“Heterosis and Combining Ability Studies in Pigeonpea (*Cajanus cajan* *(L.)* Millsp.)”

BY

JAYBHAYE DNYANESHWAR BHAGWAN
(Reg. No. 2018A08MB)

DEPARTMENT OF AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)
COLLEGE OF AGRICULTURE, BADNAPUR
VASANTRAO NAIK MARATHWADA KRISHI
VIDYAPEETH, PARBHANI - 431 402 (M.S.) INDIA

2020

“Heterosis and Combining Ability Studies in Pigeonpea (*Cajanus cajan* (*L.*) Millsp.)”

DISSERTATION

Submitted to the
Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani
in partial fulfillment of the requirement
for the award of the degree of

MASTER OF SCIENCE
(Agriculture)

IN

AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

BY

JAYBHAYE DNYANESHWAR BHAGWAN
(Reg. No. 2018A08MB)

DEPARTMENT OF AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)
COLLEGE OF AGRICULTURE, BADNAPUR
VASANTRAO NAIK MARATHWADA KRISHI VIDYAPEETH, PARBHANI - 431 402 (M.S.) INDIA
2020

CANDIDATE'S DECLARATION

I hereby declare that this dissertation or part thereof has not been previously submitted by me for a degree of any other institution or university.

Place: BADNAPUR

Date: 8 /12/ **2020**

(JAYBHAYE.D.B.)

Reg. No. 2018A08MB

Dr. J. E. Jahagirdar
Head
Dept. of Agril. Botany,
VNMKV, Parbhani -431 402.

CERTIFICATE – I

This is to certify that the dissertation entitled **"Heterosis and Combining Ability Studies in Pigeonpea (*Cajanus cajan* (L.) Millsp.)"** submitted by **Mr. JAYBHAYE DNYANESHWAR BHAGWAN** to the College of Agriculture, Badnapur in partial fulfilment of the requirements for the degree of MASTER **OF SCIENCE (AGRICULTURE)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** is record of original and bonafide research work carried out by her under my guidance and supervision. It is of sufficiently high standard to warrant its presentation for the award of the said degree.

I also certify that the dissertation or part thereof has not been previously submitted by her for a degree of any university.

(J. E. Jahagirdar)
Research Guide and
Chairman of
Advisory Committee

Place: Badnapur
8 /12/2020

CERTIFICATE-II

This is to certify that the dissertation entitled **"Heterosis and Combining Ability Studies in Pigeonpea (*Cajanus cajan* (L.) Millsp.)"** Submitted by **Mr. JAYBHAYE DNYANESHWAR BHAGWAN (Reg. No. 2018A08MB)** to the College of Agriculture, Badnapur, Jalna in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** has been approved by the student's Advisory Committee after *viva-voce* examination in collaboration with external examiner.

External Examiner
(H.V. Kalpande)

(J. E. Jahagirdar)
Research Guide and
Chairman of Advisory Committee

Member of Advisory committee

(D. K. Patil)

(S. B. Sarode)

(P.H. Ghante)

Associate Dean and Principal
College of Agriculture, Badnapur

Associate Dean(P.G)
College of Agriculture,
VNMKV, Parbhani

PLAGIARISM CLEARANCE CERTIFICATE

Date: 8/12/2020

This is to certify that thesis entitled **"HETEROSIS AND COMBINING ABILITY STUDIES IN PIGEONPEA (*Cajanus cajan (L.) Millsp.)*"** submitted by **Mr. JAYBHAYE DNYANESHWAR BHAGWAN Reg. No. 2018A08MB** has been properly examined by using URKUND: Anti Plagiarism Software.

No sentence, equation, diagram, table, paragraph or section has been copied Verbatim from previous work unless it is placed under quotation marks duly referenced. The work presented is original and own work of the researcher (i.e. there is no plagiarism). No ideas, process, result or words of other have been presented as Researcher's own work.

Signature and Name of the
Research Student

Signature and Name of the
Research Guide.

URKUND

Document Information

Analyzed document	Final Theis for Plagarism 24.09.2020 (1).pdf (D79896897)
Submitted	9/25/2020 12:50:00 PM
Submitted by	Dr. Jagdish E. Jahagirdar
Submitter email	jagdishjahagirdar@gmail.com
Similarity	8%
Analysis address	jagdishjahagirdar.vnmkv@analysis.urkund.com

Sources included in the report

W	URL: https://www.arccjournals.com/uploads/articles/lr302009.pdf Fetched: 9/25/2020 12:53:00 PM	⊞	3
SA	**introduction, review of literature, materials and methods, results and discussion, ...** Document introduction, review of literature, materials and methods, results and discussion, ... (D54543072)	⊞	3
SA	**VNM Krishi Vidyapeeth / Pratik final Thesis.pdf** Document Pratik final Thesis.pdf (D78926005) Submitted by: drammisal15@gmail.com Receiver: drammisal15.vnmkv@analysis.urkund.com	⊞	8
SA	**"PRIYANKA CHOUDHARY_GPB-RCA_17-01-02-09-21_M.Sc._JUNE_2019".pdf** Document "PRIYANKA CHOUDHARY_GPB-RCA_17-01-02-09-21_M.Sc._JUNE_2019".pdf (D54253979)	⊞	7
SA	**"Amit Kumar Meena_GBP-RCA_16-01-02-09-19_M.Sc._Feb._2019 (1).pdf** Document "Amit Kumar Meena_GBP-RCA_16-01-02-09-19_M.Sc._Feb._2019 (1).pdf (D48479654)	⊞	10
W	URL: https://www.researchgate.net/publication/303307565_Genetic_architecture_of_dual_pu ... Fetched: 8/23/2020 6:08:06 AM	⊞	2
SA	**VNM Krishi Vidyapeeth / Anjali Talpe M Sc.pdf** Document Anjali Talpe M Sc.pdf (D79527342) Submitted by: silkroutepb@rediffmail.com Receiver: silkroutepb.vnmkv@analysis.urkund.com	⊞	1
SA	**Heterosis and Combining Ability Studies in Mungbean Vigna radiata L.Wilczek by KAK ...** Document Heterosis and Combining Ability Studies in Mungbean Vigna radiata L.Wilczek by KAK ... (D54727920)	⊞	17
W	URL: https://core.ac.uk/download/pdf/219475025.pdf Fetched: 7/17/2020 6:54:26 AM	⊞	9
W	URL: https://www.researchgate.net/figure/Heterosis-and-combining-ability-effects-in-sel ... Fetched: 3/17/2020 9:52:44 AM	⊞	1
SA	**New Microsoft Word Document.docx** Document New Microsoft Word Document.docx (D64139895)	⊞	16

ACKNOWLEDGEMENT

A successful venture is not only the efforts of an individual but also it is an artistic creation with the help of eminent persons. During my career and the completion of this work I have face both weal and woe, but inspiration and guidance given by my parents, teachers, friends and dear- ones has helped me to make the work into reality. Words would probably be insufficient to express my gratitude, but words are all have as a medium of my expression.

I have immense pleasure in expressing my whole hearted sense of gratitude and indebtedness towards my Research Guide ***Dr. J.E. Jahagirdar*** *Head Dept. of Agril. Botany, VNMKV, Parbhani, for his inspiring guidance, keen interest, his activeness and sharpness. I take this opportunity to express my deep and sincere feeling of gratitude to him for suggesting research topic, valuable guidance, constant inspiration, constructive criticism, talented versatile advice and untiring efforts in preparation of the manuscript of this dissertation.*

I wish to express my sincere thanks to ***Dr. A. S. Dhawan****, Hon. Vice-chancellor, VNMKV, Parbhani,* ***Dr. V.D. Patil*** *Ex-Director of Instruction and Dean Faculty of Agriculture, VNMKV, Parbhani,* ***Dr. P. G. Ingole*** *Director of Instruction and Dean Faculty of Agriculture, VNMKV, Parbhani,* ***Dr. D.P. Waskar*** *Director of Research, VNMKV, Parbhani and* ***Dr. G.M. Waghmare*** *Associate Dean and Principal, College of Agriculture, Badnapur.*

It is my great privilege and pleasure to record my deep sense of gratitude to the members of my advisory committee, ***Dr. D.K, Patil*** *Principal Scientist (Plant Breeding) & I/c Agricultural Research Station, Badnapur,* ***Dr. S.B. Sarode*** *Assistant Professor (Agril. Botany) College of Agriculture, Badnapur,* ***Dr.P.H.*** *Ghante Scientist (Plant Pathology) Agricultural Research Station, Badnapur, and especially thankful to* ***Mr. V.K, Gite*** *Scientist (Plant Breeding) Agricultural Research Station, Badnapur for their valuable guidance and help during my course of investigation.*

I am extremely thankful and grateful to Abbu, Ghayal, Ginare Vishnu, Aarke

Vishal, Mahindra Ragde and Narayan kakade and the whole Ars team, for their valuable guidance during research work and for their cooperation during my research work.

I wish to express my heartfelt, cordial, sincere and inherent thanks to my Department senior Lokhande Mangesh, Jadhav Akshsay, Kale Balu, Dhawane Jayashree, Shedge Pranjal, Waghmare vaishali, Panchal vasant and my beloved juniors Sandip, Nitin, Anirudh, Shivaji for their everlasting vibrant encouragement during carrying out this experimentation and untiring help was rendered with cheerful smiling gestures.

It gives me immense pleasure to acknowledge the vote of thanks to my colleagues Dipak, Altaf, Yogesh, Snehal, Sable Suraj, Temak Shrirang, Bhangare Akshay, More Pryandnyashil for their moral support and co-operation throughout this academic programme for their invaluable cooperation, endless help and moral support during my course of study.

And most important, it would be impossible to express in words or phrases to convey my respect and wholesome gratitude to my parents who are the pillars of strength and inspiration. Who through their efforts, sacrifices, encouragement in educating me at the cost of their comfort and consolation and humbly express deepest sense toGrandfather Shree **Kundalik A Jaybhaye** and Grandmother **Subhidrabai K Jaybhaye** and my Father Shree **Jaybhaye Bhagwan Kundlik**, Mother Shreemati **Jaybhaye Mahananda Bhagwan** and my Brother **Gopal**, Sister **Minakshi G Mundhe**, and lastly my wife **Mrs. Dipali D Jaybhaye.**

"No love is greater than mother's love and No care is greater than father's care."

I am especially grate to **Jagananth Gaware** (Samarth Computers) who carried out the immense help made me possible to complete this manuscript.

Lastly, I express my regards to those whose names I have forgotten to mention here.

Place: Badnapur

Date: 8/ 12/ 2020

(JAYBHAYE. D.B)

Reg.No.2018A08MB

CONTENTS

LIST OF PLATES

LIST OF TABLES

ABBREVIATIONS

/	:	per
%	:	per cent
$\sum$	:	Summation
σ^2	:	Variance
cm	:	Centimeter (s)
CV	:	Coefficient of variation
d.f.	:	Degree of freedom
EMSS	:	Error mean sum of squares
et al.	:	*et alia* (and others)
etc.	:	Etcetera’s
Fig.	:	Figure
g	:	Gram (s)
G	:	Genotypic correlation
GM	:	General mean
GCA	:	General combining ability
i.e.	:	ld. est (that is)
kg	:	Kilogram (s)
m	:	Meter
MSS	:	Mean sum of squares
P	:	Phenotypic correlation
No.	:	Number
R	:	Residual effect
RH	:	Relative Heterosis
S.E.	:	Standard error
SC	:	Standard Check
SCA	:	Specific combining ability
viz.,	:	Videlicet (namely)
SH	:	Standard Heterosis
FS	:	Full Sibs
HS	:	Half Sibs
CD at 5%	:	Critical difference at
5 per cent CD at 1%	:	Critical
difference at 1 per cent		

CHAPTER-I

INTRODUCTION

1.1 Background information

Pigeonpea *[Cajanus cajan (L.) Mill Spaugh]* is an often-cross pollinated crop (20 - 70%) with diploid (2n = 2x) chromosome number of 22 and genome size of 1C = 858 Mbp. It is commonly known as tur, red gram or Arhar. It belongs to family Leguminosae, sub family *Papilionaceous*. It is a short-lived perennials Rubin which plants may grow for about five years and turn into small trees. It is a hardy, widely adapted and drought tolerant crop with a large temporal variation (90-300 days) for maturity. These traits allow its cultivation in a range of environments and cropping systems. It is the most versatile food legume with diversified uses as food, feed, fodder and fuel. It is one of the important pulse crops of India and ranks second to chickpea in area and production. Invariably, the traditional pigeonpea cultivars and landraces are of long duration and grown as intercrop with other earlier maturing cereals and legumes. It is an important pulse mostly grown in Asia, Africa, Latin America and the Caribbean islands. Considering the vast natural genetic variability in local germplasm and presence of various wild relatives, India is considered as the primary center of origin of pigeonpea *(Van der Masen, 1990*). Globally, pigeonpea is mainly traded for food use. It is a rich source of protein, carbohydrate, and certain minerals. Protein content of commonly grown pigeonpea cultivars ranges between 17.9 to 24.3 g per 100 g for whole grain sample and split grains. Pigeonpea seed also contains about 57.3 to 58.7 per cent carbohydrate, 1.2 to 8.1 per cent crude fiber and 0.6 to 3.8 per cent lipids. Seeds pigeonpea is a good source of iron and iodine and rich in es essential amino acids like lysine, tyrosine, cysteine and arginine. Pulses constitute an important ingredient predominantly in vegetarian diet and are important source of protein that nutritionally balances the proteins from cereal grains. They supply minerals and vitamins and provide an abundance of food energy. Pulses provide a cheaper source of proteins as they generally contain nearly twice as much protein as that of cereals and hence correctly called poor man's meat. Pulses are also important for sustainable agriculture and enriching of the soil through biological nitrogen fixation.

They enrich the soil with nitrogen up to 20-40 kg N/ha and organic matter through leaf fall and profuse underground root growth (Hariprassanna and Bhatt, 2002). Its roots help in releasing soil-bound phosphorus to make it available for plant growth (Ae et al 1990) with so many benefits at low cost Pigeonpea has become an ideal crop for sustainable agriculture systems in rain dependent areas.

In India pigeonpea is grown on an area of 4.45 M. ha with average total production of 4.18 M. tones and productivity about 937 kg/ha during 2018- 19(Anonymous, 2018). In Maharashtra, it having largest role in an area, production and productivity. In Maharashtra in year of 2018-19 pigeonpea grown in an area of 12.20 lakh ha, production of 10.56 lakh tons and yield about 866 kg/ha. In Marathwada region, in year 2018-19 pigeon pea grown in area of 4.46 lakh ha, production of 3.95 lakh tons and yield about 855 kg/ha. The pigeon is a woody, short lived perennial shrub that is cultivated widely in the tropics and subtropics. Combining ability studies are very useful for the breeders as it helps in the selections of parents and hybrids, provide the superior inbreed for character. It also gives the information on gene effects of genetic variances present in material for character under study. Main aim of this investigation is to identify good general & specific combiners for yield and yield contributing traits in pigeon pea. In recent years the importance of this crop has increased due to growing shortage of irrigation, erratic rainfall and increased need for protein rich food. The multiple uses and its role in sustainable agriculture make pigeonpea a favorite crop of small land holder. Significantly progress has been made over the last few decades through breeding for reducing crop duration, improving seed quality and overcoming the constraints of major diseases like wilt and sterility mosaic. These milestones have helped to increase the production and area of pigeonpea, even though yield per unit land area has remained as low as ever. Since the demand for pigeonpea is increasing and land area available for expansion is limited, research now needs to focus on the genetic enhancement of yield. The higher pigeonpea yield per unit land area can be obtained by introducing new evolved varieties of different duration, with high yielding potential under specific agroecological situation followed by improved management practices. The numbers of varieties are evolved by the ICRISAT, Hyderabad, IARI New Delhi, ARS, Badnapur and other institutes.

However, in order to increase the productivity, exploitation of heterosis is essential.

IMPORTANCE AND NEED OF STUDY

Information about the genetic architecture of parents and understanding the mode of gene action controlling seed yield and its related components are of major importance in devising suitable breeding procedures for polygenic traits. The knowledge of heterosis for economic traits can be effectively utilized in selecting the desired characters in crop improvement programmes. Combining ability is the most effective tool for identifying the appropriate parents for hybridization. For heterosis breeding, it is necessary to select the cross combination with high degree of specific combining ability (SCA) and preferably the parents involved with high general combining ability (GCA) effect. It also gives the information on gene effects of genetic variances present in material for character under study. Therefore, present investigation is undertaken to identify good general and specific combiners and better heterotic combination for yield and yield contributing characters in pigeonpea (Singh and Singh, 2009).

1 .3 Objective of the study

Keeping in view the above facts, the present study was undertaken with the following objectives: -

1) To estimate the standard heterosis for yield and yield contributing traits.
2) To estimate the combining ability effects of parents and hybrids.

CHAPTER -II

REVIEW OF LITERATURE

A brief review of related literature has been illustrated in this chapter under the following headings: -

2.1 Combining ability

2.2 Heterosis

2.1 Combining ability

Combining ability can 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 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.

Line x tester analysis is a precise approach to estimate the general and specific combining ability effects of parents and crosses respectively. It is also useful in estimating various types of gene effects. Kempthome (1957) proposed line x tester analysis technique which is analogous to North Carolina mating Design II.

North Carolina mating design II of Comstock and Robinson (1952): In this analysis, a random sample off's' sizes were taken and all of them were mated to each of 'd' dams. They also precisely expressed the variance due to general combining ability (σ^2GCA) and variance due to specific combining ability (σ^2SCA) in terms of the covariance of half-sibs (Cov (HS) and covariance of full- sibs (Cov (FS) respectively.

σ2gca= Cov (HS)

σ 2sca = Cov (FS)-2 Cov (HS)

The available literature pertaining to combining ability in pigeonpea has been reviewed here as under:

Sharma *et al*. (1973) found that GCA variances were higher than SCA variances for the characters *viz*., plant height, days to flowering, days to maturity, 100 seed weight and yield per plant

Dahiya and Barar (1977) reported low GCA for flowering time and high GCA for pod number, 100 seed weight and yield per plant.

Krishna Rao and Nagur (1979) observed a variety namely Jawahar 45 as consistently exhibiting good GCA for grain yield.

Reddy *et al*. (1979a) reported the predominance of SCA effects. The GCA effect for most of the characters were generally negative for early and medium parents and positive for late parents. They also inferred that specific mid late x late and early x late combinations are likely to give recombination of economic worth.

Chaudhari *et al.* (1980) reported the predominance of both additive and non-additive gene action. GCA effect was significant for days to 50 per cent flowering in No. 148. In the cross No.148 x Hyderabad, they found negative significant SCA effect for days to 50 per cent flowering. The cross C 11 x No-148 was best cross in terms of yield in pigeonpea.

Venkateshwarlu and Singh (1982) reported that variances due to both GCA and SCA were highly significant indicating the presence of both additive and dominance gene effects. The parent NP (WR)-15, T 7 and C 11 were the best general combiners for number of pods per plant, seeds per pod and 100 seed weight in pigeonpea.

Singh *et al.* (1983) reported that UPAS 120, Mukta and S 103 were promising for breeding early maturing hybrids since they are best combiners for earliness and yield components in pigeonpea.

Omanga (1985) found C 11 to be the best general combiner for seal yield while ICP 7035 and ICP 9150 showed highest GCA effect for hundred seed weight in pigeonpea.

Patel *et al.* (1987) analyzed 30 hybrids involving 3 genetic male sterile lines and reported significant positive SCA mainly for number of pods and pod length in pigeonpea.

Hazarika *et al* (1988) observed significant GCA and SCA effects for yield components in pigeonpea. They reported 477, 219, ICPL 96 and ICPL 87 as good combiner for majority of characters. Determinate plants were generally good combiners for seeds per pod and seed size. Indeterminate plants were generally good for pods and yield per plant.

Patel *et al* (1992) analyzed 10 hybrids involving three GMS lines and reported that hybrids showing significant positive SCA effects mainly involved good and other poor combining parents. This was especially noted in respect of pod and branches per plant in pigeonpea.

Ghodke *et al.* (1993) reported that the GCA effect were highly significant for all characters. Whereas, SCA effects were highly significant for days to maturity and 100 seed weight They further reported 9 hybrids exhibiting good SCA effects for yield and other characters. Two hybrids showing high SCA effects involved both parents with low GCA in pigeonpea.

Khapre *et al.* (1993) studied combining ability for grain yield and its components in diallel crosses involving seven divers pigeonpea cultivars. The study revealed the predominance of additive gene effects for the yield and yield contributing characters.

Parents, BDN 2, ICP 6997, PBNA 54 and Daithna local were the best general combiners for all characters except days to maturity. Prabhat showed consistent desirable GCA effects for days to maturity. The hybrids ICP 6997*PBNA 54 and ICP 6997x BDN 2 showed significant SCA for grain yield.

Khapre *et al.* (1996) studied heterosis and combining ability analysis for grain yield and its components in pigeonpea and revealed a significant role of non-additive gene action for all the characters. The parents MS Hy 9, MS small leaf, Igithana local, BDN 2 and ICPL 87 were the best general combines. Seven hybrids showed significant positive SCA effects and high per se performance for grain yield and other yield attributes.

Narladkar and Khapre (1997) studied combining ability in pigeonpea and found that out of 24 hybrids, 10 hybrids showed significant positive SCA effects and high per se performance for grain yield and also showed significant SCA effects for other related morpho-physiological traits.

