18 m ha), Karnataka (0.68m ha), Madhya Pradesh (0.53 m ha), Andhra Pradesh (0.47 m ha), Uttar Pradesh (0.31 m ha) and Gujarat (0.22 m ha). The area, production and productivity of pigeonpea during 2017-18 were 44.59 lac ha, 41.80 lac tons and 793 kg/ha, respectively (GOI 2019), showing a stagnation trend in productivity over the last few decades.

In India about 70% of the total area and production of pigeonpea is only from these six states (FAO, 2012) indicating scope for further improving genetic potential for yield enhancement. Lack of genetically superior varieties, poor crop husbandry and exposure to several biotic (diseases and insect pests) and abiotic (drought, salinity and water logging) stresses has lead to relatively low crop yields (Varshney *et al*., 2010).

As per the Indian Council of Medical Research (ICMR) the optimum pulses requirement per capita per day to maintain normal health is 104 g (Anonymous, 2011). However, the quantity available to the people of India is not even half. The per capita availability of protein in our country is already one-third of its normal requirement (Paul *et al.,* 2011) and if the production is not increase to an optimum level, it will further increase malnutrition problem among the poor community. By increasing the area or productivity of the crop this problem could be alleviated, it is important to enhance the productivity by a significant margin because the opportunities of horizontal increase in the cultivated areas are limited.

Pods of pigeonpea are consumed as green vegetable in many countries. Dry seeds are consumed as split dhal. Pigeonpea straws are palatable and green leaves can used as fooder, it is also used as ration for milch cattle. Pigeonpea sticks are used for various purposes such as thatch and basket making. Its use as a fodder crop has increased recently. Seed and fodder contains approx, 20-22% protein. Seeds are rich in iron, iodine, and essential amino acids like lycine, cystine and arginine. Pigeonpea plant is capable of fixing atmospheric nitrogen being a leguminous and thereby capable of restoring lot of nitrogen in the soil. Pigeonpea is a well recognized as a valuable source of dietary proteins; in addition to its nutritional value, it also has a unique property of biological nitrogen fixation and restoring soil fertility thereby improving physical properties of the soil by virtue of its deep root system in addition to its nutritional value. In southeastern U.S.A it is also grown as forage crop.

Polysaccharides and lower crude fiber content in vegetable type pigeonpea is higher than *dal*, irrespective of its seed size. The crude fiber content in vegetable type pigeonpea and garden pea (*Pisum sativum* (L.)) are almost similar. Pigeonpea has higher trypsin inhibitor activity than garden pea but soybean (*Glycine max* [L.] Merr) has higher magnitude than pigeonpea. With respect to starch and protein pigeonpea *dal* is superior to vegetable type, whereas vegetable pigeonpea grains had higher crude fiber, fat, and protein digestibility. Green pigeonpea is better in potassium by 17%, phosphorus by 28.2%, zinc by 48.3%, copper by 20.9%, and iron by 14.7%. On contrary, the *dal* hads 19.2% more calcium, and 10.8% more manganese (Saxena et al 2010) while researchers have identified genotypes such as ICP7035, with a sugar content as high as 8.8% at ICRISAT. Frozen green pigeonpea is usually combined with rice or served as soup In the Caribbean region; therefore there is a persistent demand for vegetable pods.

Large pods and seeds are primary characteristics of vegetable type pigeonpea varieties. These two traits are linked together and has been generally observed in most germplasm and such line are invariably photo-sensitive, and long duration (>180 days at 17^{o}N) in term of maturity, and perennial in nature. The onset of short photo-periods required to flower for these cultivars and landraces and fresh pods are produces in about 40-50 days, the pods setting is extended up to 60 days in some varieties. A major constraint from the processing and marketing points of view is short and limited periods of fresh green pods. Besides these attributes vegetable type pigeonpea should be good in appearance, sweet in taste and have desirable organoleptics properties to fetch a good price in the market beside other attributes. Therefore, the objective in a vegetable-type pigeonpea breeding programme, besides yield, revolves around such traits.

For collection of pigeonpea germplasm, characterization, maintainance and distribution for further improvement ICRISAT has a global responsibility. A total of 13 germplasm and 548 accessions collected from over 70 countries have been assembled for use in future breeding programme. Due to several biotic and abiotic stresses, pigeonpea productivity in comparison to cereals is very low and stagnant. Traditional long duration types have been continually replaced by short and medium duration varieties over time. These varieties are low yielding although improved as compared to long duration types. Genetic improvement of pigeonpea has been emphasized for more than five decades by researchers and has developed number of cultivars. However, the improved cultivars have failed to enhance productivity of the crop, because progress made in the genetic improvement of yield has been limited. Therefore, to enhance the yield of pigeonpea for ensuring food and nutritional security use of hybrid technology as an alternative approach is necessary.

Gene action and its interaction for yield and yield components are governed by gene having small effects with large of number of gene and greatly influenced by environment. Selection of gene effect is not possible for the small individual. For predicting the effectiveness of selection in a population information on the nature of gene action could be useful. Good knowledge on type of gene effect, and its magnitude and composition of genetic variance is essential. Estimation of gene effects involved in the inheritance of yield contributing quantitative characters is helpful in planning breeding programme.

Breeding of pigeonpea is more challenging as compared to other food legumes; this may be attributed to various crop specific traits and high sensitivity to changes in environment. It is essential to identify the parents as well as crosses which can be exploited to bring about further genetic improvement in yield and systematic breeding programme. To decide appropriate breeding procedures that could be used for crop improvement, knowledge on the types of gene action of quantitatively inherited traits is important. Genetic mechanism governing yield and its components is important since breeding for improved varieties is a continuous process and requires thorough knowledge. It is mandatory for the breeders to isolate desirable genotypes that will contribute favourable genes or combination of genes for yield and other agronomic traits for development of superior hybrids. Therefore to understand the nature of gene action, knowledge of genetic variances, levels of dominance, and the importance of genetic effects is necessary.

Combining ability analysis is a powerful tool to discriminate good as well as poor combiners and selection of an appropriate parental material. It also gives information on the nature of gene action involved in the inheritance of various traits. Since it helps in developing improved hybrids and high

yielding varieties and also aids to identify the best combiner in the breeding procedure. Combining ability as the concept of a measure of gene action was proposed by Sprague and Tatum (1942). The line x tester analysis technique has been extensively used as compared to other methods because, it provides a systematic approach to assess parents and crosses combining ability for different quantitative characters as well as heterosis to study the extend of yield and yield contributing characters. In addition, it gives overall genetic picture of the materials under investigation in a single generation.

The concept of generation mean analysis was developed by Hayman (1958) and Hayman and Jinks (1958) for the estimation of genetic components. The knowledge of generation mean analysis is helpful in understanding inter and intra allelic gene effect controlling various economic traits. Generation mean analysis is one of the genetic models which were developed for the estimation of different genetic effects. Generation mean analysis greatest merit lay in its ability to estimate epistatic gene effects such as dominance × dominance, additive × additive, and additive × dominance effects. Besides gene effects, Generation mean analysis is important for breeders to know how much of the variation present in a crop is genetic and to what extent this variation is heritable, since efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and environment.

Hence the present investigation was conducted to study the following aspects.

1. To study the combining ability effects and variances for different metric traits.
2. To study the pattern of inheritance and gene effects for different metric traits in number of pigeonpea crosses.

CHAPTER II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Combining ability may be defined as the relative ability of a genotype to transmit superiority to its crosses. The term general combining ability (gca) is defined as the average performance of a line in a series of crosses and a specific combining ability (sca) of a cross is the performance of a cross combination to do relative better or worse than would be expected on the basis of average performance of the parents involved. The concept of general and specific combining ability was first given by Sprague and Tatum (1942). They suggested that general combining ability is expected to be the result of genes, which are largely additive in their effects and specific combining ability largely depends on genes with dominance or epistatic effects. On the other hand, Griffing (1956) suggested that general combining ability is due to both additive as well as additive x additive gene interactions.

The available literature in combining ability pertaining to 10 quantitative characters of present studies in pigeon pea has been reviewed here.

Plant height

Sindhu *et al.* (2000) and Kumar *et al*. (2009) reported parents with good gca did not necessarily produce superior hybrids with good sca. Srinivas *et al.* (2002), Pandey (2004), Phad *et al.* (2007), Sarode *et al.* (2009) and Punam and Rupa (2011) reported inheritance pattern for some polygenic traits and reported that estimates of gca variance were higher than their corresponding sca variance indicating predominant of additive gene effects for expression of plant height. Jayamala and Rathnaswamy (2000), Khorgade *et al*. (2000), Pandey and Singh (2002), Banu *et al.* (2006), Kumar *et al*. (2003) and Suresh (2014) reported significant differences among the parents for all characters and observed that non additive gene effects were predominant for plant height in

mungbean, whereas Sunilkumar *et al.* (2003), Banu *et al.* (2006) and Yadav *et al.* (2008) reported variance due to gca and sca and revealed predominance of non-additive gene action for plant height and concluded that line and tester were found to be good combiners for plant height and cross combinations exhibited significant sca effects. Kandalkar (2006) and Bhavani and Bhlla (2010) reported the important of both additive and non-additive genetic action in governing the expression of plant height and reveled that expression in plant height is under controlled of both additive and non additive gene action. Baskaran and muthiah (2009), Arbad *et al.* (2013), Saroj *et al*. (2014) and Patil *et al*. (2015) observed significant differences for genotype, general combining ability and specific combining ability for plant height under assessment. However, general combining ability variances were lower than the specific combining ability variances for all the evaluated parameters including plant height and reported highest general combining ability effects in the desired directions for plant height. Sekhar *et al*. (2004) and Jahagirdar (2003) revealed that both additive and non-additive variances were important for plant height and other traits studied although additive variance was preponderant for plant height. Estimates of gca effects revealed significant for all characters including plant height indicating that gca of parents and sca of the hybrids were influenced by environment and concluded that both additive and non-additive gene effects were equally important for plant height. Raju and muthiah (2007), Kumar *et al.* (2009) and Patel and Acharya (2011) reported that mean squares due to general and specific combining ability effects were significant for plant height, revealing importance of both additive and non-additive gene actions with preponderance of non-additive type of gene effects in the expression of these traits. Mhasal (2015), Sudhir *et al*. (2017) and Shrivarsha *et al.* (2017) reported higher magnitude of sca variance over gca variance for this trait which indicated preponderance of non-additive gene action.

Days to 50% flowering

Pandey (2004) and Sarode *et al.* (2009) reported the ratio of genetic components indicating the additive genetic effects for days to 50% flowering and concluded that variances for general and specific combining abilities revealed the predominance of additive gene action for days to flowering. The lines were good combiners for days to 50% flowering, while among the testers one tester was a good combiner for days to 50% flowering. Yadav *et al.* (2008) and Marappa (2008) observed both general and specific combining ability effects were significant for days to 50% flowering and revealed non-additive gene action for the expression of days to 50% flowering with good general combiners for days to 50% flowering and observed three crosses have good combinations for days to 50% flowering. Similarly significant non additive gene action for days to 50% flowering was also reported by Jayamala and Rathnaswamy (2000), Khorgade *et al*. (2000), Pandey and Singh (2002), Sunil kumar *et al.* (2003), Banu *et al.* (2006), Raju *et al*. (2007), Yadav *et al.* (2008), Kumar *et al*. (2009) and Patel *et al*. (2011), whereas Pandey *et al.* (2014) and Yamanura *et al.* (2014) reported parents and crosses with positive gca and sca effects, respectively for days to 50% flowering. Arbad *et al*. (2013) and Mhasal (2015) conducted studies on combining ability effects and observed higher magnitude of sca variance over gca variance for all the traits which indicated preponderance of non-additive gene action. Sudhir *et al*. (2017) and Shrivarsha *et al*. (2017) reported higher magnitude of sca variance over gca variance for this trait, which indicated preponderance of non-additive gene action. Kandalkar *et al.* (2005) observed highly significant gca and sca variances for this trait indicating the importance of both additive and non-additive gene action for days to 50% flowering. Sunilkumar *et al.* (2003), Banu *et al.* (2006) and Yadav *et al.* (2008) reported variance due to gca and sca and revealed predominance of non-additive gene action for days to 50% flowering and

concluded that line and tester were found to be good combiners for days to 50% flowering and cross combinations exhibited significant sca effects.

Number of primary branches

Kandalkar (2006) and Sarode *et al.* (2009) reported that line and tester crosses differ in their general combining ability for almost all the traits and additive gene effects were predominant for the inheritance of number of primary branches and revealed that additive gene effects were predominant for the inheritance and combiner for number of primary branches. Sudhir *et al*. (2017) and Shrivarsha *et al*. (2017) reported non-additive gene action for the expression of number of primary branches. Singh *et al*. (2001), Pandey *et al*. (2002) and Banu *et al.* (2006) reported that non additive gene effects were predominant for inheritance of number of primary branches. Shoba and Balan (2010), Bhavani and Bhalla (2010), Patil *et al*. (2015) and Mhasal (2015) also reported significant role of non-additive gene action for number of primary branches per plant. Yadav *et al.* (2008) conducted experiments on crosses of pigeon pea and reported that both additive and non-additive genetic components of variance were important in governing the expression of number of primary branches. Yamanura *et al.* (2014), Saroj *et al*. (2014) and Patil *et al*. (2015) estimated the nature of gene action for yield and yield contributing characters. They observed predominance of non-additive gene action for almost all the characters including number of primary branches which was under the influence of additive gene action, the estimates of specific combining ability revealed that all crosses exhibited significant positive *sca* effects for number of primary branches in desired direction. Meshram *et al*. (2013) observed that lines were good combiners for number of branches and few component traits, while among the testers one tester was a good combiner for number of primary branches and the majority of yield component characters studied. The hybrids exhibited desirable sca effects for number of branches and

few component traits. Khorgade *et al*. (2000) reported that additive gene effects were predominant for the inheritance of number of branches and revealed desirable and positive *sca* effects for number of primary branches.

Number of secondary branches

Yadav *et al.* (2008) carried out experiment on crosses of pigeon pea and reported highly significant gca and sca variances for number of secondary branches under study indicating the importance of both additive and non-additive gene action for the expression of this trait. They also concluded that most of the crosses with significant sca effects involved one good and one poor general combiner in respect to number of secondary branches. Khorgade *et al*. (2000) and Parmar (2012) reported that additive gene effects were predominant for the inheritance of number of secondary branches and revealed high general combining ability effects for number of secondary branches and concluded that desirable and positive *sca* effects for number of secondary branches were good specific combiners. Meshram *et al*. (2013) reported that line were good general combiner and revealed desirable sca effects for number of secondary branches and few component traits. Mhasal (2015), Sudhir *et al*. (2017) and Shrivarsha *et al*. (2017) reported significant role of non-additive gene action for number of secondary branches and revealed the predominance of non-additive gene action for number of secondary branches and most of the characters in the study. Whereas Pandey (2004), Phad *et al.* (2007) and Sarode *et al.* (2009) reported significant differences among the parents for number of secondary branches and predominance of non additive gene action in expression of this traits. Meshram *et al*. (2013) and Yamanura *et al*. (2014) reported the nature of gene action for yield and yield contributing characters. They observed predominance of non-additive gene action for almost all the characters including number of secondary branches which was under the influence of additive gene action, the estimates of specific combining ability revealed that all crosses exhibited

significant positive *sca* effects for number of secondary branches in desired direction. Arbad *et al*. (2013) reported sca genetic variances were greater than gca for number of secondary branches. Bhavani *et al*. (2010) reported highly significant gca and sca variances for number of secondary branches indicating the importance of both additive and non-additive gene action.

Days to pods initiation

Jayamala and Rathnaswamy (2000), Ajay Kumar *et al.* (2001) and Sarode, *et al.* (2009) reported that parent and crosses have high and good general combining ability effects for days to pods initiation. Pandey and Singh (2002), Sekhar *et al.* (2004), Banu *et al.* (2006), Patil *et al*. (2015) and Mhasal (2015) reported that non additive gene action was more prevalent for day to pods initiation, as the variances due to general combining ability were lower than the specific combining ability variances for days to pods initiation. Shoba and Balan (2010), Saroj *et al.* (2014) and Shrivarsha *et al*. (2017) also reported predominant role of non additive gene action for days to pods initiation, Sunilkumar *et al.* (2003), Lohithaswa *et al.* (2003) and Sujatha and Kajjidoni (2013) reported predominant role of additive gene action for days to pods initiation. Yadav *et al.* (2008) reported that mean squares due to general and specific combining ability effects were significant for days to pods initiation, exhibiting importance of both additive and non-additive gene actions in the inheritance of these traits. Raju and Muthiah (2007) conducted studies in pigeonpea to understand nature of gene action in pigeon pea and reported significant role of non-additive gene action for days to pods initiation, and predominant role of additive gene action was confirmed through the study. One line was found to be a good general combiner for important traits like days to pods initiation. Pandey *et al.* (2014) reported that estimates of sca variance were higher than their corresponding gca variance for days to pods initiation 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. Bhavani *et al*. (2010) and Yamanura *et al.* (2014) reported highly significant gca and sca variances for days to pods initiation indicating the importance of both additive and non-additive gene action, and most of the crosses with significant sca effects involved one good and one poor general combiner. Meshram (2013) reported significant positive *sca* effects for days to pods initiation and the cross combination exhibited significant *sca* effects coupled with higher standard heterosis for days to pods initiation. Saroj *et al*. (2014) reported significant differences among the parents for all characters and for hybrids except for days to pods initiation and concluded that non additive gene effects were predominant for days to pods initiation.

Days to 80% pods maturity

Pandey *et al*. (2002), Sunilkumar *et al.* (2003), Banu *et al.* (2006), Yadav *et al.* (2008) and Bhavani and Bhalla (2010) studied general combining ability and specific combining abilities in pigeon pea hybrids along with their parents with special emphasis on maturity and reported the pre-dominance of non additive gene action for days to 80% pods maturity. Bhavani *et al*. (2010) reported highly significant gca and sca variances for days to 80% pods maturity and revealed the importance of both additive and non-additive gene action. Baskaran *et al*. (2009), Saroj *et al*. (2014) and Patil *et al*. (2015) reported significant differences among the parents for days to pods initiation and non additive gene effects were predominant for days to 80% pods maturity. Praveen *et al*. (2014) and Yamanura *et al*. (2014) reported that estimates of sca variance were higher than their corresponding gca variance for days to 80% pods maturity and revealed the important of non-additive gene action. Phad *et al.* (2007) reported that variances due to additive gene effects

were higher than variances due to non additive gene effects for days to 80% pods maturity indicating the importance of additive gene action governing for these traits. Pandey (2004) also reported the predominance of additive gene action for days to 80% pods maturity as compared to other character. Kandalkar (2005), Yadav *et al.* (2008) and Bhavani *et al*. (2010) reported that both additive and non-additive genetic components of variance governed the expression in days to 80% pods maturity and concluded that this trait was predominantly under the control of additive genetic components with significant role of non-additive genetic component. Patil *et al.* (2015), Mhasal (2015), Sudhir *et al*. (2017), Shrivarsha *et al.* (2017) and Meshram (2013) reported significant role of non-additive gene action for days to 80% pods maturity.

Number of pods per plant

Bhavani and Bhalla (2010), Sudhir *et al*. (2017) and Shivarsha *et al*. (2017) reported that variance due to sca was highly significant for number of pods per plant and magnitude of gca variances were relatively lower than the sca variances. Similarly, Sekhar *et al.* (2004), Banu *et al.* (2006) and Raju and Muthiah (2007) reported the mean square due to sca were highly significant for number of pods per plant. Pandey *et al*. (2002), Jahagirdar (2003), Sunil kumar *et al.* (2003), Raju and Muthiah (2007), Phad *et al.* (2007), Shoba and Balan (2010) and Praveen *et al*. (2014) reported that estimates of sca variance were higher than their corresponding gca variance for number of pods per plant and the values of average degree of dominance were more than unity and predictability ratio was less than unity for number of pods and other character signifying non-additive gene action which resulted from dominance, over dominance, epistatic and various other interaction effects. Yamanura *et al*. (2014), Saroj *et al*. (2014) and Patil *et al*. (2015) observed significant differences for genotype, general combining ability and specific combining

ability for all the characters under assessment. However, general combining ability variances were lower than the specific combining ability variances for all the evaluated parameters and reported highest general combining ability effects in the desired directions for number pods per plant. Kandalkar (2005) reported that general and specific combining ability effects were significant for number of pods per plant exhibiting importance of both additive and non-additive gene actions in the inheritance of these traits and revealed that both additive and non-additive variances were important for number of pods per plant and other traits studied although additive variance was preponderant for number of pods per plant. Punam and Roopa (2011) also reported importance of both additive and non-additive gene actions with preponderance of non-additive type of gene effects in the expression of this trait.

Pod length

Meshram *et al*. (2013) and Yamanura *et al*. (2014) observed predominance of non-additive gene action for almost all the characters including pods length which was under the influence of additive gene action. The estimates of specific combining ability revealed that all crosses exhibited significant positive *sca* effects for pods length in desired direction. Kandalkar (2006) and Phad *et al.* (2007) reported variance due to gca and sca and revealed pre-dominance of additive gene action for pod length. Similarly Sudhir *et al*. (2017) and Shrivarsha *et al*. (2017) also reported that none of parent was good general combiner for pods length and other traits however; each was superior combiner for pods length. In most of the characters sca effects were high in magnitude indicating the presence of non additive genetic variation for inheritance of pods length. Whereas Khorgade *et al*. (2000), Singh and Srivastava (2001), Pandey and Singh (2002), Sunil kumar *et al.* (2003) and Shoba and Balan (2010) observed non-additive components of genetic variation for different characters including pods length. Banu *et al.* (2006),

Saroj *et al*. (2014) and Patil *et al*. (2015) reported non-additive gene effects for pods length. Meshram (2013) reported that magnitude of gca variances for pods length and for other characters was greater than that of gca variances, which suggest considerable non additive genetic effects. Bhavani *et al*. (2010) reported both additive and non-additive genetic variances components were important for controlling inheritance of these traits. Yadav *et al.* (2008) reported that gca and sca variances were highly significant for pods length indicating the presence of both additive and non-additive type of gene action. However predominance of non-additive gene action was observed for these traits. Meshram *et al*. (2013) observed that hybrids exhibited desirable sca effects for pods length and few component traits. Sujatha and Kajjidoni (2013**)** reported that additive gene effects were predominant for the inheritance of pods length and hybrids also exhibited high general combining ability effects for pods length and concluded that desirable and positive *sca* effects for pods length were good specific combiners for pods length. Lohithaswa *et al.* (2003), Raju and Muthiah (2007) and Sujatha and Kajjidoni (2013**)** also recorded good general combiner for pods length and other traits. In most of the characters gca effects were high in magnitude indicating the presence of additive genetic variation for inheritance in pods length.

100-seed weight

Raju and Muthiah (2007) and Sujatha and Kajjidoni (2013) reported predominance of additive gene action in expression of 100-seed weight. Similarly Kumar *et al.* (2003) and Lohithaswa *et al*. (2003) also recorded good general combiner for 100-seed weight and other traits. In most of the characters gca effects were high in magnitude indicating the presence of additive genetic variation for inheritance in 100-seed weight. Sathya and Jayamani (2011), Sudhir *et al*. (2017) and Shrivarsha *et al.* (2017) reported predominance of non-additive gene action for all traits and concluded 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 100-seed weight. Similarly Kumar *et al.* (2003), Banu *et al.* (2006), Sarode, *et al.* (2009), Shoba and Balan (2010) and Saroj *et al.* (2014) reported the estimates of variances of gca and sca for 100-seed weight and concluded that gene action was predominantly of non additive type for 100-seed weight. However Punam and Roopa (2011) reported that general and specific combining ability effects were significant for 100-seed weight exhibiting importance of both additive and non-additive gene actions in the inheritance of these traits. Meshram *et al*. (2013) and Yamanura *et al*. (2014) observed predominance of non-additive gene action for 100-seed weight which was under the influence of additive and non additive gene action, the estimates of specific combining ability revealed that all crosses exhibited significant positive *sca* effects for 100-seed weight in desired direction**.** Meshram *et al*. (2013) revealed that additive gene effects were predominant for the inheritance of 100-seed weight and hybrids exhibited high general combining ability effects for 100-seed weight and concluded that desirable and positive *sca* effects for 100-seed weight. Acharya *et al.* (2009) reported that mean squares due to general and specific combining ability effects were significant for100-seed weight, revealing importance of both additive and non-additive gene actions for this trait.

Seed yield per plant

Kandalkar (2005) and Punam and Roopa (2011) reported that gca and sca variances were highly significant for all the traits indicating the presence of both additive and non-additive type of gene action for inheritance of seed yield in pigeon pea. Raju and Muthiah (2007) and Sujatha and Kajjidoni (2013) also reported that, in most of the characters gca effects were high in magnitude indicating the presence of additive genetic variation for inheritance in seed

yield per plant. Srivastava *et al*. (2001) reported that out of six lines one line showed good general combiner yield per plant and one tester was found to be a good general combiner for yield per plant. Yamanura *et al.* (2014), Saroj *et al*. (2014), Patil *et al*. (2015) and Mhasal (2015) reported significant role of non-additive gene action for yield per plant and yield attribute and predominant role of additive gene action was confirmed through the study. Pandey *et al*. (2002), Jahagirdar (2003), Sunilkumar *et al.* (2003), Sudhir *et al*. (2017) and Shivarsha *et al*. (2017) reported that estimates of sca variance were higher than their corresponding gca variance for seed yield per plant indicating important of non-additive gene action for seed yield per plant. Pandey *et al*. (2014) reported that estimates of sca variance were higher than their corresponding gca variance for yield per plant signifying non-additive gene action for yield per plant. Punam and Roopa (2011) reported highly significant gca and sca variances for yield per plant and revealed importance of both additive and non-additive gene action and most of the crosses with significant sca effects. Similarly Sekhar *et al.* (2004), Banu *et al.* (2006), Baskaran and Muthiah *et al.* (2007), Phad *et al.* (2007), Kumar *et al*. (2009), Sarode, *et al.* (2009), Shoba and Balan (2010), Bhavani and bhalla (2010) and Mhasal (2015) also reported non-additive gene action was more prevalent for seed yield per plant as the variances due to specific combining ability were higher than the general combining ability variances for seed yield per plant. Baskaran and Muthiah (2009) reported significant differences among the parents for all characters and for hybrids except for yield per plant where non additive gene effects were predominant for all characters.

Gene effects

The knowledge of nature of gene effects involve in the expression of quantitative traits of economic importance will be helpful in formulating a systematic breeding methodology for the genetic enhancement for trait(s). The

information regarding the genetic control of quantitative traits was first established by Johannsen (1909). Fisher (1918) was the first to partition the genetic variance into three components *i.e.* additive, dominance and epistatic variance. Hayman and Mather (1955) further divided the espistatic variance into three components (1) additive x additive, (2) additive x dominance and (3) dominance x dominance interactions. The studies on estimation of gene effects in pigeon pea are reviewed as under

Plant height

Raut *et al.* (2000), Hooda *et al.* (2003), Vinay *et al.* (2002), Dixit *et al*. (2006), Sarode *et al*. (2009), Kumar *et al*. (2009), Payasi *et al.* (2010), Ravinder *et al.* (2012) and Singh (2016) reported that dominance gene effects made a significant contribution in the inheritance of plant height but magnitude of dominance effects was slightly higher than that of the additive gene effects and dominant gene effects (h) contributed significantly for most of the characters including plant height and concluded that dominance x dominance (l) was more important than additive x additive (i) for these traits. Sharma *et al*. (2012), Khodambashi *et al.* (2012) and Ashutosh *et al.* (2017) reported that among the epistatic components, dominance x dominance gene effects were higher for plant height. Kandalkar *et al.* (2006), Sreelakshmi *et al*. (2013), Sharma *et al.* (2001), Singh *et al*. (2009) and Singh *et al*. (2010) reported both dominance x dominance (l) and additive x additive (i) interaction for plant height and Parmar *et al*. (2015) also studied the nature and magnitude of gene effects for yield and yield components in pigeon pea crosses and reported the presence of additive and dominance gene effects and epistatic interaction in almost all crosses indicating the importance of both additive and non additive gene action in the expression of plant height. Raut (2002), Singh *et al.* (2003), Gohil *et al*. (2006), Yadav (2007), Rahangdale *et al*. (2012) and Ajay *et al.* (2012) reported that plant height showed additive gene effect and duplicate

epistasis were significantly important in the inheritance of plant height. Singh *et al*. (2005) and Preeti *et al*. (2008) also observed predominance of additive gene effects and concluded that additive gene effects (d) contributed significantly for different traits like plant height. Whereas Oommen *et al*. (2000) and Kandalkar *et al.* (2006) observed that plant height was under the control of both additive (d) and dominance (h) gene effects. Singh (2016) reported that dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for these traits. This could be exploited by selecting individuals based on their performance in recurrent selection. Maloo *et al*. (2005) reported the presence of additive gene effects (i) in plant height, indicating importance of additive gene effects (i) in the expression of plant height.

Days to 50% flowering

Vinay *et al.* (2002), Dixit *et al*. (2006), Kumar *et al.* (2009), Sarode *et al*. (2009), Ravinder *et al.* (2012) and Singh (2016) reported the presence of additive, dominance and epistatic gene effects. Among nonallelic interactions dominance x dominance (l) was of greater magnitude than main gene effects for days to 50% flowering. Singh *et al.* (2003), Singh *et al*. (2005) and Ajay *et al.* (2012) reported that additive gene effects (i) contributed significantly for days to 50% flowering. Similarly Tyagi and Srivastava (2001), Raut (2002), Gohil *et al*. (2006), Yadav (2007) and Preeti *et al*. (2008) also reported that additive gene action contributed significantly in the inhiritance of day to 50% flowering and presence of both non-allelic interactions *i.e* duplicate and complementary. Hooda *et al.* (2000), Hooda *et al.* (2001), Rahangdale *et al*. (2012) and Ajay *et al.* (2012) reported the importance of additive gene action for days to 50% flowering. Sharma *et al*. (2001), Singh *et al*. (2009)**,** Singh *et al*. (2010), Sreelakshmi *et al.* (2013) and Parmar *et al*. (2015) reported presence of duplicate epistasis and significant additive, dominance and non-

allelic interactions for days to 50% flowering. Duplicate type of epistasis for days to 50% flowering was also reported by Singh (2016) and Ashutosh *et al*. (2017), whereas complementary type of epistasis for days to flowering was reported by Ajay *et al.* (2012) and Atungwu *et al*. (2005). Sandeep *et al*. (2005) also reported presence of additive, dominance and epistatic gene effects and concluded that dominance x dominance (l) was of greater magnitude than main gene effects for days to 50% flowering. Oommen *et al*. (2000) and Kandalkar *et al.* (2006) revealed significant contribution of both additive and dominance gene effects for days to 50% flowering. Atungwu *et al*. (2005) and Sharma and Sharma (2012) and Khodambashi *et al.* (2012) concluded that both epistatic gene effects play an important role for the inheritance of days to 50% flowering and other traits. Khodambashi *et al.* (2012) reported days to 50% flowering with significant and higher magnitude of dominance, and concluded that epistatic effect of additive x additive and dominance x dominance components for days to 50% flowering were significant in one or more crosses which indicated that epistasis played an important role in determining the inheritance of these characters. Hooda *et al.* (2000) and Hooda *et al.* (2001) reported that epistatic/digenic interactions were observed in all the crosses for days to 50% flowering and revealed that additive gene effects were significant for days to 50% flowering.

Number of primary branches

Oommen *et al*. (2000), Kandalkar *et al.* (2006) and Singh *et al*. (2010) observed additive (d) and dominance (h) components of genetic variation were significant for number of primary branches**.** Sharma *et al*. (2001), Singh *et al.* (2009) and Sreelakshmi *et al*. (2013) reported the presence of additive, dominance gene effects and epistatic interaction in almost all crosses indicating the importance of both additive and non additive gene action in the expression of these characters. However Hooda *et al.* (2000), Hooda *et al.* (2001), Singh

et al. (2003), Singh and Bajpai (2005) and Ajay *et al.* (2012) reported that additive × additive (i) contributed significantly in the inheritance of number of primary branches. Singh and Singh (2016) and Ashutosh *et al*. (2017) reported duplicate type of non-allelic interaction for number of primary branches. Tyagi and Srivastava (2001) and Preeti *et al*. (2008) reported the importance of additive, dominance as well as epistatic effects in the genetic control for number of primary branches and revealed that among epistatic gene effects, additive × additive (i) type epistasis was significant for number of primary branches. Sarode *et al*. (2009), Singh (2016) and Ashutosh *et al*. (2017) observed dominance x dominance inter-allelic interactions (l) was more important than additive x additive (i) for number of primary branches. Sreelakshmi *et al.* (2013) and Parmar *et al*. (2015) conducted experiment on crosses of pigeonpea and revealed significant contribution of both additive and dominance gene effects in number of primary branches**,** whereas Sandeep *et al*. (2005) and Khodambashi *et al.* (2012) reported that additive, dominance and at least one of the epistatic effect were involved in the inheritance of number of primary branches However, significant dominance (h) and dominance x dominance (l) interactions were observed for number of primary branches and concluded that dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for number of primary branches per plant with predominant of duplicate type of epistasis. Sharma *et al*. (2001), Singh *et al.* (2009)**,** Singh *et al*. (2010) and Parmar *et al*. (2015) observed that number of primary branches was under the control of both additive (d) and dominance (h) gene effects.

Number of secondary branches

Raut *et al.* (2000), Sarode *et al*. (2009), Payasi *et al.* (2010), Ravinder *et al.* (2012), Kumar *et al.* (2009), Singh (2016) and Ashutosh *et al*. (2017) reported higher magnitude of dominance x dominance (l) gene effects for

number of secondary branches. The estimates of (h) and (l) components were significant with opposite signs in all the crosses, with higher magnitude of dominance x dominance (l) effects with duplicate type of epistasis in the inheritance of number of secondary branches. Singh *et al.* (2003), Singh *et al*. (2005), Singh *et al*. (2005) and Ajay *et al.* (2012) reported the presence of additive and dominance gene effects and epistatic interaction in almost all crosses indicating the importance of both additive and non additive gene action in the expression of these characters. However, the fixable gene effect additive × additive (i) contributed significantly in the inheritance of number of secondary branches. Tyagi and Srivastava (2001), Preeti *et al*. (2008), Singh *et al*. (2009) and Singh *et al*. (2010) reported duplicate type of non-allelic interaction for number of secondary branches, and reported importance of additive, dominance as well as epistatic effects in the genetic control for number of secondary branches and revealed that among epistatic gene effects, additive × additive (i) type epistasis was significant for number of secondary branches. Dixit *et al*. (2006) and Atungwu *et al*. (2005) observed that dominance x dominance inter-allelic interactions (l) was more important than additive x additive (i) for number of secondary branches. Parmar *et al*. (2015) reported significant contribution of both additive and dominance gene effects for number of secondary branches; whereas Oommen *et al*. (1999) reported that additive, dominance and at least one of the epistatic effects were involved in the inheritance of number of secondary branches. Hooda *et al.* (2000) and Hooda *et al.* (2001) reported that epistatic/digenic interactions were observed in all the crosses including number of secondary branches and revealed that additive gene effects were significant for number of secondary branches. Khodambashi *et al.* (2012) reported that dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for number of secondary branches per plant with predominant of duplicate type of epistasis in lentil.

Days to pod initiation

Raut *et al*. (2000), Singh *et al.* (2003), Singh and Bajpai (2005), and Ajay *et al.* (2012) reported that additive gene effects were more important than dominant gene effects in all the crosses for days to pods initiation and revealed that most of the characters appeared to be complex in the expression of gene effects in different crosses and additive x additive were important in most crosses for majority of the traits including days to pods initiation. Similarly Dixit *et al*. (2006) and Atungwu *et al*. (2005) also reported that dominance gene effects were important in most crosses for days to pods initiation and revealed predominant positive and significant dominance (h) effects with higher magnitude in this trait. This was also reported by Kumar *et al*. (2009). However, Kandalkar *et al.* (2006), Singh *et al*. (2009)**,** Singh *et al*. (2010), Sreelakshmi *et al*. (2013) and Parmar *et al*. (2015) reported the importance of both additive and non-additive gene actions in the expression of day to pods initiation and concluded that there is contribution of components of genetic variance *i.e*. additive (d), dominance (h) and epistatic (i, j and l) towards the mean for days to pods initiation. On the other hand, Hooda *et al.* (2003), Kumar *et al*. (2009), Payasi *et al.* (2010), Ravinder *et al.* (2012), Singh (2016) and Ashutosh *et al*. (2017) reported that additive, dominance and at least one of the epistatic effect were involved in the inheritance of days to pods initiation and concluded that dominance x dominance inter-allelic interaction (l) was more important than additive x additive type (i) for this traits. Also according to Sarode *et al*. (2009), Ravinder *et al.* (2012) and Khodambashi *et al.* (2012) dominance gene effect (h) was more predominant for days to pods initiation and dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for days to pods initiation. However, to exploit additive as well as non- additive gene effects, reciprocal recurrent selection procedure may be adopted .Raut *et al.* (2000), Payasi *et al.* (2010), Singh (2016) and Ashutosh *et al*. (2017) revealed the importance of domimance x

dominance effects for this trait with duplicate type of epistasis. Hooda *et al.* (2000) and Hooda *et al.* (2001) reported that epistatic/digenic interactions were observed in all the crosses revealed that additive gene effects were significant for days to pods initiation.

Days to 80% pod maturity

Oommen *et al*. (2000), Sharma *et al*. (2001), Kandalkar *et al.* (2006), Sreelakshmi *et al.* (2013), and Parmar *et al*. (2015) reported the importance of both additive and non-additive gene actions in the expression of day to 80% pods maturity and concluded that there is contribution of components of genetic variance *i.e*. additive (d), dominance (h) and epistatic (i, j and l) towards the mean for days to 80% pods maturity, on the other hand according to Vinay *et al.* (2002), Dixit *et al*. (2006) and Atungwu *et al*. (2005) Sharma and Sharma (2012), Khodambashi *et al.* (2012), Kumar *et al*. (2009), Singh (2016) and Ashutosh *et al*. (2017) dominance gene effect (h) was more predominant for days to 80% pods maturity and dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for this trait and concluded that dominant gene effect (h) contributed significantly for this character in the crosses and selection in segregating generations of these crosses will be effective for the development of this trait. However, to exploit additive as well as non- additive gene effects, reciprocal recurrent selection procedure may be adopted. Raut *et al.* (2000), Hooda *et al.* (2003), Sarode *et al*. (2009), Payasi *et al.* (2010) and Ravinder *et al.* (2012) reported that dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for this trait. Kandalkar *et al.* (2006) and Parmar *et al* . (2015) revealed the importance of both additive and non-additive type of gene actions for this trait with duplicate type of epistasis. Hooda *et al.* (2000), Hooda *et al.* (2001), Raut (2002), Singh *et al.* (2003), Singh *et al*. (2005) and Ajay *et al.* (2012) reported that additive gene effect was more

important than dominant gene effect in all the crosses for days to 80% pods maturity and revealed that most of the characters appeared to be complex in the expression of gene effects in different crosses and additive x additive effects were important in most crosses for days to 80% pods maturity. Similarly, Tyagi and Srivastava (2001), Gohil *et al*. (2006), Preeti *et al*. (2008), Yadav (2007) and Rahangdale *et al*. (2012) also reported that additive gene effects were important in most crosses for days to 80% pods maturity with predominant and significant dominance (h) effects with higher magnitude of dominance x dominance (l) effects. This was also reported by Vinay *et al.* (2002), Dixit *et al*. (2006), Atungwu *et al*. (2005), Dashiell *et al*. (2002), Sandeep *et al*. (2005), Kumar *et al.* (2009), Sharma *et al*. (2012) and Khodambashi *et al.* (2012).

Number of pods per plant

Sharma *et al*. (2001), Singh *et al.* (2003), Singh *et al*. (2005) and Ajay *et al.* (2012) reported that both additive and non-additive gene effects contributed for inheritance of this trait with predominance of additive x additive (i) effects and concluded that significant effects were observed in opposite direction indicating the duplicate nature of epistasis in the genetic control of number of pods per plant. Similar results were reported by Tyagi and Srivastava (2001), Raut (2002), Gohil *et al*. (2006),Yadav (2007), Preeti *et al*. (2008) and Rahangdale *et al.* (2012). The significant of additive × additive (i) effects for number of pods per plant was also reported by Ajay *et al.* (2012). Also duplicate nature of epistasis in the genetic control for inheritance in number per pods per plant was reported by Kumar *et al*. (2009), Payasi *et al.* (2010), Ravinder *et al.* (2012), Singh (2016) and Ashutosh *et al*. (2017), they also reported highly significant and positive dominance x dominance (l) gene effects for number of pods per plant. Hooda *et al.* (2003), Singh (2005) and Sarode *et al*. (2009) also reported presence of additive, dominance and

epistatic gene effects and concluded that dominance x dominance (l) was of greater magnitude than main gene effects for number of pods per plant indicating the importance of non-additive gene effects. Raut *et al.* (2000), Kumar *et al.* (2009), Sharma *et al*. (2012) and Khodambashi *et al.* (2012) also reported additive gene effect (d) was significant for pod per plant and concluded that dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for number of pods per plant. Gohil *et al*. (2006),Yadav (2007) and Rahangdale *et al*. (2012) reported that additive gene effects were more important than dominant gene effects in all the crosses for number of pods per plant and revealed that most of the characters appeared are to be complex in the expression of gene effects in different crosses. Singh *et al*. (2009), Singh *et al*. (2010) and Sreelakshmi *et al*. (2013) observed that additive (d) and dominance (h) components of genetic variation were significant for number of pods per plant in the crosses with complementary type of non-allelic interaction. Whereas Parmar *et al*. (2015) reported presence of additive, dominance gene effects and epistatic interaction in number of pods per plant.

Pod length

Raut (2002), Gohil *et al*. (2006), Yadav (2007), Kumar *et al*. (2009), Rahangdale *et al*. (2012), Singh (2016) and Ashutosh *et al*. (2017) reported that dominant x dominant (l) gene action was significant for pod length and concluded that dominance × dominance (l) gene effect mainly governed the inheritance of pod length and among non-allelic interactions, dominance x dominance (I) had greater magnitude than main gene effects for pods length indicating the additive gene effects and revealed that additive gene effects (d) also contributed significantly for pods length. Sarode *et al*. (2009),Vinay *et al.* (2002), Dixit *et al*. (2006) and Atungwu *et al*. (2005) observed that dominance epistatic gene effects in almost all the crosses, indicating

importance of dominance gene actions in the expression of pods length and duplicate type of epistasis was prevalent in most of the crosses for pods length. Tyagi and Srivastava (2001), Gohil *et al*. (2006) and Preeti Massey *et al*. (2008) reported that additive × additive (i) type of epistasis was significant in all the crosses for pods length and concluded that additive x additive gene effect (i) inter-allelic interactions was more important for this trait. Oommen *et al*. (2000) and Kandalkar *et al.* (2006) reported the presence of additive, dominance gene effects and epistatic interaction in pod length in all the crosses indicating the importance of both additive and non additive gene action in the expression of this character. Similar result was also reported by Parmar *et al.* (2015) with duplicate type of epistasis in most of the crosses for pod length. Singh *et al.* (2003), Singh *et al*. (2005) and Ajay *et al.* (2012) reported the importance of additive and dominance gene effects in the expression of this character. However, the fixable gene effect additive × additive (i) contributed significantly in the inheritance of pod length.

100-Seed weight

Singh and Singh (2016) reported duplicate gene action for 100-seed weight. Kandalkar (2006), Singh and Bajpai (2005), Kumar *et al*. (2009) also reported duplicate type of epistasis for inheritance in 100-seed weight. Kandalkar (2006), Singh *et al*. (2009), Singh *et al*. (2010), Sreelakshmi and Shivani (2013) and Parmar *et al.* (2015) also studied the nature and magnitude of gene effects for yield and yield components in pigeon pea crosses and reported the presence of additive, dominance gene effects and epistatic interaction in 100- seed weight indicating the importance of both additive and dominance gene sffects and interaction in the expression of this character. Sharma and Sharma (2012), Khodambashi *et al.* (2012), Ravinder *et al.* (2012), Singh (2016) and Ashutosh *et al*. (2017) reported that among the epistatic components, dominance x dominance gene effects were higher for 100-seed

weight. Singh and Bajpai (2005) and Ajay *et al.* (2012) reported that 100-seeds weight showed additive gene effect and duplicate epistasis were significantly important in the inheritance of this traits. Oommen *et al*. (2000) and Kandalkar (2006) reported that dominance x dominance (l) showed ambidirectional dominance but the positive sign of additive x additive reflects the association of alleles in the parental lines. Indicating the importance of dominance x dominance (l) and additive x additive (i) for the trait, Tyagi and Srivastava (2001), Gohil *et al*. (2006), Yadav (2007), Rahangdale and Raut (2002) and Preeti *et al*. (2008) also observed predominance of additive gene effects and concluded that additive gene effects (d) contributed significantly for different traits like 100-seed weight, whereas Khodambashi *et al.* (2012) observed that 100-seed weight was under the control of both additive (d) and dominance (h) gene effects. However, dominance x dominance inter-allelic interactions (l) was more important than additive x additive type (i) for most of the traits studied which could be exploited by selecting individuals based on their performance in recurrent selection. Singh and Bajpai (2005) reported the presence of additive (i) epistatic gene effects in 100-seed weight, indicating importance of additive (i) gene effects in its expression. Dixit *et al*.(2006) and Atungwu *et al*. (2005) reported that dominance gene effects made a significant contribution to the inheritance of 100-seed weight but the magnitude of the dominance effects was slightly higher than that of the additive gene effects and concluded that dominance gene effects (h) contributed significantly for most of the characters and recommended selection in segregating generations of these crosses which will be effective for the development of this trait.