Kumar and Srivastava (1998) reported KPMS 1050 and MSNP (WR) 15 among the lines and PR 5149, PDA 92-1, KPP 1034-1, KPP 1034-5 and KPP 1034-7 among the testers as good general combiners for seed yield. They also concluded that gene action was predominantly non- additive for the characters studio! in pigeonpea.

Wanjari *et al.* (1998) found that among males, AK 22 and AK 30 had been good general combiners. The MS P3 x AK 22 has been found to have high SCA. They also concluded that a hybrid MS P9 x AK 31 is expected to be with complementary epistasis.

Singh and Srivastava (2001) studied combining ability variances and effects using four lines of the wild species Cajanus sericeus and four testers of cultivated species Cajanus cajan in a line x tester fashion and found that among the lines, C. sericeus (ICPW 160) proved to be a good general combiner for days to flowering, plant height, number of primary branches per plant, pod length, number of seed per pod, 100 seed weight and seed yield per plant. Among the testers Cajanus cajan proved to be a good general combiner.

Pandey and Singh (2002) evaluated three genetic male sterile lines (DAMS 1, ICPMS 3783 and KPMS 1050) and 12 diverse genotypes of the long duration group of (Cajanus cajan (L.) Millsp.) along with their hybrids for general and specific combining ability, variance components and standard heterosis. Among the lines, DA 32, DA 34, DA 37, DA 46, DA 93-4, DA 93-2, DA 94-6 and Bahar mutant and among the testers DAMS 1 and ICPMS 3783 were found to be good general combiners for seed yield/plant and other yield contributing traits such as secondary branches/plant, clusters/plant and number of pods/plants the tester DAMS 1 was also a good general combiner for primary branches/plant and per cent pod setting.

Jahagirdar (2003) reported the parents BDN 2, ICPL 87, BSMR 736 and ICPL 87119 were the best general combiner for the grain yield and other yield contributing characters. Ten out of 24 F1's showed significant positive SCA effects and high per se performance for grain yield in pigeonpea.

Lohithaswa and Dharmaraj (2003) reported the predominance of non-additive gene effects for all the characters except days to 50 per cent flowering, 100 seed weight and protein content for which additive gene action was predominant. The parents BSMR 380, ICPL 87119 and TS 3 were the best general combiners for grain yield in pigeonpea.

Pawar and Tikka (2003) studied 64 hybrids and revealed higher magnitude of SCA variances over GCA variances for all the traits which indicated preponderance of non-additive gene action. The parents MS 228, MS Pusa 33, SKNP 9256 and AL 15 were good general combiners for seed yield and its yield contributing traits in pigeonpea.

Pandey (2004) reported two lines *viz.,* DAMS 1 and ICMS 3783 and nine testers were found to be good general combiners among three genetic male sterile lines and 12 testers for yield and yield contributing characters. The estimates of σ^2GCA, σ^2SCA and σ^2 GCA/σ^2SCA were exhibited partial dominance of additive genetic action for yield and other yield contributing characters in pigeonpea.

Banu *et al*. (2006) studied the general (GCA) and specific combining ability (SCA) effects in 45 pigeonpea hybrids along with their parents for days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per plant, seeds per pod, pod length, 100-seed weight and single plant yield. The components of variance due to GCA and SCA revealed pre-dominance of non-additive gene action for most of the characters studied. The parents ICP 13201 and ICP 13207 were found to be the best general combiners for yield attributing traits. The hybrid ICP 11967 x CO 5 was identified as the best combination and could be exploited for improving seed yield in pigeonpea.

Baskaran and Muthaih (2007) studied in pigeonpea through line x tester analysis revealed the preponderance of non-additive gene action over additive for all the characters studied. The parent's CO 5, VBN 1 and ICPL 83027 were found to be good general combiners for majority of characters. The hybrids VBN 1 X ICPL 83027, ICPL 87 X ICPL 83024, CORG 9701 X APK I, CORG 9904 X ICPL 83027 had good SCA effects for most of the traits including seed yield and can be utilized in heterosis breeding programmes.

Phad *et al* (2007) revealed that the parents ICPL 87119, BDN 2004, AKT 8811, BSMR 736 and BSMR 853 had good general combining ability whereas among the crosses, BDN 2 x BDN 2010, BDN 2 x BSMR 853 and BSMR 736 x AKT 8811 were the best specific cross combinations for grain yield/plant, plant spread, number of primary branches/plant, number of secondary branches/plant and number of pods/plant in pigeonpea.

Sameer Kumar *et al.* (2009) estimated the variances due to GCA and SCA effect and found the predominance of non-additive gene action for most of the characters in the present study. Among female parents, PRG 100 and LRG 30 and among the testers, ICP 8863 and ICPL 87119 were found to be good combiners for most of the characters studied. The cross combinations viz., LRG 30 x ICP 8863, PRG 100 x ICP 8863, LRG 30 x ICP 87119, ICPL 85063 x ICP 87119 and PRG 100 x ICP 87119 exhibited significant SCA effects coupled with appreciable amounts of relative heterosis, heterobeltiosis and standard heterosis for yield and its attributes in pigeonpea.

Singh and Singh (2009) crossed ten pods fly resistant lines with each of three pods fly susceptible varieties in a line x tester mating design. MA2, PDA 93-1E, SL 21-9-3, Bahar and T 7 were identified as good general combiners for seed yield per plant. The heterosis to the extent of 73.77% and 168.42% over the standard check (Bahar) and better parent, respectively were observed for seed yield per plant Five hybrids i.e., MA 2 x Bahar, PDA 93-1E x T 7, PDA 93-1E x Bahar, SL 219-3 x T7 and ICP 8102-5-SI x T 7 exceedingly above 45% standard heterosis for yield were spotted out as promising heterotic crosses in pigeonpea.

Beckham and Umaharan (2010) revealed that pod length, pod width, seeds per pod, shelling percentage and phenolic content were under the control of additive genetic effects with the non-additive effects generally being either not significant or much smaller compared to the additive genetic effects. 100 seed weight was controlled by both additive and non-additive effects.

Gedam (2010) recorded that non additive gene action was more prevalent for almost all traits, as the SCA variance (σ^2 SCA) were higher than GCA variance (σ^2 GCA) for all the characters under studies except for days to 50% flowering.

Gupta *et al*. (2011) studied combining ability and found that the lines CMSGT 33A, CMSGT 100A, CMSGT 288A, CMSGT 301A and CMSGT 311A among females (A lines) and GTR 27 and GTR 29 among males (R lines) were good general combiners for seed yield and one or more other characters. CMSGT 311A x GTR 29, CMSGT 310A x GTR 27, CMSGT 288A x GTR 26, CMSGT 301A x GTR 27, CMSGT 301A x GTR 30 and CMSGT 100A x GTR 28 showed desired higher SCA effects for seed yield per plant in pigeonpea.

Thiruvengadam and Muthiah (2012) studied combining ability in pigeonpea using genetic male sterile lines and estimated the nature of gene action for yield and its component traits. Based on overall GCA effects, the lines MS CO 9701, MS CO 5 and the testers ICPL 87, CORG 9302 and TAT 93-47 were identified as potential parents as they exhibited significant GCA effects for most of the traits. Among the number of crosses with high SCA values, the hybrids MS CO 9701 x ICPL 87, MS CO 9701 x CORG 9302, MS CO 5 x CORG 9302, MS CO 5 x TAT 93-47 were the most promising as they were early, dwarf and high yielding in pigeonpea.

Arbad *et al*. (2013,) studied the combining ability and genetic variance for nine quantitative traits in pigeonpea nonadditive gene effects were pre dominant for all characters. Two crosses exhibiting high SCA effects for grain yield per plants and some parents were good combiner for grain yield and pod per plants.

Meshram *et al*. (2013) predominance of non-additive gene action for almost all the characters including seed yield except plant height which was under the influence of additive gene action. None of the parents exhibit significant GCA effects for all the characters under study, however among the lines AKCMS 10A, AKCMS 13A and AKCMS 09A and among the testers AKPR 8, AKPR 359 and AKPR 292 were identified as potential parents as they exhibited significant GCA effects for most of the traits. Among the hybrid combinations AKCMS 09A x AKPR 8, AKCMS 10A x ICPR 2740, AKCMS 11A x AKPR 319, AKCMS 09A x AKPR 374 and AKCMS 06A x AKPR 359 might be exploited for the improvement of respective traits as found to possess desirable genes for most of the important characters including seed yield in pigeonpea.

Pandey *et al*. (2014) reported that estimates of SCA variance were higher than their corresponding GCA variance for all the traits except plant height. The eight crosses estimate good specific combining ability effects for yield and its major attributes hence, it may be considered for hybrid breeding programmes.

Saroj *et al.* (2014) evaluated 26 F1 hybrids involving two CMS lines and 13 restorers in line x tester fashion and revealed first four cross combinations viz., ICPA 2043 x Azad, ICPA 2043 x ICPR 4105, ICPA 2092 x ICPR 3760 and ICPA 2092 x MA 6 exhibited significantly high SCA effects for seed yield and the parents involved having high x high and low x low GCA effects in pigeonpea.

Yamanura *et al.* (2014) reported that the parents ICPA 2078, GT 308A, PKV TARA, ARCCV 2 and GPHR 08-11 were good general combiners for seed yield and its direct components. The estimates of SCA effects revealed that nine experimental hybrids had significant, desirable and positive SCA effects for seed yield. The cross combination ICPA 2092 x Vipula, ICPA 2078 x BSMR 856 and ICPA 2078 x ARCCV 2 were good specific combiners for number of secondary branches, number of pods per plant and seed yield per plant in pigeonpea.

Mhasal *et al.* (2015) reported female parent, ICPA-2047A recorded significant general combining ability (GCA) effect for maximum six characters such as grain yield per plant, plant height, number of clusters, number of seeds per pod, 100 seal weight and days to 50 percent flowering. The male parent AKPR-324 achieved the highest GCA effect for plant height, number of clusters, 100 seed weight and grain yield per plant. The cross ICPA-2047A x AKPR-324 depicted high mean performance (33.67), positive specific combining ability (SCA) effect and both the parents involved revealed high GCA effects in pigeonpea.

Patil *et al*. (2015) studied seven obcordate A- lines and four known fertility restorers in line X tester mating design to estimate general combining ability mid specific combining ability. Higher magnitude of SCA effect showed that hybrid vigour under the control of non-additive genes. Among A- lines, ICPA 2204 and among testers, ICPL 20116 were the best combiner. Among hybrids ICPA 2208 x ICPL 20108 a crass between high GCA parents was the best with positive significant SCA effect and higher mean performance for grain yield, 100-seed mass, number of seeds/pods in pigeonpea.

Tikle *et al*. (2016) reported that the male parent ICPL 87119 was good general combiner for days to maturity and pollen fertility and among the female parent ICP 2043 was good general combiner.

Kumar *et al.* (2017) to ascertain combining ability 30 hybrids were made from 13 parents in a line X tester mating design during *Kharif,2012-13* and tested in a Randomized Block Design with two replications during *Kharif,2013-14.* Analysis of variance for quantitative traits revealed that all accessions were significantly different and a wide range of variability exists for most of the traits studied. Most promising combinations for seed yield per plant were ICPA 2047, ICPL 20126, ICPA 2048, X ICPL 20106, ICPA 2047 X ICPL 20108 and ICPA 2047 X ICPL 20098. The general combining ability revealed that among the testers, ICPL 20126 and ICPL 20108 were good general combiners for seed yield /plant. The results also revealed that some crosses exhibited higher order significant and desirable SCA effects for different characters involved parents having different GCA effects.

Srivarsha *et al.* (2017) to estimate combining ability, twenty-seven hybrids were made from 12 parents in a line X tester mating design during *Kharif 2015-16* and tested in a Randomized block design with three replications during *Kharif 2016-17.* Among these parents ICPL 161 and ICPL 149 had desirable GCA effect for grain yield per plant and its contributing characters. Ten crosses exhibited significant positive SCA effect for grain yield. Out of them most promising crosses in terms of grain yield were ICPA 2039 X ICPL 161, ICPA 2156 X ICPL 86022 and ICPA 2039 ICPL 88039, ICPL 161 and ICPL 149 can be used for future hybridization programmes.

Mallikarjuna *et al.* (2018a) four cytoplasmic genetic male sterile lines were crossed with six restorer lines in Line x Tester design. The resultant 24 hybrids were evaluated along with their parents during *Kharif* 2017-18. The lines ICPB 2043, ICPB 2047 and ICPL 87119 were good general combiners for seed yield and its components. Six out of 28 hybrids showed significant positive sca effects for seed yield and its two or more component traits.

Mohan, and Sheeba (2019) the study was conducted in line x tester mating design using 40 hybrids, 14 parents to estimate the combining ability effects and heterosis for yield and yield attributing traits in green gram. Considering the per se performance and gca effects VBN 2 and ADT 3 (lines) and IPM-02-03, Pusa 0871 and EC 398897 (testers) were adjudged as the best parents and crosses involving these are expected to throw desirable segregants.

2.2 Heterosis

The term heterosis was first used by Shull (1914). Heterosis refers to tie increased or decreased vigour exhibited by hybrids in F1 generation over the mean of both parents or over better parent. The heterosis is the genetic expression of the beneficial effects of hybridization. In common usage, the terms heterosis and hybrid vigour is synonymous and it has been more precisely suggested by Whaley (1952) as the developed superiority of the hybrids as hybrid vigour and the mechanism by which the superiority is developed as heterosis.

In a particular cross, heterosis is measured in terms of two parameters i.e. heterosis over mid parental value (relative heterosis) and heterosis over better parent value (heterobeltiosis). However, in plant breeding programmes, heterosis is also estimated in terms of heterosis over check or standard variety/hybrid (useful or standard heterosis). In terms of combining ability for quantitative characters, heterosis is highly associated with specific combining ability effects of the cross. Although the basic meaning of heterosis was clear, yet there was disagreement regarding the situation to which the term should be applied. Shull (1948) strictly reserved heterosis to describe an increase in a characteristic arising from hybridity. On the other hand, Mackey (1976) considered heterosis as a two-way phenomenon. Similarly, Mayo (1987) considered 'negative heterosis' in addition to positive heterosis in the sense that it may be of value for certain characteristics such as maturity period. In pigeonpea there are many reports to present the possibility of good amount of heterosis for grain yield and its components in experimental hybrids. This information may be useful for exploitation of heterosis on commercial scale.

Soloman *et al.* (1957) gave first report on heterosis in pigeonpea by studying the extent of heterosis in ten hybrids in respect of fourteen morphological characters. Considerable heterosis was observed in several growth parameters and yield components. Fairly conspicuous vigour (24.5%) was noticed in few best hybrid combinations though it did not out yield the highest yielding variety.

Veeraswamy *et al.* (1973) recorded that the interparietal hybrids in red gram between CO 1 (a short duration high yielding strain) and 19 diverse varieties expressed heterosis for plant height, plant spread, number of branches, number of clusters, number of pods and days to 50 per cent flowering. The maximum heterosis was recorded for number of clusters (179.6 %) and number of pods (188.5 %) over the superior parent in pigeonpea.

Shrivastava *et al.* (1975) studied the extent of heterosis in 17 Fi hybrid combinations involving 14 genotypes for yield and observed 96 per cent heterosis for secondary branches and 80 per cent heterosis for number of pods per plant. In most of the crosses, low x medium and low x low parental combinations had maximum heterosis for individual characters. In case of secondary branches, heterosis was maximum in high x high as well as low x low crosses indicating the role of genetic diversity for obtaining high hybrid vigour in pigeonpea

Reddy *et al.* (1979b) observed high heterotic effects in crosses involving diverse parents of different maturity groups. Specifically, mid late x late and early x late cross combinations were of economic worth and negative heterosis was exhibited for traits viz., plant height and protein content while positive heterosis was observed in respect of pod number and yield in pigeonpea.

Venkateswarlu *et al.* (1981) observed the mean heterosis of 39 per cent for yield and about 16 per cent for days to flowering as well as pods per plant. In general, early x and midlate x late combinations resulted in high heterosis for yield in pigeonpea.

Marekar (1982) observed overall heterosis of 17.85 and 6.75 per cent for yield over mid parent and better parent respectively. For other traits viz., plant height, days to flower, number of primary branches, pod weight and hundred seed weight overall heterosis over mid-parent was 17.7, 0.4, 12.0, 6.6 and 5.6 per cent respectively. Negative heterobeltiosis over better parent was obtained for plant height, days to flower, number of primary branches and 100 seal weight in pigeonpea.

Singh *et al.* (1983) observed the maximum heterotic response up to 221 per cent for grain yield in line x tester studies of pigeonpea. The best heterotic cross, Mukta x Upasl20 was identified as potential cross for early maturing hybrids.

Omanga (1985) studied the heterosis in seven fertile lines crossed in line x tester design and reported high heterosis percentage over mid parent for yield and other three related characters in pigeonpea. High magnitude of heterosis was seen with MS-Prabhat than with MS 3 A.

Saxena *et al.* (1986) observed the heterosis for yield and six yield contributing traits which ranged between 24 and 26 per cent in pigeonpea.

Tuteja *et al.* (1989) reported high heterosis in a best cross A2 x EE 76 for yield, number of clusters and pods among thirty hybrids in pigeonpea.

Patel *et al.* (1991) using line x tester design including 3 male sterile lines, 10 medium and 10 early maturity pollinators recorded heterosis for seed yield per plant in pigeonpea. Out of these 60 combinations, heterosis for seed yield over better parent was highest for crosses MS 3A x DL 781 (80%) and MS Prabhat x ICPL 684 (78%).

Tuteja *et al.* (1992) showed that a single cross Aged x EE 76 and a three-way cross (ICPL 87 x EE76) x UPAS 120 was significantly better for days to maturity in negative direction in pigeonpea.

Khapre *et al.* (1996) studied 24 hybrids along with 11 parents and ICPH 8 and BDN 2 as standard hybrid and standard variety respectively as a check. They found that crosses with line MSHY 9 showed marked heterosis for height at first effective branches, number of primary branches, pods per plant and grain yield per plant followed by line MS Prabhat Male parents BDN 2, Daithna local, ICPL 87 and BDN 7 gave marked heterosis for yield and its components in pigeonpea

Paul *et al.* (1996) studied heterosis for yield and yield components in hybrid pigeonpea in 28 late maturing pigeonpea experimental hybrids and found that hybrids gave better heterotic response against T 7 as compared to Bahar which varied from - 27.7 to 91.2 per cent. They also concluded that pods per plant in association with number of secondary branches and dry matter at maturity were found to be the chief contributing characters.

Verulkar and Singh (1997) studied heterosis in pigeonpea and found that the standard heterosis for seed yield per plant ranged from 16.5 pa- cent in cross ICPL 151 x ICPL 84023 to 54.6 per cent in cross UPAS 120 x ICPL 84023. These crosses also exhibited significant desirable heterosis for days to flower, days to maturity, number of pods and 100 seed mass.

Kumar and Srivastava (1998) observed heterosis over better parent for seed yield which ranged from -77.91 to 110.97 per cent at DPR, Kanpur using line x tester design involving three male sterile lines and twelve male fertile parents of longer duration in pigeonpea.

Wanjari *et al.* (1998) studied exploitation of heterosis in pigeonpea and found that MST 21 was better female line and AK 22 and AK 30 among males had been identified as good general combiners. The MS P3 x AK 22 have been found to have high sea.

Wankhede (1998) studied heterosis for yield and yield components for 24 crosses in pigeonpea developed by crossing three male sterile lines and eight testers and revealed that the phenomenon of heterosis was of general occurrence for most of the traits, except plant height. The cross AKMA 11 x AKT 9221 showed highest seed yield per plant and exhibited high heterosis (63.19 %) and useful heterosis over BDN 2 (83.84 %). They concluded that the mean squares due to parents and crosses were highly significant for all the characters. AKMS 11 x AKT 9221 and AKML 11 x C 11 were the best crossed followed by AKMS 21 x C 11 for seed yield, number of clusters, number of pods and protein content and AKMS 21 x BDN 2 for number of clusters and pods per plant.

Hooda *et al.* (1999) reported heterosis in 40 crosses using line x tester design. Maximum heterosis for pods per plant over standard check Manak was obtained for crosses QMS 1 x TAT 10 (38.1 %), QMS 1 x H 88-43 (28%), heterosis, for seed yield per plant was observed within range of 21.2 to 28.9 per cent

Singh *et al.* (1999) studied 16 inter specific hybrids involving four lines of Cajanus sericeus and four testers of Cajanus cajan and observed 85.96%, 45.43%, and 25.54% average heterosis for branches per plant, pods per primary branch and pods per plant respectively.

Srinivas *et al.* (2000) studied 22 experimental hybrids derived from two male sterile lines viz., ICP MS 288 and MS 3783 as female and 11 mediums to late genotypes as male in line x tester mating design. Out of these crosses, the crosses involving ICP MS 3783 line showed heterosis for seed yield and most of component characters. The cross ICP MS 3783 x LRG 30 was best hybrid combination.

Chandrikala and Raveendran (2002) studied 30 pigeonpea hybrids derived from three QMS lines and ten tester lines. The cross with MS Prabhat DT showed marked heterosis for pods per plant, clusters per plant, 100 seed weight and grain yield per plant Highest positive heterosis ova- mid, better and standard parents was observed in MS 0-5 x ICPL 88009 for number of branches per plant and in MS Prabhat NDT x ICPL 88009 and MS Prabhat DT x ICPL 84023 for grain yield per plant.

Pandey and Singh (2002) reported highly significant positive heterosis for seed yield per plant, number of primary branches and number of secondary branches per plant in pigeonpea.

Kalaimagal and Ravikesavan (2003) reported heterosis for seed yield and its components in 63 crosses obtained by crossing 3 genetic male sterile lines with 21 testers in L×T fashion. The heterosis was ranged from 9.13 to 404.57 per cent, 10.11 to 57.92 per cent and 10.42 to 106.17 per cent over mid parent, better parent and standard check respectively in pigeonpea.

Aher *et al.* (2006) studied the performance of three crosses viz., BDN 2 x BDN 2010, BDN 2 x Nirmal 2 and BSMR 736 x Nirmal 2 and observed maximum positive heterosis over mid parent, better parent (45.5%, 26.0%) respectively for number of pods per plant and grain yield per plant Similar trend of heterosis over better parent was recorded for these traits in pigeonpea.

Saxena *et al*. (2006) studied the yield of new CMS-based pigeonpea hybrids and found hybrids on Ai cytoplasm i.e. ICPH 2319 (3017 kg/ha) was the best with standard heterosis of 61.3 per cent over the best check ICPL 360. On A2 cytoplasm-based hybrids, ICPH 3172 (2725 kg/ha) was found to be best with 33-36% superiority over controls and on A4 cytoplasm-based hybrids, ICPH 2438 (3414 kg/ha) was the best performing hybrids with 61 per cent superiority.

Anantha and Muthian (2007) studied combining ability and heterosis for seed yield and its components using line x tester mating design and observed high degree of heterosis for seed yield per plant and other yield components over standard check (CO 5) in pigeonpea.

Wanjari *et al.* (2007) studied heterosis in CMS based 136 hybrids in pigeonpea and found maximum heterosis in hybrid No. 230407 (GT 288 A x 220751-5) with 212.26 per cent heterosis over check followed by hybrid No. 230466 (AKV 2 A x 22076-29) and hybrid No. 230405 (GT 288 A x 220682-55) with heterosis of 140.94 per cent and 131.92 per cent over check respectively.

Acharya *et al.* (2009) reported that out of 45 crosses, 30 and 19 crosses exhibited significant positive heterobeltiosis and standard heterosis for seed yield per plant Ten best crosses exhibited significant desirable standard heterosis for seed yield per plant as well as yield contributing characters in pigeonpea.

Sarode *et al.* (2009) studied the estimates of heterosis for yield and yield traits in long duration pigeonpea. Out of fifteen crosses, the maximum standard heterosis was recorded in a cross Pusa 9 x Bahar (55.32 %) followed by MAL 8 x ICPL 7035 (47.94 %) for yield per plant and pods per plant.

Chandirakala *et al.* (2010) reported that two hybrids viz. MS Prabhat DT x ICPL 88009 and MS Prabhat DT x ICPL 84023 showed highly significant and positive heterosis over mid, better and standard parent in general, the proportion of hybrids exhibiting significant heterotic effect for grain yield with genetic male sterile line MS Prabhat DT was greater as compared to lines, MS Prabhat NOT and CO 5.

Shoba and Balan (2010) studied the heterosis over standard variety for single plant yield varied from -25.0 % (CORG 990047 A x ICPL 87) to 325 % (MS CO 5 x PA 128). While considering mean performance, SCA effects and standard heterosis the promising hybrids namely CORG 990047 A x APK 1 and MS CO 5 X ICPL 83027 which were found to be superior for plant height(cm), number of pods/plant and single plant yield in pigeonpea.

Sameer Kumar *et al.* (2012) reported in all the four crosses for seed yield per plant and for most of its attributes in pigeonpea.

Gedam *et al.* (2013) studied heterosis for seed yield and its components in 40 crosses obtained by crossing 4 female lines with ten male testers in LXT fashion. Nonadditive gene effects were predominant for all the characters, except for days to 50% flowering. The cross ICPL 20106 x ICPR 3477 showed high heterosis over mid parents and better parent with 144.98 % and 61.31 % over the standard check 'BSMR 736 and ICPH 2671 respectively for grain yield per plant in pigeonpea.

Patel *et al*. (2013) studied diallel analysis in pigeonpea for estimation of heterosis including seed yield per plant and its component characters. Significant heterobeltiosis and high per se performance with regards to seed yield per plant and its components were recorded by the crosses GT 102 x ICPL 87119 (33.80% and 95.00g), BSMR 853 x GT 102 (25.35% and 85.00 g) and ICPL 87119 x AGT 2 (25.23% and 92.67g) in positive direction respectively.

Gite *et al.* (2014) reported standard heterosis in pigeonpea for seed yield ranged from 53.31 to 77.94 per cent. On the basis of heterosis over standard check, first five hybrids *viz,* (ICPA 2043 x ICPR 2671), (ICPA 2043 x ICPR 3473), (ICPA 2043 x ICPR 3477), (ICPA 2043 x ICPR 3514) and (ICPA 2048 x ICPR 2671) out yielded BSMR 736 to the extent of 77.94%, 72.54%, 64.95%, 61.02% and 60.29%, respectively. Whereas, these five hybrids also had highest better parent heterosis to the extent of 53.81%, 58.92%, 42.58%, 48.64% and 31.58%, respectively.

Patil *et al.* (2014) studied heterobeltiosis for seed yield and its components with protein content. Highly significant positive heterosis was over better parent for seed yield and its components with protein. The cross GT 102 x ICPL 87119 shows highest heterosis over better parents with high seed yield/plant followed by crosses ICPL 87119 x AGT 2, BSMR 853 x ICPL 87119 and BSMR 853 x GT 102. The cross GT 102 x AGT 2 reported significant positive heterobeltiosis for protein content followed by the cross AGT 2 x GTR11 and ICPL 87119 x AGT 2.

Saroj *et al.* (2014) reported that the four hybrids viz., ICPA 2043 x Asha, ICPA 2092 x Asha, ICPA 2043 x Azad and ICPA 2043 x ICPR 4105 showed significant heterosis, over mid parent, better parent and MPH, BPH and EH, over commercial variety i.e. MAL 13. Further, two hybrids (ICPA 2043 x Azad and ICPA 2043 x Asha) could manage to out yield the check MAL 13 significantly with the margin of > 20 % and thus, may be exploited for heterosis breeding in pigeonpea.

Gadekar *et al*. (2015) studied 48 hybrids developed by crossing with four diversified based male sterile lines viz., oval leaf, sesamum leaf, obcordifoliate leaf and small leaf with twelve diverse fertility restorer lines of pigeonpea for estimation of economic heterosis over two checks PKV -Tara and AKT- 8811. Hybrids viz., Obcordifoliate leaf x AKPR-178 (M), Obcordifoliate leaf x AKPR-344 and Obcordifoliate leaf x AKPR-210 exhibited highest significant economic heterosis effects over two checks PKV-TARA and AKT-8811.

Pandey *et al.* (2015) studied sixty Fi hybrids developed by crossing three CMS lines with 20 elite genotypes/restorers. Sixty Fi hybrids for various morphological traits and the crosses derived from high diversity group showed high positive significant heterosis for seed yield. However, some crosses gave very high negative heterosis for seed yield although their parents belong to a high diversity group. The reason for this possibly could be linkage of alleles for complex genetic traits as biomass and yield. Among the top fifteen heterotic hybrids for seed yield, ten crosses were resulted from crossing between parents of low diversity while five from the high diversity group.

Reddy *et al*. (2015) revealed presence of significant levels of heterosis in pigeonpea hybrids for yield and yield component characters. Concerning individual trait, maximum heterosis over mid parent, better parent and standard check were observed for seed yield per plant, followed by number of secondary branches and pods per plant High heterosis, more than 100 per cent over the check Asha more than 50 per cent over mid-parent and more than 30 percent over better parent were noticed in the hybrids, ICPH 3762 and ICPH 3474. These promising mid-late hybrids with improved per se performance, high heterosis for seed yield and other major yield attributing traits were identified here for large scale commercial cultivation.

Singh and Singh (2015) studied heterosis, twelve hybrids having diverse background was developed to understand the heterosis and inbreeding depression in late maturity group of pigeonpea (*Cajanus cajan L.*) More than 100% significant economic heterosis were revealed in crosses, MAL-17 x NDA 4906 (266.32%), BHUA 96-13-3 x NDA 49-6 (249.98%), BHUA 96-13-3 x MAL-19 (190.41%), MAL-17 x NDA59-1 (136.27%) and MAL-17 x MAL- 19 (103.46%) for seed yield per plant. The cross MAL-17 x NDA 49-6 and BHUA 96-13-3 X NDA 49-6, showed better performance in Fi, low/even negative inbreeding depression in Fa and involved parents with high per se performance. Two crosses namely, BHUA 96-13-3 X MAL-19 and BHUA 96-21-4 X NDA 99-1.

Srivarsha *et al.* (2017) Twenty-seven pigeonpea *[Cajanus cajan (L.) Millsp.]* hybrids were developed by hand pollination using three CMS lines (A lines) and nine testers (R lines). These hybrids along with their parents and two standard checks (VL Arhar 1 and ICPL 161) were evaluated in a randomized block design with three replications during kharif 2016-17 for the heterosis studies .Results indicated that the crosses ICPA 2039 X ICPL 90048 had manifested significant heterobeltiosis and standard heterosis over two checks viz., VL Arhar1 and ICPL 161 for grain yield per plant and yield contributing characters .The stability of these promising crosses can be studied across the different environments and feasibility for their commercial utilization could be tested in further generations.

Soni and Patel (2017) evaluated thirty CGMS based pigeonpea *[Cajanus cajan (L.) Millsp]* hybrids by crossing six CMS lines with five 'R' lines and for yield potential. The range of standard heterosis over GTH1 for seed yield per plant was from -27.29 (CMS GT 301 A X GTR 52) to 69.79 per cent (CMS GT 603 A X GTR 52). The best cross combinations for seed yield were CMS GT 603 A X GTR 52 (69.79), CMS GT 603A X GTR 23 (64.59%), and CMSGT 288A X GTR 95(57.22%).

Mallikarjuna *et al.* (2018b) in this context, four cytoplasmic male sterile lines were crossed with six genotypes of pigeonpea in a line x tester mating design. Thus, the resultant 24 hybrids along with their parents and two standard checks ASHA (ICPL 87119) and ICPH 2740 and evaluated during *Kharif* 2017-18. The results indicated that the manifestation of relative heterosis for seed yield per plant was significantly superior of nine hybrids ranging from -35.93% - 49.93%, four hybrids ranging from -44.45% - 36.14%, one hybrid over standard variety ranging from - 44.45% - 15.82% and one hybrid over standard hybrid ranging from - 52.04% - 21.31% most of the cross combinations the significant positive heterosis was observed for seed yield per plant was mainly due to the manifestation of heterosis for its component characters. The best cross combinations in order of merit seed yield and other yield components were ICPA 2043 x ICPL 20096, ICPA 2047 x ICPL 20098 and ICPA 2078 x ICPL 87119.

Mohan and Sheeba (2019) the study was conducted in line x tester mating design using 40 hybrids, 14 parents to estimate the combining ability effects and heterosis for yield and yield attributing traits in green gram. Considering the per se performance, significant sca effects and desirable heterosis, the hybrids ADT 3 x IPM-02-03, ADT 3 x IPM-02-14, ADT 3 x PDM 139, ADT 3 x TM-11-34, were found to be superior for number of pods per plant, number of pod clusters per plant. The hybrids can be utilized to develop high yielding varieties with desirable traits.

CHAPTER – III

MATERIAL AND METHODS

The present investigation was undertaken to study "Heterosis and Combining Ability Studies in Pigeonpea" (*cajanus cajan (L.) Millsp.*)". The experiment was conducted at Agri cultural Research Station, Badnapur.

3.1 Experimental materials

3.1.1 Description of Breeding Materials: The experiment consisted of 20 crosses developed by using 5 female and 4 male parents along with Vipula and Asha as checks.

The details of the female and male parents are given in below:

Parents-

Female parents-

(Line)	1) BDN 708	2) BDN 711
	3) BDN 716	4) BSMR 736
	5) BSMR 853	

Male parents-

(Tester)	1) LRG-41	2) TJT-501
	3) AL-882	4) TS3R

Checks-	1) Asha	2) Vipula

3.2 Crossing programme

The set of 20 hybrids were developed during monsoon season of 2019-2020 by crossing five female lines with four male parents.

3.2 Experimental methods

3.3.1 Study of crosses and its parent

31 treatments comprising 20 hybrids along with 9 parents and 2 checks were studied during *Kharif* of 2019-20 at the Agricultural Research station, Badnapur.

3..3.2 Details of experiment.

1) Mating design : Line x tester
2) Design : RBD
3) No. of Replication : Two
4) Treatments : 20 F_1's +9 Parents +2 checks
5) Plot size : 0.90 x 4m
6) Spacing : 90 x 20cm
7) Fertilizer dose : 25:50:0 NPK (kg/ha)
8) Season : *Kharif* 2019-20
9) Location : Agricultural Research Station, Badnapur

Cultural practices

The crop was given a uniform basal dose of 25 kg N and 50 kg P_2O_5/ha. Cultural practices like weeding and plant protection measures were followed as and when required.

3.4 Observations

3.4.1 Observations on yield and yield contributing characters

Five competitive plants were selected randomly from each row in each replication for recording the observations. Average value of the line for each character was computed from these plants for the characters given below.

3.4.1.1 Plant height (cm)

At maturity, plant height was measured in cm from base of the plant to tip of the main stem.

3.4.1.2 Days to 50 per cent flowering

Number of days from sowing to 50 per cent flowering in a plot was recorded and average number of days to flowering was worked out.

3.4.1.3 Pollen fertility (%)

For testing the pollen fertility in the hybrids **2 per cent aceto-carmine** solutions was used to stain and differentiate the fertile and sterile pollen grains. Three plants were selected randomly from each hybrid and five buds from each plant were collected to record its pollen fertility. Anthers from each flower bud were squashed on a slide and the count of fertile and sterile pollen grains in three microscopic fields was noted.

Per cent pollen fertility of hybrids was calculated on mean of all the from a hybrid.

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

3.4.1.4 Days to maturity

Days required from sowing to maturity of 80 per cent of plants in a plot were recorded as days to maturity.

3.4.1.5 Number of primary branches per plant

The total effective pod bearing branches per plant on the main stem were recorded.

3.4.1.6 Number of secondary branches per plant

Total effective pod bearing branches per plant on primary branches were noted.

3.4.1.7 Number of pods per plant

The numbers of pods without any damage on plant were counted. Total number of pods bearing seeds were counted per plant at maturity.

3.4.1.8 Number of seeds per pod

The number of seeds in each of 10 pods of selected five plants were recorded and average was worked out as number of seeds per pods on each plant.

3.4.1.9 **Pod length (cm)**.

Pod length of five selected plant was recorded in cm.

3.4.1.10 100 seeds weight (g)

Healthy 100 seeds were counted and weight recorded in grams.

3.4.1.11 Grain yield per plant (g)

The grain yield was recorded in grams (g) per plant

3.5. Statistical method

Data in each experiment of all entries was subjected to analysis of variance (Panse and Sukhatme, 1967) for testing the significance of treatments.

3.6 Estimation of heterosis

The heterosis was calculated as per the procedure suggested by Fonseca and Patterson (1968).

3.6.1 Standard heterosis

The heterosis effects in terms of per cent increase or decrease over standard check (useful heterosis) were measured for all the eleven characters.

$$\text{Per cent heterosis over standard check} = \frac{\overline{F_1} - \overline{SC}}{SC} \; 100$$

Where,

F1 = Mean of F1 hybrid

SC = Mean value of standard check

Heterosis was tested by least significance difference (LSD) as below:

$$\text{L.S.D. for standard check} = \left(\frac{\text{2 x pooled error mean square of the RBD}}{\text{Number of replications at p = 0.05 and 0.01}} \right)$$

3.7 Line x tester analysis

The genetic analysis was carried out for line x tester mating design as suggested by Kempthorne (1957).

The treatment SS was partitioned to source attributed to parents, crosses and parent vs crosses.

Table 3.1 ANOVA for line x tester mating design

Sr. No.	Sources of variation	DF	SS	MSS
1.	Replication	(r - 1)	-	-
2.	Genotype/treatments	(g - 1)	-	-
3.	Lines (females)	(l – 1)	-	$\sigma2+rl\frac{1}{t-l}\Sigma_{i} gi^2$
4.	Testers (Males)	(t - 1)	-	$\sigma2+rt\frac{1}{l-l}\Sigma_{j} gj^2$
5.	Lines x Testers	(l - 1) (t - 1)	-	$\sigma2+r\frac{1}{(t-l)(i-i)}\Sigma_{i}\Sigma_{j} Sij^2$
6.	Error	(r - 1) (lt - 1)	-	$\sigma 2e$

The standard error and critical difference between two means were calculated as follows

$$\text{S.E. of mean} = \sqrt{\text{EMSS / No. of replications}}$$

$$\text{S.E. difference} = \text{S.E. of mean} \times \sqrt{2}$$

Critical difference (C.D.) = S.E. difference x 't' value

('t' value at 5 and 1 per cent level of probability for error degrees of freedom)

3.7.1 Analysis of variance for combining ability in line x tester

The line x tester analysis to estimate general and specific combining ability in respect of the character in F_1 under the study was carried out according to the procedure given by Kempthorne (1957). The analysis of variance will take the following form.

Table 3.2 ANOVA for combining ability analysis.

Sr. No.	Source of variation	Degree of freedom (d.f.)	Mean square	Expectations
1.	Lines (l)	(l-1)	M_1	σ^2e+ (CovFS-2CovHS) + (tr CovHS)
2.	Tester (t)	(t-1)	M_2	σ^2e+ r (CovFS-2CovHS) + (tr CovHS)
3.	Line x tester	(l-1) (t-1)	M_3	σ^2e+ r (CovFS-2CovHS)
4.	Error	(r-1) (tl-1)	M_4	σ^2e

Where,

lr = Line x Replication

tr = Tester x Replication

Cov HS = Covariance half sibs

Cov FS = Covariance of full Sibs

3.7.2 Estimation of general and specific combining ability effects

One of the major objectives of the present study was to estimate the general combining ability effect of the lines and the testers and the specific combining ability effect between the lines and the testers. The combining ability effects and their standard errors were estimated as follows.

The mean used to estimate the general and specific combining ability effects of the ijk observations was

$$X_{ijx} = m + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

X_{ijx} = Any character measured on cross i x j in k^{th} replication

m = Population mean

g_i = gca effect of i^{th} female parent

g_j = gca effects of j^{th} male parent

s_{ij} = sca effects of ij^{th} combination

e_{ijk} = Error associated with the observation xijk

i = Number of female parents

j = Number of male parents

k = Number of replications

individual effects were estimated as indicated below

i) $$m = \frac{X\ldots}{mfr}$$

Where

x = The total of all hybrids

m = Number of males

f = Number of females

r = Number of replications

$$\text{ii)}\quad g_i = \frac{X_{i..}}{fr} - \frac{X_{...}}{mfr}$$

Where

$X_{i.}$ = Total of i^{th} male parent over all female parents and réplications.

$$\text{iii)}\quad g_j = \frac{X_{j..}}{mr} - \frac{X_{...}}{mfr}$$

Where

X_j = Total of j^{th} female parent over all male parents and réplications.

$$\text{iii)}\quad S_{ijgj} = \frac{X_{(ij)}}{r} - \frac{X_{j..}}{fr} - \frac{X_{j..}}{mr} + \frac{X_{...}}{fmr}$$

Where

$x_{(ij)}$ = $(ij)^{th}$ combination total over all replication.

The restriction $g_i = 0$, $s_{ij} = 0$ is imposed on the elements of model

The covariance for half sib and full sib were obtained by following relation.

$$\text{i) Cov HS} = (\sigma^2\text{gca line}) = \frac{M_l - M_{l \times t}}{r \times t}$$

$$\text{ii) Cov HS} = (\sigma^2\text{ gca tester}) = \frac{M_t - M_{l \times t}}{r \times l}$$

$$\text{iii) Cov HS} = (\sigma^2\text{ gca ave.}) = \frac{M_l + M_t - 2\,M_{l \times t}}{r\,(L + T)}$$

Where,

M_l = MSS of lines

M_t = MSS of testers

$M_{l \times t}$ = MSS of line x tester

r = Replication

l = Lines

t = Testers

iv) $$\text{Cov FS} = \frac{(M_l - M_e) + (M_t - M_e) + (M_{lxt} - M_e)\ 6r\ (\text{Cov HS ave.}) - r\ (l \times t)\ \text{Cov HS ave}}{3r}$$

v) $\sigma^2 \text{sca} = \text{Cov. FS}$

vi) $\sigma^2 \text{sca} = \text{Cov. FS} - 2\ \text{Cov. HS}$

vii) $$\sigma^2 \text{sca} = \frac{M_{l \times t} - Me}{r}$$

Where,

M_e = Error mean sum square

The standard error for GCA and SCA effects were calculated as follows

i) $$\text{S.E. (GCA line) gi} = \frac{M_e}{r \times t}^{1/2}$$

ii) $$\text{S.E. (GCA tester) gi} \left\{ \frac{M_e}{r \times l} \right\}^{1/2}$$

iii) $$\text{S.E. (sij - skl)} = \left(\frac{2M_e}{r} \right)^{1/2}$$

Where,

Me = Error mean sum of squares

r = Replications

t = Testers

l = Lines

Per cent contribution of lines, testers and crosses

The proportional contribution of lines, testers and their interactions were determined by following formulae

i) Contribution of males = $\dfrac{\text{SS (m)}}{\text{SS (crosses)}}\ 100$

ii) Contribution of females = $\dfrac{\text{SS (f)}}{\text{SS (crosses)}}\ 100$

iii) Contribution of females x males = $\dfrac{\text{SS (m x f)}}{\text{SS (crosses)}}\ 100$

CHAPTER- IV

RESULTS

In this study five lines BDN 708, BDN 711, BDN 716, BSMR 853, BSMR 736) were crossed with four testers (LRG-41, TJT501, TS3R, AL882) and twenty crosses were developed following line x tester mating design. These twenty crosses along with their parents and checks *viz*., Asha and Vipul were grown during *Kharif* 2019 at Agricultural Research Station, Badnapur. Observations were recorded on different quantitative characters and genotypes were analyzed as per line x tester mating design, while mean data on 31 genotypes (5 lines, 4 testers, 20 crosses and 2 checks) was used for estimation of standard heterosis.