Seed yield per plant

Raut (2002), Singh *et al.* (2003), Singh and Bajpai (2005), Gohil *et al*. (2006), Yadav (2007), Rahangdale *et al*. (2012) and Ajay *et al.* (2012) reported that fixable gene effect *i.e.* Additive × additive (i) contributed

significantly in the inheritance of seed yield per plant. Tyagi and Srivastava (2001) and Preeti *et al*. (2008) also reported that additive gene effects (i) contributed significantly for seed yield per plant. Similarly, Hooda *et al.* (2001) and Hooda *et al.* (2000) also reported that additive gene action contributed significantly in the inhiritance of seed yield per plant and presence of both non-allelic interactions *i.e*. duplicate or complementary was also reported. Raut *et al.* (2000), Sarode *et al*. (2009), Kumar *et al*. (2009), Payasi *et al.* (2010), Ravinder *et al.* (2012), Singh (2016) and Ashutosh *et al*. (2017) reported the presence of additive, dominance and epistatic gene effects. Among nonallelic interactions dominance x dominance (l) was of greater magnitude than main gene effects for seed yield indicating the importance of heterosis breeding to utilize non- additive gene effects. Kumar *et al.* (2009) and Sreelakshmi *et al*. (2013) revealed significant contribution of both additive and dominance gene effects in controlling of this trait and concluded that both epistatic gene effects play an important role for the inheritance of seed yield. Hooda *et al.* (2001) and Hooda *et al.* (2000) reported the importance of additive gene action for seed yield. Singh (2016) and Ashutosh *et al*. (2017) reported presence of duplicate epistasis and significant additive, dominance and non-allelic interactions for seed yield. Duplicate type of epistasis for seed yield was also reported by Kumar *et al*. (2009) while complementary type of epistasis was reported by Sharma *et al.* (2012) and Khodambashi *et al.* (2012) and concluded that dominance x dominance (I) was of greater magnitude than main gene effects for seed yield indicating the importance of nonadditive gene effects. Oommen *et al*. (1999) and Kandalkar (2006) reported that epistatic/digenic interactions were observed in all the crosses for seed yield and revealed that additive gene effects were significant for seed yield and other character and complementary type gene action was observed in seed yield. Sharma *et al*. (2001), Singh *et al*. (2009)**,** Singh *et al*. (2010) and Parmar *et al*. (2015) reported the presence of additive, dominance gene effects and epistatic interaction in seed yield in all

the crosses indicating the importance of both additive and non additive gene action in the expression of this character .Similar result was also reported by Kandalkar (2006) and suggested the important of both additive and non-additive type of gene actions with duplicate type of epistasis for seed yield per plant.

CHAPTER III

MATERIALS AND METHODS

MATERIALS AND METHODS

The details of experimental site, period of experiment, meteorological data during the experimental period, materials used, methods adopted for conducting of experiments and analysis of data during the course of investigation are described in this chapter as follows.

3.1. General information

3.1.1. Site of experiment

The present investigation was undertaken to study the "**Combining ability and gene effects in vegetable-type pigeonpea [(*Cajanus Cajan* (L.) Millsp.)]**" under foothill of Nagaland" The experimental study was conducted at farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences And Rural Development, Medziphema Campus, Nagaland University, during 2015 and 2016. The experimental farm is located at 25 degree 45' 43" N latitude and 93 degree 53' 04" E longitude at an altitude of 310 m above mean sea level.

3.1.2 Meteorological data

The data pertaining to the weekly rainfall, minimum and maximum temperature, relative humidity for the main experiment season (Kharif 2015 and 2016) has been presented in table 3.1 and 3.2

Table 3.1. Meteorological data during the period of investigation (June-December 2015)

Month	Temperature		Relative Humidity		Total Rainfall (mm)
	Max.Temp. (^{o}C)	Min.Temp. (^{o}C)	Max.RH (^{O}C)	Min.RH (^{O}C)	
June	31.50	24.50	82.00	58.00	188.80
July	31.90	24.80	85.00	59.00	322.90
August	31.50	25.10	83.00	61.00	177.90
September	31.90	24.30	85.00	59.00	232.80
October	31.70	20.80	92.00	63.00	61.30
November	28.20	15.00	93.00	59.00	20.70
December	24.60	9.90	92.00	52.00	9.60

(Source: ICAR research complex for NEHR Jharnapani)

Table 3.2. Meteorological data during the period of investigation (July-December 2016)

Month	Temperature		Relative Humidity		Total Rainfall (mm)
	Max.Temp. (^{o}C)	Min.Temp. (^{o}C)	Max.RH (^{O}C)	Min.RH (^{O}C)	
July	32.58	24.84	91.2	71.4	57.04
August	33.79	24.36	92.37	69.05	82.4
September	32.56	23.95	93.82	73.07	69.4
October	32.12	22.05	93.60	69.46	6.1
November	28.21	16.91	94.67	66.17	35.37
December	26.53	11.55	94.44	54.38	1.28

(Source: ICAR research complex for NEHR Jharnapani)

3.2 EXPERIMENTAL DETAIL

3.2.1. Experimental material

The experimental material used in the present study comprised of four lines (female parent), three testers (male parent), F_1 and advance generation (F_2 and F_3) maintained through generation.

Table 3.3: List of parents used in Line x Tester and Generation mean analysis

Parents	Character
BRG-2	High yielding and bold-seeded pigeon pea variety for dhal and vegetable purpose, the seed are large with creamy white colour.
B3-13	Plant is tall in nature, bold seeded and seed are light brown in colour with medium seed size.
B2-10	Bold-seeded pigeon pea with medium sized seeds, green pods with slight to moderate pods constriction.
B2-5-2-1	It has medium size seed and brownish in colour, bold-seeded, pods are green with streak mark.
BRG-1	High yielding pigeon pea cultivar, resistant to pods borer, the seed are large with creamy white seed colour.
BRG-3	Early to medium duration variety with indeterminate growth habit. The flowers of this variety are yellow and pods are green in colour. It has medium to large seed sized.
B1-169-1	These varieties has medium to large seed size with creamy seed colour and pods are green with streak mark.

3.3 Experimental method

EXPERIMENT NO. 1 (2015): Analysis of combining ability variances and effects and generation advancement from F2 to F3

3.3.1. Planting of F_1 generation and parents

The 12 hybrids and seven parents (4 lines and 3 testers) were sown in well-prepared field in *Kharif* 2015, in Randomized Block Design (RBD) with three replications. The plants were spaced 45 cm within rows and 60 cm between rows, in a plot size of 3 m x 1.5 m (length x breadth). In the beginning of the experiment 2-3 seeds were dibbled at each hill, thus consisting of 25 plants in each plot. After two weeks of germination, thinning was carried out to maintain single plant at each hill. The fertilizer applied at the rate of 15kg N, 20 kg P and 15 kg K/ha. All the recommended cultural practices were followed to raise good crop during the period of study. Field experiment for study of combining ability analysis for (Parents + F1s) of pigeonpea was conducted as detailed below:

3.3.2. Technical Programme

1. Design	:	Randomized Block Design (RBD).
2. No. of Replications	:	3
3. Row - Row Distance	:	60 cm.
4. Plant -Plant Distance	:	45 cm.
5. No. of Rows	:	3
6. Row length	:	4

At the same time to generate material for generation mean analysis, crosses were made during 2015, where emasculation and pollination was done

at morning 6.30-8.00 a.m. The process of hybridization programme comprises of 4 female and 3 male to generate a total set of hybrids in a line x tester fashion as proposed by Kempthorne (1957). Emasculation and pollination was carried out on 12 hybrids during 2015 rainy season. Sufficient numbers of hand pollinated seeds were produced during emasculation process. The bud most likely to shed pollen the next day was selected. The buds were tightly closed and approximately 6% the size of a mature bud. Two buds per inflorescence was selected for emasculation and about two to ten buds are emasculated and other buds are removed .After emasculation pollination was done immediately. Buds were tagged with thread for easy identification in pollinated flower. Until sufficient numbers of crossed pods were obtained hybridization process was carried out. Each of the lines *viz*. BRG-2 , B3-13, B2-10 and B2-5-2-1were crossed with each of four testers *viz.* BRG-1, BRG-3 and B1-169-1 in a Line × Tester mating design to generate F1 seed of 12 cross combinations during kharif, 2016. At the same time experimental materials of F2 generation already maintained and present were collected from AICRP for pigeonpea, Medziphema center, this F2 from the previous generation was raised to produce F3 population and some F2 were sun dried and stored and saved for next year. Thus materials for generation mean studies was generated simultaneously, and five basic generations *viz*. P1, P2, F1, F2, and F3 was developed for each of the 12 crosses and were evaluated during 2016.

Table 3.4: Parent and their 12 crosses

Lines		Sources
L1	BRG-2	UAS, Bangalore, Karnataka
L2	B3-13	UAS, Bangalore, Karnataka
L3	B2-10	UAS, Bangalore, Karnataka
L4	B2-5-2-1	UAS, Bangalore, Karnataka
Testers		
T1	BRG-1	UAS, Bangalore, Karnataka
T2	BRG-3	UAS, Bangalore, Karnataka
T3	B1-169-1	UAS, Bangalore, Karnataka
Crosses (Line x Tester)		
1	B2-5-2-1 x BRG-1	
2	B2-5-2-1 x BRG-3	
3	B2-5-2-1 x B1-169 -1	
4	B3-13 x BRG-1	
5	B3-13 x BRG-3	
6	B3-13 x B1-169 -1	
7	B2-10 x BRG-1	
8	B2-10 x BRG-3	
9	B2-10 x B1-169 -1	
10	BRG-2 x BRG-1	
11	BRG-2 x BRG-3	
12	BRG-2 x B1-169 -1	

EXPERIMENT No. 2 (2016)

Study of components of genetic variances for yield and yield traits through generation means analysis using five parameters model

3.3.3. Generation mean analysis

The experimental material comprising of five populations *viz*. P1, P2, F1, F2 and F3 of 12 cross combinations *viz*. BRG-2 x BRG-1, BRG-2 x BRG-3, BRG-2 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3 and B2-5-2-1 x B1-169-1 generated from the previous year were evaluated in a Randomized Block Design (RBD) with three replications during *Kharif* 2016 to estimate the nature of gene action and its effects. Recommended dose of fertilizer was applied as previous year.

3.3.4. Technical Programme

1. Design	:	Randomized Block Design (RBD).
2. No. of Replication	:	3
3. Row - Row Distance	:	60 cm.
4. Plant -Plant Distance	:	45 cm.
5. No. of Rows	:	3
6. Row length	:	4 m

Table 3.5: Details of parents and cross combinations for generation mean analysis

Parents (P1)	**Genotype**
1	BRG-2
2	B3-13
3	B2-10
4	B2-5-2-1
Parents (P2)	
1	BRG-1
2	BRG-3
3	B1-169-1
Crosses	
1	B2-5-2-1 x BRG-1
2	B2-5-2-1 x BRG-3
3	B2-5-2-1 x B1-169 -1
4	B3-13 x BRG-1
5	B3-13 x BRG-3
6	B3-13 x B1-169 -1
7	B2-10 x BRG-1
8	B2-10 x BRG-3
9	B2-10 x B1-169 -1
10	BRG-2 x BRG-1
11	BRG-2 x BRG-3
12	BRG-2 x B1-169 -1

3.4 Observations to be recorded

3.4.1. Quantitative character

Five plants among the competitive population were taken from each plot in each replication randomly for recording data of the traits. The list of the traits studied and their methods for recording the observations are given below:

3.4.1.1. Days to 50% flowering

Numbers of days were recorded from the date of sowing till the date when 50 percent flower appeared in plot basis.

3.4.1.2. Plant height (cm)

The height of the plant was recorded in centimeter from the ground level to tip of main stem at the time of maturity.

3.4.1.3. Primary branches per plant

The number of primary branches per plant was recorded as total number of primary branches on the main stem.

3.4.1.4. Secondary branches per plant

The number of secondary branches per plant was recorded as total number of sub-branches on branches of the main stem.

3.4.1.5. Days to pods initiation

The number of days was counted from the date of sowing to appearance of first pod on the plant.

3.4.1.6. Days to 80% pods maturity:

This was noted in terms of days from the date of sowing to the stage when over 80% percent pods have matured.

3.4.1.7. Number of pods per plant

All the effective pods from each selected plant at physiological maturity were counted and averaged.

3.4.1.8. Pod length (cm)

Length of pod was measured in centimetre. Mean length of five pods from each plant was considered and averaged.

3.4.1.9. 100- Seed weight (g)

The test weight of counted 100 seeds in grams at 10 percent (air dry) moisture content was recorded for individual genotype.

3.4.1.10. Seed yield per plant (g)

The selected plants were harvested, threshed and winnowed separately. Finally the seeds were weighed in grams after sun dried them to appropriate moisture level.

3.4.2 Qualitative character

3.4.2.1. Pods colour: Recorded as main colour of the pods

3.4.2.2. Pods pubescence: Recorded at near maturity

3.4.2.3. Pods surface constriction: Recorded at near maturity

3.4.2.4. Pods size: Recorded at pods maturity

3.4.2.5. Pods waxiness: Recorded at near maturity

3.4.2.6. Pods surface stickiness: Recorded at near maturity

3.4.2.7. Seed coat pattern; recorded after harvest

3.4.2.8. Seed shape: Recorded within three months of harvesting

3.4.2.9. Seed colour: Recorded after harvest

3.5 Statistical analysis

The data collected on the characters were statistically analyzed for various genetical parameters.

3.5.1. Analysis of variance and combining ability

Analysis of combining ability was carried out as per method suggested by Kempthorne (1957). Mean sum of squares that arises due to different sources of variation were estimated and their expected genetic values were calculated. A model analysis of variance (ANOVA) table for Line x Tester analysis is given below:

ANOVA for combining ability

Source of variation	Degrees of freedom	Mean sum of squares	Expected mean sum of squares
Replication	(r-1)	_	
Hybrids	(lt-1)	_	
Lines	(l-1)	M_1	$\sigma^2_e + r$ [Cov(FS) - 2Cov(HS) + rt[Cov(HS)]
Testers	(t-1)	M_2	$\sigma^2_e + r$ [Cov(FS) - 2Cov(HS) + rl [Cov(HS)]
Line× tester	(l-1) (t-1)	M_3	$\sigma^2_e + r$[Cov(FS) - 2Cov(HS)]
Error	(r-1) (lt-1)	M_4	σ^2_e

Where,

r = Number of replications

l = Number of lines (males)

t = Number of testers (females)

Cov (HS) = Covariance of half sibs

Cov (FS) = Covariance of full sibs

M1 = Mean sum of squares due to females

M2 = Mean sum of squares due to males

M3 = Mean sum of squares due to female x male

M4 = Mean sum of squares due to error

3.5.2. Estimation of variance

The GCA and SCA variances were expressed in terms of covariance full sibs (FS) and half sibs (HS) as indicated below.

$$\text{Cov (HS)} = \frac{M_1 + M_2 - 2M_3}{r\,(l + t)}$$

$$\text{Cov (FS)} = 1/3r\,[M_1+M_2+M_3 - 3M_4 + 6r\ \text{Cov (HS)} - r\,(l+t)\ \text{Cov (HS)}]$$

$\square\ ^2$gca= Cov (HS)

$\square\ ^2$sca= Cov (FS) – 2 Cov (HS)

$$\text{GCA variance for lines} = \text{Cov (HS) lines} = \frac{M_1 - M_2}{r\,t}$$

$$\text{GCA variance for testers} = \text{Cov (HS) testers} = \frac{M_2 - M_3}{r\,l}$$

$$\text{SCA variance for hybrids} = \frac{M_3 - M_4}{r}$$

3.5.3. Estimation of combining ability effects

The model used to analyse the GCA and SCA effects is given below.

Yijk = $\square$ + gi + gj + sij + eijk

Yijk = any character measured of the cross (i x j) in the kth replication

□ = Population mean

gi = gca effect of ith (male) parent

gj = gca effect of jth (female) parent

sij = Sca effect of (i x j)th cross

eijk = Error associated with observation ijk

i = Number of female parents

j = Number of male parents

k = Number of replications

The individual effects were estimated as indicated below

(A) General combining ability effects (gca)

i) Lines : $gi = \frac{Xi..}{tr} - \frac{X...}{rlt}$

Where,

Xi.. = Total of i^{th} female parent over all parents and replications

Population mean = $= \frac{X...}{rlt}$

ii) Testers = gj = $= \frac{X.i.j.}{lr} - \frac{X...}{lrt}$

Where,

X.j. = Total of jth male parent over all female parents and replications

(B) Specific combining ability effects (sca)

$$sij = = \frac{Xij..}{r} - \frac{Xi..}{tr} - \frac{Xj..}{rl} - \frac{X..}{rlt}$$

Where,

Xij = Total of ijth combinations over all replications

Sij = sca effect of the ijth combination

The standard error (SE) and critical difference (CD) pertaining to the gca effects of male and female parents and sca effects of different combinations

$$SE\ (gca\ for\ line) = \sqrt{\frac{M4}{rt}}$$

$$SE\ (gca\ for\ tester) = \sqrt{\frac{M4}{rl}}$$

SE (sca effect) =√ (M4/r)

Where,

M4 = Error variance (eMSS)

r = Replication

l = Lines

t = Testers

Proportional contribution of lines, testers and their interaction

$$a)\ Contribution\ of\ lines\ (\%) = \frac{SS\ (lines) \times 100}{SS\ (crosses)}$$

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

$$\text{c) Contribution of L x T} = \frac{\text{SS (lines x testers)} \times 100}{\text{SS (crosses)}}$$

Where,

SS = Sum of squares

3.5.4. Generation mean analysis (Five parameter models)

3.5.4.1. Generation Means and Variances

The standard statistical procedures were used to calculate mean and variances of each generation for each character. Mean (x) = $\frac{\sum xi}{n}$

Variance = $\frac{1}{n-1}\left[\sum x_i^2 - \frac{(\sum xi)^2}{n}\right]$

Variance of mean (V_m) = $\frac{\text{Variance}}{n}$

Standard error mean (S.E) = $\sqrt{\frac{\text{Variance}}{n}}$

n = Total number of observations recorded for respective generation.

3.5.4.2. Scaling tests

In the presence of simple additive-dominance situations, there exists a simple relationship between the expected values of different generation means. Mather (1949) and Hayman and Mather (1955) constructed scaling test A, B, C and D based on this concept which were used to test the adequacy of simple additive-dominance model and to detect the presence of epistatic interaction. The significance of either of tests would indicate failure of simple additive-

dominance model to explain variation in generation means. The calculations of scaling tests are as here under

A = 2 $\bar{B}_1 - \bar{P}_1 - \bar{F}_1$

B = 2 $\bar{B}_2 - \bar{P}_2 - \bar{F}_1$

C = 4 $\bar{F}_2 - 2\ \bar{F}_1 - \bar{P}_1 - \bar{P}_2$

D = 4 $\bar{F}_3 - 2\ \bar{F}_2 - \bar{P}_1 - \bar{P}_2$

Since in the present study there were five generations *viz*. P_1, P_2, F_1, F_2 and F_3, hence the estimation of scales C and D were done.

The variances of the estimates were computed using following formulae

V_C = 16V ($\bar{F}_2$) + 4V ($\bar{F}_1$) + V ($\bar{P}_1$) + V ($\bar{P}_2$)

V_D = 16V ($\bar{F}_3$) + 4V ($\bar{F}_2$) + V ($\bar{P}_1$) + V ($\bar{P}_2$)

The standard error of each scaling test was calculated as under

S.E. (C) = $(V_C)^{\frac{1}{2}}$

S.E. (D) = $(V_D)^{\frac{1}{2}}$

The testing of individual scaling test was carried out by using t-test as follows:

t (C) = C/S.E. (C)

t(D) = D/S.E.(D)

The degree of freedom for t-test was equal to the sum of degree of freedom of all the generations involved in the respective scaling test as shown below

d.f. (C) = d.f of F_2 + d.f. of F_1 + d.f. of P_1 + d.f. of P_2

d.f. (D) = d.f of F_3 + d.f. of F_2 + d.f. of P_1 + d.f. of P_2

However, the calculated values of't' were compared with the tabulated values of 't' at 5% and 1% levels of significance. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction.

3.5.4.3. Estimation of genetic components

Five-parameter model for estimation of various genetic components proposed by Hayman (1958) was applied using following formula.

Mean (m) = $\bar{F}_2$

Additive effect (d) = $\frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2$

Dominance effect (h) = $(4\bar{F}_1 + 12\bar{F}_2 - 16\bar{F}_3) / 6$

Dominance x Dominance (l) = $(8\bar{F}_1 - 24\bar{F}_2 + 16\bar{F}_3) / 3$

Additive x Additive (i) = $\bar{P}_1 - \bar{F}_2 + \frac{1}{2}(\bar{P}_1 - \bar{P}_2 + h) - \frac{l}{4}l$

The variance of each estimate was computed as follows

$V_m = V(\bar{F}_2)$

$V_d = \frac{1}{4}[V(\bar{P}_1) + V(\bar{P}_2)]$

$V_h = \frac{1}{36}[16V(\bar{F}_1) + 144V(\bar{F}_2) + 256V(\bar{F}_3)]$

$V_l = = \frac{1}{9}[256V(\bar{F}_3) + 576V(\bar{F}_2) + 64V(\bar{F}_1)]$

$V_i = V(\bar{P}_1) + V(F_2) + \frac{1}{4}[V(\bar{P}_1) + V(\bar{P}_2) + V_h] + \frac{1}{16}(V_l)$

The standard error of each of the gene effect was computed as follows

S.E. (m) = $(V_m)^{\frac{1}{2}}$

S.E. (d) = $(V_d)^{\frac{1}{2}}$

S.E. (h) = $(V)^{\frac{1}{2}}$

S.E. (i) =$(V_i)^{\frac{1}{2}}$

S.E. (l) = $(V_l)^{\frac{1}{2}}$

The significance of each parameter was tested by using t-test

t (m) = (m)/S.E.(m)

t (i) = (i)/S.E. (i)

t (d) = (d)/S.E.(d)

t (h) = (h)/S.E. (h)

t (l) = (1)/S.E. (1)

The calculated t value of each parameter was compared with tabulated values of t at 5% and 1% levels of significance.

CHAPTER IV

RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

4.1. Qualitative character

Qualitative character was not subjected to statistical analysis. Nine characters were observed for qualitative character of various pigeon pea genotypes as presented in Table 4.1.

4.1.1. Pods colour

Two different types of pods colour were recorded. They are green with brown streak and green with black streak. Among parent five genotypes BRG-2, B3-13, B2-10, B2-5-2-1 and BRG-3 recordedgreenwith brownstreak andBRG-1 and B1-169-1 recorded green with black streak and among the crosses all the crosses recorded green with brown streaks.

4.1.2. Pods pubescence

Pods pubescence is the presence of hairy growth on pods surface. Pods pubescence was found in all the genotypes, both parents and crosses.

4.1.3. Pods constriction

Two different types of pods constriction were recorded. They are slight and prominent type of pods constriction. The parents BRG-2, B3-13, B2-10, BRG-1 and B1-169-1 have slight type of pods constriction, whereas parents B2-5-2-1 and BRG-3 have prominent type of constriction. Among the crosses BRG-2 X BRG-1, BRG-2 X B1-169-1,B3-13 x BRG-1, B3-13 X B1-169-1, B2-10 X BRG-1 and B2-10 X B1-169-1 have slight type of pods constriction and crosses BRG-2 X BRG-3, B3-13 X BRG-3, B2-10 X BRG-3, B2-5-2-1 X BRG-1, B2-5-2-1 X BRG-3 and B2-5-2-1 X B1-169-1 recorded prominent type.

4.1.4. Pods waxiness

Pods waxiness is the presence of wax on the surface of pods. Pods waxiness was found in all the genotypes for both parent and crosses.