The results of the present investigation are presented under the following major heading.

1. **Analysis of variance**
2. **Mean performance of genotypes for yield and yield components**
3. **Line x tester analysis**
4. **Combining ability of parent and crosses for yield and yield components**
5. **Estimation of standard heterosis**

4.1 Analysis of variance

The analysis of variance showed significant differences among the genotypes for all the characters studied. (Table 4.1)

4.2 Mean performance of genotypes for yield and yield components

Mean performance of different characters studied along with check is presented in (Table 4.2).

4.2.1 Plant height (cm)

The range of plant height was 77.60 cm to 243.00 cm with general mean of 190.94 cm.

Among the lines and testers, BSMR 853 (205.60 cm) and LRG-41 (208.10 cm) were the tallest. Among the crosses, BDN 716 x LRG-41 (243.00 cm) showed highest plant height followed by BSMR 853 x LRG-41 (222.00cm) and BSMR 736 x LRG-41 (219.00 cm).

4.2.2 Days to 50 per cent flowering

The range of days to 50 per cent flowering was 96.50 to 120 days with general mean of 111.08 days.

Among the lines and testers AL882 (96.50 days) was earliest in flowering, followed by BDN 711 (111 days). Among the crosses, BSMR 853 x TS3R (103.50), BDN 716 x AL882 (104.50 days), BSMR 853 x AL882 (105 days) and BDN 711 x AL88 (106 days) took minimum days to flower. Among the lines, BSMR 853 (120 days), BSMR 736 (119.50 days) and testers LRG-41 (117.50 days) was late in flowering. Among crosses BDN 716 x LRG-41 (118 days), BSMR 853 x LRG-41 (117 days), was late in flowering.

4.2.3 Pollen fertility (%)

The range of pollen fertility recorded was 77.50 to 92.50 per cent with the general mean of 85.93 per cent.

Among the lines, BSMR 853 (92.50%) recorded highest pollen fertility and highest pollen fertility among the testers was recorded by LRG-41 (87.50%). Among the crosses BDN 708 x LRG-41(92.50%), BSMR 853 x LRG-41 (90.50) % recorded highest pollen fertility followed by BSMR 736 A x LRG-41 (87.50%).

4.2.4 Days to maturity

Days to maturity ranged from 143.00 to 181.00 days with general mean 169.17 days.

Among the lines and testers, BDN 711 (157 days) and the tester, AL882 (143 days) were early in maturity. Among the crosses BDN 711 x AL882 (144 days) was earliest followed by BDN 716 x AL882 (160 days), BDN 711 x tjt-501 (166.50 days), BDN 708 x TJT-501 (169.50 days). Among the lines, BSMR 853 (177 days) and testers LRG-41 (176.50 days), was late in flowering. Among crosses BDN 716 x LRG-41(181 days), BSMR 736 x LRG- 41 (177 days), BSMR 853 x LRG-41 (176 days) was late in flowering.

Table 4.1 ANOVA for different yield and yield contributing characters in Pigeon pea.

Sources of Variation	d. f.	Mean sum of squares										
		Plant height (cm)	Days to 50 % flowering	Pollen fertility (%)	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
Replications	1	11.41	3.16	47.90	0.25	0.01	0.15	5.34	0.006	0.02	0.07	4.08
Genotype	30	1718.06**	66.72**	35.12	183.82**	1.65**	13.70**	9024.12**	0.25	0.46	1.80	430.17**
Error	30	4.27	3.26	11.70	3.32	0.04	1.60	10.25	0.05	0.01	0.09	6.29

*** -Significant at 5 % level of significance**

**** -Significant at 1 % level of significance**

Table 4.2 Mean values of parents, hybrids and check for yield and yield contributing characters in pigeonpea.

Sr. No.	Parents/Crosses	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
	LINES											
1.	BSMR 853	205.60	120.00	92.50	177.0	8.60	19.50	109.10	3.40	5.35	10.95	40.13
2.	BSMR 736	180.50	119.50	92.50	175.00	7.60	15.50	106.00	4.10	5.15	11.57	40.28
3.	BDN 716	188.40	114.50	87.50	169.00	7.30	13.00	124.50	3.30	4.65	10.68	63.35
4.	BDN 711	146.70	111.00	82.50	157.50	6.10	13.50	114.00	3.20	5.10	11.38	62.24
5.	BDN 708	192.20	112.00	83.75	165.00	5.70	13.50	170.00	3.30	4.60	10.82	52.45
	TESTERS											
6.	LRG-41	208.10	117.50	87.50	176.50	6.30	16.00	142.70	3.70	6.10	12.43	60.99
7.	TS3R	176.00	104.00	87.50	155.00	7.10	13.50	127.85	3.30	4.30	12.18	34.93
8.	AL882	77.60	96.50	82.50	143.00	5.30	9.00	67.75	3.50	5.10	7.80	26.25
9.	TJT-501	177.50	113.50	77.50	175.50	6.10	17.00	145.80	3.30	4.35	12.38	31.32
	CROSSES											
10.	BSMR 853 x AL882	197.00	105.00	85.50	166.00	6.30	13.50	283.50	3.30	4.75	9.94	54.04
11.	BSMR 853 x TS3R	209.00	103.50	77.50	168.00	7.50	15.00	150.90	5.10	4.15	11.80	34.65
12.	BSMR 853 x TJT-501	206.00	107.00	87.50	167.00	6.60	12.50	274.00	3.30	4.50	12.30	47.16
.13.	BSMR 853 x LRG-41	222.00	117.00	90.50	176.00	8.30	16.00	303.80	3.50	5.50	11.82	69.37

Cont.…

Sr. No.	Parents/Crosses	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
14.	BSMR 736 x AL882	193.50	111.50	82.50	166.00	6.70	13.00	138.65	3.40	5.70	11.77	30.41
15.	BSMR 736 x TS3R	199.10	113.00	87.50	173.00	7.60	15.50	176.75	3.40	5.10	12.45	55.05
16.	BSMR 736 x TJT501	203.60	109.00	92.50	166.00	7.30	14.57	166.50	3.30	4.60	12.29	34.98
17.	BSMR 736 x LRG-41	219.00	114.00	87.50	177.50	7.30	12.50	291.65	3.90	5.30	12.16	68.43
18.	BDN 716 x AL882	190.50	104.50	87.50	160.50	7.40	16.00	243.05	3.40	4.30	11.96	65.88
19.	BDN 716 x TS3R	203.00	106.50	87.50	171.00	7.30	16.00	185.40	3.70	5.10	12.81	61.28
20.	BDN 716 x TJT501	211.00	119.50	82.50	176.00	6.40	13.00	146.50	3.60	4.85	12.34	37.31
21.	BDN 716 x LRG-41	243.00	118.00	87.50	181.00	7.30	20.50	275.50	3.60	5.15	12.38	76.50
22.	BDN 711 x AL882	171.00	106.00	82.50	144.00	6.10	13.00	124.95	3.40	4.50	11.10	29.88
23.	BDN7 11 x TS3R	182.50	115.50	87.50	183.00	5.60	12.50	116.80	3.60	4.75	11.65	35.27
24.	BDN 711 x TJT-501	206.50	107.50	87.50	166.50	7.90	15.50	126.05	3.70	4.55	11.08	37.10
25.	BDN 711 x LRG-41	180.10	113.00	87.50	178.50	8.40	18.60	147.45	3.60	5.75	11.34	67.16
26.	BDN 708 x AL882	146.00	111.00	77.50	174.50	5.90	12.50	117.15	3.50	4.55	11.46	34.82
27.	BDN 708 x TS3R	186.60	113.00	82.50	172.00	5.70	15.00	153.10	3.30	5.30	11.40	31.69
28.	BDN 708 x TJT501	207.00	103.50	85.00	169.50	8.10	21.00	256.40	3.40	4.75	10.65	50.65
29.	BDN 708 x LRG-41	209.10	115.00	92.50	176.50	8.20	17.50	147.00	3.30	5.10	11.31	40.70
	CHECKS											
30.	Asha	206.10	117.00	82.50	173.50	7.30	15.50	109.80	3.60	4.35	11.72	41.26
31.	Vipula	212.50	114.50	87.50	175.50	7.10	17.20	136.90	3.70	5.35	11.45	35.26
	Parental Mean	172.43	112.05	85.97	165.94	6.67	14.50	118.07	3.45	4.96	11.13	46.88
	Mean of crosses	199.27	110.65	85.92	170.62	7.09	15.18	191.25	3.56	4.91	11.70	48.14
	General Mean	190.94	111.08	85.93	169.17	6.96	14.97	168.54	3.53	4.92	11.52	47.75
	S.E. +	1.46	1.27	2.41	1.28	0.14	0.89	2.26	0.16	0.08	0.21	1.77
	C.D. 5%	4.22	3.68	6.98	3.72	0.42	2.59	6.53	0.46	0.25	0.62	5.12
	C.V.	1.07	1.62	3.98	1.07	2.99	8.42	1.93	6.48	2.53	2.64	5.32

4.2.5 Number of primary branches per plant

Number of primary branches per plant ranged from 5.30 to 8.60 with general mean of 6.96.

Maximum number of primary branches per plant was observed in line, BSMR 853 (8.60) and tester TS3R (7.10). Among the crosses, BDN 711 x LRG-41 (8.40) had relatively maximum number of primary branches per plant followed by BSMR 853 x LRG-41 (8.30).

4.2.6 Number of secondary branches per plant

The range of number of secondary branches per plant was 9.00 to 21.00 with general mean of 14.97.

Among the parent's line BSMR 853 (19.50) and tester TJT501 (17.00) showed highest number of secondary branches per plant. Among the crosses, BDN 708 x TJT 501 (21.00) recorded highest number of secondary branches per plant followed by BDN 716 x LRG-41 (20.50) and BDN 711 x LRG-41 (18.60).

4.2.7 Number of pods per plant

Number of pods per plant ranged from 67.75 to 303.80 with general mean of 168.54.

Among the lines and testers maximum number of pods per plant was recorded by BDN 708 (170.00) and TJT-501 (145.00). Among the crosses, BSMR 853 x LRG4(303.80) had recorded highest number of pods per plant followed by BSMR 736 x LRG-41 (291.65), BSMR 853 x AL882 (283.50), BDN 716 x LRG-41 (275.50), BSMR 853 x TJT-501 (174.00).

4.2.8 Number of seeds per pod

Number of seeds per pod ranged from 3.20 to 5.10 with general mean 3.53.

Among the parent lines, BSMR 736 (4.10) and tester LRG-41 (3.70) recorded maximum number of seeds per pod. Among the crosses, BSMR 853 x TS3R (5.10) showed highest number of seeds per pod followed by BDN 736 x LRG-41 (3.90), BDN 716 x TS3R (3.70).

4.2.9 Pod length (cm):

The range of pod length was from 4.15 to 6.10 cm with general mean of 4.92.(cm). Among the lines and testers, BSMR 853 (5.30 cm) and LRG-41 (6.10 cm) had highest pod length. Among the crosses, BDN 711 x LRG-41 (5.75 cm) recorded highest pod length followed by BSMR 736 x AL882 (3.70).

4.2.10 100 seed weight (g)

The range of 100 seed weight was from 7.80 to 12.81 (g) with general mean of 11.52 (g). Among the lines and testers line, BSMR 736 (11.57 g) and testers LRG-41 (12.43 g) had highest 100 seed weight. In the crosses, BDN 716 x TS3R (12.81g) recorded highest test weight followed by BSMR 736 x TS3R (12.45g) and BDN 716 x LRG-41 (12.38 g).

4.2.11 Grain yield per plant (g):

The range of yield per plant was 26.25 (g) to 76.50 (g) with general mean of 47.75 (g). Among the parents, line BDN 716 (63.35 g) and tester LRG-41 (60.99 g) recorded highest grain yield per plant. In the crosses, BDN 716 x LRG-41 (76.50 g) showed highest grain yield per plant followed by BSMR 853 x LRG-41 (69.37g), BSMR 736 x LRG-41 (68.43g).

4.3 Line x tester analysis

Total of twenty crosses were developed by crossing five lines with four testers. These twenty crosses were grown along with their parents. Data were collected for eleven characters. The data was analyzed following the line x tester design. The results obtained for eleven characters are presented in Table 4.3 below.

4.3.1 Analysis of variance for line x tester analysis

The analysis of variance (Line x tester) due to different sources for eleven characters is summarized in Table 4.3. The analysis of variance indicated that the differences due to crosses were significant for all of the characters. The analysis of variance due to lines were significant for all the characters except plant height and 100 seed weight. The analysis of variance due to testers were significant for all the characters except plant height, days to maturity and grain yield per plant. The analysis of variance due to line x tester were significant for all the characters.

Table 4.3 ANOVA for Line x Tester analysis

Sources of Variation	**d. f.**	Mean sum of squares										
		Plant height (cm)	**Days to 50 % flowering**	**Pollen fertility (%)**	**Days to maturity**	**No. of primary branches per plant**	**No. of secondary branches per plant**	**No. of pods per plant**	**No. of seeds per pod**	**Pod length (cm)**	**100 seed weight (g)**	**Grain yield per plant (g)**
Replications	1	5.47	6.40	12.10	0.02	0.001	0.76	14.16	0.009	0.01	0.34	7.40
Crosses	19	831.43**	50.58**	33.64*	147.25**	1.56**	13.44**	8883.98**	0.31**	0.40**	0.95**	476.08**
Parents (Line)	4	1227.61*	20.15	11.10	34.56	0.09	11.54	17400.31	0.19	0.21	2.27*	533.74
Parents (Tester)	3	2301.93*	112.70	70.82	447.49*	3.93	20.14	10179.59	0.34	0.97	1.07	1187.91*
Line x Tester	12	331.74**	45.20**	31.86*	109.76**	1.45**	12.40**	5721.30**	0.35**	0.32**	0.48**	278.90**
Error	19	4.19	3.34	13.62	3.44	0.04	1.69	13.78	0.05	0.01	0.07	6.12

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

4.3.2 Proportional contribution of lines, testers and line x testers

The proportional contribution of lines, testers, and line x testers for various characters are presented in Table 4.4. The data revealed that contribution of line x tester was higher than both lines and testers for characters Days to 50% flowering(56.43%), Pollen fertility (59.81%), no. of primary branches per plant (58.97%), no. of secondary branches per plant (58.26%), no. of pods per plant (40.67%), number of seed per pod (70.03%), pod length (50.83%), grain yield per plant (36.99%). The contribution of tester was highest for plant height (43.71%) and days to Maturity (47.98%) than line and line x tester. The contribution of lines was more than testers and line x tester for the characters 100 seed weight (50.28%) and number of pods per plant (41.23%).

Table 4.4 Proportional contribution of lines, testers and line x tester

Sr. No.	Characters	Line (%)	Tester (%)	line x tester (%)
1.	**Plant height (cm)**	31.08	43.71	25.20
2.	**Days to 50 per cent flowering**	8.38	35.17	56.43
3.	**Pollen fertility (%)**	6.94	33.23	59.81
4.	**Days to maturity**	4.94	47.98	47.07
5.	**Number of primary branches per plant**	1.26	39.76	58.97
6.	**Number of secondary branches per plant**	18.07	23.66	58.26
7.	**Number of pods / plants**	41.23	18.09	40.67
8.	**Number of seeds / pods**	12.74	17.21	70.03
9.	**Pod length (cm)**	11.24	37.92	50.83
10.	**100 seed weight (g)**	50.28	17.71	32.00
11.	**Grain yield per plant (g)**	23.60	39.39	36.99

4.4 Analysis of variance for combining ability

Line x tester analysis of 20 crosses obtained by crossing 5 lines with 4 testers was carried out and the total variance due to crosses was partitioned into portions attributable to GCA, SCA and error. Analysis of variance for combining ability is presented in Table 4.5.

The mean squares of GCA effect were significant for all characters. The mean square of SCA effect were significant for all the characters. This indicated the presence of significant differences between males and females for these traits.

4.4.1 General Combining Ability (GCA) effect

General combining ability (GCA) effect for parents is presented in Table 4.5.1 and described character wise as below.

4.4.1.1 Plant height (cm)

Among female lines highest positive significant GCA effect was exhibited by BDN 716 (12.60) followed by BSMR 853 (9.22) and BSMR 736 (4.52); while significant negative GCA effect was exhibited by BDN 711 (-14.25) and BDN 708 (-12.10). Among the testers significant positive GCA effect was showed by TJT-501 (15.36) and AL882 (7.54), while significant negative GCA effect is exhibited by LRG-41 (-19.67) and TS3R (-3.23).

4.4.1.2 Days to 50 per cent flowering

For trait, days to 50% flowering BSMR 853 (-2.52) exhibited significant negative GCA effect. Out of the four testers LRG-41(-3.05) showed significant negative GCA effect.

4.4.1.3 Pollen fertility (%)

For this trait none of the lines showed significant positive or negative GCA effects. Among testers, TJT-501 (3.17) recorded significant positive GCA effect. Whereas, tester LRG- 41 (-2.82) recorded significant negative GCA effect.

Table 4.5 ANOVA for combining ability analysis

Sources of Variation	d.f.	Mean sum of squares										
		Plant height (cm)	Days to 50 per cent flowering	Pollen fertility (%)	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 seed weight (g)	Grain yield per plant (g)
GCA	8	3187.41**	116.05**	48.26**	283.68**	2.19**	17.50**	3384.48**	0.16**	0.64**	4.01**	433.38**
SCA	12	331.74**	45.20**	31.86*	109.76**	1.45**	12.40**	5721.30**	0.35**	0.32**	0.48**	278.90**
Error	28	4.26	3.41	12.14	3.52	0.04	1.59	10.82	0.05	0.01	0.08	6.68

*** -Significant at 5 % level of significance**

**** -Significant at 1 % level of significance**

Table 4.5.1 General combining ability of parents in pigeon pea

Sr. No.	Parents	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility	Days to maturity	No. of primary branches per plant	No. of secondary branches plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
	Female parents (Lines)											
1.	BSMR 853	9.22**	-2.52**	-0.67	-1.37	0.08	-0.93	61.79**	0.23**	-0.18**	-0.23*	3.28**
2.	BSMR 736	4.52**	1.22	1.57	1.42	0.13	-1.29**	2.13	-0.06	0.26**	0.46**	-0.92
3.	BDN 716	12.60**	1.47*	0.32	1.50*	0.00	1.19*	21.35**	0.01	-0.06	0.67**	12.10**
4.	BDN 711	-14.25**	-0.15	0.32	-2.62**	-0.09	-0.28	-62.44**	0.01	-0.02	-0.40**	-5.78**
5.	BDN 708	-12.10**	-0.02	-1.55	2.50**	-0.12	1.31**	-22.84**	-0.19*	0.01	-0.49**	-8.67**
	Male parents (Testers)											
6.	LRG-41	-19.67**	-3.05**	-2.82*	-8.42**	-0.61**	-1.58**	-9.75**	-0.16*	-0.15**	-0.45**	-5.03**
7.	TS3R	-3.23**	-0.35	-1.42	2.77**	-0.35**	-0.38	-34.66**	0.25**	-0.03	0.32**	-4.55**
8.	AL882	7.54**	-1.35*	1.07	-1.62*	0.16*	0.13	2.63*	-0.10	-0.26**	0.03	-6.70**
9.	TJT-501	15.36**	4.75**	3.17**	7.27**	0.80**	1.83**	41.82**	0.01	0.44**	0.10	16.29**
	C.D. 5% GCA (Line)	**2.08**	**1.86**	**3.52**	**1.89**	**0.21**	**1.27**	**3.32**	**0.23**	**0.13**	**0.29**	**2.61**
	C.D. 5% GCA(Tester)	**1.86**	**1.67**	**3.15**	**1.69**	**0.19**	**1.14**	**2.97**	**0.20**	**0.11**	**0.26**	**2.33**

*** -Significant at 5 % level of significance**

**** -Significant at 1 % level of significance**

4.4.1.4 Days to maturity

Among five lines, BDN 711 (-2.62) showed significant negative GCA effects. While, BDN 708 (2.50) exhibited significant positive GCA effect. Among the testers, TJT-501 (7.27) and TS3R (2.77) exhibited significant positive GCA effect and LRG-41(-8.42) showed significant negative GCA effect for the trait days to maturity.

4.4.1.5 Number of primary branches per plant

For this trait none of the lines exhibited significant positive GCA effect. Among the tester's LRG-41 (-0.61) and TS3R (-0.35) showed significant negative GCA effects and TJT- 501(0.80) showed significant positive GCA effects.

4.4.1.6 Number of secondary branches per plant

Among the lines, BDN 708 (1.31) expressed significant positive GCA effect while BSMR 736 (-1.29) recorded significant negative GCA effect. Among testers, TJT-501 (1.83) showed significant positive GCA effect while significant negative GCA effect is exhibited by LRG-41 (-1.58) for the trait number of secondary branches per plant.

4.4.1.7 Number of pods per plant

For the trait number of pods per plant lines, BSMR 853 (61.79) recorded significant positive GCA effect followed by BDN 716 (21.35) whereas, line BDN 711 (-62.44) and BDN 708 (-22.84) recorded significant negative GCA effect. Among testers, TJT-501 (41.82) highest significant positive GCA effect while significant negative GCA effect is exhibited by TS3R (- 34.66).

4.4.1.8 Number of seeds per pod

Among the lines, BSMR 853 (0.23) exhibited significant positive GCA effect, whereas, line BDN 708 (-0.19) exhibited significant negative GCA effect. Among testers LRG- 41(-0.16) showed significant negative GCA effect and TS3R (0.25) recorded significant positive GCA effect.

4.4.1.9 Pod length (cm)

of five lines, BSMR 736 (0.26) showed significant positive GCA effect and BSMR 853 (-0.18) showed significant negative effect. Among the testers TJT-501(0.44) showed significant positive GCA effect while AL882 (-0.26) and LRG-41(-0.15) showed negative GCA effects.

4.4.1.10 100 seed weight (g)

For trait 100 seed weight line, BDN 716 (0.67) and BSMR 736 (0.46) recorded significant positive GCA effect while, line BDN 708(-0.49) and BDN 711(-0.40) recorded significant negative GCA effect. Among testers TS3R (0.32) showed significant positive GCA effect while tester, LRG-41(-0.45) had significant negative GCA effect.

4.4.1.11 Grain yield per plant (g)

For trait grain yield per plant, the lines BDN 716 (12.10) exhibited significant positive GCA effect followed by BSMR 853 (3.28) while line, BDN 708(-8.67) and BDN 711(-5.78) exhibited significant negative GCA effect. Among testers, TS3R (16.29) showed significant positive GCA effect while tester, AL882 (-6.70), LRG-41(-5.03) and TS3R (-4.45) had significant negative GCA effect.

4.4.2 Specific Combining Ability (SCA) effects

Specific combining ability (SCA) effect is generally considered as the best criterion for selection of superior hybrid combination. Specific combining ability (SCA) effects were estimated for eleven characters in 20 crosses. Estimates of specific combining ability effects are presented in Table 4.5.2 and described characters wise as below.

4.4.2.1 Plant height (cm)

Among the 20 crosses, four crosses *viz.,* BDN 716 x LRG-41 (15.76), BDN 711 x TJT- 501 (13.93), BDN 708 x TJT-501 (12.38), BSMR 736 x AL882(9.37) exhibited significant positive SCA effects. While three crosses *viz.,* BDN 708 x AL882 (-21.50), BDN 711 x LRG- 41 (-20.29) followed by BSMR 853 x TJT-501 (-10.04) showed significant negative SCA effects.

4.4.2.2 Days to 50 per cent flowering

Among twenty crosses, three crosses *viz.*, BDN 708 x TJT-501 (-5.77), BDN 716 x TS3R (-5.27) followed by BSMR 853 x TS3R (-4.27) showed significant negative SCA effect.

4.4.2.3 Pollen fertility (%)

Among 20 crosses one cross showed significant negative SCA effect for pollen fertility, BSMR 853 x TS3R (-6.32). None of the crosses showed significant positive SCA effect.

4.4.2.4 Days to maturity

Out of twenty crosses, five crosses *viz.,* BDN 711 x AL882 (-15.57), BSMR 853 x TS3R (- 4.02), BDN 716 x TS3R (-3.90), BDN 708 x TS3R (-3.90) followed by BSMR 736 x TJT-501 (-3.00) showed significant negative SCA effects for trait days to maturity.

4.4.2.5 Number of primary branches per plant

Among twenty crosses, four crosses exhibited significant positive SCA effect *viz.,* BDN 708 x TJT-501 (0.96), BDN 716 x AL882 (0.91), BDN 711 x TJT-501 (0.73) followed by BSMR 853 x TS3R (0.68). The crosses BDN 711 x TS3R (-1.04), BDN 708 x TS3R (-0.92), BDN 716 x TJT-501 (-0.86) followed by BSMR 853 x TJT-501 (-0.74) exhibited significant negative SCA effects.

4.4.2.6 Number of secondary branches per plant

For trait no. of secondary branches per plant, two crosses BDN 708 x TJT-501 (4.37) followed by BSMR 736 x TS3R (1.99) showed significant positive SCA effects. The crosses BDN 716 x TJT-501 (-3.50), BSMR 736 x LRG-41 (-3.22) BDN 708 x AL882 (-2.47) followed by BDN 711 x TS3R (-2.01) exhibited significant negative SCA effect.

Table 4.5.2 Specific combining ability of crosses in Pigeon pea

Sr. No.	Crosses	Plant height (cm)	Days to 50 per cent flowering	Pollen fertility	Days to maturity	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100 Seed weight (g)	Grain yield per plant (g)
1.	BSMR 853 x AL882	8.17**	-0.07	3.07	5.17**	-0.26	0.83	40.24**	-0.33	0.17	-1.07**	8.14**
2.	BSMR 853 x TS3R	3.75*	-4.27**	-6.32*	-4.02**	0.68**	1.13	-67.48**	1.04**	-0.54**	0.01	-12.22**
3.	BSMR 853 x TJT-501	-10.04**	0.22	1.17	-0.62	-0.74**	-1.88*	18.31**	-0.39*	0.03	0.80**	2.43
4.	BSMR 853 x LRG-41	-1.86	4.15**	2.07	-0.52	0.32*	-0.08	8.92**	-0.31	0.32**	0.25	1.65
5.	BSMR 736 x AL882	9.37**	2.67	-2.17	3.80**	0.09	0.69	-44.94**	0.06	0.67**	0.05	-11.77**
6.	BSMR 736 x TS3R	-1.46	1.47	1.42	-0.40	0.73**	1.99*	18.02**	-0.35*	-0.04	-0.03	12.38**
7.	BSMR 736 x TJT-501	-7.74**	-1.52	3.92	-3.00*	-0.09	0.54	-29.52**	-0.09	-0.31**	0.09	-5.53**
8.	BSMR 736 x LRG-41	-0.16	-2.62	-3.17	-0.40	-0.73**	-3.22**	56.43**	0.38*	-0.32**	-0.10	4.92*
9.	BDN 716 x AL882	-1.70	-4.57**	4.07	-3.20*	0.91**	1.20	40.23**	-0.01	-0.39**	0.04	10.67**
10.	BDN 716 x TS3R	-5.64**	-5.27**	2.67	-3.90**	0.55**	0.009	7.45**	-0.13	0.28**	0.11	5.59**
11.	BDN 716 x TJT-501	-8.42**	8.72**	-4.82	5.50**	-0.86**	-3.50**	-68.74**	0.13	0.26**	-0.06	-16.23**
12.	BDN 716 x LRG-41	15.76**	1.12	-1.92	1.60	-0.60**	2.28*	21.06**	0.01	-0.14	-0.09	-0.03
13.	BDN 711 x AL882	5.65**	-1.45	0.92	-15.57**	-0.28	-0.31	5.93*	-0.01	-0.23*	0.26	-7.43**
14.	BDN 711 x TS3R	0.71	5.35**	2.67	12.22**	-1.04**	-2.01*	22.65**	-0.23	-0.10	0.03	-2.53
15.	BDN 711 x TJT-501	13.93**	-1.65	0.17	0.12	0.73**	0.46	-5.39*	0.23	-0.07	-0.24	1.44
16.	BDN 711 x LRG-41	-20.29**	-2.25	-1.92	3.22*	0.59**	1.86	-23.18**	0.01	0.41**	-0.05	8.52**
17.	BDN 708 x AL882	-21.50**	3.42*	-4.05	9.80**	-0.46**	-2.41*	-41.46**	0.29	-0.22*	0.70**	0.39

18.	BDN 708 x TS3R	2.66	2.72	-0.45	-3.90**	-0.92**	-1.11	19.35**	-0.33	0.40**	-0.12	-3.22
19.	BDN 708 x TJT-501	12.28**	-5.77**	-0.45	-2.00	0.96**	4.37**	85.35**	0.13	0.08	-0.58*	17.88**
20.	BDN 708 x LRG-41	6.56**	-0.37	4.95	-3.90**	0.42*	-0.83	-63.23**	-0.09	-0.27**	0.003	-15.05**
	CD 5%	**4.17**	**3.73**	**7.04**	**3.79**	**0.42**	**2.55**	**6.65**	**0.46**	**0.26**	**0.58**	**5.22**

*** -Significant at 5 % level of significance**

**** -Significant at 1 % level of significance**

4.4.2.7 Number of pods per plant

For trait no. of pods per plant significant positive SCA effect was observed in three crosses BDN 708 x TJT-501 (85.35), BSMR 736 x LRG-41 (56.43) followed by BSMR 853 x AL882 (40.24). Four crosses showed significant negative SCA effect for number of pods per plant *viz.,* BDN 716 x TJT-501 (-68.74), BSMR 853 x TS3R (-67.48), BDN 708 x LRG-41 (- 62.23) followed by BSMR 736 x AL882 (-44.94).

4.4.2.8 Number of seeds per pod

Among the twenty crosses BSMR 853 x TS3R (1.04) exhibited significant positive SCA effect. While significant negative SCA effect for number of seeds per pod was exhibited by BSMR 853 x TJT-501 (-0.39) followed by BSMR 736 x TJT-501 (-0.35).

4.4.2.9 Pod length (cm)

Out of forty crosses, four crosses exhibited significant positive SCA effects *viz.,* BSMR 736 x AL882 (0.67), BDN 711 x LRG-41 (0.41), BDN 708 x TS3R (0.40) followed by BDN 716 x TS3R (0.28). While three crosses BSMR 853 x TS3R (-0.54), BDN 716 x AL882 (-0.39) followed by BSMR 736 x LRG-41 (-.032) showed significant negative SCA effects for the trait pod length.

4.4.2.10 100 Seed weight (g)

Among twenty crosses BSMR 853 x TJT-501 (0.80), and BDN 708 x AL882 (0.70) showed significant positive SCA effects while, the cross BSMR 853 x AL882 (-1.07) followed by BDN 708 x TJT-501 (-0.58) exhibited significant negative SCA effects.

4.4.2.11 Grain yield per plant (g)

Among twenty crosses three crosses showed significant positive SCA effects *viz.,* BDN 708 x TJT-501 (17.88), BSMR 736 x TS3R (12.38) followed by BDN 716 x AL882 (10.67). While four crosses BDN 716 x TJT-501 (-16.23), BDN 708 x LRG-41 (-15.05), BSMR 853 x TS3R (-12.220 followed by BSMR 736 x AL882 (-11.77) exhibited significant negative SCA effects.

4.5 Estimation Standard Heterosis

In the present investigation, standard heterosis is estimated for all the twenty crosses for eleven yield and yield contributing characters and expressed as per cent increase or decrease over standard checks ASHA and VIPULA. The percentage of standard heterosis over the standard checks for the characters studied is presented in Table 4.6.

4.5.1 Plant height (cm)

For trait plant height the standard heterosis range over standard checks Vipula and Asha is -31.29 to 14.35 and -29.16 to 17.90 per cent respectively. The crosses, BSMR 853 x LRG-41 (4.47%, 7.71%), BSMR 736 x LRG-41 (3.06%, 6.26%) followed by BDN 716 x LRG-41 (14.35%, 17.90%) exhibited significant positive heterosis over standard checks Vipula and Asha respectively. While the crosses BSMR 853 x AL882 (-7.29%, -4.42%), BSMR 736 x AL882 (-8.94%, -6.11%), BDN 716 x AL882 (-10.35%, -7.57%), BDN 711 x LRG-41 (-15.25%, -12.62%) followed by BDN 708 x AL882 (-31.29%, -29.16%) exhibited highest significant negative standard heterosis over the checks Vipula and Asha respectively.

4.5.2 Days to 50 per cent flowering

The standard heterosis range over checks Vipula and Asha is -9.61 to 4.37 and -11.54 to 2.14 per cent for the trait days to 50 per cent flowering. The crosses BSMR 853 x TS3R (- 9.61%, -11.54%), BSMR 736 x TJT-501 (-4.80%, -6.84%), BDN 716 x AL882 (-8.73%, -10.68%), BDN 711 x TJT-501 (-6.11%, -8.12%) followed by BDN 708 x TJT-501 (-9.61%, -11.54%) exhibited highest significant negative standard heterosis over the checks Vipula and Asha respectively.

4.5.3 Pollen fertility (%)

The standard heterosis for pollen fertility over standard checks Vipula and Asha ranged from -11.43 to 5.71 and -6.06 to 12.12 per cent respectively. The crosses exhibited significant negative heterosis for standard check Vipula viz., BSMR 853 x TS3R (-11.43) and BDN 708 x AL882 (-11.43). For the standard check Asha, the crosses BSMR 736 x TJT -501 (12.12), BDN 708 x LRG-41 (12.12) showed significant positive heterosis.

Table 4.5 Estimation of standard heterosis over checks VIPULA and ASHA.

Sr. No.	Crosses	Plant height		Days to 50% flowering		Pollen fertility		Days to maturity		No. of Pri- branches per plant	
		SC1	SC2	SC1	SC2	SC1	SC2	SC1	SC2	SC1	SC2
1.	BSMR 853 x AL882	-7.29**	-4.42**	-8.30**	-10.26**	-2.29	3.64	-5.41**	-5.95**	-11.27**	-13.70**
2.	BSMR 853 x TS3R	-1.65	1.41	-9.61**	-11.54**	-11.43**	-6.06	-4.27**	-4.82**	5.63	2.74
3.	BSMR 853 x TJT-501	-3.06**	-0.05	-6.55**	-8.55**	0.00	6.06	-4.84**	-5.38**	-7.04*	-9.59**
4.	BSMR 853 x LRG-41	4.47**	7.71**	2.18	0.00	3.43	9.70*	0.28	-0.28	16.90**	13.70**
5.	BSMR 736 x AL882	-8.94**	-6.11**	-2.62	-4.70**	-5.71	0.00	-5.41**	-5.95**	-5.63	-8.22*
6.	BSMR 736 x TS3R	-6.31**	-3.40**	-1.31	-3.42*	0.00	6.06	-1.42	-1.98	7.04*	4.11
7.	BSMR 736 x TJT-501	-4.19**	-1.21	-4.80**	-6.84**	5.71	12.12**	-5.41**	-5.95**	2.82	0.00
8.	BSMR 736 x LRG-41	3.06**	6.26**	-0.44	-2.56	0.00	6.06	1.14	0.57	2.82	0.00
9.	BDN 716 x AL882	-10.35**	-7.57**	-8.73**	-10.68**	0.00	6.06	-8.55**	-9.07**	4.23	1.37
10.	BDN 716 x TS3R	-4.47**	-1.50	-6.99**	-8.97**	0.00	6.06	-2.56*	-3.12**	2.82	0.00
11.	BDN 716 x TJT-501	-0.71	2.38*	4.37*	2.14	-5.71	0.00	0.28	-0.28	-9.86**	-12.33**
12.	BDN 716 x LRG-41	14.35**	17.90**	3.06	0.85	0.00	6.06	3.13*	2.55*	2.82	0.00
13.	BDN 711 x AL882	-19.53**	-17.03**	-7.42**	-9.40**	-5.71	0.00	-17.95**	-18.41**	-14.08**	-16.44**
14.	BDN 711 x TS3R	-14.12**	-11.45**	0.87	-1.28	0.00	6.06	4.27**	3.68**	-21.13**	-23.29**
15.	BDN 711 x TJT-501	-2.82**	0.19	-6.11**	-8.12**	0.00	6.06	-5.13**	-5.67**	11.27**	8.22*
16.	BDN 711 x LRG-41	-15.25**	-12.62**	-1.31	-3.42*	0.00	6.06	1.71	1.13	18.31**	15.07**

17.	BDN 708 x AL882	-31.29**	-29.16**	-3.06	-5.13**	-11.43**	-6.06	-0.57	-1.13	-16.90**	-19.18**
18.	BDN 708 x TS3R	-12.19**	-9.46**	-1.31	-3.42*	-5.71	0.00	-1.99	-2.55*	-19.72**	-21.92**
19.	BDN 708 x TJT-501	-2.59*	0.44	-9.61**	-11.54**	-2.86	3.03	-3.42**	-3.97**	14.08**	10.96**
20.	BDN 708 x LRG-41	-1.60	1.46	0.44	-1.71	5.71	12.12**	0.57	0.00	15.49**	12.33**
	SE	**2.06**	**2.06**	**1.84**	**1.84**	**3.48**	**3.48**	**1.87**	**1.87**	**0.21**	**0.21**
	SD5%	**4.32**	**4.32**	**3.86**	**3.86**	**7.29**	**7.29**	**3.93**	**3.93**	**0.44**	**0.44**
	SD1%	**5.90**	**5.90**	**5.28**	**5.28**	**9.96**	**9.96**	**5.37**	**5.37**	**0.60**	**0.60**

Table 4.5 cont.…

Sr. No	**Crosses**	**No. of sec- branches per plant**		**No. of pods per plant**		**No. of seed per pod**		**Pod length**		**100 seed wt.**		**Grain Yield**	
		SC1	**SC2**	**SC1**	**SC2**	**SC1**	**SC2**	**SC1**	**SC2**	**SC1**	**SC2**	**SC1**	**SC2**
1.	BSMR853 x AL882	-21.51**	-12.90	107.09**	158.20**	-10.81	-8.33	-11.21**	9.20**	-13.19**	-15.19**	54.68**	32.17**
2.	BSMR 853 x TS3R	-12.79	-3.23	10.23**	37.43**	37.84**	41.67**	-22.43**	-4.60	3.06	0.68	-1.73	-16.03*
3.	BSMR853 x TJT-501	-27.33**	-19.35*	100.15**	149.54**	-10.81	-8.33	-15.89**	3.45	7.42**	4.95	33.75**	14.29*
4.	BSMR 853 x LRG-41	-6.98	3.23	121.91**	176.68**	-5.41	-2.78	2.80	26.44**	3.23	0.85	96.74**	68.11**
5.	BSMR 736 x AL882	-24.42**	-16.13	1.28	26.28**	-8.11	-5.56	6.54*	31.03**	2.79	0.43	-13.74	-26.29**
6.	BSMR 736 x TS3R	-9.88	0.00	29.11**	60.97**	-8.11	-5.56	-4.67	17.24**	8.73**	6.23*	56.13**	33.41**
7.	BSMR736 x TJT-501	-15.29	-6.00	21.62**	51.64**	-10.81	-8.33	14.02**	5.75	7.34**	4.86	-0.79	-15.23*
8.	BSMR 736 x LRG-41	-27.33**	-19.35*	113.04**	165.62**	5.41	8.33	-0.93	21.84**	6.20*	3.75	94.07**	65.83**
9.	BDN 716 x AL882	-6.98	3.23	77.54**	121.36**	-8.11	-5.56	-19.63**	-1.15	4.50	2.09	86.85**	59.66**
10.	BDN 716 x TS3R	-6.98	3.23	35.43**	68.85**	0.00	2.78	-4.67	17.24**	11.92**	9.34**	73.79**	48.50**
11.	BDN 716 x TJT-501	-24.42**	-16.13	7.01**	33.42**	-2.70	0.00	-9.35**	11.49**	7.77**	5.29*	5.81	-9.58

12.	BDN 716 x LRG-41	19.19*	32.26**	101.24**	150.91**	-2.70	0.00	-3.74	18.39**	8.12**	5.63*	116.96**	85.39**
13.	BDN 711 x AL882	24.42**	-16.13	-8.73**	13.80**	-8.11	-5.56	-15.89**	3.45	-3.06	-5.29*	-15.24	-27.58**
14.	BDN 711 x TS3R	-27.33**	-19.35*	-14.68**	6.38*	-2.70	0.00	-11.21**	9.20**	1.75	-0.60	0.03	-14.53*
15.	BDN 711 x TJT-501	-9.88	0.00	-7.93**	14.80**	0.00	2.78	-14.95**	4.60	-3.23	-5.46*	5.22	-10.09
16.	BDN 711 x LRG-41	8.14	20.00*	7.71**	34.29**	-2.70	0.00	7.48**	32.18**	-0.96	-3.24	90.48**	62.77**
17.	BDN 708 x AL882	-27.33**	-19.35*	-14.43**	6.69*	-5.41	-2.78	-14.95**	4.60	0.09	-2.22	-1.23	-15.61*
18.	BDN 708 x TS3R	12.79	-3.23	11.83**	39.44**	-10.81	-8.33	-0.93	21.84**	-0.44	-2.73	-10.12	-23.20**
19.	BDN 708 x TJT-501	22.09**	35.48**	87.29**	133.52**	-8.11	-5.56	-11.21**	9.20**	-6.94*	-9.09**	43.65**	22.74**
20.	BDN 708 x LRG-41	1.74	12.90	7.38**	33.88**	-10.81	-8.33	-4.67	17.24**	-1.22	-3.50	15.43*	-1.37
	SE±	**1.26**	**1.26**	**3.28**	**3.28**	**0.22**	**0.22**	**0.12**	**0.12**	**0.28**	**0.28**	**2.58**	**2.58**
	CD5%	**2.64**	**2.64**	**6.88**	**6.88**	**0.48**	**0.48**	**0.26**	**0.26**	**0.60**	**0.60**	**5.41**	**5.41**
	CD1%	**3.61**	**3.61**	**9.41**	**9.41**	**0.65**	**0.65**	**0.36**	**0.36**	**0.82**	**0.82**	**7.39**	**7.39**

*** -Significant at 5 % level of significance ** -Significant at 1 % level of significance*Note: - SC1: - Vipula; SC2: - Asha**

4.5.4 Days to maturity

The standard heterosis for days to maturity over standard checks Vipula and Asha ranged from -17.95 to 4.27 and -18.41 to 3.68 per cent respectively. Out of 20 crosses the crosses BSMR 853 x AL882 (-5.41%, -5.95%), BSMR 736 x AL882 (-5.41%, -5.95%), BDN 716 x AL882 (-8.55%, -9.07%), BDN 711 x AL882 (-17.95%, -18.41%) followed by BDN 708 x TJT-501 (-3.42%, -3.97%) exhibited highest significant negative standard heterosis for the checks Vipula and Asha respectively.