4.1.5. Pod surface stickiness

Pod surface stickiness is the presence of stickiness on the surface of pods. Pods surface stickiness was found in all the genotype for both parent and crosses.

4.1.6. Seed size

Two type of seed size was recorded namelylarge and medium. The parents BRG-2, BRG-1 and BRG-3 have large type of seed size, whereas parents B3-13, B2-10, B2-5-2-1 and B1-169-1 have medium type of seed size. Among the crosses BRG-2 X BRG-1, BRG-2 X BRG-3, BRG-2 X B1-169-1, B3-13 X BRG-1, B3-13 X BRG-3, B2-10 X BRG-1, B2-10 X BRG-3, B2-5-2-1 X BRG-1and B2-5-2-1 X BRG-3 have large type of seed size and crosses B3-13 X B1-169-1, B2-10 X B1-169-1 and B2-5-2-1 X B1-169-1have medium type of seed size.

Table 4.1: Qualitative character in pigeon pea for both parental genotype and crosses

Genotype	Pods colour	Pods pubescence	Pods constriction	Pods waxiness	Pods surface stickiness	Seeds size	Seed colour pattern	Seed shape	Seed colour
BRG-2	Green with brown streak	Present	Slight	Present	Present	Large	Speckled and molted	Oval	Creamy
B3-13	Green with brown streak	Present	Slight	Present	Present	Medium	Speckled	Globular	Light brown
B2-10	Green with brown streak	Present	Slight	Present	Present	Medium	Plain	Globular	Dark purple
B2-5-2-1	Green with brown streak	Present	Prominent	Present	Present	Medium	Plain	Globular	Brownish
BRG-1	Green with black streak	Present	Slight	Present	Present	Large	Speckled	Oval	Creamy
BRG-3	Green with brown streak	Present	Prominent	Present	Present	Large	Molted	Oval	Creamy
B1-169-1	Green with black streak	Present	Slight	Present	Present	Medium	Molted	Oval	Creamy
BRG-2 X BRG-1	Green with brown streak	Present	Slight	Present	Present	Large	Speckled and molted	Oval	Creamy
BRG-2 X BRG-3	Green with brown streak	Present	Prominent	Present	Present	Large	Speckled and molted	Oval	Creamy
BRG-2 X B1-169-1	Green with brown streak	Present	Slight	Present	Present	Large	Speckled and molted	Oval	Creamy
B3-13 X BRG-1	Green with brown streak	Present	Slight	Present	Present	Large	Speckled	Oval	Creamy
B3-13 X BRG-3	Green with brown streak	Present	Prominent	Present	Present	Large	Speckled	Oval	Creamy
B3-13 X B1-169-1	Green with brown streak	Present	Slight	Present	Present	Medium	Speckled	Oval	Creamy
B2-10 X BRG-1	Green with brown streak	Present	Slight	Present	Present	Large	Speckled	oval	Dark purple
B2-10 X BRG-3	Green with brownstreak	Present	Prominent	Present	Present	Large	Molted	Oval	Dark purple
B2-10 X B1-169-1	Green with brown streak	Present	Slight	Present	Present	Medium	Molted	Oval	Dark purple
B2-5-2-1 X BRG-1	Green with brown streak	Present	Prominent	Present	Present	Large	Speckled	Oval	Brownish
B2-5-2-1 X BRG-3	Green with brown streak	Present	Prominent	Present	Present	Large	Molted	Oval	Brownish
B2-5-2-1 X B1-169-1	Green with brown streak	Present	Prominent	Present	Present	Medium	Molted	Oval	Brownish

4.1.7. Seed colour pattern

Four type of seed coat colour were recorded, they were speckled, molted, speckled and molted and plain. The parents BRG-2 have speckled and molted type of seed colour pattern and parents B3-13 and BRG-1 have speckled type of seed colour pattern followed by parent BRG-3 and B1-169-1which have molted type of seed colour pattern and B2-10 and B2-5-2-1which have plain type of seed colour pattern. Among the crosses BRG-2 X BRG-1, BRG-2 X BRG-3 and BRG-2 X B1-169-1 have speckled and molted type of seed colour pattern followed by B3-13 X BRG-1, B3-13 X BRG-3, B3-13 X B1-169-1, B2-10 X BRG-1 and B2-5-2-1 X BRG-1which have speckled type of seed colour pattern and B2-10 X BRG-3, B2-10 X B1-169-1, B2-5-2-1 X BRG-3 and B2-5-2-1 X B1-169-1 have molted type of seed colour pattern.

4.1.8. Seed shape

Two type of seed shape were recorded. They are oval and globular. Oval type was found in all the genotypes both parent and crosses except in parent B3-13, B2-10 and B2-5-2-1 which has globular type of seed shape.

4.1.9. Seed colour

Four type of seed colour were reported. They are creamy, brownish, light brown and dark purple. The parents BRG-2, BRG-1, BRG-3 and B1-169-1 have creamy type of seed colour. Whereas parents B2-10 have dark purple type of seed colour and parent B2-5-2-1 have brownish type of seed colour followed by B3-13 which has light brownish seed colour. Among the crosses B2-10 X BRG-1, B2-10 X BRG-3 and B2-10 X B1-169-1 have dark purple type of seed colour and crosses BRG-2 X BRG-1, BRG-2 X BRG-3, BRG-2 X B1-169-1, B3-13 X BRG-1, B3-13 X BRG-3 and B3-13 X B1-169-1 have creamy type of seed colour and crosses B2-5-2-1 X BRG-1, B2-5-2-1 X BRG-3 and B2-5-2-1 X B1-169-1 have brownish type of seed colour.

4.2. Combining ability

General combining ability estimate provides information regarding additive gene action whereas; specific combining ability refers to the combination performance and thus reflects non-additive type of gene action. General combining ability includes additive and additive x additive interaction and specific combining ability is the sum total effects of dominance, dominance x dominance and additive x dominance interaction. Data pertaining to yield and its components traits were recorded on 7 parents and 12 crosses which were analysis by following the line x tester approach for combining ability (Kempthome, 1957).

The concept of general and specific combining ability provides information to breeder for assessing parents in the production of superior hybrid by selecting suitable line. Exploitation of heterotic effect including additive and nonadditive genetic variability is provided by hybrid development. Variability and combining ability of parents influence the magnitude of heterosis. Many mating designs have been develop to provide information on combining ability and nature of gene action. However, the simplest and efficient methods of evaluating large number of inbreds for combining ability have been the line × tester analysis (Kempthorne, 1957). Combining ability plays a significant role for breeder in determining the nature and magnitude of gene action involved in the inheritance of the traits for crop improvement. Combining ability is useful in selection of desirable parents since, performance of the hybrids helps in exploitation of heterosis. The best combiners to be hybridized either to exploit heterosis or to select method to be followed in breeding programmes through proper selection method is provided by gene action and combining ability analysis. screening and selection of available germplasm is important for exploitation of heterosis that could produce better combination of genetically important characters, the entire

genetic variability observed in the analysis for each trait was partitioned into its components *i.e.*general and specific combining ability as defined by Sprague and Tatum (1942). General combining ability is used to designate the average performance of a line in hybrid combinations and the term specific combining ability to define those cases in which certain combinations do relatively better or worse than expected on the basis of the average performance of the lines involved.

4.2.1. Analysis of variances for combining ability

Results of analysis of variance for combining ability Table 4.2 revealed that mean squares due to parents were found to be significant for all the traits except number of primary branches. And analysis of variance for combining ability revealed significant for all the traits for mean squares due to crosses. Similarlysignificant for all the traits except number of primary branches and days to 80% pod maturity were found in mean squares due to parent *vs.* crosses.

Results of analysis of variance for combining ability were found significant due to mean squares due to lines for all the traits except number of primary branches per plant and plant height. Also results of analysis of variance for combining ability revealed that mean squares due to testers found to be significant for all the traits except number of secondary branches per plant and 100-seed weight. Line x tester mean squares was found to be significant for all the traits except number of primary branches, number of secondary branches and plant height.

4.2.2. GCA and SCA variance

The gca variance and sca variance are presented in Table 4.3 for different characters. Which are basic criteria for the selection or hybridization programme, the comparative variances due to general combining ability and

specific combining ability for different characters under study are as follow. The ratio of variance due to gca/sca was less than unity for most of traits except days to 50% flowering, number of primary branches and pods length, indicating the greater role of non additive gene action for inheritance of character.

4.2.3. Combining ability (GCA and SCA effects)

The combining ability estimation for gca and sca effects are presented in table 4.4 for gca effect and table 4.6 for sca effects. Parent are classified based on the combining ability effects as good (G), average (A) and poor (P) combiners as presented in table 4.5. The gca effects is considered as good general combiner if the significant gca effects is towards desirable direction (G) and considered as average general combiner (A) if the sca effects is nonsignificant and the parent is designated as poor general combiner (P) with significant negative gcaeffect. The estimate of gcaeffects of parental lines for different characters (Table 4.4) showed that none of the parental line was excellent in gca effects for all the characters studied. This suggested use of multiple parent participation through multiple crossing to effect substantial improvement in yield and its components.

Table 4.2: Analysis of variance for combining ability (Line X Tester) in pigeon pea for different characters

Source of variation	DF	Mean square of the character									
		Day to 50% flowering	Plant height (cm)	No of pri. branches	No of sec. branches	Day to pods initiation	Day to 80% pod maturity	Number of pods/plant	Pods length (cm)	100-seed weight (g)	Seed yield (g)
Replication	2	7.62	98.72	4.65	2.52	1.83	19.38	45.60	0.51	0.25	0.21
Treatment	18	709.62**	288.40**	2.65	26.78**	24.49**	1691.49**	4865.18**	0.35**	2.44**	551.78**
Parent	6	516.81**	2647.61**	2.67	4.97	29.12**	638.45**	3579.47**	0.67**	3.79**	211.22**
Line	3	89.66**	116.48	6.43	38.70*	133.04**	240.14**	674.01**	0.68**	1.85**	190.16**
Tester	2	163.94**	513.97**	5.99**	12.46	107.34**	417.7**	2739.62**	0.53**	0.29	295.54**
L x T	6	622.04**	16.15	14.36	1.63	37.80**	1581.00**	12521.54**	0.61**	3.98**	709.48**
Crosses	11	64.45**	245.98**	12.82**	18.67**	93.35**	205.23**	1854.95**	0.78**	2.37**	1021.15**
Parent vs.Crosses	1	288.62**	406.38**	0.08	21.49**	113.56**	2.79	21747.00**	0.48**	66.48**	254.47**
Error	36	4.65	37.76	2.49	2.78	6.72	10.76	108.56	0.13	0.23	41.23

Table 4.3: Estimation of genetic components of variance for seed yield and its attributing characters

Source of variation	DF	Day to 50% flowering	Plant height (cm)	No of pri. branches	No of sec. branches	Day to pods initiation	Day to 80% pod maturity	Number of pods/plant	Pods length (cm)	100-seed weight (g)	Seeds yield (g)
Variance due to GCA	**2**	3.23	5.52	1.54	1.87	8.54	9.86	20.42	0.12	0.06	19.61
Variance due to SCA	**3**	1.56	64.37	1.23	3.38	34.23	16.65	698.32	0.07	0.26	593.46
Variance due to GCA/Variance due to SCA	**6**	2.07	0.08	1.25	0.55	0.25	0.59	0.03	1.72	0.23	0.03

Table 4.4: GCA effects of lines and testers

Parent	Character									
	Day to 50% flowering	**Plant height (cm)**	**No of pri. branches**	**No of sec. branches**	**Day to pod initiation**	**Day to 80% pod maturity**	**Number of pods per plant**	**Pod length (cm)**	**100-seed weight (g)**	**Seed yield/plant (g)**
LINE										
BRG-2	-2.38**	8.42**	1.18**	1.21**	-3.62**	-4.56**	10.12**	0.67**	0.51*	6.25*
B-3-13	0.95	5.36*	-2.29**	0.31	0.77	1.45	-22.44**	-0.58**	-0.62*	-13.86**
B2-10	-4.15**	-8.24**	1.47*	-2.55**	1.53**	-4.61**	11.23**	0.39**	0.65*	6.14*
B2-5-2-1	5.66**	-6.29*	-0.68	0.74	-0.68	7.37**	1.09	-0.46**	-0.45*	0.87
SE	0.72	2.05	0.52	0.55	0.86	1.09	3.47	0.12	0.16	2.14
		TESTER								
BRG-1	-0.82	-2.45**	1.14**	2.44*	-2.58**	-4.58**	2.63**	0.30**	0.47**	5.03**
BRG-3	-2.52**	5.75**	2.46**	1.23**	-0.48	3.12**	2.57**	0.18**	0.57**	2..41*
B1-169-1	3.31**	-3.21**	-3.61**	-3.65**	2.37**	1.31	-5.61**	-0.41**	-0.81*	-7.81**
SE	0.62	1.77	0.45	0.48	0.75	0.95	3.00	0.10	0.14	1.85

Table 4.5: SCA performance of crosses involving particular parental combination

Crosses	Day to 50% flowering		Plant height (cm)		No of primary branches/plant		No of sec branches/plant		Day to pods initiation	
	Parent involved	SCA	Parent involved	SCA	Parent involved	SCA	Parent involved	SCA	Parent involved	SCA
B2-5 -2-1 X BRG-1	P x A	P	G X G	P	A X G	P	A X G	P	A X G	A
B2-5-2-1 X BRG-3	P x G	A	G X P	P	A X G	P	A X G	A	A X A	A
B2-5-2-1 X B1-169-1	P X P	P	G X G	A	A X P	P	A X P	G	A X P	A
B3-13 X BRG-1	A X A	P	P X G	A	P X G	P	A X G	P	A X G	P
B3-13 X BRG-3	A X G	P	P X P	G	P X G	P	A X G	P	A X A	P
B3-13 X B1-169-1	A X P	P	P X G	G	P X P	A	A X P	P	A X P	A
B2-10 X BRG-1	G X A	G	G X G	P	G X G	G	P X G	G	P X G	G
B2-10 X BRG-3	G X G	G	G X P	A	G X G	G	P X G	G	P X A	P
B2-10 X B1-169-1	G X P	A	G X G	G	G X P	P	P X P	P	P X P	A
BRG-2 X BRG-1	G X A	G	P X G	P	G X G	G	G X G	G	G X G	G
BRG-2 X BRG-3	G X G	G	P X P	P	G X G	G	G X G	G	G X A	A
BRG-2 X BI-169-1	G X P	G	P X G	G	G X P	G	G X P	G	G X P	G

Where, P= Poor G=good A=average

Cont…

Crosses	Day to 80% pods maturity		Number of pods per plant		Pods length (cm)		100-seed weight (gm)		Seed yield/plant	
	Parents involved	SCA	Parents involved	SCA	Parents involved	SCA	Parents involved	SCA	Parents involved	SCA
B2-5 -2-1 X BRG-1	P X G	P	A X G	G	P X G	A	P X G	A	A X G	P
B2-5-2-1 X BRG-3	P X P	A	A X G	A	P X G	A	P X G	P	A X G	A
B2-5-2-1 X B1-169-1	P X A	P	A X P	P	P X P	G	P X P	P	A X P	P
B3-13 X BRG-1	A X G	G	P X G	A	P X G	P	P X G	G	P X G	A
B3-13 X BRG-3	A X P	P	P X G	P	P X G	A	P X G	A	P X G	A
B3-13 X B1-169-1	A X A	A	P X P	A	P X P	A	P X P	A	P X P	A
B2-10 X BRG-1	G X G	G	G X G	G	G X G	G	G X G	G	G X G	G
B2-10 X BRG-3	G X P	P	G X G	G	G X G	G	G X G	G	G X G	A
B2-10 X B1-169-1	G X A	A	G X P	A	G X P	A	G X P	A	G X P	A
BRG-2 X BRG-1	G X G	G	G X G	G	G X G	G	G X G	G	G X G	G
BRG-2 X BRG-3	G X P	A	G X G	G	G X G	G	G X G	G	G X G	G
BRG-2 X BI-169-1	G X A	G	G X P	G	G X P	P	G X P	G	G X P	G

Where, P= Poor G=good A=average

Table 4.6: SCA effects of the crosses

Crosses	Character									
	Day to 50% flowering	Plant height (cm)	No of primary branches/plant	No of secondary branches/plant	Day to pod initiation	Days to 80% pods maturity	Number of pods per plant	Pod length (cm)	100-seed weight (g)	Seed Yeld/plant(g)
B2-5 -2-1 X BRG-1	7.17**	5.11**	-1.34**	-0.63*	-2.54	6.04**	11.65**	-0.05	-0.17	-4.91**
B2-5-2-1 X BRG-3	2.31	4.40**	-1.09*	-0.21	2.60	2.54	3.46	-0.02	-0.63**	2.88
B2-5-2-1 X B1-169-1	4.12**	1.89	-1.86**	1.30*	0.40	4.34**	-7.04**	0.43**	-0.41*	-5.41**
B3-13 X BRG-1	4.65**	1.89	-1.38**	-0.91**	4.26**	-5.91**	2.10	-0.36*	0.54**	2.71
B3-13 X BRG-3	4.92**	-4.25*	-1.12**	-0.76**	3.73**	4.75**	-18.00**	-0.22	-0.09	2.67
B3-13 X B1-169-1	6.67**	-1.87	-0.76	-0.65*	2.43	-0.32	2.63	-0.04	-0.21	-1.14
B2-10 X BRG-1	-5.81**	7.78**	1.45**	1.34**	-4.13**	-7.70**	16.34**	0.54**	0.82*	9.71**
B2-10 X BRG-3	-6.24**	1.54	2.34**	1.61**	4.14**	4.49**	8.97**	0.39*	0.46*	1.56
B2-10 X B1-169-1	0.26	-2.75**	-1.18**	-0.79**	-2.55	-2.57	3.49	-0.12	-0.11	-3.42
BRG-2 X BRG-1	-7.01**	5.55**	1.83**	1.14**	-3.83**	-4.52**	17.60**	0.48**	1.07**	12.31**
BRG-2 X BRG-3	-4.77**	11.70**	1.10**	1.10**	1.70	2.07	11.28**	0.51**	0.56**	6.01**
BRG-2 X BI-169-1	-2.39**	-8.67**	0.78**	0.76**	-4.78**	-5.53**	15.12**	-0.53**	0.92**	7.93**
SE	1.24	3.55	0.91	0.96	1.49	1.89	6.01	0.20	0.28	3.71

4.2.3.1. Days to 50% flowering

The highest significant negative gca effects for parents was recorded in BRG-2 and B2-10 for line followed by BRG-3 in tester, which exhibit negative significant gca Effects. However, the significant positive gca effects were exhibited by B2-5-2-1 in line followed by B1-169-1 in tester. The negative gca effects indicate their usefulness in breeding for early flowering lines which are desirable for earliness and may be considered as parents in crop improvement programmes for development of short duration genotypes.

Among the twelve hybrids significant negative sca effects was evidenced by number of crosses *viz*. BRG-2 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, which were desirable for earliness and may be considered as parents in crop improvement programmes for development of short duration genotypes. Positive sca effects was recorded for crosses B2-5 -2-1 x BRG-1, B3-13 x B1-169-1, B3-13 x BRG-3, B3-13 x BRG-1 and B2-5-2-1 x B1-169-1.

The cross combination BRG-2 x BRG-1 (good × average), BRG-2 x BI-169-1 (good × poor) and B2-10 x BRG-1(good × average) was the best specific combiner for earliness with highly significant negative sca effects. Indicating the role of non-additive gene action for this trait and is expected to produce desirable transgressive segregants in subsequent generations. Diallel mating or intermating in segregating populations followed by cyclic selection can be practiced for improving this trait in this cross.

The cross combination B2-10 x BRG-3 (good x good) and BRG-2 x BRG-3 (good x good) exhibited highly significant negative sca effect, this might be due to accumulation of undesirable and desirable alleles from the parents in respective cross combinations. The ratio of variance due to gca/sca was greater than unity for these traits, indicating the greater role of additive gene action for inheritance of this character.Similar findings were also reported

earlier by Sunilkumar *et al.* (2003), Lohithaswa *et al*. (2003), Raju and Muthiah (2007) and Sujatha and Kajjidoni (2013).

4.2.3.2. Plant height at maturity (cm)

The lines BRG-2 and B3-13 showed positive significant gca effects. In case oftesters, BRG-3 showed positive significant gca effects. Also line B2-10 and B2-5-2-1 showed negative gca effects, whereas in tester B1-169-1 showed negative significant gca effects .The negativegca effects indicate their usefulness in breeding for dwarf hybrids.

Among the cross combination five hybrid BRG-2 x BRG-3 followed by B2-10 x BRG-1 , B2-5-2-1 x BRG-3, BRG-2 x BRG-1 and B2-5 -2-1 x BRG-1 showed positive significant sca effects and three cross combinations BRG-2 x BI-169-1 followed by B3-13 x BRG-3 and B2-10 x B1-169-1 exhibited negative significant sca effects.

The cross B2-10 x B1-169-1(good x good) exhibited highly significant negative sca effect in desirable direction. Hence, there are possibilities of complimentary epistatic effects acting in the direction of additive effects of the good combiners. In these crosses, as the parents had high gca effects and there is a greater chance to get desirable transgressive segregants that can be handled through simple pedigree method whereas, cross BRG-2 x B1-169-1 (poor x good) indicate the importance of non-additive gene action. These crosses can be handled through breeding methods involving selection, intermating the selections and reselection for the improvement of these traits. On the contrary, B3-13 x BRG-3 (poor x poor) combining ability parents exhibited significant sca effect in desirable direction. Hence, cross performance cannot be accurately adjudged by assessing their parents gca effects alone and it is not always the case that high sca affects results from the combination of high gca parents. In this case improvement of this trait for these crosses appeared to be difficult as simple pedigree breeding will not be able to fix up useful

segregants in the early generation. Hence, one or two cycles of recurrent selection followed by pedigree breeding would be more effective and useful for improvement of this character. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character. These results are in accordance with the findings of Khorgade *et al*. (2000), Banu *et al.* (2006), Kumar *et al*. (2009), Bhavani and bhalla (2010), Mhasal (2015) and Sudhir *et al.* (2017).

4.2.3.3. Number of primary branches per plant

Among the lines B2-10 and BRG-2 showed positive significant gca effects, while BRG-1 and BRG-3 in testers exhibited positive significant gca effects, the positive gca effects indicate their usefulness in breeding for higher number of primary branches. Thus B2-10 and BRG-2 among the lines and BRG-1 and BRG-3 among the testers were considered to be desirable genotypes as these genotypes exhibited significantly high positive gca effects for number of primary branches per plant.

Among the 12 hybrids, eleven hybrids showed significant sca effects. Among them five hybrids B2-10 x BRG-3 followed by BRG-2 x BRG-1, B2-10 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1 exhibited positive significant sca effects. Negative significant sca effects were recorded in the cross B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3 and B2-10 x B1-169-1.

The cross B2-10 x BRG-3 (good × good), BRG-2 x BRG-1 (good x good), B2-10 x BRG-1 (good x good) and BRG-2 x BRG-3(good x good) exhibited highly significant positive sca effect. Hence, there are possibilities of complimentary epistatic effects acting in the direction of additive effects of the good combiners. In these crosses, as the parents had high gca effects and there is a greater chance to get desirable transgressive segregants that can be handled through simple pedigree method. On the

contrary the cross combination BRG-2 x BI-169-1(good x poor) exhibited positive significant sca effects indicating the role of non-additive gene action, diallel mating or intermating in segregating populations followed by cyclic selection can be practiced for improving this character. The ratio of variance due to gca/sca was greater than unity for these traits, indicating the greater role of additive gene action for inheritance of this character. Similar findings were also reported earlier by Sunilkumar *et al.* (2003), Lohithaswa *et al*. (2003), Raju and Muthiah (2007) and Sujatha and Kajjidoni (2013).

4.2.3.4. Number of secondary branches per plant

The estimate of gcaeffects among the lines showed that BRG-2 exhibited positive significant gca effects. Among the testers BRG-1 and BRG-3 showed positive significant gca effects, these genotypes exhibited significantly high positive gca effects for number of secondary branches per plant.

The positive gca effects indicate their usefulness in breeding for higher number of secondary branches in lines. Thus BRG-2 among the lines and BRG-1 and BRG-3 among the testers were considered to be desirable genotypes as these genotypes exhibited significantly high positive gca effects for number of secondary branches per plant.

Among the 12 hybrids, eleven hybrids showed significant sca effects. The hybrids B2-10 x BRG-3 followed by B2-10 x BRG-1, BRG-2 x BRG-1,B2-5-2-1 X B1-169-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1 showed positive significant sca effects and five hybrids B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1 and B2-10 x B1-169-1 exhibited negative significant sca effects.

The cross combinations B2-10 x BRG-3 (poor x good), B2-10 x BRG-1(poor x good) and BRG-2 x BI-169-1 (good x poor) indicate the importance

of non-additive gene action. These crosses can be handled through breeding methods involving selection, intermating the selections and reselection for the improvement of these traits. The crosses BRG-2 x BRG-1 (good x good) and BRG-2 x BRG-3 (good x good) indicated that the cross showing (good × good) combination may be exploited through the simple pedigree method while the other combination through diallel selective mating or intermating in segregating populations followed by cyclic selections for improvement of this character. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character. This finding is similar to the findings of Banu *et al.* (2006), Shoba and Balan (2010), Saroj *et al.* (2014), Patil *et al*. (2015) and Mhasal (2015).

4.2.3.5. Day to pod initiation

Among the lines B2-10 showed positive significant gca effects and among the testers B1-169-1 showed positive significant gca effects. The negative significant gca was recorded in BRG-2 in line and BRG-1 in tester which indicated their usefulness in breeding for day to pods initiation.

Among the 12 hybrids, three hybrids B2-10 x BRG-1 followed by BRG-2 x BI-169-1 and BRG-2 x BRG-1 exhibited negative significant sca effects followed by hybrids B2-10 x BRG-3, B3-13 x BRG-1 and B3-13 x BRG-3 exhibited significant positive sca effects.

The cross combination B2-10 x BRG-1 (poor x good) and BRG-2 x BI-169-1(good x poor) was the best for earliness with highly significant negative sca effects. Indicating the role of non-additive gene action for this trait and is expected to produce desirable segregants in subsequent generations. Diallel mating in segregating populations followed by cyclic selection can be practiced for improving this trait in this cross. On the other hand BRG-2 x BRG-1 (good x good) showed significant positive sca effects indicating the possibilities of

complimentary epistatic effects acting in the direction of additive effects of the good combiners. In these crosses, the parents had high gca effects, thus there is a greater chance to get desirable transgressive segregants that can be fixed through simple pedigree method. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character. Similar findings were also reported earlier by Yadav *et al.* (2008), Marappa (2008), Arbad *et al*. (2013), Mhasal (2015), Sudhir *et al*. (2017) and Shivarsha *et al*. (2017).

4.2.3.6. Days to 80 % pods maturity

The estimate of significant gca effects among the lines showed that BRG-2 and B2-10 exhibited negative significant gca effects. Among the testers BRG-1 showed negative significant gca effects. Also B2-5-2-1 in line and BRG-3 in tester recorded the positive significant gca effects .The negative gca effects indicated their usefulness in breeding for early maturing lines.

Out of 12 hybrids, eight hybrids showed significant sca effects, among them four hybrids B2-10 x BRG-1, B3-13 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-1 exhibited negative significant sca effects, indicating the possibility to get early maturing segregants. Whereas B2-5 -2-1 x BRG-1, B3-13 x BRG-3, B2-5-2-1 x B1-169-1 and B2-10 x BRG-3 registered significant positive sca effects indicating late maturity.

The cross combinations B2-10 x BRG-1 (good x good) and BRG-2 x BRG-1 (good x good) had displayed highest significant sca effects and both the parents involved were good general combiners for this trait. Hence, there is a greater chance to get desirable transgressive segregants that can be fixed through simple pedigree method in early generations. These crosses can be handled through recombination breeding for improving this trait.

On the contrary the cross combinations B3-13 x BRG-1(average x good) and BRG-2 x BI-169-1 (good x average) involving one or none good general combiners showed significant positive sca effects indicating the role of non-additive gene action. Diallel mating or intermating in segregating populations followed by cyclic selection can be practiced for improving this trait. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character. These findings of gca and sca are similar to observations of Saroj *et al*. (2014), Patil *et al*. (2015) and Shivarsha *et al.* (2017).

4.2.3.7. Number of pods per plant

Among the lines BRG-2 and B2-10 showed positive significant gca effects, and among the testers BRG-1 and BRG-3 showed positive significant gca effects. The positive gca effects indicate their usefulness in breeding for higher number of pods per plant.

Among the 12 hybrids, eight hybrids exhibited significant sca effects. Among them six hybrids BRG-2 x BRG-1 followed by B2-10 x BRG-1, BRG-2 x BI-169-1, B2-10 x BRG-3, B2-5-2-1 x BRG-1 and BRG-2 x BRG-3 exhibited positive significant sca effects and recorded highest number of pods per plant and two hybrids B3-13 x BRG-3 and B2-5-2-1 x B1-169-1 exhibited significant negative sca effects.

The cross combination BRG-2 x BRG-1 (good x good), B2-10 x BRG-1(good x good), B2-10 x BRG-3(good x good) and BRG-2 x BRG-3(good x good) exhibited highest positive sca effects for number of pods, hence there are possibilities of complementary epistatic effects acting in the direction of additive effects of the good combiners. In these crosses, as the parents had high gca effects and there is a greater chance to get desirable transgressive segregants that can be handled through simple pedigree method.

On the other hand BRG-2 x BI-169-1 (good x poor) and B2-5-2-1 x BRG-1 (average x good) exhibited significant positive sca effects for number of pods, indicating the role of dominance gene action responsible for the expression of this trait in these crosses, which could be exploited through biparental mating followed by selection in later generations. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character. The findings are in general agreement with the results reported by Raju and Muthiah (2007), Phad *et al.* (2007), Shoba and Balan (2010),Sudhir *et al*. (2017) and Shivarsha *et al*. (2017).

4.2.3.8. Pod length (cm)

The significant gca effect was reported in both line and tester,in case ofline BRG-2 and B2-10 showed positivesignificant gca effects. In testers BRG-1 and BRG-3 showed positive significant gca effects. The positive gca effects indicate their usefulness in breeding for maximum pod length.

Out of 12 hybrids, seven hybrids have shown significant sca effects of which five hybrids B2-10-x BRG-1followed by BRG-2 x BRG-3, BRG-2 x BRG-1, B2-5-2-1 x B1-169-1 and B2-10 X BRG-3 showed positive significant sca effects with maximum pod length and two hybrids BRG-2 x BI-169-1and B3-13 x BRG-1 exhibited negative significant sca effects.

The cross combination B2-10-x BRG-1 (good x good), BRG-2 X BRG-3 (good x good), BRG-2 x BRG-1 (good x good) and B2-10 x BRG-3(good x good) showed highest positive sca effects. Hence, there are possibilities of complementary epistatic effects acting in the direction of additive effects of the good combiners. In these crosses, as the parents had high gca effects and there

is a greater chance to get desirable transgressive segregants that can be handled through simple pedigree method in early generations.

The cross B2-5-2-1 x B1-169-1 (poor x poor) with poor combining ability parents exhibited significant positive sca effect in desirable direction. In this case improvement of this trait also appeared to be difficult as simple pedigree breeding will not be able to fix up useful segregants in the early generation. Hence, one or two cycles of recurrent selection followed by pedigree breeding would be more effective and useful for improvement of this character. The cross B2-10 x B1-169-1 (good x poor) exhibited highly significant positive sca effect in desirable direction, indicating the role of non-additive gene action for these traits. Diallel mating or intermating in segregating populations followed by cyclic selection can be practiced for improving this trait in this cross. The ratio of variance due to gca/sca was greater than unity for these traits, indicating the greater role of additive gene action for inheritance of this character. Similar findings were also reported earlier by Sunilkumar *et al.* (2003), Lohithaswa and Dharmaraj (2003) and Sujatha and Kajjidoni (2013).

4.2.3.9. 100-seed weight (g)

Among the lines, positive significant gca effects were observed in BRG-2 and B2-10, among the testers, BRG-1 and BRG-3 showed positive significant gca effects. The positive gca effects indicate their usefulness in breeding for higher 100-seed weight.

Among the 12 hybrids, eight hybrids showed significant sca effects, six hybrids BRG-2 x BRG-1 followed by BRG-2 x BI-169-1, B2-10 x BRG-1, B3-13 x BRG-1, BRG-2 x BRG-3 and B2-10 x BRG-3 exhibited positive significant sca effects and showed maximum 100-seeds weight and two

hybrids B2-5-2-1 x BRG-3 and B2-5-2-1 x B1-169-1 exhibited negative significant sca effects.

The cross combination BRG-2 x BRG-1(good x good), B2-10 x BRG-1 (good x good), BRG-2 x BRG-3 (good x good) and B2-10 x BRG-3 (good x good) were among the best combiners for 100-seed weight with desirable positive significant sca effects. Hence, there are possibilities of complementary epistatic effects acting in the direction of additive effects of the good combiners. In these crosses, as the parents had high gca effects and there is a greater chance to get desirable transgressive segregants that can be handled through simple pedigree method.

The cross combination BRG-2 X BI-169-1(good x poor) and B3-13 x BRG-1 (poor x good) were also among the best combiners for 100-seed weight with desirable positive significant sca effects, indicating the role of dominance gene action responsible for the expression of this trait in these crosses, which could be exploited through biparental mating or intermating of selects followed by selection in later generations. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character. The findings are in general agreement with the results reported by Raju and Muthiah (2007), Phad *et al.* (2007), Shoba and Balan (2010),Sudhir *et al*. (2017) and Shivarsha *et al*. (2017).

4.2.3.10. Seed yield per plant (g)

Among the lines, significant and positive gca effects was recorded in BRG-2 and B2-10. Among the testers, BRG-1 and BRG-3 showed positive significant gca effects. The positive gca effects indicate their usefulness in breeding for higher seeds yield.

The significant sca effects among the 12 hybrids revealed that six hybrids were significant for sca effects. Among the hybrids, four hybrids BRG-2 x BRG-1 followed by B2-10 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3 showed positive significant sca effects and two hybrids B2-5 -2-1 X BRG-1 and B2-5-2-1 x B1-169-1 showed negative significant sca effects. The hybrids BRG-2 x BRG-1 followed by B2-10 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3 were recorded highest for seed yield per plant.

The cross combination BRG-2 x BRG-1 (good x good), B2-10 x BRG-1 (good x good), BRG-2 x BRG-3(good x good) had displayed high significant sca effects and the parents involved were good general combiners for seed yield per plant. Hence, there is a greater chance to get desirable transgressive segregants that can be handled through simple pedigree method in early generations.

Dominance gene action was found to be responsible for the expression of this trait in the crossBRG-2 x BI-169-1 (good x poor) which could be exploited through biparental mating or intermating of selects followed by selection in later generations for isolation of breeding lines with high seed yield. The ratio of variance due to gca/sca was less than unity for these traits, indicating the greater role of non additive gene action for inheritance of this character.These results are in accordance with the findings of Jahagirdar (2003), Sunilkumar *et al.* (2003), Sudhir *et al*. (2017) and Shrivarsha *et al.* (2017).

4.3. Generation mean analysis

Genetic variability present in the population and understanding the type and relative magnitude of gene action involved for different characters are prerequisites for manipulating quantitatively inherited characters in a systematic breeding programme. Its success depends upon both the amount of

variability present in a population with which plant breeder is dealing and so it's efficient management and utilization.

Fisher (1918) first partitioned the continuous variation into additive, dominance and epistasis. In 1932, Fisher *et al.* suggested the method for separation of fixable and non-fixable components of variation in segregating population by the use of second and third degree statistics. The earlier methods of determining the genetic components of quantitative variability were based on the assumption that the non-allelic interactions among genes have a rather negligible bias on the estimates of additive and dominance components of variation. To analyses the role of epistasis, however, a genetic model was developed by Hayman (1958) and Jinks and Jones (1958) which partitioned epistatic effects into different components from the means of six generations of a cross, *viz*. P1, P2, F1, F2 B1and B2, the P1 and P2 being two homozygous parents. Likewise the procedure for analysis of first degree statistics was developed by Mather (1949).

With a view to studying the nature and mode of gene action of yield and its components, generation mean analysis was carried out utilizing mean data of five basic generations *viz*. P1, P2, F1, F2, and F3 of twelve selected crosses. The significance of C and D scales indicates the presence of two types of non-allelic interactions *viz*. additive × additive (i) and dominance × dominance (l). The significance of C scale suggests dominance × dominance (l) type of interaction. The significance of D scale reveals additive × additive (i) type of gene interaction and significance of both C and D scales indicates additive × additive and dominance × dominance type of gene interactions. In the present investigation the calculated values of C and D scaling test were highly significant for all the twelve crosses under study, except few crosses. Assuming the presence of non allelic interactions for all the characters, data were subjected to further analysis using five parameter models as suggested by Hayman (1958). The mean performance of five generations with respect to

yield associated traits along with standard errors and the estimates of individual scaling tests (C and D) and genetic effects *viz*. additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) were collated in Tables 4.7 to 4.19, and presented character wise.

The means of P1, P2, F1, F2 and F3 generation in each cross was used to estimates various gene effects. Since the back cross generations were not available, d' and 'j' could not be estimated separately and a combined estimate of (d-j) symbolized, as'd' was only available. Hayman (1958) and Jinks and Jones (1958) have developed independently the method of estimation of five genetic parameters using generation means. These models are based on certain assumptions such as (i) diploid inheritance (ii) multiple allelism is absent (iii) linkage is absent (iv) absence of lethal genes (v) constant variability for all genotypes and (vi) environmental effects are additive with the genotypic value. Some of these assumptions like diploid inheritance, random distribution of environment effects and constant variability of all genotypes can be satisfied. However, some of them like the absence of multiple allelism and epistasis are hardly realistic assumption, though unavoidable, if any analysis is at all to be possible.

Method suggested by Mather (1949) is based on the assumption that epistasis is absent, while Hayman's (1958) method using generation means allows accommodation of epistasis. Among the interaction effects additive x additive type of interaction effects are more useful for the breeders. The two interaction effects namely, i = sum of additive x additive effects of genes and l = sum of dominance x dominance effects of genes were estimated in five parameter model along with m, d and h. As Hayman (1958) pointed out that in the presence of epistatic effects, estimation of parameters from different crosses is not readily comparable. It will therefore, be convenient to present the results of this analysis separately for each cross combination. Crosswise for all the ten characters of seven crosses have been presented in Table 4.10 to Table

4.19 character wise and discussions on the results obtained with regard to nature of gene action are reported here cross and character wise.

4.3.1. Analysis of Variance

Analysis of variance for five generations of every cross was carried out and has been presented in Table 4.7 to Table 4.9. The analysis of variance for five generation of twelve crosses showed significance mean square due to population for all the crosses indicating the existence of considerable amount of genetic variability for yield and its components in all the crosses.To determine gene interaction presence in twelve pigeon pea crosses simple scaling test was applied as given by Mather. Result on scaling test indicate that C and D were significant in each of the twelve crosses for most of the traits studied, suggesting the presence epistatic components i and l involvement either one or both of the two. Five parameter models was fitted to the observed components of mean in each of the twelve crosses On the basis of simple scaling test for epistasis,

The C and D scaling tests (Mather, 1949) were applied prior to the use of the five parameter model (Hayman, 1958) for the estimation of various genetic components.

4.3.2. Mean effect (m)

The‘t’ values were tested against‘t’ table value to estimate the significance of mean effect for various traits. The estimates of mean (m) was significant for all the traits under study *viz*, days to 50% flowering, number of primary branches/plant, number of secondary branches/plant, days to pods initiation, days to 80 % pods maturity, plant height at maturity (cm), pod length (cm), number of pods per plant, 100-seed weight (g) and seed yield per plant (g) which is presented in Table 4.10 to Table 4.19.

Table 4.7: Analysis of variance (generation mean and standard error) for yield and its components in twelve crosses of pigeon pea

Source of variation	DF	Day to 50% flowering	Plant height (cm)	No. of pri. branches	No. of sec. branches	Day to pods initiation	Day to 80% pods initiation	No. of pods per plant	Pods length (cm)	100-seed weight (g)	Seed yield per plant (g)
BRG-2 X BRG-1											
Replication	2	3.92	41.55	0.025	0.21	4.53	5.46	21.57	0.024	0.043	1.64
Generation	4	8.56**	187.21**	0.76**	2.76**	12.22**	35.76**	187.22**	0.076**	0.507**	7.87**
Error	8	2.20	11.03	0.081	0.51	1.57	8.23	14.43	0.018	0.042	1.08
BRG-2 X BRG-3											
Replication	2	5.45	32.53	0.063	0.42	3.46	1.76	28.87	0.053	0.32	2.89
Generation	4	11.81**	213.22**	1.21**	3.81**	19.31**	45.45**	165.82**	0.046**	0.73**	6.89**
Error	8	1.42	13.01	0.05	0.75	6.32	6.28	12.65	0.011	0.036	0.67
BRG-2 X B1-169-1											
Replication	2	0.088	22.54	0.07	0.51	9.19	3.56	49.76	0.044	0.67	0.76
Generation	4	7.45**	165.43**	1.67**	1.72**	54.22**	49.67**	178.23**	0.0589**	1.32**	8.93**
Error	8	0.81	12.33	0.04	0.33	4.68	7.59	16.53	0.017	0.68	0.89
B3-13 X BRG-1											
Replication	2	0.22	27.34	0.07	0.53	0.81	1.65	8.46	0.09	0.12	0.56
Generation	4	10.21**	145.27**	1.35**	5.67**	16.35**	38.59**	211.04**	0.056**	0.67**	6.28**
Error	8	0.68	11.02	0.031	0.47	1.06	7.86	21.38	0.04	0.03	0.73
B3-13 X BRG-3											
Replication	2	1.53	12.34	0.021	0.75	0.78	1.59	24.22	0.24	0.56	2.67
Generation	4	9.45**	187.42**	0.671**	4.83**	7.76**	29.65**	193.07**	0.062**	1.32**	9.03**
Error	8	2.46	16.34	0.052	0.71	0.55	2.088	13.76	0.07	0.37	0.76

Table 4.8: Analysis of variance (generation mean and standard error) for yield and its components in twelve crosses of pigeon pea

Source of variation	DF	Day to 50% flowering	Plant height (cm)	No. of pri. branches	No. of sec. branches	Day to pods initiation	Day to 80% pods initiation	No. of pods per plant	Pods length (cm)	100-seed weight (g)	Seed yield per plant (g)
B3-13 X B1-169-1											
Replication	2	0.81	38.52	0.027	0.74	2.69	3.05	6.76	0.044	0.67	0.76
Generation	4	7.92**	254.31**	0.92**	2.56**	43.39**	24.67**	178.23**	0.0589**	1.41**	8.93**
Error	8	0.76	17.51	0.067	0.35	8.88	8.59	18.53	0.016	0.28	0.89
B2-10 X BRG-1											
Replication	2	0.78	31.23	0.07	0.66	8.86	4.86	35.54	0.043	0.19	1.22
Generation	4	9.32**	211.65**	1.64**	6.76**	139.53**	33.43**	119.06**	0.075**	0.92**	9.36**
Error	8	1.81	11.27	0.08	0.69	14.87	5.83	19.41	0.028	0.0312	0.73
B2-10 X BRG-3											
Replication	2	4.45	16.54	0.018	0.39	0.61	7.73	17.64	0.039	0.31	0.78
Generation	4	7.055**	169.11**	1.61**	4.47**	13.42**	41.35**	184.66**	0.54**	0.79**	7.01**
Error	8	2.31	15.33	0.08	0.43	1.86	6.54	13.98	0.026	0.016	0.82
B2-10 x B1-169-1											
Replication	2	3.59	27.31	0.16	0.23	0.44	4.65	6.02	0.062	0.08	0.85
Generation	4	11.32**	191.16**	1.19**	2.48**	21.18**	38.29**	90.02**	0.079**	1.69**	5.84**
Error	8	1.54	14.17	0.03	0.51	2.07	8.033	13.41	0.013	0.022	0.71
B2-5-2-1 X BRG-1											
Replication	2	4.76	41.34	0.06	0.025	1.39	10.47	7.33	0.043	0.065	1.21
Generation	4	34.75**	145.56**	1.23**	1.56**	18.87**	28.73**	189.77**	0.069**	1.022**	9.55**
Error	8	2.34	15.64	0.07	0.053	4.97	6.87	19.06	0.05	0.027	0.79

Table 4.9: Analysis of variance (generation mean and standard error) for yield and its components in twelve crosses of pigeon pea

Source of variation	DF	Day to 50% flowering	Plant height (cm)	No. of pri. branches	No. of sec. branches	Day to pods initiation	Day to 80% pods initiation	No.of pods per plant	Pods length (cm)	100-seed weight (g)	Seed yield per plant (g)
B2-5-2-1 X BRG-3											
Replication	2	0.28	41.34	0.018	0.26	6.43	5.68	12.65	0.053	0.0373	0.81
Generation	4	12.53**	128.65**	0.621**	2.68**	16.88**	36.02**	186.64**	0.086**	0.83**	8.48**
Error	8	0.91	12.06	0.081	0.33	3.72	4.43	14.98	0.031	0.0127	0.73
B2-5-2-1 X B1-169-1											
Replication	2	0.91	31.26	0.76	0.68	0.83	6.34	20.28	0.081	0.069	0.16
Generation	4	9.28**	164.27**	1.59**	3.93**	15.93**	23.81**	179.56**	0.072**	0.92**	6.23**
Error	8	1.39	16.46	0.05	0.41	5.47	3.70	16.06	0.034	0.028	0.51

4.3.3. Main effect

The scaling test and main effect of ten characters for different crosses (twelve crosses) is presented from Table 4.10 to Table 4.19.

4.3.3.1. Days to 50 % flowering

The D scaling test was non significant in cross B2-10 X BRG-3whereas both C and D scaling test were non significant for crosses B2-5-2-1 X BRG-3, which indicated the adequacy of both additive x additive and dominance x dominance model for this cross, while the remaining crosses exhibit significant C and D individual scaling test.