4.5.5 Number of primary branches per plant

The standard heterosis over standard checks Vipula and Asha ranged from -21.13 to 18.31 and -23.29 to 15.07 per cent respectively. Out of 20 crosses, the crosses BSMR 853 x LRG-41 (16.90%, 13.70%), BDN 711 x LRG-41 (18.31%, 15.07%), BDN 708 x TJT-501 (14.08%, 10.96%) followed by BDN 708 x LRG-41 (15.49%, 12.33%) exhibited significant positive standard heterosis over the checks Vipula and Asha respectively. While the crosses BSMR 853 x AL882 (-11.27%, -13.70%), BDN 711 x AL882 (-14.08%, -16.44%), BDN 711 x TS3R (-21.13%, -23.29%), BDN 708 x AL882 (-16.90%, -19.18%) followed by BDN 708 x TS3R (-19.72%, -21.92%) exhibited significant negative standard heterosis over the checks Vipula and Asha respectively.

4.5.6 Number of secondary branches per plant

The standard heterosis over standard checks Vipula and Asha ranged from -27.33 to 24.42 and -19.35 to 35.48 per cent respectively. Among the 20 crosses BDN 716 x LRG-41 (19.19%, 32.26%) followed by BDN 708 x TJT-501 (22.09%, 35.48%) exhibited significant positive standard heterosis over the checks Vipula and Asha respectively. While the crosses BSMR 853 x TJT-501 (-27.33%, -19.35%), BSMR 736 x LRG-41 (-27.33%, -19.35%), BDN711 x TS3R (-27.33%, -19.35%) followed by BDN 708 x AL882 (-27.33%, -19.35%) exhibited significant negative standard heterosis over the checks Vipula and Asha respectively.

4.5.7 Number of pods per plant

The standard heterosis range over checks Vipula and Asha is -14.68 to 121.91 and 13.80 to 176.68 per cent respectively. Out of 20 crosses, BSMR 853 x LRG-41 (12191%, 176.68%), BSMR 736 x LRG-41 (113.04%, 165.62%), BDN 716 x LRG-41 (101.24%, 150.91%), BDN 711 x LRG-41 (7.71%, 34.29%) followed by BDN 708 x TJT-501 (87.29%, 133.52%) exhibited highest significant positive standard heterosis over the checks Vipula and Asha respectively. While the cross BDN 711 x TS3R (-14.68%) followed by BDN 708 x AL882 (- 14.43%) exhibited significant negative standard heterosis over the check Vipula.

4.5.8 Number of seeds per pod

The standard heterosis over standard checks Vipula and Asha ranged from -10.81 to37.84 and -8.33 to 41.67 per cent for the trait number of seeds per pod respectively. Out of 20 crosses, only BSMR 853 x TS3R (37.84%, 41.67%) exhibited significant positive standard heterosis over checks Vipula and Asha respectively. None of the crosses exhibited significant standard negative heterosis for the check Vipula and Asha respectively.

4.5.9 Pod length (cm)

The standard heterosis over standard checks Vipula and Asha ranged from -19.63 to14.02 and -1.15 to 32.18 per cent for trait pod length respectively. Out of 20 crosses, the crosses exhibited positive standard heterosis over checks Vipula and Asha were BSMR 736 x AL882 (6.54%, 31.03%) followed by BDN 711 x LRG-41 (7.48%, 32.18%) respectively. The crosses BSMR 853 x AL882 (-11.21%) BSMR 853 x TS3R (-22.43%), BSMR 853 x TJT-501 (- 15.89%), BDN 716 x AL882 (-19.63%), BDN 711 x TJT-501 (-14.95%), BDN 708 x TJT-501 (-11.21%) showed significant negative standard heterosis for the check Vipula. None of the crosses showed significant negative standard heterosis over standard check Asha.

4.5.10 100 seed weight (g)

For trait 100 seed weight, standard heterosis range over checks Vipula and Asha is -13.19 to 11.92 and -15.19 to 9.34 per cent. Out of 20 crosses, the crosses BSMR 736 x TS3R (8.73%, 6.23%), BDN 716 x TS3R (11.92%, 9.34%), BDN 716 x TJT-501 (7.77%, 5.29%) followed by BDN 716 LRG-41 (8.12%, 5.63%) exhibited significant positive standard heterosis over the checks Vipula and Asha respectively. While, the cross BSMR 853 x AL882 (-13.19%, -15.19%) followed by BDN 708 x TJT-501 (-6.94%, -9.09%) exhibited significant negative standard heterosis over the checks Vipula and Asha respectively.

4.5.11 Grain yield per plant (g)

The standard heterosis over standard checks Vipula and Asha ranged from -15.24 to16.96 and -27.58 to 85.39 per cent for trait grain yield per plant respectively. Out of 20 crosses, the crosses *viz.,* BDN 716 x LRG-41 (85.39%,116.96%) exhibited highest standard heterosis over the checks Asha and Vipula respectively, followed by the crosses BSMR 853 x LRG-41 (68.11%, 96.74%), BSMR 736 x LRG-41 (65.83%, 94.07%), BDN 711 x LRG-41 (62.77%, 90.48%), BDN 716 x AL882 (59.66%, 86.83%), and BDN 716 x TS3R (48.50%, 7 3.79%).

CHAPTER-V

DISCUSSION

Information on heterosis and combining ability is helpful in planning of future breeding programmes. Heterosis breeding aims to exploit the phenomenon of hybrid vigour to increase yield potential and yield stability. It gathers genes that perform well under heterozygous condition (F_1). The main breeding strategy for crop improvement in pigeon pea is the selection of parents for hybridization on the basis of per se performance for hybrid and yield contributing characters. The superiority of parents may not depend much on their superior per se performance but it depends upon their ability to combine well. In any sound breeding programmed the proper choice of parents based on their combining ability is a prerequisite. Hybrid vigour serves as key to the problem of enhancing the yield of many self- and cross- pollinated crops.

Therefore, the present investigation was undertaken with a view to explore the possibility of exploring heterosis and find out the combining ability of parents and crosses in a line x tester mating design involving 5 lines and 4 testers.

The results of the present findings are discussed in the following sub – headings: -

1. **Analysis of variance.**
2. **Mean performance of parents and crosses for yield and yield contributing characters.**
3. **Line x tester analysis.**
4. **Combining ability analysis.**
5. **Estimation of standard heterosis.**

5.1.1 Analysis of variance

The analysis of variance showed significant differences among the genotypes for all the eleven yield and yield contributing characters under study.

5.1.2 Mean performance of parents and crosses for yield and yield contributing characters.

The mean performance of nine parents and twenty crosses studied is presented in Table 4.2.

For plant height, the line BSMR 853 (205.60) and the tester LRG-41 (208.10 cm) recorded highest plant height. Among the crosses BDN 716 x LRG-41 (243.00 cm) showed highest plant height followed by BSMR 853 x LRG-41 (222.00 cm).

In the present investigation the line BDN 711(111.00 days) was earlier in flowering, while in testers it was AL882 (96.50 days). Among the crosses BSMR 853 x TS3R (103.50), BDN 716 x AL882(104.50), BDN 711 x AL882 (106.00 days) and BDN 708 x TJT-501 (103.50 days) was earlier to flower.

The line BSMR 853 (92.50%) and among the tester LRG-41 (87.50%) recorded highest pollen fertility. Among the crosses, BSMR 736 x TJT-501 (92.50%) showed highest pollen fertility followed by BSMR 853 x LRG-41 (90.50%).

Maturity duration is a very important factor which determines the adaptation., The line BDN 711 (157.50 days) and tester AL882 (143) days) were early in maturity. Out of crosses, the cross BDN 711 x AL882 (144 days) followed by BDN 716 x AL882 (160.50) exhibited early maturity.

Among the 9 parents, line BSMR 853 (8.60) and tester TS3R (7.10) recorded maximum number of primary branches per plant. The cross, BDN 711 x LRG-41 (8.40) followed by BSMR 736 x TS3R (7.60), BSMR 853 x TS3R (7.50)) had maximum number of primary branches per plant.

The highest number of secondary branches were registered by line BSMR 853 (19.50) and tester LRG-41 (16.00). Among the crosses, BDN 708 x TJT-501 (21.00) followed by BDN 716 x LRG-41 (20.50) were with highest number of secondary branches per plant.

Among the lines and testers highest number of pods per plant is recorded by BDN 708 (170.00) and TJT-501 (145.80) respectively. Out of the crosses, 736 x LRG-41(291.65), BSMR 853 x LRG-41 (283.50), BDN 716 x LRG-41 (275.50), BDN 708 x TJT-501 (256.40) had highest number of pods per plant.

BSMR 736 (4.10) and LRG-41 (3.70) recorded maximum number of seeds per pod among the lines and testers respectively. The cross BSMR 853 x TS3R (5.10) followed by BSMR 736 x LRG-41 (3.90) was with maximum number of seeds per pod among the crosses.

Among the lines, testers, and crosses highest pod length has been recorded by BSMR 853 (5.35), LRG-4 (6.10cm) and BDN 711 x LRG-41 (5.75cm), BSMR 736 x AL882(5.70), BSMR 853 x LRG-41 (5.50) respectively.

Among lines BDN 711 (11.38) and testers LRG-41(12.43), TS3R (12.18) and the cross BDN 716 x TS3R (12.81), BSMR 736 x TS3R (12.45), followed by BDN 711 x LRG-41 (11.34) showed maximum seed weight.

Among the lines BDN 716 (63.35 g) has manifested highest grain yield per plant while among the testers, LRG-41 (60.99 g) has shown highest grain yield per plant. Out of the crosses evaluated, highest grain yield was recorded by BDN 716 x LRG-41 (76.50 g) followed by BSMR 853 x LRG-41 (69.37), BSMR 736 x LRG-41 (68.43).

5.1.3 Line x Tester Analysis

5.1.4 Analysis of variance for line x tester analysis

The analysis of variance (Line x Tester) due to different sources for eleven characters is summarized in Table 4.3. The analysis of variance indicated that the differences due to crosses were significant for all of the characters. The analysis of variance due to lines were not significant for any of the characters except plant height and 100 seed weight. The analysis of variance due to testers were also not significant for any of the characters except plant height, days to maturity and grain yield. The analysis of variance due to line x tester were significant for all the characters.

5.4. Combining Ability Analysis

Combining ability is the capacity of an individual to transmit superior performance to its offspring. Combining ability enables the plant breeder to select the potential combinations either to exploit it in F1 hybrid commercially or to select progenies from the cross combinations in succeeding generations for improvement in one or more characters.

Combining ability analysis on one hand is useful in the identification of potential parents for developing commercial hybrids while on other side it helps to select parents to develop base population for further crop improvement programmes. There were significant differences among the genotypes for characters, which led to the combining ability analysis. Therefore, were partitioned genetic effects between genotypes into general combining ability and specific combining ability.

The mean squares of GCA and SCA effect were significant for all characters indicating the presence of significant differences between males and females for these traits.

5.4.1 General combining ability (GCA effects):

The parental lines showing high GCA effects for yield and yield contributing characters are presented in table 5.1

Table 5.1: Parents showing high desirable GCA effects.

Sr. No.	Characters	Parents
1.	**Plant height (cm)**	BSMR 853, BDN 716, TJT-501, AL882
2.	**Days to 50 per cent flowering**	BSMR 853, LRG-41
3.	**Pollen fertility (%)**	----------------------------------
4.	**Days to maturity**	BDN 711, LRG-41, AL882
5.	**Number of primary branches per plant**	TJT-501
6.	**Number of secondary branches per plant**	BDN 708, TJT-501
7.	**Number of pods per plant**	BSMR 853, BDN 716, TJT-501
8.	**Number of seeds per pod**	BSMR 853, TS3R
9.	**Pod length (cm)**	BSMR 736, TJT-501
10.	**100 seed weight (g)**	BSMR 736, BDN 716, TS3R
11.	**Grain yield per plant (g)**	BSMR 853, BDN 716, TJT-501

Investigation of GCA effects revealed that the parents BSMR 853 and BDN 716 among lines, TJT-501among testers were the good general combiners for yield and most of the yield contributing characters. Hence these good general combiners of males and females may be extensively used in future for pigeonpea breeding programmes. The negative GCA effect was desirable in days to 50 per cent flowering and days to maturity, which was observed in BSMR 853 among lines and among testers it was observed in LRG-41. In general, good general combiners for grain yield also had good or average combining ability for one or more yield components. In most of the parents high GCA effects were associated with high *per se* mean for yield and yield components. It is important to mention here that the parents which showed good GCA effects for grain yield per plant also indicated significantly positive GCA effects for number of pods per plant. The results were earlier reported by Singh and Srivastava (2001), Banu *et al.* (2006), Baskaran and Muthiah (2007), Phad *et al.* (2007), Acharya *et al.* (2009), Singh *et al.* (2009), Shoba *et al.* (2010), Gupta *et al.* (2011), Thiruvengadam *et al.* (2012), Meshram *et al.* (2013), Pandey *et al.* (2015) Mhasal *et al.*(2015), Tikle *et al.* (2016), Kumar *et al.* (2017), Srivarsha *et al.* (2017).

5.4.2 Specific Combining Ability (SCA) effect of crosses:

In crop improvement programmes specific combining ability is important to pinpoint specific cross combination for commercial exploitation or varietal development. Specific combining ability effect is the index to determine usefulness of a particular combination in the exploitation of heterosis.

The specific combining effects of the present investigation (table 5.2) are discussed below:

For the trait plant height, four crosses *viz.,* BDN 716 x LRG-41 (15.76), BDN 711 x TJT-501 (13.93), BDN 708 x TJT-501 (12.38), BSMR 736 x AL882(9.37) exhibited significant positive SCA effects. While three crosses *viz.,* BDN 708 x AL882 (-21.50), BDN 711 x LRG- 41 (-20.29) followed by BSMR 853 x TJT-501 (-10.04) showed significant negative SCA effects. The results are in agreement with the earlier results reported by Sharma et al (1973), Saxena et al (1980), Sindhu et al (1992) and Singh and Srivastava (2001).

For days to 50 per cent flowering negative SCA effects are desirable. Three crosses *viz.*, BDN 708 x TJT-501 (-5.77), BDN 716 x TS3R (-5.27) followed by BSMR 853 x TS3R (-4.27) showed significant negative SCA effect. These results are in agreement with the earlier results reported by Singh and Srivastava (2001), Banu *et al.* (2006), Shoba *et al.* (2010), Meshram *et al.* (2013) and Yamamura *et al.* (2014).

None of the cross showed significant positive SCA effect for the trait pollen fertility.

For days to maturity negative SCA effects are desirable. five crosses *viz.,* BDN 711 x AL882 (-15.57), BSMR 853 x TS3R (-4.02), BDN 716 x TS3R (-3.90), BDN 708 x TS3R (-3.90) followed by BSMR 736 x TJT-501 (-3.00) showed significant negative SCA effects for trait days to maturity. These results are in agreement with the earlier results reported by Singh and Srivastava (2001), Banu *et al.* (2006), Shoba *et al.* (2010), Meshram *et al.* (2013) and Yamamura *et al.* (2014).

For trait no. of primary branches per plant, out of twenty crosses, four crosses exhibited significant positive SCA effect *viz.,* BDN 708 x TJT-501 (0.96), BDN 716 x AL882 (0.91), BDN 711 x TJT-501 (0.73) followed by BSMR 853 x TS3R (0.68). The crosses BDN 711 x TS3R (-1.04), BDN 708 x TS3R (-0.92), BDN 716 x TJT-501 (-0.86) followed by BSMR 853 x TJT-501 (-0.74) exhibited significant negative SCA effects. The results are in close agreement with earlier results revealed by Phad *et al*. (2007), Thiruvengadam *et al*. (2012), and Pandey *et al* (2014).

For the trait number of secondary branches per plant, out of 20 crosses two crosses BDN 708 x TJT-501 (4.37) followed by BSMR 736 x TS3R (1.99) showed significant positive SCA effects. The crosses BDN 716 x TJT-501 (-3.50), BSMR 736 x LRG-41 (-3.22) BDN 708 x AL882 (-2.47) followed by BDN 711 x TS3R (-2.01) exhibited significant negative SCA effect. These findings were in perfect agreement with Phad *et al.* (2007), Thiruvengadam *et al.* (2012) and Pandey *et al.* (2015)

For the trait number of pods per plant three crosses BDN 708 x TJT-501 (85.35), BSMR 736 x LRG-41 (56.43) followed by BSMR 853 x AL882 (40.24) exhibited significant positive standard heterosis. Four crosses showed significant negative SCA effect for number of pods per plant *viz.,* BDN 716 x TJT-501 (-68.74), BSMR 853 x TS3R (-67.48), BDN 708 x LRG-41 (-62.23) followed by BSMR 736 x AL882 (-44.94). Present observations are in close agreement with the earlier reports of Pandey *et al.* (2015) and Yamamura *et al.* (2014).

For the trait number of seeds per pod BSMR 853 x TS3R (1.04) exhibited significant positive SCA effect. While significant negative SCA effect for number of seeds per pod was exhibited by BSMR 853 x TJT-501 (-0.39) followed by BSMR 736 x TJT-501 (-0.35) the findings are in close agreement with earlier results reported by Acharya *et al.* (2009), Baskaran and Muthiah (2007), Thiruvengadam *et al.* (2012). and Pandey *et al.*(2014).

For the trait pod length out of forty crosses, four crosses exhibited significant positive SCA effects *viz., BSMR* 736 x AL882 (0.67), BDN 711 x LRG-41 (0.41), BDN 708 x TS3R (0.40) followed by BDN 716 x TS3R (0.28). While three crosses BSMR 853 x TS3R (-0.54), BDN 716 x AL882 (-0.39) followed by BSMR 736 x LRG-41 (-.032) showed significant negative SCA effects for the trait pod length.

For the trait 100 seed weight BSMR 853 x TJT-501 (0.80), and BDN 708 x AL882 (0.70) showed significant positive SCA effects while, the cross BSMR 853 x AL882 (-1.07) followed by BDN 708 x TJT-501 (-0.58) exhibited significant negative SCA effects. These results are in agreement with the earlier results reported by Ghodke *et al.* (1993), Shoba *et al.* (2010), Meshram *et al.* (2013) and Yamamura *et al.* (2014).

For the trait grain yield three crosses showed significant positive SCA effects *viz.,* BDN 708 x TJT-501 (17.88), BSMR 736 x TS3R (12.38) followed by BDN 716 x AL882 (10.67). While four crosses BDN 716 x TJT-501 (-16.23), BDN 708 x LRG-41 (-15.05), BSMR 853 x TS3R (-12.220 followed by BSMR 736 x AL882 (-11.77) exhibited significant negative SCA effects. These results are in agreement with the findings of Khapre *et al.* (1993), Phad *et al.* (2007), Sarode *et al.* (2009), Gupta *et al.* (2011), Arbad *et al.* (2013), Yamamura *et al.* (2014) and Srivarsha *et al.* (2017) for grain yield per plant.

Table 5.2 Crosses showing desirable SCA effects.