Among major gene effects, additive (d) component exhibits negative significant for day to 50% flowering in crosses *viz*. BRG-2 x BI-169-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, BRG-2 x BRG-1, B3-13 x BRG-1, BRG-2 X BRG-3and B2-10 x B1-169-1,whereas the dominance (l) component exhibit negative significantfor the crosses B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BI-169-1 and BRG-2 x BRG-1 followed by B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-5 -2-1 X BRG-1 and BRG-2 x BRG-3, which exhibit positive dominance (h) effects. The estimates of additive (d) and dominant (h) gene effects were significant in eleven and ten crosses. However, negatively significant additive and dominant gene effects were observed in seven and five crosses respectively. The magnitude of dominant (h) component was comparatively higher than additive (d) gene effects in majority of the crosses. Similar results were presented by Sarode *et al*. (2009),Kumar *et al*. (2009) and Singh and Singh (2016).

4.3.3.2. Plant height at maturity

Among the 12 crosses studied both C and D scales were non-significant in crosses B3-13 x BRG-3, which indicated the adequacy of additive-dominance model for this cross followed byB3-13 X B1-169-1, which

exhibited non significant for D scaling test, while the remaining crosses exhibit significant for both C and D scaling test.

The additive (d) gene effects were significant and positive for plant height in crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas cross combinations B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3 and B2-10 x B1-169-1 showed negative significant additive (d) effects. Significant and negative dominance (h) effects was recorded in crosses B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-3, BRG-2 x BI-169-1 and BRG-2 x BRG-1. Among the main gene effect, the additive component was positively significant in six crosses and negatively significant in six crosses, whereas dominance gene effect was positively significant in two crosses and negatively significant in ten crosses besides having much higher magnitude than additive gene effects, but the magnitude of dominance gene effect was mostly negative. Similar results were recorded by Sarode *et al*. (2009) and Kumar *et al*. (2009).

4.3.3.3. Number of primary branches

Significance of one or more scaling tests suggested the presence of non-allelic interactions. For number of primary branches per plant B2-5-2-1 x B1-169-1recorded non significant for D scaling test indicating the adequacy of dominance x dominance model.

Significant and positive dominance (h) effects were recorded in crosses B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BI-169-1, whereas the cross combination B2-5-2-1 x BRG-3, B3-13 X B1-169-1, B2-10 x BRG-3, B2-10 x BRG-1,BRG-2 x BRG-1 and BRG-2 x BRG-3 showed negative significant dominance (h) effects. Significant and negative additive (d) effects were recorded in the crosses B3-13 x BRG-3, B2-

10 x BRG-3 and BRG-2 x BRG-1. Positive and significant additive (d) effects are observed in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 X BRG-3and BRG-2 x BI-169-1. Additive and dominant gene effects were significant in all the crosses. However dominant component was mostly negatively significant in all the crosses and its magnitude was usually higher than that of additive component. Singh and Singh (2016) and Ashutosh *et al*. (2017)also reported similar results.

4.3.3.4. Number of secondary branches

Among the 12 crosses studied D scaling test were non significant for the crossesB3-13 X B1-169-1, which indicated the adequacy of additive x additive model for this cross.

Among major gene effectpositive and significant dominance (h) effect was recorded in B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1, whereas significant negative dominance (h) effects was recorded in the crosses BRG-2 x BRG-3. Significant and negative additive (d) effects were recorded in the crosses B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas significant and positive additive (d) effects were recorded in B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BRG-1. The estimates of additive (d) and dominant (h) gene effects were significant in eleven and nine crosses, respectively but the magnitude of dominant (h) gene effect was comparatively higher than additive (d) gene effect in majority of the crosses. This was also reported by Kandalkar (2006), Singh and Bajpai (2005), Kumar *et al*. (2009) and Singh and Singh (2016).

4.3.3.5. Days to pod initiation

Among the 12 crosses studied the C scale was non-significant in the case of B3-13 x BRG-3, which indicated the adequacy of dominance x dominance model for this cross, whereas the cross combination B3-13 x B1-169-1 exhibit non significant for D scaling test indicating the adequacy of additive x additive model for this cross.

Among the major gene effects additive (d) gene effects were significant and positive in the crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 X BRG-3,B2-10 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BRG-3, whereas the cross combination B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-1, B2-10 x BRG-1and BRG-2 x BI-169-1 showed negative significant additive (d) effects. Highly significant and negative dominance (h) effects were recorded in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3 and BRG-2 x BRG-3, whereas positive and significant dominance (l) effects observed in the crosses B3-13 x BRG-3, B2-10 x B1-169-1,BRG-2 X BI-169-1 and BRG-2 x BRG-1. The estimates of additive (d) and dominant (h) gene effects were significant in all thecrosses, negatively in six and eight crosses, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects in majority of the crosses. Singh and Bajpai (2005), Kumar *et al*. (2009) and Singh and Singh (2016) also reported role of dominance component in the expression of days to pod initiation.

4.3.3.6. Days to 80% pods maturity

The C scaling test for days to 80% pod maturity were non significant for crosses B3-13 x BRG-3 indicating the adequacy of dominance x dominance model for the cross, whereas crosses B3-13 X B1-169-1and BRG-2 X BRG-3exhibit

non significant for D scaling test indicating the adequacy of additive x additive model for this cross.

The additive (d) gene effects were significant and positive in crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3 and BRG-2 x BRG-3, whereas the cross combination B3-13 X B1-169-1, BRG-2 x BI-169-1, BRG-2 x BRG-1, B2-5-2-1 x B1-169-1, B2-5-2-1 x BRG-3, B2-10 x BRG-1 and B2-10 x B1-169-1 showed negative significant additive (d) effects. Highly significant and negative dominance (h) effects were recorded in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1,B3-13 X B1-169-1, B2-10 X BRG-3, BRG-2 X BRG-3and BRG-2 X BI-169-1whereas positive and significant dominance (h) effects was observed in the crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 X B1-169-1 and BRG-2 x BRG-1. The estimates of additive (d) and dominance (h) gene effects were significant in eleven and twelve crosses. Negatively in seven crosses for both additive and dominance components, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects in majority of the crosses.This is in conformity with the result of Kandalkar (2006) and Kumar *et al*. (2009).

4.3.3.7. Number of pods per plant

Among the 12 crosses studied the C and D scale were significant for all the crosses. Significant and positive dominance (h) effects were recorded in crosses BRG-2 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, B2-10 x B1-169-1, B2-5-2-1 x BRG-1 and B2-5-2-1 x B1-169-1, whereas significant negative dominance (h) effects are recorded in the crosses B2-5-2-1 x BRG-3, B3-13 X B1-169-1, B2-10 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1. Significant and negative additive (d) effects were recorded in the crosses B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B2-10 x BRG-1, B3-13 X BRG-3, B2-10 X BRG-3 and BRG-2 x BRG-3 on the other hand positive significant

additive (d) effects were observed in the crosses B2-5-2-1 x BRG-3, BRG-2 x BRG-1, B2-10 x B1-169-1, B3-13 x B1-169-1 and BRG-2 x BI-169-1. The estimates of additive (d) and dominant (h) gene effects were significant in eleven and twelve crosses, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects in majority of the crosses. Predominance of dominance effects for number of pods was also reported byKumar *et al*. (2009), Singh and Singh (2016) and Ashutosh *et al*. (2017).

4.3.3.8. Pod length (cm)

Significance of one or more scaling tests suggested the presence of non-allelic interactions. C scaling test recorded non significant for crossB2-5-2-1 X B1-169-1 and B3-13 X BRG-3indicating the adequacy of dominance x dominance model for this cross.

Among the major gene effect additive (d) gene effects were significant and positive in crosses B2-5-2-1 x B1-169-1, B3-13 x B1-169-1, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1 whereas the cross combination B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-1 and B2-10 x BRG-3 showed negative significant additive (d) effects. Highly negative and significant dominance (h) effects were recorded in the crosses B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-1, BRG-2 x BRG-3, BRG-2 x BI-169-1, B3-13 x BRG-3 and B3-13 x BRG-1, the positive significant dominance (h) effects observed in the crosses B2-5 -2-1 x BRG-1. Among the main gene effect, additive (d) and dominant (h) gene effects were significant in eleven crosses, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects. Kandalkar (2006), Singh and Bajpai (2005), Kumar *et al*. (2009) and Singh and Singh (2016) also reported the importance of dominance (h) effect for this trait.

4.3.3.9. 100-seed weight (g)

Among the 12 crosses studied the scaling test C and D were significant for all the crosses. Significant scaling tests suggested the presence of non-allelic interactions. Additive (d) gene effects were positive and significant for crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-1 and B2-10 x B1-169-1, Significant negative additive (d) effect for this traits was recorded in crosses B3-13 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas the cross combination B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x B1-169-1, B2-10 x BRG-1 and BRG-2 x BRG-1 showed negative dominance (h) effects. Significant and positive dominance (h) effects were recorded in crosses B2-5 -2-1 X BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3,BRG-2 X BI-169-1 and BRG-2 x BRG-3. Among the main gene effect, magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects. Similar result of predominance of dominance effects for 100-seed weight was also reported by Kumar *et al*. (2009), Singh and Singh (2016) and Ashutosh *et al*. (2017).

4.3.3.10. Seed yield per plant (g)

Among the 12 crosses studied the scaling test C and D scales were significant for all the crosses. Among the main effects the additive (d) gene effects were positive and significant in the crosses B2-5-2-1 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BRG-3, whereas the cross combination B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1 and BRG-2 x BI-169-1 exhibited negative significant additive (d) effects, whereas dominance (h) effects were negative and significant for crossesB2-5 -2-1 X BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x B1-169-1 and BRG-2 x BRG-1. The positive and significant dominance (h) were recorded in B3-13 x BRG-1, B3-

13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1. Among the main gene effect, additive (d) and dominant (h) gene effects were significant in all the crosses, respectively but the magnitude of dominant (h) gene effects was comparatively higher than additive (d) gene effects. Kandalkar (2006), Singh and Bajpai (2005), Kumar *et al.* (2009), Singh and Singh (2016) and Ashutosh *et al*. (2017)also reported predominance of dominance (h) effect for seed yield.

4.4. Interaction effects

The interaction effect (epitasis) for ten characters in 12 crosses are presented from table 4.10 to table 4.19.

4.4.1. Days to 50 % flowering

As regards to digenic interaction for days to 50 per cent flowering, estimates of additive x additive (i) gene effects were negative and significant for the crosses B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BRG-1. While positive and significant additive x additive (i) gene effects were recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BI-169-1. Dominance x dominance (l) interaction effects were positive and significant in crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B2-10 x BRG-3, and BRG-2 x BRG-1, whereas crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1, BRG-2 x B1-169-1, BRG-2 x BRG-3 and B2-10 x B1-169-1 exhibited negative and significant dominance x dominance (l) effects.

The dominance (h) and dominance x dominance (l) effects sign for all the crosses were in opposite direction, suggesting presence of duplicate type of epistasis in the genetic control of this trait except B2-5-2-1 x B1-169-1, B2-10 x B1-169-1 and BRG-2 x B1-169-1 which showed complementary type of epistasis. Positive sign of additive x additive (i) gene effects in cross revealed

that early segregating generation selection could be practiced. In case of negative sign of additive x additive (i) gene effects in the crosses selection can be deferred to later generations when suitable recombinants become available in the crosses.

Additive x additive (i) interaction were significant in eleven crosses, and negative and highly significant in six crosses, indicating the major contribution of additive x additive (i) interaction for the expression of this trait, as it highly significant in many crosses. Likewise, though dominance x dominance (l) effects were significant in ten crosses, but its magnitude were mostly positive and higher than additive x additive (i) interaction for the expression of this character. Positive and significance dominance x dominance gene effects for days to 50% flowering was also reported by Kumar *et al.* (2009), Sarode *et al*. (2009),and Singh and Singh (2016).

4.4.2. Plant height at maturity (cm)

As regard to epistasis negative and significant dominance x dominance (l) effects is recorded in crosses B3-13 x BRG-1 and B3-13 x B1-169-1, positive and significant dominance x dominance (l) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1. Hence, selection can be delayed until later generations when the dominance effects would have diminished.

Additive x additive (i) effects were negative and significant for the crosses B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-3 and BRG-2 x BRG-1. Negative and significant additive x additive (i) effects suggest that selection can be deferred to later generations when suitable recombinants become available in the crosses. Positive and significant additive x additive (i) effects recorded in crosses B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x B1-169-1, B2-10 x B1-169-1 and

BRG-2 x B1-169-1, positive sign of additive x additive (I) effects in cross revealed that selection could be practiced in early segregating generations.

Among the interaction components, dominance x dominance (l) effects was positive and significant in most of the crosses except B3-13 x BRG-1 and B3-13 x B1-169-1, which were negatively significant. Similar results of dominance x dominance (i) effect were reported by Sarode *et al*. (2009), Kumar *et al*. (2009) and Singh and Singh (2016). The dominance (h) and dominance x dominance (l) effects sign for all the crosses were in opposite direction, suggesting presence of duplicate type of epistasisfor plant height. Recurrent selection for specific combining ability is suggested to exploit duplicate epistasis and in order to exploited dominance epistatic gene effects.

Dominance x dominance gene effect was mostly positive, whereas additive x additive gene effect was mostly negative, and magnitude of dominant x dominant (l) gene effects was comparatively higher than additive x additive gene effects for plant height. This is in conformity with the finding of Sarode *et al*. (2009),Kumar *et al*. (2009), Singh and Singh (2016) and Ashutosh *et al*. (2017).

Table 4.10:Scaling tests and estimates of gene effects for days to 50% flowering in crosses

Sl.No	Crosses	Scaling test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-26.67**	-11.00**	126.01**	7.21**	11.86**	18.12**	-11.34**	D
2	B2-5-2-1 X BRG-3	0.87	-0.77	132.43**	-10.58**	5.34	1.43	3.42	
3	B2-5-2-1 X B1-169-1	-27.53**	-5.00**	126.65**	-2.13**	9.56**	6.23**	7.34**	C
4	B3-13 X BRG-1	11.67**	10.00**	134.57**	-3.58**	-21.00**	-21.00**	31.45**	D
5	B3-13 X BRG-3	-9.67**	-3.47**	126.12**	-0.76	6.43**	7.34**	-4.34	
6	B3-13 X B1-169-1	13.81**	-3.53**	131.13**	4.67**	-2.75	-5.36**	-0.36	
7	B2-10 X BRG-1	-45.23**	-7.53**	126.11**	2.94**	15.58**	-11.45**	-14.68**	D
8	B2-10 X BRG-3	8.57**	4.33	124.76**	4.86**	-12.76**	-8.37**	19.12**	D
9	B2-10 X B1-169-1	-25.33**	-8.33**	154.24**	-0.87**	-7.56**	6.17**	-11.25**	C
10	BRG-2 X BRG-1	-25.03**	1.43*	120.25**	-1.55**	-6.43**	-2.87*	10.37**	D
11	BRG-2 X BRG-3	26.53**	6.10**	122.24**	-0.87**	7.56**	-5.67**	-7.25**	D
12	BRG-2 X BI-169-1	-3.63**	-19.77**	129.45**	-11.47**	-15.65**	14.43**	-12.68**	c

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

Table 4.11: Scaling tests and estimates of gene effects for Plant height in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-191.54**	-20.71**	182.76**	-16.76**	-62.09**	38.45**	83.34**	D
2	B2-5-2-1 X BRG-3	67.39**	80.67**	214.67**	-25.31**	-31.74**	-12.76**	67.54**	D
3	B2-5-2-1 X B1-169-1	23.22**	14.14**	215.76**	21.65**	-31.76**	-25.35**	30.64**	D
4	B3-13 X BRG-1	-89.36**	-55.67**	191.64**	12.54**	24.86**	110.54**	-113.35**	D
5	B3-13 X BRG-3	-2.39	1.74	205.65**	-14.03**	-19.61**	-7.32	8.06	
6	B3-13 X B1-169-1	-32.56**	-1.98	211.71**	12.56**	38.12**	28.65**	-17.78**	D
7	B2-10 X BRG-1	23.63**	28.65**	217.83**	-24.76**	-57.65**	-54.53**	68.65**	D
8	B2-10 X BRG-3	49.19**	39.59**	216.45**	-22.43**	-73.54**	-79.56**	98.85**	D
9	B2-10 X B1-169-1	31.35**	50.80**	224.76**	-24.54**	-105.67**	101.45**	256.47**	D
10	BRG-2 X BRG-1	11.22*	29.25**	199.56**	23.45**	-57.34**	-56.63**	98.37**	D
11	BRG-2 X BRG-3	-76.52**	-14.51**	183.65**	19.85**	-31.55*	-43.85**	131.45**	D
12	BRG-2 X BI-169-1	85.73**	-15.71**	216.65**	22.54**	-73.32**	62.79**	158.8**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

4.4.3.Number of primary branches

Among the interaction effects negative and significant additive x additive (i) effects were recorded in crosses B2-5-2-1 x BRG-3, B2-10 x BRG-3 and BRG-2 x BRG-3, whereas positive significant additive x additive (i) effects were observed in crosses B-2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1. The negative sign of additive x additive (i) gene effects in the crosses suggested selection can be deferred to later generations when suitable recombinants become available in the crosses. Positive and significant dominance x dominance (l) effects are recorded in crosses B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, BRG-2 x BRG-3, B2-10 x BRG-3, BRG-2 x BRG-1and B3-13 x B1-169-1. On the other hand significant and negative dominance x dominance (i) effect are recorded in crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BI-169-1.

The dominance (h) and dominance x dominance (l) effects sign for all the crosses were in opposite direction, suggesting presence of duplicate nature of epistasis in the genetic control of this trait. Positive sign of dominance x dominance (l) effect in crosses indicated that dominance direct was unidirectional, which suggests that intermatting the selects in segregating generations to exploit components of genetic variability *i.e* additive and non-additive in number of primary branches per plant would lead to desirable improvement. Whereas positive sign of additive x additive (i) effects in crosses revealed that selection is possible in early segregating. Both additive x additive (i) and dominance x dominance (l) effects were significant for all the crosses irrespective of sign in all the crosses. However the relative contribution of dominance x dominance gene effects (l) was much higher than additive x additive gene effects (i) coupled with duplicate type of epistasis.

Among epistatic interaction additive x additive gene effects was positive and significant in seven crosses and negative and significant in three crosses, in case of dominance x dominance gene interaction, it was negative and significant in four crosses and positively significant in seven crosses, and its magnitude was comparatively higher than additive x additive gene effects. This is in conformity with the finding of Sarode *et al*. (2009), Singh and Singh (2016) and Ashutosh*et al*. (2017).

4.4.4. Number of secondary branches

Among the epistatic gene effects positive and significant additive x additive (i) gene effects was recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1.Whereas negative and significant additive x additive (i) gene effects was significant for the crosses B2-5-2-1 x BRG-3and B3-13 x B1-169-1.

The positive and significant dominance x dominance (l) effects were significant in crosses B3-13 x BRG-1, B3-13 x B1-169-1and BRG-2 x BRG-3. Negative and significant dominance x dominance (i) gene effects was recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 X BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 X BRG-1, B2-10 X BRG-3, B2-10 X B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1.

The estimates of dominance (h) and dominance × dominance (l) components were opposite in signs and significant in all the crosses. Maximum of the crosses exhibited positive and significant additive x additive (i) effect except B2-5-2-1 x BRG-3 and B3-13 x B1-169-1 which were negatively significant for additive x additive (i) effect. Therefore, selection should be deferred to later generations for these two crosses when desirable recombinants become available. The positive and significant additive x additive (i) effect, indicate the possibility of selection in early segregating generation. On the

other hand negative and significant dominance x dominance (i) gene effects was recorded in most of the crosses except B3-13 x BRG-1, B3-13 x B1-169-1 and BRG-2 x BRG-3 which were positively significant for number of secondary branches. Therefore, delay in selection until later generations when the dominance effects would have diminished. Importance of dominance x dominance (i) gene effects for inheritance of number of secondary branches was also reported by Kandalkar (2006) and Kumar *et al*. (2009).

Among the non-allelic interaction, the magnitude of dominance × dominance gene effects was much higher than additive x additive gene effects, but mostly negatively significant. This is in conformity with the finding ofSinghand Singh (2016) and Ashutosh *et al.* (2017).

Table 4.12: Scaling tests and estimates of gene effects for number of primary branches in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-27.34**	-8.30**	12.45**	12.49**	21.34**	14.37**	-2.79	
2	B2-5-2-1 X BRG-3	16.28**	15.63**	19.57**	2.56**	-27.56**	-29.45**	22.56**	D
3	B2-5-2-1 X B1-169-1	-6.57**	-0.34	19.37**	7.34**	-2.34*	0.25	5.21**	D
4	B3-13 X BRG-1	-7.75**	-7.12**	16.47**	5.47**	16.36**	12.47**	-19.74**	D
5	B3-13 X BRG-3	-12.55**	5.66**	18.34**	-6.36**	12.67**	14.81**	-16.48**	D
6	B3-13 X B1-169-1	-6.85**	6.77**	19.25**	4.36**	-4.34**	-1.37	9.35**	D
7	B2-10 X BRG-1	-10.67**	6.34**	20.45**	7.67**	-17.76**	16.85**	23.26**	D
8	B2-10 X BRG-3	15.22**	6.84**	21.35**	-12.56**	-14.45**	-11.57**	13.01**	D
9	B2-10 X B1-169-1	16.06**	-9.81**	17.64**	15.12**	21.45**	18.46**	-21.43**	D
10	BRG-2 X BRG-1	-9.24**	-1.87**	17.98**	-10.35**	-17.45**	13.27**	19.26**	D
11	BRG-2 X BRG-3	21.52**	8.16**	16.36**	11.36**	-18.45**	-17.43**	21.65**	D
12	BRG-2 X BI-169-1	-13.21**	-11.28**	18.86**	5.57**	14.65*	19.68**	-12.27**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

Table 4.13: Scaling tests and estimates of gene effects for number of secondary branches in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-31.54**	-18.13**	15.45**	4.61**	21.53**	31.47**	-32.56**	D
2	B2-5-2-1 X BRG-3	33.22**	3.67*	18.35**	3.76**	-0.65	-6.87*	-18.68**	
3	B2-5-2-1 X B1-169-1	9.12**	-4.84**	13.37**	1.87	11.56**	9.34**	-27.68**	D
4	B3-13 X BRG-1	-20.39**	-6.45**	14.26**	-7.45**	6.04	0.85	17.56**	
5	B3-13 X BRG-3	-12.54**	-15.72**	16.66**	-6.65**	39.32**	31.64**	-57.84**	D
6	B3-13 X B1-169-1	7..67**	1.22	20.23**	-6.13**	6.54	-8.54*	17.56**	
7	B2-10 X BRG-1	-46.76**	-17.35**	20.75**	9.47**	45.68**	38.75**	-22.56**	D
8	B2-10 X BRG-3	5.50**	6.31**	18.78**	8.62**	21.34**	13.86**	-30.57**	D
9	B2-10 X B1-169-1	-92.84**	-7.32**	17.46**	5.36**	28.51**	14.82**	-19.48**	D
10	BRG-2 X BRG-1	-25.87**	-11.64**	19.63**	15.86**	46.81**	36.65**	-21.45**	D
11	BRG-2 X BRG-3	13.05**	4.45**	17.35**	-14.43**	-21.06**	17.94**	21.46**	D
12	BRG-2 X BI-169-1	5.71**	-4.87**	15.63**	-6.52**	18.71**	10.46**	-26.86**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

4.4.5. Days to pod initiation

The epistatic gene interaction for days to pods initiation revealed that aditive x additive (i) effects was negative and significant in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x B1-169-1and BRG-2 x BRG-1 showed positive and significant additive x additive (i) effect.