Sr. No.	Character	Crosses
1.	**Plant height (cm)**	BSMR 853 x AL882, BSMR 736 x AL882, BDN 716 x LRG-41, BDN 708 x TJT-501
2.	**Days to 50 per cent flowering**	BSMR 853 x TS3R, BSMR 736 x TS3R, BDN 708 x TJT-501
3.	**Pollen fertility (%)**	---
4.	**Days to maturity**	BSMR 853 x TS3R, BDN 716 x TS3R, BDN 711 x AL882, BDN 708 x TS3R
5.	**Number of primary branches per plant**	BSMR 853 x TS3R, BSMR 736 x TS3R, BDN 716 x AL882, BDN 711 x TJT-501, BDN 708 x TJT- 501
6.	**Number of secondary branches per plant**	BSMR 736 x TS3R, BDN 708 x TJT-501
7.	**Number of pods per plant**	BSMR 853 x AL882, BSMR 736 x LRG-41, BDN 716 x AL882, BDN 711 x TS3R, BDN 708 x TJT-501
8.	**Number of seeds per pod**	BSMR 853 x TS3R, BSMR 736 x LRG-41
9.	**Pod length (cm)**	BSMR 853 x LRG-41, BSMR 736 x AL882, BDN 716 x TS3R, BDN 711 x LRG-41, BDN 708 x TS3R
10.	**100 seed weight (g)**	BSMR 853 x TJT-501, BDN 708 x AL882
11.	**Grain yield per plant (g)**	BDN 708 x TJT-501, BSMR 853 x AL882, BDN 711 x LRG-41, BSMR 736 x TS3R, BDN 716 x AL882

Plate 1: Crossing block - kharif 2018

Plate 2: General view of exp. field 2019

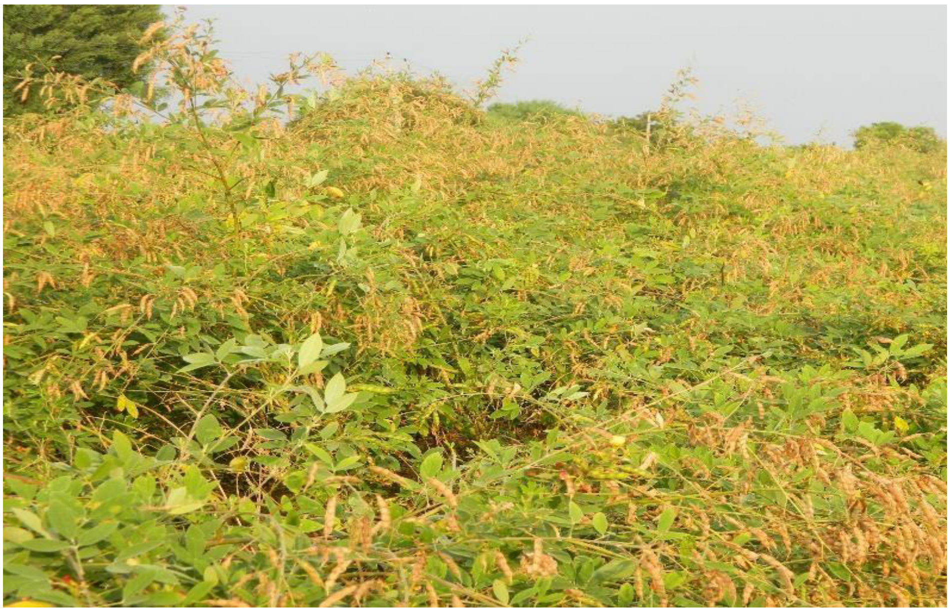

Plate 3: Promising F1 crosses

5.5 Estimation of standard heterosis

In the present research work, percent heterosis was calculated over standard checks VIPULA and ASHA (standard heterosis) in twenty crosses developed by crossing five lines with four testers. The magnitude of heterosis varied from trait to trait and cross to cross.

In pigeonpea plant height is desirable character for achieving high yield as vigour in plant height may lead to increase biomass as well as source-sink capacity for obtaining optimum yield. For trait plant height the standard heterosis range over standard checks Vipula and Asha is -31.29 to 14.35 and -29.16 to 17.90 per cent respectively. The crosses, BSMR 853 x LRG-41 (4.47%, 7.71%), BSMR 736 x LRG-41 (3.06%, 6.26%) followed by BDN 716 x LRG-41 (14.35%, 17.90%) exhibited significant positive heterosis over standard checks Vipula and Asha respectively. While the crosses BSMR 853 x AL882 (-7.29%, -4.42%), BSMR 736 x AL882 (-8.94%, -6.11%), BDN 716 x AL882 (-10.35%, -7.57%), BDN 711 x LRG-41 (-15.25%, -12.62%) followed by BDN 708 x AL882 (-31.29%, -29.16%) exhibited highest significant negative standard heterosis over the checks Vipula and Asha respectively. Similar results were also reported earlier by Veeraswamy *et al.* (1973), Wankhede *et al.* (2005), Baskaran and Muthiah (2006), Patel and Tikka, (2008), Sarode *et al.* (2009), Chandrikala *et al.* (2010), Shoba and Balan (2010), Vaghela *et al.* (2011), Pandey *et al.* (2013), Gite *et.al.* (2014).

Early maturing hybrids are generally preferred therefore, negative heterosis for days to 50 per cent flowering is considered as useful parameter. The standard heterosis range over checks Vipula and Asha is -9.61 to 4.37 and -11.54 to 2.14 per cent for the trait days to 50 per cent flowering. The crosses BSMR 853 x TS3R (-9.61%, -11.54%), BSMR 736 x TJT-501 (- 4.80%, -6.84%), BDN 716 x AL882 (-8.73%, -10.68%), BDN 711 x TJT-501 (-6.11%, -8.12%) followed by BDN 708 x TJT-501 (-9.61%, -11.54%) exhibited highest significant negative standard heterosis over the checks Vipula and Asha respectively. Same results have also been reported by Wankhede *et al.* (2005), Baskaran and Muthiah (2006), Wanjari*et al.* (2007), Patel and Tikka (2008), Sarode *et al.* (2009), Chandrikala *et al.* (2010), Vaghela *et al.* (2011), Pandey *et al.* (2013), Gite *et.al.* (2014) and Patil et al. (2015).

The standard heterosis for pollen fertility over standard checks Vipula and Asha ranged from -11.43 to 5.71 and -6.06 to 12.12 per cent respectively. The crosses exhibited significant negative heterosis for standard check Vipula viz., BSMR 853 x TS3R (-11.43) and BDN 708 x AL882 (-11.43). For the standard check Asha, the crosses BSMR 736 x TJT -501 (12.12), BDN 708 x LRG-41 (12.12) showed significant positive heterosis.

The standard heterosis for days to maturity over standard checks Vipula and Asha ranged from -17.95 to 4.27 and -18.41 to 3.68 per cent respectively. Out of 20 crosses the crosses BSMR 853 x AL882 (-5.41%, -5.95%), BSMR 736 x AL882 (-5.41%, -5.95%), BDN 716 x AL882 (-8.55%, -9.07%), BDN 711 x AL882 (-17.95%, -18.41%) followed by BDN 708 x TJT-501 (-3.42%, -3.97%) exhibited highest significant negative standard heterosis for the checks Vipula and Asha respectively. These results are in agreement with earlier results reported by Veeraswamy *et al.* (1973), Hooda *et al.* (1999), Kalaimagal and Ravikesavan (2003), Aher *et al.* (2006), Sarode *et al.* (2009), Gupta *et al.* (2011), Pandey *et al.* (2013), Gite *et al.* (2014) and Patil *et al.* (2015).

More primary branches per plant are believed to be closely associated with high seed yield per plant resulting high productivity. The standard heterosis over standard checks Vipula and Asha ranged from -21.13 to 18.31 and -23.29 to 15.07 per cent respectively. Out of 20 crosses, the crosses BSMR 853 x LRG-41 (16.90%, 13.70%), BDN 711 x LRG-41 (18.31%, 15.07%), BDN 708 x TJT-501 (14.08%, 10.96%) followed by BDN 708 x LRG-41 (15.49%, 12.33%) exhibited significant positive standard heterosis over the checks Vipula and Asha respectively. While the crosses BSMR 853 x AL882 (-11.27%, -13.70%), BDN 711 x AL882 (-14.08%, -16.44%), BDN 711 x TS3R (-21.13%, -23.29%), BDN 708 x AL882 (-16.90%, -19.18%) followed by BDN 708 x TS3R (-19.72%, -21.92%) exhibited significant negative standard heterosis over the checks Vipula and Asha respectively. Similar results were earlier reported by Pandey and Singh (2002), Pandey (2004), Arher *et al.* (2006).

For the trait number of secondary branches per plant, the standard heterosis over standard checks Vipula and Asha ranged from -27.33 to 24.42 and -19.35 to 35.48 per cent respectively. Among the 20 crosses BDN 716 x LRG-41 (19.19%, 32.26%) followed by BDN 708 x TJT-501 (22.09%, 35.48%) exhibited significant positive standard heterosis over the checks Vipula and Asha respectively. While the crosses BSMR 853 x TJT-501 (-27.33%, -19.35%), BSMR 736 x LRG-41 (-27.33%, -19.35%), BDN711 x TS3R (-27.33%, -19.35%) followed by BDN 708 x AL882 (-27.33%, -19.35%) exhibited significant negative standard heterosis over the checks Vipula and Asha respectively. Similar results were also reported earlier by Pandey and Singh (2002), Aher *et al.,* (2006), Gite *et al,* (2014) and Patil *et al.* (2014).

For the trait pods per plant the standard heterosis range over checks Vipula and Asha is -14.68 to 121.91 and 13.80 to 176.68 per cent respectively. Out of 20 crosses, BSMR 853 xLRG-41 (12191%, 176.68%), BSMR 736 x LRG-41 (113.04%, 165.62%), BDN 716 x LRG-41 (101.24%, 150.91%), BDN 711 x LRG-41 (7.71%, 34.29%) followed by BDN 708 x TJT-501 (87.29%, 133.52%) exhibited highest significant positive standard heterosis over the checks Vipula and Asha respectively. While the cross BDN 711 x TS3R (-14.68%) followed by BDN 708 x AL882 (-14.43%) exhibited significant negative standard heterosis over the check Vipula. These results are in agreement with the finding of Hooda *et al* (1999), Aher *et al.* (2006), Baskaran and Muthiah (2006), Patel and Tikka (2008), Sarode *et al.* (2009), Chandrikala *et al.* (2010), Gupta *et al.* (2011), Vaghela *et al.* (2011), Pandey *et al.* (2013), Gite *et al.* (2014) and Patil *et al.* (2015).

The hybrids with positive heterosis for number of seeds per pod are desirable to increase the yield. The standard heterosis over standard checks Vipula and Asha ranged from -10.81 to 37.84 and -8.33 to 41.67 per cent for the trait number of seeds per pod respectively. Out of 20 crosses, only BSMR 853 x TS3R (37.84%, 41.67%) exhibited significant positive standard heterosis over checks Vipula and Asha respectively. None of the crosses exhibited significant standard negative heterosis for the check Vipula and Asha respectively. These findings were in agreement with the findings of Banu *et al.* (2006), Patel and Tikka (2008), Sarode *et al.* (2009), Kumar *et al.* (2012), Pandey *et al.* (2013), Patil *et al.* (2015), Mhasal *et al.* (2015).

The standard heterosis over standard checks Vipula and Asha ranged from -19.63 to 14.02 and -1.15 to 32.18 per cent for trait pod length respectively. Out of 20 crosses, the crosses exhibited positive standard heterosis over checks Vipula and Asha were BSMR 736 x AL882 (6.54%, 31.03%) followed by BDN 711 x LRG-41 (7.48%, 32.18%) respectively. The crosses BSMR 853 x AL882 (-11.21%) BSMR 853 x TS3R (-22.43%), BSMR 853 x TJT-501 (-15.89%), BDN 716 x AL882 (-19.63%), BDN 711 x TJT-501 (-14.95%), BDN 708 x TJT-501 (-11.21%) showed significant negative standard heterosis for the check Vipula. None of the crosses showed significant negative standard heterosis over standard check Asha. These results were in agreement with earlier results reported by Patel *et al.,* (2013) and Patil *et al.,* (2014).

For the trait 100 seed weight, standard heterosis range over checks Vipula and Asha i s -13.19 to 11.92 and -15.19 to 9.34 per cent. Out of 20 crosses, the crosses BSMR 736 x TS3R (8.73%, 6.23%), BDN 716 x TS3R (11.92%, 9.34%), BDN 716 x TJT-501 (7.77%, 5.29%) followed by BDN 716 LRG-41 (8.12%, 5.63%) exhibited significant positive standard heterosis over the checks Vipula and Asha respectively. While, the cross BSMR 853 x AL882 (-13.19%, -15.19%) followed by BDN 708 x TJT-501 (-6.94%, -9.09%) exhibited significant negative standard heterosis over the checks Vipula and Asha respectively. The findings were in agreement with Wankhede *et al.* (2005), Baskaran and Muthiah (2006), Patel and Tikka (2008), Sarode *et al.* (2009), Vaghela *et al.* (2011), Kumar *et al.* (2012), Pandey *et al.* (2013), Gite *et al.* (2014), Patel *et al.* (2014) and Patil *et al.* (2015).

Ultimate aim of breeding is to gain the heterotic yield associated with other heterotic characters. Grain Yield is the complex character of all other yield contributing characters. The standard heterosis over standard checks Vipula and Asha ranged from -15.24 to 16.96 and -27.58 to 85.39 per cent for trait grain yield per plant respectively. Out of 20 crosses, the crosses *viz.,* BDN 716 x

LRG-41 (85.39%,116.96%) exhibited highest standard heterosis over the checks Vipula and Asha respectively, followed by the crosses BSMR 853 x LRG-41 (68.11%, 96.74%), BSMR 736 x LRG-41 (65.83%, 94.07%), BDN 711 x LRG-41 (62.77%, 90.48%), BDN 716 x AL882 (59.66%, 86.83%), and BDN 716 x TS3R (48.50%, 73.79%). These findings were in close agreement with the results of earlier workers Hooda *et al.* (1999), Pandey and Singh (2002), Wankhede*et al.* (2005), Anantha and Muthiah, (2007), Wanjari *et al.* (2007), Solanki *et al.* (2008), Patel and Tikka, (2008), Sarode *et al.* (2009), Singh and Singh, (2009), Deva *et al.* (2009), Bharate *et al.* (2010), Chandrikala *et al.* (2010), Vaghela *et al.* (2011), Gupta *et al.* (2011), Kumar *et al.* (2012), Pandey *et al.* (2013), Patil *et al.* (2015) and Mhasal *et al.* (2015).

Table 5.3 crosses showing high desirable standard heterosis

Sr. No.	Characters	Standard Heterosis	
		ASHA	**VIPULA**
1.	**Plant height (cm)**	BDN 716 x LRG-41, BSMR 853 x LRG-41, BSMR 736 x LRG-41.	BDN 716 x LRG-41, BSMR 853 x LRG-41, BSMR 736 x LRG-41.
2.	**Days to 50 per cent flowering**	BSMR 853 x TS3R, BDN 708 x TJT-501, BSMR853 x TJT-501, BSMR853 x AL882, BSMR 736 x TJT-501, BDN 716 x AL882, BDN 716 x TS3R, BDN 711 x TJT-501.	BSMR 853 x TS3R, BDN708 x AL882, BSMR 853 x TJT-501, BSMR 736 x AL882, BDN716 x TS3R, BDN711 x TJT-501, BDN 708 x AL882, BDN711 x AL882.
3.	**Pollen fertility (%)**	---------------------------------------	BSMR 736 x TJT-501, BDN 708 x LRG-41
4.	**Days to maturity**	BDN716 x AL882, BDN711 x TJT- 501, BDN708 x TJT-501, BDN711 x AL882, BSMR853 x AL882, BSMR853 x TS3R, BSMR853 x TJT-501, BSMR736 x AL882.	BDN716 x AL882, BDN711 x AL882, BDN711 x TJT-501, BDN708 x TJT-501, BSMR853 x AL882, BSMR853 x TS3R, BSMR853 x TJT-501, BSMR36 x AL882.
5.	**Number of primary branches per plant**	BSMR 853 x LRG-41, BDN 708 x TJT-501, BDN 711 x TJT-501, BDN 711 x TJT-501, BDN 708 x LRG-41, BDN 711 x LRG-41	BSMR 853 x LRG-41, BDN 708 x LRG-41, BDN 711 x LRG-41, BDN 708 x TJT-501.
6.	**Number of secondary branches per plant**	BDN 708 x TJT-501, BDN 711 x AL882.	BDN 708 x TJT-501, BDN 716 x LRG-41.

7.	**Number of pods per plant**	BSMR 853 x LRG-41, BSMR 736 x LRG-41, BDN 708 x TJT-501, BDN 716 x LRG-41.	BSMR 853 x LRG-41, BSMR 736 x LRG-41, BDN 708 x TJT-501, BDN 716 x LRG-41, BDN711 x LRG-41.
8.	**Number of seeds per pod**	BSMR 853 x TS3R.	BSMR 853 x TS3R.
9.	**Pod length (cm)**	BDN 711 x LRG-41, BSMR 736 x TJT-501.	BDN 711 x LRG-41, BSMR 736 x AL882.
10.	**100 seed weight (g)**	BDN716 x LRG-41, BSMR736 x TJT-501, BSMR736 x TS3R, BSMR853 x TJT-501, BDN716 x TJT-501.	BDN 716 x TS3R.
11.	**Grain yield per plant (g)**	BDN 716 x AL882, BSMR 853 x LRG-41, BSMR 736 x LRG-41, BDN 716 x LRG-41, BDN 716 x TS3R, BDN 711 x LRG-41, BDN 708 x TJT-501.	BDN 716 x LRG-41, BSMR 853 x LRG-41, BSMR 736 x LRG-41, BDN 708 x TJT-501.

The crosses BDN 716 x LRG-41, BSMR 853 x LRG-41, BSMR 736 x LRG-41, BDN 711, LRG-41, BDN 716 x AL882, and BDN 716 x TS3R had exhibited significant positive standard heterosis over the check VIPULA and ASHA for yield and most of the yield contributing characters. Hence, the cross can be further handled in future breeding programme for the improvement of pigeonpea.

CHAPTER- VI

SUMMARY AND CONCLUSIONS

The present research was undertaken with the objectives to study the heterosis and combining ability for yield and yield contributing characters in pigeonpea (*Cajanus cajan* (L.) Millsp.). It was carried out through a line x tester mating design involving 5 lines and 4 testers. A total of 31 genotypes (5 lines, 4 testers, 20 crosses and 2 standard checks) were sown in a randomized block design with two replications during *Kharif* 2019 at Agricultural Research station, Badnapur. Mean data of genotypes (excluding standard check) were analyzed as per line x tester mating design while mean data of 31 genotypes (including standard check) was used for the estimation of heterosis.

The concept of combining ability as measure of gene action was proposed by Kempthorne (1957) and estimation of heterosis was done as per Fonseca and Patterson's (1968). The results obtained are summarized as follows,

The parents BSMR 736, BDN 711, BDN 716, LRG-41, TJT-501 and TS3R had higher grain yield as well as better values for most of the yield contributing characters.

The analysis of variance shows that the differences due to crosses were significant for all of the characters. The analysis of variance due to lines were significant only for the characters *viz.,* plant height and 100 seed weight. The analysis of variance due to testers were significant for the characters *viz.,* plant height, days to maturity and grain yield. The analysis of variance due to line x tester were significant for all the characters.

The mean squares of GCA effect were significant for all characters. The mean square of SCA effect were significant for all the characters. This shows the presence of significant differences between males and females for these traits.

The estimates of GCA effects revealed that BDN 716, BSMR 853 and TJT-501 were the good general combiners for grain yield per plant and most of the yield contributing characters. The lines BSMR 853 and tester LRG-41 have recorded significant negative GCA effects for days to 50 per cent flowering and days to maturity. High GCA due to additive gene effects of parents helps for further selection of parents.

Among the crosses the *per se* performance and SCA effects were different. However, the crosses BSMR 853 x TJT-501, BSMR 736 x TJT-501, BSMR 736 x LRG-41, BDN 711 x TJT-501 and BDN 708 x TJT-501 had high *per se* performance and desirable significant SCA effects for grain yield and other components. On the basis of *per se* performance and general combining ability of parents, BSMR 853, BDN 716, and TJT-501, are good to use in potential breeding programmes and their crosses may be exploited in near future after studying their stability in different environments.

The heterosis breeding has been used extensively in improving yield potential through development of hybrid cultivars in most of the crops including pigeonpea. Out of twenty hybrids, the lines BSMR 853, BDN 716, and BDN 711 crossed with tester LRG-41, and TJT-501 has shown significant superiority over the standard checks Vipula and Asha. It is essential to judge the potential of hybrids along with stability across the location. Hence it is suggested to evaluate hybrid combination at multilocation.

LITERATURE CITED

Acharya, S., Patel, J.B., Tank, C.J. and Yadav, A.S. 2009. Heterosis and combining ability studies in indo-African crosses of pigeonpea. J. Food Legumes, **22**(2): 91-95.

Aher, G.U., Madrap, I.A., Tike, M.A. and Gore, R. 2006. Heterosis and inbreeding depression in Pigeonpea. J. Maharashtra Agric. Univ. **31**(1): 33-37.

Anantha, R. P. And Muthian, A.R. 2007. Euheterosis and combining ability for quantitative and qualitative traits in pigeonpea. Research on Crops, **8**(3): 140-143.

Arbad, S.K., Madrap. I. A., and Jadhav, P. 2013. Combining ability for yield and yield contributing characters in pigeonpea. Internat. J. Agril. Sci, **9**(1): 252- 255.

Arunachalam, V. 1974. The fallacy behind the use of modified Line x tester design. Indian J. Genet, **34**(2): 281-287.

Banu, M. R., Muthaiah, A.R. and Ashok, S. 2006. Combining ability studies in pigeonpea. Crop Research, **31**(3): 102-107.

Baskaran, K. and Muthiah, A.R. 2006. Variability studies in Pigeonpea (*Cajanus* cajan (L.) Millsp.*)*. Res. Crops, **7**:249-252.

Baskaran, K. and Muthiah, A.R. 2007. Studies on combining ability in Pigeonpea (*Cajanus cajan* (L.) Millsp.*)*. Legume Res.**30** (1): 67 - 69.

Beekham, A.P. and Umaharan.2010. Inheritance and combining ability studies of pod physical and biochemical quality traits in vegetable pigeonpea. Euphytica **176**:36-47.

Bharate, B.S., P. B. Wadikar and S. P. Pole, 2010. Heterosis in pigeonpea. Ann. Plant Physiol.,**24**: 68-71.