Among twelve crosses dominant x dominant (l) effect was positive and significant for crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3 and BRG-2 x BRG-3 for days to pods initiation. On the other hand significant and negative dominant x dominant (l) effect was recorded in the crosses BRG-2 x BRG-1 and BRG-2 x BI-169-1. Opposite sign of dominance (h) and dominance x dominance (l) indicated duplicate type of epistasis for days to pod initiation, Recurrent selection for specific combining ability can be adopted in order to exploit dominance and epistatic gene effects. Additive x additive (i) effects exhibited negative and significance in most the crosses suggesting that selection can be deferred to later generations when suitable recombinants become available. On the other hand, dominance x dominance (l) effects were positively significant for days to pod initiation, therefore selection for these crosses can be delayed until later generations when the dominance effect would have diminished.

Additive x additive (i) interaction was observed to be highly significant in eleven crosses, and negatively in seven crosses. This is in conformity with the findingof Singh *et al.* (2003), Singh and Bajpai(2005) and Ajay *et al.* (2012).Whereas dominance (l) components were significant in seven crosses and negatively significant in two crosses, respectively, however the magnitude of dominance x dominance (i) gene interaction was mostly positive. Similar

result was also reported by Kandalkar *et al.* (2006), Kumar *et al*. (2009)and Ashutosh *et al*. (2017).

4.4.6. Days to 80% pods maturity

As regards to digenic interaction, the negative and significant additive x additive (i) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 x B1-169-1and BRG-2 x BRG-3, whereas negatively significant dominance x dominance (l) gene effects were recorded in crosses B2-5-2-1 x B1-169-1, BRG-2 x BRG-1and BRG-2 x BI-169-1 for days to 80% pods maturity. The positive and significant additive x additive (i) effects are recorded in crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-3, BRG-2 x BI-169-1 and BRG-2 x BRG-1 and positive significant dominance x dominance (i) effects are observed in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 X B1-169-1 and BRG-2 x BRG-3.

Most of the crosses exhibited duplicate types of epistasis with significant opposite signs of dominance (h) and dominance x dominance (l) components indicating presence of duplicate type of epistasis in the inheritance of days to 80% pods maturity except B2-10 x BRG-1 and BRG-2 x BI-169-1 which showed complementary type of epistasis. The relative magnitude of additive x additive (i) over dominance x dominance (l) irrespective of sign indicated the preponderance of additive gene action, therefore, pedigree method of selection can be used to improve this trait, however most of the crosses exhibited negatively significant additive x additive (i) effects which suggest that selection may be deferred to later generations till desirable recombinants become available**.** On the other hand dominance x dominance (l) effect exhibited positive significance for most the crosses except B2-5-2-1 X B1-169-1, BRG-2 X BRG-1 and BRG-2 X BI-169-1 indicating that selection

can be delayed until dominance effects would have been diminished in later generations.

The major contribution of additive x additive (i) interaction was obvious for the expression of this trait as it was observed to be highly significant in eleven crosses, negatively in seven crosses. This is in conformity with the findingof Singh *et al.* (2003) and Ajay *et al.* (2012);whereas dominance x dominance (l) components were significant in ten crosses and negatively significant in three crosses, respectively, however the magnitude of dominance x dominance (l) gene interaction was mostly positive.

4.4.7. Number of pods per plant

Among the interaction effects negative and significant additive x additive (i) effects were recorded in crosses B2-5 -2-1 x BRG-1 and B2-5-2-1 x BRG-3. Positive and significant additive x additive (i) effects was recorded for crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1. Positive and significant dominance x dominance (l) gene effects are recorded for the crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1and BRG-2 x BRG-3, whereas negative and significant dominance x dominance (l) gene effects were recorded for the cross B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 X B1-169-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1.

Table 4.14: Scaling tests and estimates of gene effects for days to pods initiation in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-6.33**	4.67*	169.65**	-1.58**	-8.45**	-7.34**	8.23	
2	B2-5-2-1 X BRG-3	-3.33*	4.53*	178.24**	-2.45**	-17.45**	-6.45**	4.36	
3	B2-5-2-1 X B1-169-1	-3.53**	-7.73**	171.34**	4.67**	-29.00**	26.47**	12.45**	D
4	B3-13 X BRG-1	9.73**	5.45**	181.35**	5.86**	-23.50**	-17.46**	7.37**	D
5	B3-13 X BRG-3	-1.67	-9.10**	194.34**	6.45**	14.83**	12.48**	1.34	
6	B3-13 X B1-169-1	-11.47**	2.06	183.24**	-10.45**	-7.68**	-2.48	-0.86	
7	B2-10 X BRG-1	-12.20**	-3.63**	167.47**	-11.67	-10.01**	-9.67**	18.34**	D
8	B2-10 X BRG-3	-10.77**	-20.87**	184.36**	4.36**	-34.68**	-29.59**	31.37**	D
9	B2-10 X B1-169-1	-4.30**	15.66**	196.88**	1.87**	6.45**	6.48**	-3.46	
10	BRG-2 X BRG-1	-10.00**	6.07**	203.45**	-6.37**	9.34**	12.48**	-5.57**	D
11	BRG-2 X BRG-3	-8.65**	-10.00**	183.47**	2.65**	-7.76**	-11.38**	12.56**	D
12	BRG-2 X BI-169-1	-11.00**	8.08**	168.43**	-4.36**	11.34**	-6.47**	-8.57**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

Table 4.15: Scaling tests and estimates of gene effects for days to 80% pods maturity in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	6.54*	3.87*	256.67**	-3.46	-11.59**	-23.32**	11.27**	D
2	B2-5-2-1 X BRG-3	11.33**	4.56**	258.00**	-6.36**	-28.84**	-17.57**	12.43**	D
3	B2-5-2-1 X B1-169-1	-35.00**	-12.37**	239.00**	-9.57**	41.47**	32.35**	-23.46**	D
4	B3-13 X BRG-1	21.73**	9.87**	249.65**	15.75**	-32.76**	-38.34**	16.47*	D
5	B3-13 X BRG-3	0.71	7.63**	253.67**	5.86**	24.84**	21.46**	3.37	
6	B3-13 X B1-169-1	5.12*	1.08	252.78**	-32.56**	-11.67**	-4.46	-2.76	
7	B2-10 X BRG-1	-11.00**	5.65**	254.81**	-8.01**	26.04**	-19.43**	27.81**	C
8	B2-10 X BRG-3	-26.65**	15.00**	249.56**	7.67**	-64.57**	-45.67**	71.54**	D
9	B2-10 X B1-169-1	-12.53**	3.77**	259.65**	-15.58*	17.18**	-48.45**	18.75**	D
10	BRG-2 X BRG-1	-18.33**	-6.67**	255.43**	-12.67**	25.67**	34.86**	-21.73**	D
11	BRG-2 X BRG-3	-8..57**	0.61	258.58**	19.81**	-14.87**	-14.47**	12.45**	D
12	BRG-2 X BI-169-1	-7.67**	6.00**	255.35**	-15.75**	-31.47**	22.48**	-18.84**	C

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

The dominance x dominance (l) effects were negatively significant for all the crosses, except B2-5 -2-1 x BRG-1, BRG-2 x BRG-3 and B2-10 x BRG-1, which indicated that selection should be resorted to when desirable recombinants become available. The estimates of dominance (h) and dominance x dominance (l) components were significant with opposite signs in all crosses indicating the predominance of duplicate epistasis for number of pods per plant, except B2-5 -2-1 x BRG-1,B3-13 X B1-169-1 and B2-5-2-1 x BRG-3 which showed complementary type of epistasis. On the other hand most of the crosses exhibited positively significant additive x additive effects except B2-5 -2-1 x BRG-1 and B2-5-2-1 x BRG-3.

Positive and significant dominance x dominance (l) effects were recorded for crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1 and BRG-2 x BRG-3 and presence of duplicate nature of epistasis in the inheritance of this trait indicated that selection can be delayed until later generations when the dominance effects would have diminished. Among epistatic interaction, dominance x dominance gene interaction was negatively significant in nine crosses and positively significant in three crosses. However, additive x additive gene effects were positively significant in ten crosses, and negatively significant in two crosses, and its magnitude was comparatively higher than dominance x dominance gene interaction. This is in conformity with the findingofSingh *et al.* (2003), Singh and Bajpai (2005) and Ajay *et al.* (2012).

4.4.8. Pod length (cm)

Among the epistatic gene effects positive additive x additive (i) gene effects were significant in the crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1, BRG-2 x BRG-1 and BRG-2 x BRG-3. Negative and significant additive x additive (i) gene effects were recorded for the crosses BRG-2 x B1-169-1, B3-13 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-3, B2-5-2-1 x BRG-3 and B2-5-2-1 x B1-169-1, whereas positive and significant dominance x dominance (l)

effects were recorded in the crosses BRG-2 x B1-169-1, BRG-2 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 X B1-169-1,BRG-2 X BRG-1andB2-5-2-1 X BRG-3whereas negative and significant dominance x dominance (l) gene effect was recorded in the crosses B2-5 -2-1 x BRG-1, B3-13 x B1-169-1, B3-13 x BRG-1 and B3-13 x BRG-3.

Almost all the crosses exhibited duplicate type of epistasis, indicating the duplicate nature of epistasis in the genetic control of this trait. However higher magnitude of dominance x dominance (l) interaction revealed the importance of dominance x dominance (l) interaction in governing these traits hence selection can be delayed until later generations when the dominance effects would have diminished. Similar results were reported by Kumar *et al*. (2011) andSingh and Singh (2016). Negative sign of additive x additive (i) interaction in crosses BRG-2 x B1-169-1, B3-13 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-3, B2-5-2-1 x BRG-3 and B2-5-2-1 x B1-169-1 indicated the dispersion of alleles in the parents and positive significance in the remaining crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1, BRG-2 x BRG-1 and BRG-2 x BRG-3indicated possibility of selection in early generation. On the other handcrosses BRG-2 x B1-169-1, BRG-2 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 X B1-169-1,BRG-2 X BRG-1andB2-5-2-1 X BRG-3exhibited positive significant dominance x dominance (l) effects for pods length which may retard the selection process in the earlier generations. Further, dominance × dominance (l) component was mostly positive whereas additive x additive was mostly negative and magnitude of dominance x dominance (l) effects was much higher than additive x additive (i) gene effects. Kandalkar (2006) and Ashutosh *et al*. (2017)also reported the similar result.

Table 4.16: Scaling tests and estimates of gene effects for number of pods per plant in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-201.44**	35.47**	185.65*	-33.56**	24.67**	-65.47**	234.65**	C
2	B2-5-2-1 X BRG-3	184.45**	33.51**	222.54**	142.46**	-50.86**	-62.86**	-133.68**	C
3	B2-5-2-1 X B1-169-1	-273.54**	-129.75**	119.67**	-14.23	331.56**	258.57**	-245.87**	D
4	B3-13 X BRG-1	-471.65**	-178.40**	116.46**	-23.86**	411.67**	257.74**	-238.64**	D
5	B3-13 X BRG-3	-159.45**	-110.87**	178.87**	-24.76**	301.46**	221.85**	-285.79**	D
6	B3-13 X B1-169-1	-34.19*	-79.76**	169.76**	75.87**	-333.76**	159.58**	-137.58**	c
7	B2-10 x BRG-1	225.12**	-64.53**	161.84**	-141.45**	-314.82**	267.64**	286.67**	D
8	B2-10 X BRG-3	231.77**	144.37**	207.85**	-143.75**	278.67**	285.76**	-271.47**	D
9	B2-10 X B1-169-1	-262.85**	-118.09**	185.35**	10.58**	465.76**	234.97**	-182.69**	D
10	BRG-2 X BRG-1	-292.07**	-89.28**	227.53**	150.76**	424.56**	556.67**	-231.81**	D
11	BRG-2 X BRG-3	-249.98**	-112.77**	209.57**	-162.87**	-387.81**	313.65**	121.59**	D
12	BRG-2 X BI-169-1	-84.79**	-37.24**	113.66**	45.98**	-127.84**	292.65**	-79.79**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

Table 4.17: Scaling tests and estimates of gene effects for pods length (cm) in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-1.05**	-1.54**	4.13**	-1.19**	2.69**	2.47**	-4.23**	D
2	B2-5-2-1 X BRG-3	1.50**	1.62**	5.67**	-0.16	-2.85**	-3.08**	4.71**	D
3	B2-5-2-1 X B1-169-1	0.02	0.44**	6.53**	0.43**	-0.56*	-0.65**	0.19	
4	B3-13 X BRG-1	3.26**	1.39**	5.79**	-0.26**	-2.26**	-2.61**	-1..56**	c
5	B3-13 X BRG-3	0.36	0.58**	5.06**	-0.43**	-0.89**	-0.91**	-1.68**	c
6	B3-13 X B1-169-1	-1.26**	-0.60**	4.76**	0.46**	1.31	1.31	-0.51**	
7	B2-10 X BRG-1	1.01**	1.75**	6.79**	-0.54**	-3.06**	3.21**	5.76**	D
8	B2-10 X BRG-3	1.61**	1.73**	5.91**	-0.19**	-2.51**	-3.12**	4.69**	D
9	B2-10 X B1-169-1	-0.74**	-0.56**	3.47**	0.11**	-0.57**	0.05	0.78**	D
10	BRG-2 X BRG-1	-2.32**	-0.82**	4.52**	0.27**	-3.08**	4.54**	5.17**	D
11	BRG-2 X BRG-3	-3.12**	-0.33*	6.47**	0.20**	-0.80**	0.58*	2.19**	D
12	BRG-2 X BI-169-1	0.68**	0.62**	4.18**	0.31**	-1.35**	-1.31**	2.49**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

4.4.9. 100-seed weight

The epistatic gene interaction for 100-seed weight revealed positive and significant dominance x dominance (l) effects in crosses B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1, whereas significant and negative dominance x dominance (l) effects in crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3 and BRG-2 x BRG-3. Additive x additive (i) effects recorded negative and significance for crosses B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1,B3-13 X BRG-3 and B2-10 x B1-169-1. Positive and significant additive x additive (i) was recorded in crosses B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, BRG-2 x BRG-3, BRG-2 x BRG-1, B3-13 x BRG-3 and BRG-2 x BI-169-1. All the crosses exhibited duplicate type of epistasis except B2-5-2-1 x BRG-1 and BRG-2 x B1-169-1 showed complementary type of epistasis. Positive sign for additive x additive (i) in crosses showed that there was association of alleles in parents for this trait.

All the crosses exhibited positive and significant dominance × dominance (l) gene effects except B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3 and BRG-2 x BRG-3which exhibited negatively significant dominance × dominance (l) gene effects. Dominance (h) and dominance × dominance (l) were opposite for eight crosses indicating the presence of duplicate type of epistasis in most of the crosses for inheritance of 100-seed weight; whereas crosses B2-5-2-1 x BRG-1 and BRG-2 x BI-169-1 exhibited complementary type of epistasis.

The relative magnitude of dominance x dominance (l) effects among interactions revealed predominance of dominance x dominance (l) effects which indicate that predominance of non-additive gene effects which may retard the selection process in the earlier generations. Therefore, superior lines may be derived upon advancing the generations letting new combination of

alleles to arise. Similar results were also reported by Kandalkar (2006), Kumar *et al*. (2009), Singh and Singh (2016) and Ashutosh *et al.* (2017).

Presence of both duplicate and complementary type of epistasis indicates that improvement of 100-seed weight mainly depends on the cross selected for improvement. Hence, biparental mating in early generations followed by selection in advance generation would be more effective than direct selection in early segregating generations. Magnitude of dominance x dominance (l) effects was much higher than additive x additive (i) gene effects for the expression of this trait. Similar results were also reported by Kandalkar (2006), Kumar *et al*. (2011), Singh (2016) and Ashutosh *et al*. (2017).

4.4.10. Seed yield per plant

Gene interaction for seed yield per plant revealed that positive and significant dominance x dominance (l) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 X B1-169-1, B3-13 x B1-169-1, B2-10 x BRG-1,BRG-2 X BRG-3and BRG-2 x BRG-1. Negative and significant dominance x dominance (l) effects are recorded in crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3,BRG-2 x B1-169-1and.B2-10 X B1-169-1.

Additive and additive (i) effects recorded negative and significant for crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1 and B3-13 X B1-169-1whereas significant positive additive x additive (i) effects was recorded in crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 X B1-169-1, BRG-2 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3. Most of the crosses exhibited duplicate typesof epistasis with significant opposite signs of (h) and (l) components indicating presence of duplicate type of epistasis in the inheritance of seed yield per plant except B2-10 X BRG-1and BRG-2 X BRG-3which showed complementary type of epistasis.

Among epistatic interaction, dominance x dominance and additive x additive component exhibited enhancing and diminishing effects for the

expression of this trait as they scored positive and negative values. However, the magnitude of dominance x dominance ˆcomponent was much higher than additive x additive component, indicating the prevalence of dominant component for the expression of this trait which is in conformity with Kandalkar (2006), Sarode *et al*. (2009),Kumar *et al*. (2009), Singh and Singh (2016) and Ashutosh *et al*. (2017).

Presence of both duplicate and complementary epistasis indicates that improvement of yield mainly depends on the cross selected for improvement. Therefore, biparental mating in early generations followed by selection in advance generation would be more effective than direct selection in early segregating generations. Predominance of dominance x dominance (l) effects in seeds yield per plant may retard the selection process in the earlier generations. Therefore, superior lines may be derived upon advancing the generations letting new combination of alleles to arise. Presence of additive, dominance and non-allelic interaction effects in seeds yield per plant suggests that intermating the selects in segregating generations to exploit both additive and non-additive components of genetic variability would be desirable to bring improvement in seed yield per plant.

Table 4.18: Scaling tests and estimates of gene effects for 100-seed weight in crosses

Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-6.76**	-4.97**	10.76**	0.76**	2.43**	-2.76**	3.89**	c
2	B2-5-2-1 X BRG-3	7.31**	3.83**	11.36**	0.81**	-7.65**	-6.59**	7.15**	D
3	B2-5-2-1 X B1-169-1	2.62**	1.28**	11.45**	-0.08	-2.08**	-2.18**	3.76**	D
4	B3-13 X BRG-1	-4.69**	-1.79**	9.79**	0.86**	3.36**	3.46**	-2.51**	D
5	B3-13 X BRG-3	1.81**	-0.89**	11.35**	-1.09**	1.29**	0.81**	-3.61**	D
6	B3-13 X B1-169-1	1.54**	0.43**	11.51**	-0.28**	-0.88**	-1.08	0.81	
7	B2-10 X BRG-1	-2.57**	-1.13**	11.64**	0.24**	-2.08**	2.02**	7.32**	D
8	B2-10 X BRG-3	1.15**	1.38**	11.73**	1.27**	3.61**	2.61**	-6.18**	D
9	B2-10 X B1-169-1	2.43**	0.55**	11.68**	0.72**	-0.57	-0.96**	1.64**	
10	BRG-2 X BRG-1	1.85**	1.08**	11.72**	0.80**	-5.67**	3.08**	6.32**	D
11	BRG-2 X BRG-3	3.49**	-1.31**	10.51**	-0.32**	2.14**	3.51**	-5.03**	D
12	BRG-2 X BI-169-1	-3.69**	-0.42**	10.27**	-0.21**	0.86**	0.72**	2.25**	c

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

Table 4.19: Scaling tests and estimates of gene effects for seed yield per plant in crosses

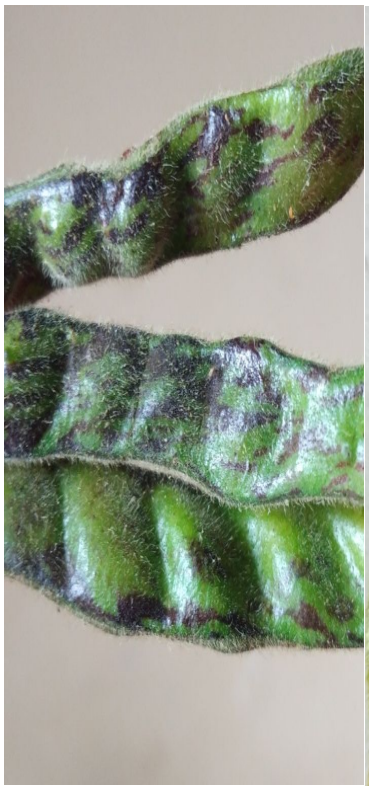
Sl.No	Crosses	Scale test		Gene effects					Type of epistasis
				Main effects			Interaction effects		
		C	D	(m)	(d)	(h)	(i)	(l)	
1	B2-5 -2-1 X BRG-1	-75.62**	3.87*	27.81**	-3.91**	-51.43**	-5.91*	18.51**	D
2	B2-5-2-1 X BRG-3	56.71**	15.85*	42.61**	39.46**	-33.12**	-29.08**	12.31**	D
3	B2-5-2-1 X B1-169-1	-47.65**	-52.77**	29.76**	-17.87**	-44.52**	-25.17**	15.09**	D
4	B3-13 X BRG-1	108.97**	-57.64**	18.46**	-20.12**	66.71**	34.61**	-20.65**	D
5	B3-13 X BRG-3	-45.58**	-22.65**	34.85**	-6.43**	71.17**	32.71**	-40.78**	D
6	B3-13 X B1-169-1	-88.83**	-8.98**	31.67**	-9.83**	-41.07**	-18.12**	24.41**	D
7	B2-10 X BRG-1	-37.74**	-16.78**	32.91**	20.76**	69.83**	29.61**	33.87**	C
8	B2-10 X BRG-3	66.83**	-19.63**	46.74**	17.34**	38.76**	38.67**	-46.62**	D
9	B2-10 X B1-169-1	-65.64**	-7.72**	42.81**	1.08*	75.81**	15.06**	-34.67**	D
10	BRG-2 X BRG-1	-69.91**	-15.91**	16.58**	9.79**	-29.73**	31.03**	81.56**	D
11	BRG-2 X BRG-3	-49.39**	-5.00**	22.61**	4.20**	25.34**	10.63**	29.31**	C
12	BRG-2 X BI-169-1	-30.63**	-12.09**	21.83**	-11.21**	34.81**	24.61**	-17.82**	D

*Significant at 5% level of probability **Significant at 1% level of probability D = Duplicate type of interaction C = Complementary type of interaction (M) =mean (d) = additive effect (h) =dominance effects (i) = additive x additive (l) = dominance x dominance

Plate 1(a). General view of reseach plot

Plate 1(b). General view of research plot

Plate 2. Overview of hybridization scheme



Pods pubescence

Pods stickiness and waxiness

Prominent pods constriction

Slight pods constriction

Green with brown streak

Green with black streak

PLATE 3. General view of pigeon pea pods

L4 (B, M, G)

L3 (DP, M, G)

T1 (C, L, O)

L1 (C, L, O)

L2 (LB, M, G)

T2 (C, L, O)

T3 (C, M, O)

Speckled

Molted

Speckled and Molted

Plain

LB= Light brown seed colour, DP= dark purple seed colour, C= Creamy seed colour, B= brownish seed colour. M=medium seed size, L= Large seed size, G= globular, O=oval seed shape

PLATE 4. General view of pigeon pea seeds

CHAPTER V

SUMMARY AND CONCLUSION

SUMMARY AND CONCLUSION

The present experiment entitled ***"Combining Ability and Gene Effect in Vegetable-Type Pigeon pea [(Cajanus cajan (L.) Millsp.)] Under Foothill of Nagaland"*** was conducted at farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Medziphema Campus, Nagaland University, during 2015 and 2016. Twelve crosses generated by crossing four lines and three testers namely BRG-2 x BRG-1, BRG-2 x BRG-3, BRG-2 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3 and B2-5-2-1 x B1-169-1. Line x Tester designwere evaluated to get the information on combining ability for yield and yield attributing traits. Further, an attempt was made to trace out best parents and crosses for future breeding programmes. The generation mean analysis was done to assess the gene action for yield and its component traits in the cross combinations. The data was subjected to line x tester analysis and generation mean analysis using five parameters model. Important findings are summarize Results of analysis of variance for combining ability Table 4.2 revealed that mean squares due to parents were found to be significant for all the traits except number of primary branches. And analysis of variance for combining ability revealed significant for all the traits for mean squares due to crosses. Similarly significant for all the traits except number of primary branches and days to 80% pod maturity were found in mean squares due to parent *vs.* crosses.

Analysis of variance for combining ability was found significant due to mean squares due to lines for all the traits except number of primary branches per plant and plant height. Also analysis of variance for combining ability revealed that mean squares due to testers found to be significant for all the

traits except number of secondary branches per plant and 100-seed weight. Line x tester mean squares was found to be significant for all the traits except number of primary branches, number of secondary branches and plant height.

The ratio of variance due to gca/sca was less than unity for most of traits except days to 50% flowering, number of primary branches and pods length, indicating the greater role of non additive gene action for inheritance of character.

The parent B2-10 and BRG-2 amongst the line and tester BRG-3 was considered to be desirable as these genotypes exhibited negative significant gca effects and was the earliest to flower.

B2-10 and B2-5-2-1among line and tester B1-169-1 exhibited negative significant gca effects for plant height.

B2-10 and BRG-2 among the lines and BRG-1and BRG-3 among the testers exhibited positive significant gca effects for number of primary branches per plant.

BRG-2 among the lines and BRG-1 and BRG-3 among the testers were considered to be desirable genotypes as these genotypes exhibited positive significant gca effects for number of secondary branches per plant.

BRG-2 in line and BRG-1 in tester exhibited negative significant gca effects for days to pods initiation.

BRG-2 and B2-10 in line and BRG-1 in tester exhibited negative significant gca effects for days to 80% pods maturity.

BRG-2 and B2-10 among the line and BRG-1 and BRG-3 among the tester exhibited positive significant gca effects for number of pods per plant.

The lines BRG-2 and B2-10 and testers BRG-1 and BRG-3 showed positive significant gca effects for pods length.

The lines BRG-2 and B2-10 and testers BRG-1 and BRG-3 exhibited highest positive significant gca effects for 100-seed weight.

Among the lines, significant positive gca was recorded in BRG-2 and B2-10 and among the testers BRG-1 and BRG-3 showed positive significant gca effects for seed yield per plant.

The cross combinations BRG-2 x BRG-1 (good × average), BRG-2 x BI-169-1 (good × poor) and B2-10 x BRG-1(good × average) were the best for early flowering with highly significant negative sca effects.

The cross combinations BRG-2 x B1-169-1 (poor × good), B3-13 X BRG-3 (poor x poor) and B2-10 x B1-169-1 (good × good) exhibited significant negative sca effect in desirable direction for plant height

The cross combinations B2-10 x BRG-3 (poor x good), B2-10 x BRG-1(poor x good) and BRG-2 x BI-169-1 (good x poor) BRG-2 x BRG-1 (good x good) and BRG-2 x BRG-3 (good x good) exhibited positive significant sca effects for number of secondary branches.

The cross combination B2-10 x BRG-1 (poor x good) and BRG-2 x BI-169-1(good x poor) was the best for earliness in days to pods initiation with highly significant negative sca effects.

The cross combinations B2-10 x BRG-1 (good x good), BRG-2 x BRG-1 (good x good), B3-13 x BRG-1(average x good) and BRG-2 x BI-169-1 (good x poor) exhibited highest significant negative sca effects for days to 80% pods maturity.

The cross combinations BRG-2 x BRG-1 (good x good), B2-10 x BRG-1(good x good), B2-10 x BRG-3(good x good), BRG-2 x BRG-3 (good x

good), BRG-2 x BI-169-1 (good x poor) and B2-5-2-1 x BRG-1 (average x good) exhibited highest positive sca effects for number of pods per plant.

The cross combinations B2-10-x BRG-1 (good x good), BRG-2 X BRG-3 (good x good), BRG-2 x BRG-1 (good x good), B2-10 x BRG-3(good x good) and B2-5-2-1 X B1-169-1 (poor x poor) exhibited highest positive sca effects for pod length.

The cross combinations BRG-2 x BI-169-1(good x poor), B3-13 x BRG-1 (poor x good), BRG-2 x BRG-1(good x good), B2-10 x BRG-1 (good x good), BRG-2 x BRG-3 (good x good) and B2-10 x BRG-3 (good x good) was best combiners for 100-seed weight with desirable positive significant sca effects.

The cross combination BRG-2 x BRG-1 (good x good), B2-10 x BRG-1 (good x good), BRG-2 x BRG-3 (good x good) and BRG-2 x BI-169-1 (good x poor), exhibited highest positive significant sca effects for seed yield per plant.

The analysis of variance for five generation of twelve crosses showed significance mean square due to population for all the crosses indicating the existence of considerable amount of genetic variability for yield and its components in all the crosses.

The estimates of mean (m) was significant for all the traits under study namely, days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, days to pods initiation, days to 80 % pod initiation, plant height at maturity (cm), pods length (cm), number of pods per plant, 100-seed weight (g) and seed yield per plant (g).

Estimation of C and D scaling tests were significance for most of the crosses indicating the present of epistasis in twelve crosses for different characters.

The D scaling test was non significant in cross B2-10 X BRG-3 whereas both C and D scaling test were non significant for crosses B2-5-2-1 X BRG-3 for days to 50% flowering.

In plant height both C and D scales were non-significant in crosses B3-13 x BRG-3 followed by B3-13 X B1-169-1 which exhibited non significant for D scaling test.

For number of primary branches per plant B2-5-2-1 x B1-169-1 recorded non significant for D scaling test.

In case of number of secondary branches per plant D scaling tests were non significant for the crosses B3-13 x B1-169-1.

For days to pods initiation C scale was non-significant in the crosses B3-13 x BRG-3 and D scale were non-significant in the cross combination B3-13 x B1-169-1.

For days to 80 % pods maturity, C scales was non-significant in the crosses B3-13 x BRG-3 and D scale were non-significant in the crosses B3-13 x B1-169-1 and BRG-2 x BRG-3.

In case of pod length C scaling test recorded non significant for crosses B2-5-2-1 X B1-169-1 and B3-13 X BRG-3.

Additive (d) component exhibits negative significant for days to 50% flowering in crosses BRG-2 x BI-169-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, BRG-2 x BRG-1, B3-13 x BRG-1, BRG-2 X BRG-3 and B2-10 x B1-169-1, whereas the dominance (l) component exhibit negative significant for the crosses B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BI-169-1 and BRG-2 x BRG-1

For plant height additive (d) component recorded negative and significant in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3 and B2-10 x B1-169-1, whereas negative and significant dominance (h) effects are recorded in the B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-3, BRG-2 x BI-169-1 and BRG-2 x BRG-1.

Additive (d) component recorded positive and significant for number of primary branches/plant in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 X BRG-3 and BRG-2 x BI-169-1,whereas positive and significant dominance (h) effects are recorded in the crosses B2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BI-169-1.

In case of number of secondary branches/plant additive (d) component recorded positive and significant for number of secondary branches/plant in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BRG-1whereas positive and significant dominance (h) effects are recorded in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1.

Additive (d) component recorded negative and significant for days to pods initiation in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-1, B2-10 x BRG-1and BRG-2 x BI-169-1,whereas negative and significant dominance (h) effects are recorded in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3 and BRG-2 x BRG-3.

For days to 80% pods maturity additive (d) component recorded negative and significant in crosses B3-13 X B1-169-1, BRG-2 x BI-169-1, BRG-2 x BRG-1, B2-5-2-1 x B1-169-1, B2-5-2-1 x BRG-3, B2-10 x BRG-1 and B2-10 x B1-169-1, whereas negative and significant dominance (h) effects are recorded in the crosses crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B3-13 X B1-169-1, B2-10 X BRG-3, BRG-2 X BRG-3 and BRG-2 X BI-169-1.

Additive (d) component recorded positive and significant for number of pods per plant in the crosses B2-5-2-1 x BRG-3, BRG-2 x BRG-1, B2-10 x B1-169-1, B3-13 x B1-169-1 and BRG-2 x BI-169-1,whereas positive and significant dominance (h) effects are recorded in the crosses BRG-2 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, B2-10 x B1-169-1, B2-5-2-1 x BRG-1 and B2-5-2-1 x B1-169-1.

In case of pods length additive (d) component recorded positive and significant in the crosses B2-5-2-1 x B1-169-1, B3-13 x B1-169-1, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1 ,whereas positive significant dominance (h) effects are recorded in the crosses B2-5 -2-1 x BRG-1.

Additive (d) component recorded positive and significant for 100-seed weight in the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-1 and B2-10 x B1-169-1, whereas positive and significant dominance (h) effects are recorded in the crosses B2-5 -2-1 X BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, BRG-2 X BI-169-1 and BRG-2 x BRG-3.

For seed yield per plant additive (d) component recorded positive and significant for the crosses B2-5-2-1 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BRG-3, whereas positive dominance (h) effects are recorded in the crosses B3-13 x BRG-1, B3-13 x

BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1.

As regards to digenic interaction for days to 50 per cent flowering estimates of additive x additive (i) gene effects were negative and significant for the crosses B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, B3-13 x B1-169-1, BRG-2 x BRG-3 and BRG-2 x BRG-1, whereas negative and significant dominance x dominance (l) effects are recorded in the crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1, BRG-2 x B1-169-1, BRG-2 x BRG-3 and B2-10 x B1-169-1.

In case of plant height estimates of additive x additive (i) gene effects were negative and significant in crosses B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-3 and BRG-2 x BRG-1, whereas negative and significant dominance x dominance (l) effects are recorded in crosses B3-13 x BRG-1 and B3-13 x B1-169-1.

For number of primary branches/plant estimates of additive x additive (i) gene effects were positive and significant for the crosses B-2-5 -2-1 x BRG-1, B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, BRG-2 x BRG-3, B2-10 x BRG-3, BRG-2 x BRG-1and B3-13 x B1-169-1.

Additive x additive (i) gene effects for number of secondary branches/plant were positive and significant for the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x B1-169-1, B3-13 x BRG-3, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B3-13 x BRG-1 , B3-13 x B1-169-1 and BRG-2 x BRG-3.

In case of days to pods initiation estimates of additive x additive (i) gene effects were negative and significant for the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-1, B2-10 x BRG-3, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas negative and significant dominance x dominance (l) effects are recorded in crosses BRG-2 x BRG-1 and BRG-2 x BI-169-1.

Additive x additive (i) gene effects for days to 80% pods maturity were negative and significant for the crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 x B1-169-1and BRG-2 x BRG-3, whereas negative and significant dominance x dominance (l) effects are recorded in crosses B2-5-2-1 x B1-169-1, BRG-2 x BRG-1and BRG-2 x BI-169-1.

As regards to digenic interaction for number of pods per plant estimates of additive x additive (i) gene effects were positive and significant for the crosses B2-5-2-1 x B1-169-1, B3-13 x BRG-1, B3-13 x BRG-3, B3-13 x B1-169-1, B2-10 x BRG-1, B2-10 x BRG-3, B2-10 x B1-169-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1and BRG-2 x BRG-3.

Additive x additive (i) gene effects for pods length were positive and significant for the crosses B2-5 -2-1 x BRG-1, B2-10 x BRG-1, BRG-2 x BRG-1 and BRG-2 x BRG-3, whereas positive and significant dominance x dominance (l) effects are recorded in crosses BRG-2 x B1-169-1, BRG-2 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 X B1-169-1, BRG-2 X BRG-1and B2-5-2-1 X BRG-3.

For 100-seed weight estimates of additive x additive (i) gene effects were positive and significant for the crosses B3-13 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, BRG-2 x BRG-3, BRG-2 x BRG-1, B3-13 x BRG-3 and

BRG-2 x BI-169-1, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B2-5-2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 x B1-169-1, B2-10 x BRG-1, B2-10 x B1-169-1, BRG-2 x BRG-1 and BRG-2 x BI-169-1.

For seed yield per plant estimates of additive x additive (i) gene effects were positive and significant for the crosses B3-13 x BRG-1, B3-13 x BRG-3, B2-10 x BRG-3, B2-10 x BRG-1, B2-10 X B1-169-1, BRG-2 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3, whereas positive and significant dominance x dominance (l) effects are recorded in crosses B2-5 -2-1 x BRG-1, B2-5-2-1 x BRG-3, B2-5-2-1 X B1-169-1, B3-13 x B1-169-1, B2-10 x BRG-1, BRG-2 X BRG-3 and BRG-2 x BRG-1.

Table 5.1: Two best *per se* performers, general combiners and specific cross combinations in Pigeon pea

Character	General combiners (desirable)	Specific cross combinations
Days to 50% flowering	BRG2, B2-10, and BRG-3	BRG-2 x BRG-1, B2-10 x BRG-3, B2-10 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1
Plant ht. at maturity(cm)	B2-10 , B2-5-2-1and B1-169-1	BRG-2 x BI-169-1,B3-13 x BRG-3 and B2-10 x B1-169-1
No of primary branches/plant	B2-10,BRG-2 ,BRG-1 and BRG-3	B2-10 x BRG-3,BRG-2 x BRG-1,B2-10 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1
No of secondary branches/plant	BRG-2, BRG-1 and BRG-3	B2-10 x BRG-3,B2-10 x BRG-1, BRG-2 x BRG-1, BRG-2 x BRG-3 and BRG-2 x BI-169-1
Day to pods initiation	BRG-2 and BRG-1	B2-10 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-1
Day to 80% pod maturity	BRG-2,B2-10 and BRG-1	B2-10 X BRG-1, B3-13 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-1
Number of pods per plant	BRG-2,B2-10,BRG-1 and BRG-3	BRG-2 x BRG-1,B2-10 x BRG-1, BRG-2 x BI-169-1, B2-10 x BRG-3, B2-5-2-1 x BRG-1 and BRG-2 x BRG-3
Pods length (cm)	BRG-2,B2-10 ,BRG-1 and BRG-3	B2-10-x BRG-1,BRG-2 x BRG-3, BRG-2 x BRG-1, B2-5-2-1 x B1-169-1 and B2-10 x B1-169-1
100-seed weight (gm)	BRG-2,B2-10, BRG-1 and BRG-3	BRG-2 X BRG-1, BRG-2 x BI-169-1, B2-10 x BRG-1, B3-13 x BRG-1, BRG-2 x BRG-3 and B2-10 x BRG-3
Seeds yield/plant	BRG-2,B2-10,BRG-1 and BRG-3	BRG-2 x BRG-1,B2-10 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3

Table 5.2: List of the crosses showing significant values (ignoring sign) for all the five components of gene effects for yield and yield components in pigeonpea

S.N.	Crosses	Yield and/or yield components
1	B2-5 -2-1 X BRG-1	Days to 50% flowering, plant height, number of primary branches ,number of secondary branches, number of pods per plant, pods length (cm) ,100-seed weight and yield per plant
2	B2-5-2-1 X BRG-3	Plant height, number of primary branches ,days to 80% pods maturity, number of pods per plant,100-seed weight and yield per plant
3	B2-5-2-1 X B1-169-1	Days to 50% flowering ,plant height, days to pods initiation, days to 80% pods maturity and yield per plant
4	B3-13 X BRG-1	Days to 50% flowering, plant height, number of primary branches ,days to pods initiation ,days to 80% pods maturity, number of pods per plant, pods length (cm) ,100-seed weight and yield per plant
5	B3-13 X BRG-3	Number of primary branches ,number of secondary branches, number of pods per plant, pods length (cm), 100-seed weight and yield per plant
6	B3-13 X B1-169-1	Plant height, number of pods per plant and yield per plant
7	B2-10 X BRG-1	Days to 50% flowering, plant height, number of primary branches, number of secondary branches, days to 80% pods maturity, number of pods per plant ,pods length (cm) ,100-seed weight and yield per plant
8	B2-10 X BRG-3	Days to 50% flowering ,plant height ,number of primary branches, number of secondary branches ,days to pods initiation ,days to 80% pods maturity, number of pods per plant ,pods length (cm), 100-seed weight and yield per plant
9	B2-10 X B1-169-1	Days to 50% flowering, plant height ,number of primary branches ,number of secondary branches, days to 80% pods maturity, number of pods per plant and yield per plant
10	BRG-2 X BRG-1	Days to 50% flowering ,plant height, number of primary branches, number of secondary branches, days to pods initiation ,days to 80% pods maturity, number of pods per plant ,pods length (cm) ,100-seed weight and yield per plant
11	BRG-2 X BRG-3	Days to 50% flowering, plant height ,number of primary branches ,number of secondary branches ,days to pods initiation, days to 80% pods maturity ,number of pods per plant , pods length (cm) ,100-seed weight and yield per plant
12	BRG-2 X BI-169-1	Days to 50% flowering, plant height ,number of primary branches ,number of secondary branches ,days to pods initiation, days to 80% pods maturity, number of pods per plant, pods length (cm) , 100-seed weight and yield per plant

CONCLUSION

On the basis of finding generated from the present investigation, following conclusion can be drawn.

1. Combining ability analysis revealed the presence of considerable variability for majority of the traits, among the lines compared to testers and substantial variability for most of the traits among crosses. Higher and significant variances due to line x tester interaction component indicated the differential behaviour of lines with testers across the traits.
2. The estimates of general combining ability in line suggested that BRG-2 and B2-10 showed positive significant gca effect for seed yield per plant and yield contributing characters *viz*. number of primary branches/plant, number of secondary branches/plant, number of pods per plant, pod length and 100-seed weight.
3. Among the testers BRG-1 and BRG-3 exhibited positive and significant GCA effect for seed yield per yield and it attributing traits namely, number of primary branches/plant, number of secondary branches/plant, number of pods per plant, pods length and 100-seed weight
4. Thus line BRG-2 and B2-10 and testers BRG-1 and BRG-3 can be used as best general combiners in the hybridization programmed.
5. The estimates of specific combining ability in crosses suggested that BRG-2 x BRG-1, B2-10 x BRG-1, BRG-2 x BRG-3, B2-10 x B1-169-1 and BRG-2 x BI-169-1 were identified as promising on the basis of specific combining ability effect.
6. Hybrids BRG-2 x BRG-1, B2-10 x BRG-1, BRG-2 x BI-169-1 and BRG-2 x BRG-3 were identified as promising on the basis of grain yield mean *per se* performance.

7. Both additive and non-additive (dominance) gene action appeared to play a significant role in controlling the expression of characters under study. Predominance of non additive gene action was observed for majority of the characters studied.
8. Predominance of non additive gene action was observed for the characters *viz*. number of secondary branches per plant, days to 80 % pods maturity, days to pod initiation, plant height at maturity (cm), number of pods per plant, 100-seed weight and seed yield per plant (g), indicating the need for exploiting the character through heterosis breeding.
9. Predominance of additive gene action was observed for the characters namely, days to 50% flowering, number of primary branches and pods length suggested the possibility of selecting better recombination through progeny selection.
10. The ratio of gca/sca variance was less than unity for most of the character except days to 50% flowering, number of primary branches and pods length indicating non additive gene action for most of the characters, thus heterosis breeding will be rewarding for improvement of these characters.
11. The choice of breeding methodology depends much upon the nature and magnitude of gene action. Inheritance of different yield contributing characters in pigeonpea revealed, that they are governed to a large extent by non-additive gene effects. However, additive genetic effect was also present in a substantial proportion. This suggests that, as the inheritance of quantitative characters becomes more complex the contribution of interacting dominant alleles becomes greater. Usually, the utilization of additive genetic variance, which is present in considerable amount in experimental

material, is comparatively easy and it can be mobilized by simple method of progeny selection. While, for the exploitation of non-additive genetic variances, heterosis breeding would be of importance to the pigeonpea breeder in improving the yield and other contributing characters in pigeonpea.

12. The estimates of the five parameters model revealed the significant values for all the components of gene effects for yield and yield components in few crosses, *viz*. hybrid B2-10 x BRG-1 and BRG-2 x BRG-1 scored significant values for all the components of gene effect for seed yield and all attributing traits whereas, cross, B2-10 x BRG-3, BRG-2 x BRG-3, BRG-2 x B1-169-1 and B3-13 x BRG-1 recorded significant values for yield and seven yield attributing traits. Similarly, in crosses, B2-10 x B1-169-1, B2-5-2-1 x BRG-1, B2-5-2-1 x B1-169 -1, B3-13 x BRG-3 and B2-5-2-1 x BRG-3 significance of ([m], [d], [h], [i] and [l]) could be visualized for few (five to six) yield traits only.
13. Two crosses namely, B2-10 x BRG-1 and BRG-2 x BRG-3 scored significant values being positively significant for all the components of gene effect ([m], [d], [h], [i] and [l]) for seed yield.
14. The relative contribution of dominance gene effect was much higher than those of additive gene effect, indicating the prevalence of dominance gene effects for the inheritance of yield and attributing characters. Further, higher frequency of duplicate type of epistasis for most of the traits including seed yield per plant, further confirms the predominance of dominant gene effects, indicated that, through effective selection, transgressive segregants could be obtained in subsequent generations.
15. Considering the magnitude and sign (positive) of the main gene effects and their interaction, the dominance (h) effects and

dominance x dominance gene effect followed by additive (d) effects and additive x additive interaction appear to play a significant role for the expression of yield per plant and its attributes. It clearly indicated that complex characters like seed yield and its attributing characters were under greater control of dominance gene effect, which indicates that as the inheritance of quantitative characters becomes more complex, the contribution of dominance gene effect for their inheritance becomes greater.

16. The magnitude of dominance (h) and dominance x dominance gene effects (ignoring the sign) was comparatively higher for seed yield and its attributing character. However, the sign of dominant x dominant gene effects were mostly negative for days to 50% flowering, number of secondary branches/plant and number of pods per plant indicating diminishing effect due to this type of gene effect could occur for the expression of these traits.
17. Based on above findings, it may be suggested that in those crosses where additive (d) and additive x additive (i) gene effects were predominant, one should follow the pedigree method of selection and recurrent selection, whereas in those crosses where dominance (h) and dominance x dominance (l) gene effect were predominant, heterosis-breeding would be effective.
18. To exploit all types of gene effects in crosses which showed significant positive effect in both additive (d) and additive x additive effects (i) and dominant (h) and dominance x dominance (l) effect, one should followed standard selection procedure which may first exploit additive gene effects. Simultaneously, care should be taken that dominant gene effects are not dissipated; rather they should be concentrate under such circumstances, inter-mating of superior segregants at

early generations followed by biparental mating and recurrent selection especially reciprocal recurrent selection. The transgressive segregants produced as a result of this will lead to the development of desirable high yielding genotypes of pigeonpea.

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