Bhatia, G.K., Gupta, S.C., Green, J.M. and Sharma, D.1981. Estimates of natural Cross-pollination in *Cajanus cajan* (L.) Millsp., Several experimental approaches. International Workshop on Pigeonpeas.pp:129-136, Vol 2, 15-19 Dec, 1980, ICRISAT, Patancheru, India.

Chandirkala, R. and Raveendran, T.S. 2002. Heterosis in pigeonpea *(Cajanus cajan* (L.) Millsp.) Annl. Agric. Res, **23**(2): 304-308.

Chandirakala, R., Subbaraman, N., Abdul Hameed and. 2010. Heterosis for yield in

Pigeonpea (*CajanusCajan*L. Millsp.). Electronic J. of plant breeding. **1**(1): 205-208.

*Comstock, R. E. and Robinson, H.F. 1952. Estimation of average dominance of genes. In J. W. Gowen (Edn.) Heterosis, Iowa State College Press, Ames, IOWA. pp. 494- 516.

Dahiya, B. S. and Barar, J.S. 1977. Diallel analysis of genetic variance in pigeonpea Expt. Agric, **13**: 193-200.

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

Dobzhaunsky, T. H. 1952. Nature and origin of heterosis. In Heterosis (Edn. Gowen, J. W.) Iowa Stage College Press, IOWA. pp. 218-223.

*East, E. M. 1936. Heterosis Genetics. **21**: 375-397.

*Fonesca, S. and Patterson, F.L. 1968. Hybrid vigour in a seven parental diallel cross in common winter wheat (*Triticum aestivum* L.). Crop Sci, **8**:85-88.

Gadekar, M. S., Nandanwar, R. S., Meshram, M. P., and Patil, A. N. (2015) a. Heterosis and combining ability analysis in cytoplasmic genetic male sterility (CGMS) system of pigeonpea height variants (*cajanus cajan* L.). *Legume Research,**38** (6)*: 717- 725.

Gadekar, M. S., Nandanwar, R. S., Meshram, M. P., Patil, A. N. and Sapkal, D. R. (2015b). Identification of heterotic hybrids and good combiner parents in leaf variants CGMS system in pigeonpea (*Cajanus cajan* L.) *Indian J. Genet*., **75**(1): 62-68.

Gedam, A.H.2010. Combining ability and heterosis in pigeonpea (*Cajanus cajan (L.)* Millsp. M.Sc. thesis, VNMKV, Parbhani.

Gedam, A.H., Jadhav, A.B., Bagade, A.B. and Madrap, I.A. 2013.Identification of heterotic hybrids for seed yield and its attributing traits in Pigeonpea. Legume Res. **36** (4): 355 – 358.

Ghodke, M. K., Patil, R.A. and Kordile, K.R. 1993. Pigeonpea News Letter, **18**: 7-8.

Gite, V. K., Madrap, I.A., Patil, D.K., Kamble, K.R. 2014. Exploitation of heterosis in CMS based hybrids in pigeonpea *(Cajanus cajan* (L.) Mill spp)., J. Agric. Res. Technol, **39**(1): 138-140.

*Grafius, J. E., 1959. Heterosis in barley. Agron. J., **51**: 554-567

*Griffing, B. 1956.Concepts of general and specific combining ability in relation to diallel crossing system. Australian J. Biol. Sci,**9**: 484-493.

Gupta, D. K., Acharya, S. and Patel, J.B. 2011. Combining ability and heterosis studies in pigeonpea using A_2 cytoplasm from *Cajanus scarabaeoids* as source of male sterility. Journal of Food Legumes, **24**(1): 58-64.

Hazarika, G. N., Singh, V.P. and Khare, R.P. 1988. Combining ability for grain yield and its components in pigeonpea. *Indian J. Pulses Research,* **1**(2): 111-117.

Hooda, J.S., Tomar, Y.S, Singh, V.P. and Singh, S. 1999. Heterosis and inbreeding depression in pigeonpea. Legume Res, **22**(1): 62-64.

Howard, A., Howard, G.L.C and Khan, A.R. (1919). Studying the pollination of Indian Crops. Memoirs. Department of Agriculture (Botanical series) **10**:195-200.

IIPR Vision 2030. Indian Institute of Pulses Research (ICAR), Kanpur, Uttar Pradesh, India.

Jadhav, B.D. And Nerkar, Y.S. 1983. Heterosis for grain yield in pigeonpea, grown under different cropping system. Indian J Agril. Sci, **53**(7):528-531.

Jahagirdar, J.E.2003. Line x tester analysis for combining ability in pigeonpea. Indian J. Pulses Research, **21**(4):56-58.

*Jones, D. F. 1917. Dominance of linked factors as a means of accounting for heterosis. Genetics, **2**: 466-497.

Kalaimagal, T. and Ravikesavan, R. 2003. Heterosis for seed yield and its components in pigeonpea *(Cajanus cajan* (L.) Millsp. International J. Tropical Agriculture, **21**: 1-4.

*Kempthorne, O. 1957. An introduction to genetic statistics, John Wiley and Son Inc. Newyork, Champman and Hall Ltd. London, pp. 468-470.

Khapre, P.R., Nerkar, Y.S. and Makne, V.G. 1993. Combining ability analysis over cropping systems for grain yield and related characteristics in pigeonpea. Indian J. Genet, **53**(2): 147-152.

Khapre, P.R., Aghav, S.B. and Madrap, I.A. 1996. Heterosis and combining ability analysis for grain yield and its components in pigeonpea. Proceeding of seminar on "Strategies for increasing pulses production in Maharashtra". pp. 7-8.

Krishna Rao and Nagur. 1979. Combining ability in pigeonpea. International Pigeonpea

News Letter, **4**: 6-8.

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

Kumar, R.V. and Saxena, K.B. (2001). Wind Pollination in Pigeonpea. Indian J.Gen.**61**:279- 280.

Kumar, C.V.S., Sreelakshmi, C.H. and Shivani, D. (2012). Gene effects, heterosis and inbreeding depression in pigeonpea (*Cajanus cajan* L.). Elect J Plant Breed. **3**:682-685.

Lohithaswa, H.S. and Dharamraj, P.S. 2003. Implications of heterosis, combining ability and Per Se Performance in Pigeonpea. Karnataka J. Agril. Sci. **16** (3): (403-407).

Mallikarjuna, S.J., Naidu, N.V., Sameer Kumar, C.V., Reddy, K.H.P., Rajarajeswari, V.and Koteswara Rao, S.R. 2018a.Combining Ability Studies in CGMS Based Hybrids of Pigeonpea [*Cajanuscajan* (L.) Millsp], *Int. J. Pure App. Biosci.* **6(5):**1223-1226.

Mallikarjuna, S. J., Naidu, N. V., Sameer Kumar, C. V., Hariprasad Reddy, K., RajaRajeswari, V. and Koteswara Rao, S.R. 2018b. Heterosis Studies for Yield and Its Components in CGMS Based Hybrids of Pigeonpea (*Cajanus cajan* (L.) Millsp), *Int. J. Pure App. Biosci.***6(5):** 1255-1263.

Manivel, P., Rangaswamy, P. and Sandur, M.Y. 1999. Heterosis studies involving GMS lines of pigeonpea: Crop Res. Hissar, **18**(2): 240-242.

Mayo, O. 1987. The theory of plant breeding. Clarendon Press Oxford, Mcrae (1985). Advanced in chemical hybridization in plant breeding Rev.**3**: 169-191.

Meshram, M.P., Patil, A. N. and Kharkar, A. 2013. Combining ability analysis in medium duration CGMS based hybrid Pigeonpea. *(Cajanus cajan* (L.) Millsp.,). J. of Food Legumes. **26**(3 & 4): 29-33.

Mhasal, G. S., Marawar, M. W., Solanke, A. C. and Tayade, S. D. 2015. Heterosis and combining ability studies in Medium duration pigeonpea F_1 hybrids. J. Agric. Res., 2015, **53**(1).

Mohan S, and A Sheeba, 2019. Heterosis and combining ability analysis for yield and yield related traits in green gram (*Vigna radiata L.) Electronic Journal of Plant Breeding 10(3), 1255-1261.*

Narladkar, V. W. and Khapre, P.R. 1997. Combining ability studies in pigeonpea. J.

Maharashtra Agric. Univ, **22**(1): 36-39.

Neetu Soni and Patel, P.T. 2017. Study of Heterosis and Pollen Fertility in CGMS Based Pigeonpea [*Cajanus cajan* (L.) Mill Spaugh] Hybrids. *Int.J.Curr.Microbiol.Ap p.Sci*.**6** (6):956-969.

Omanga, P. A. 1985. The use of male sterile lines to measure the nature and magnitude of hybrid vigour in pigeonpea. East African Agric. Forestry Journal, **48**(1): 51-55.

Onim, J.F.M.,1981, Pigeonpea Improvement in Kenya. Proceedings of International Workshop on Pigeonpea,15-19 December 1980, Vol 1, ICRISAT Centre, Patancheru,A.P 502324,India.pp:427-436.

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

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

Pandey, P., Rajesh, K., Pandey, V. R, Jaiswal, K. K. and Tripathi, M., 2013. Studies on heterosis for yield and its component traits on CGMS based pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids. Int. J. Agric. Res. DOI: 10.3923.

Pandey, P., Pandey, V. R., Ashutosh Kumar, Yadav, S., Tiwari, D. and Rajesh Kumar. 2015. Relationship between heterosis and genetic diversity in Indian pigeonpea [*Cajanus cajan* (L.) Millspaugh] accessions using multivariate cluster analysis and heterotic grouping. AJCS **9**(6):494-503.

Panse, V.G. and Sukhatme, P.V. 1967. Statistical Methods for Research Workers, I.C.A.R., New Delhi. 220-240.

Patel, J.A., Pathak, A.R. Zaveri, P.P. and Shah, R.M. 1987. Combining ability in pigeonpea. Indian J. Genet, **47**(2): 183-188.

Patel, G.V., Zaveri, P.P. and Pathak, A.R. 1991. Use of male sterility to measure heterosis in pigeonpea *(Cajanus cajan* (L.) Millsp.) Indian J. Genet, **51**(2): 208-213.

Patel, G.V., Zaveri, P.P. and Pathak, A.R. 1992. Combining ability analysis of parents and hybrids using genetic male sterility in pigeonpea. Indian J. Genet, **52**(3): 292- 296.

Patel, M. P. and Tikka, S. B. S., 2008. Heterosis for yield and yield components in pigeonpea. Food Legumes, **2**: 65-66.

Patel, S.R., Nizama, J.R. and Chauhan, D.A. 2013. Heterosis study in Pigeonpea (*Cajanus cajan* (L.) Millsp.) Asian resonance **24**: 49-50.

Patil, S.B., Hingane, A.J., Sameer Kumar, C. V., Mula Myer, R. Vijaya Kumar and Saxena, I. B. 2015. Combining ability studies of pigeonpea CGMS lines with an obcordate leaf Marker. Journal of Food Legumes**28**(2): 7-12.

Paul, P. R., Singh, R.M. and Nandan, R. 1996. Heterosis for yield and yield components in hybrid pigeonpea. Indian J. Pulses Res, **9**(2): 145-148.

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

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

Reddy, R.P., Azeem, M.A., Rao, V.K. and Rao, N.G.P. 1979a. Combining ability and index selection in F2 generation of pigeonpea crosses. Indian J. Genet, **39**: 247-254.

Reddy, R.P., Rao, V.K. and Rao, N.G.P. 1979b. Heterosis and combining ability in pigeonpea. Indian J. Genet, **39**: 240-246.

Sameer Kumar, C.V., Sreelakshami, C.H. and Kishore, P. 2009. Studies on combining ability and heterosis in pigeonpea. Legume Res, **32**(2): 92-97.

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

Saroj, S. K., Singh, M. N., Singh, T. 2014. Combining ability, heterosis and inbreeding depression analysis for using CMS lines in long duration Pigeonpea. Internet J. of Res. Studies in Biosciences (IJRSB). **2** (10): PP 7-15.

Saxena, K. B., Faris, D.G., Reddy, L.J. Sharma, D., Reddy, B.V.S. Gupta S.C. and Green, J.M. 1986. Prospects for hybrid pigeonpea: In new frontiers inbreeding researches. Proceedings of the 5th International Congress SABRO, 25 to 29 Nov. 1995. Bangkok, Thailand. pp 379-388.

Saxena, K.B., Singh, L. and Gupta, M.D. 1990. Variation for natural out crossing in pigeonpea. Euphytica, **56**: 143-148.

Saxena, K.B., Chauhan, V.S., Johansen, C. and Singh, L.,1992. Recent Developments in Hybrid Pigeonpea Research. Proc.Workshop on'New Frontiers in Pulses

Research and Development.'November10 to 12, 1989, Kanpur, India, pp: 58- 69.

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

Saxena, K.B., and Sawargaonkar, S.L.2014. First information on heterotic groups in Pigeonpea (*Cajanus cajan (L.*) Millsp.). Euphytica **200**(2):187-196.

Saxena, K.B., and Nadarajan N.2010.Prospects of Pigeonpea hybrids in Indian Agriculture. Elect. J. Plant Breed. **1**:1107-1117.

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

Shoba, D. and Balan, A. 2010. Heterosis in CMS/GMS based Pigeonpea [*cajanus cajan* (L.) Millsp.] Hybrids. Agric. Sci. Digest.**30** (1): 32 – 36.

Shrivastava, M. P., Singh, L. and Singh, R.P. 1975. Heterosis in pigeonpea. Indian J. Genet, **36**(2): 197-200.

*Shull, G. H. 1914. Duplicate genes for capsule form in Bursa bursa Paster Zeischr. In dukt. Abstamm. U. Verebungsi, **12**: 97-149.

Shull, G.H. 1948. What is heterosis? Genetics, **33:**439-446.

Singh, S.P., Govil, J.N. and Ram, A. 1983. Combining ability and heterosis in early pigeonpea hybrids. Indian J. Genet, **43**(3): 481-486.

Singh, I.P., Dixit, G.P. and Srivastava, D.P. 1999. Heterosis in interspecific hybrid in pigeonpea. Indian J. Pulses Res, **12**(2): 176-179.

Singh, I.P. and Srivastava, D.P. 2001. Combing ability analysis in inter specific hybrids of pigeonpea. Indian J. Pulses Res, **14**(1): 27-30.

Singh, O. and Singh, M.N. 2009. Combining ability analysis in pigeonpea. J. Food Legumes, Vol. **22**(1).

Singh, R. S. and Singh, M. N. 2015. Heterosis and Inbreeding Depression for Yield and Yield Traits in Pigeonpea (*Cajanus cajan* L.) Environment & Ecology **34** (1A): 395— 399.

Solanki, S. D., Jaimini, S.N., Patel. J. B. and Chauhan. R. M., 2008. Heterosis study in interspecific cross of pigeonpea [*Cajanus scarabaeoides* x *Cajanus cajan (*L.) Millsp.]. Biosci. Rep., **6**: 95-98.

Soloman, R. N., Argikar, S.G.P., Solanki, M.S. and Murbad, I.R. 1957. A study of heterosis in *Cajanus Cajan*. Indian J. Genet, **17**: 90-95.

Sprague, G.F. and Tatum, L.A. 1942. General and specific combining ability effect of single crosses of crops Agro J, **34**: 923-932.

Srinivas, T., Jain, K.C., Reddy, M.V. and Reddy, M.S. 2000. Heterosis for grain yield and its component characters in pigeonpea (*Cajanus cajan* (L.) Millsp). Res. on Crop, **1**(3): 302-306.

Srivarsha, J., Jahagirdar, J.E., Kumar, S., Hingane, A.J., Paitl, D.K., Shruthi, H.B., Bhosle, T.M. 2017. Studies on CGMS based short Duration Hybrids pigeonpea (*Cajanus cajan* (L.) Millsp.) In terms of Combining Ability. Int.J.Curr.Microbiol.App.Sci., **6**(10): 3128-3136.

Srivarsha, J., Jahagirdar, J.E., Kumar, S., Hingane, A.J., Paitl, D.K., Gite, V.K., Shruthi, H.B., Bhosle, T.M. 2017. Study of CGMS based short Duration Hybrids pigeonpea (*Cajanus cajan* (L.) Millsp.) In terms of Heterosis. Int.J.Curr.Microbiol.App.Sci., **6**(11): 682-692.

Stebbins, 1957. Self-fertilization and Population variability in higher plants. The American Naturalist. pp.no.861.

Sudhir Kumar., Debnath, M. K., Sameer Kumar, C. V., Singh, P. K., and Sultana, R. (2015). Study of heterosis and pollen fertilityin CGMS based pigeonpea [*Cajanus cajan* (L.) Millspaugh] hybrids. *Res.Environ. Life.sci.,**9**(1):107-110.*

Sudhir Kumar., Singh. P.K., Sameer Kumar, C. V. and Saxena, K. B. 2017. Study of CGMS based pigeonpea [*Cajanus cajan (l.) Millsp*] hybrids in terms of combining ability. Int. J. of Agri. Sci and Res. (IJASR) pp.no.129-134.

Thiruvengadam, V., Muthiah, A.R. 2012. Combining ability analysis for yield and its components in Pigeonpea using GMS lines. J. of Food Legumes. **25**(3): 171- 174.

Tikle, A. N., Kumar, S., Kumar, R. V., & Saxena, K. B. (2016). Gene action and combining ability estimates using cytoplasmic-genic male sterile lines to develope pigeonpea hybrids for rainfed condition. *International Journal of scientific and Research Publication*,**6**(1):502-506.

Tuteja, O. P., Malik, B.P.S. and Singh, V.P. 1989. Heterosis in pigeonpea and its possibilities for utilization Phytobreedon. **4**: 54-58.

Tuteja, O. P., Malik, B.P.S. and Singh, V.P. 1992. Heterosis in single- and three-way crosses in pigeonpea. Indian J. Genet, **52**(1): 100-102.

Van der Maesen L. J. G., 1980. Pigeonpea: Origin, History, evolution and taxonomy. In the pigeonpea (Y. L. Nene, S. D. Hall and V. K. Sheila eds.) CAB International, Wallingford, U.K. pp 15-46.

Vaghela, K. O., Desai, R. T., Nizama, J. R., Patel, J. D., and Kodappully, V. C., 2011. Heterosis study for yield and yield components in pigeonpea (*Cajanus cajan* (L.) Millsp.]. Res.Crops, **12**: 192-194.

*Vavilov, N. I. 1951. The origin, variation, immunity and breeding of cultivated plants. Chranica Botanica. **13**(1/6): 1-366.

Veeraswamy, R. Palaniswamy, G.S. and Rathnaswamy, R. 1973. Natural cross pollination in pigeonpea. Madras Agric. J, **60**(9-12): 18-28.

Venkateswarlu, S., Reddy, A.R. and Singh, R.M. 1981. Heterosis in pigeonpea and the implication in production hybrids on commercial basis. Madras Agric. J, **68**(8): 496-501.

Venkateswarlu, S. and Singh, R.B. 1982. Combining ability for earliness in pigeonpea. Indian J. Genet, **41**(2): 252-254.

Verulkar, S.B. and Singh, D.P. 1997. Heterosis in pigeonpea. ICPN, **4**: 33-34.

Wanjari, K.B., Patil, A.N. and Prema Manapure, 1998. Selection of male sterile population for development of parental lines for exploitation of heterosis in pigeonpea. Indian J. Pulses, **11**(2): 6-10.

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

Wankhede, R.R. 1998. Combining ability analysis in pigeonpea using male sterile lines. M Sc. Thesis, Dr. PDKV, Akola.

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

Whaley, W. G., 1952. Physiology of gene action in hybrids. IOWA State College Press. Pp: 98-113.

Yamumura, Lokesha, R., Dharmaraj, P. S., Muniswamy, S. and Diwan, J.R. 2014. Estimation of heterosis, combining ability and gene action in Pigeonpea

(*Cajanus cajan* (L.) Millsp.). Electronic Journal of plant Breeding, **5**(2): 173-178.

*- original not seen.

THESIS ABSTRACT

a) Title of the Thesis : **"Heterosis and Combining Ability studies in Pigeonpea (*Cajanus cajan (L.) Millsp.*)"**

b) Name of student : **Jaybhaye Dnyaneshwar Bhagwan**

c) Degree to be awarded : M.Sc. (Agriculture)

d) Year of award of degree : 2020

e) Major subject : Genetics and Plant breeding

f) Total No. of pages in the thesis : 76

g) Number of words in abstract : 308

h) Signature of the student :

(Jaybhaye Dnyaneshwar Bhagwan)

i) Name and address of Major Advisor :

Dr. J. E. Jahagirdar

Head
Dept. of Agril. Botany VNMKV,
Parbhani -431 402

j) Signature Name and address of forwarding authority :

Dr. B. G. Kamble

Head of section,
Department of Agriculture Botany,Badnapur.

ABSTRACT

The present investigation was undertaken for "Heterosis and Combining ability studies in Pigeonpea (*Cajanus cajan (L.) Millsp.*)" The objective of present study is to estimate the standard heterosis and combining ability effects among parents and crosses to find out promising cross combinations for seed yield and its components. The experimental material comprised of 20 crosses along with 9 parents (5 lines and 4 testers) and standard checks Asha and Vipula. The experiment was laid out in Randomized Block Design with two replications. The observations were recorded on eleven characters *viz.,* plant height, days to 50 per cent flowering, pollen fertility, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and grain yield per plant.

The analysis of variance revealed that there were significant differences among the parents and crosses for all the characters studied. The estimates of GCA effects revealed that BSMR 853, BDN 716 and TJT-501 were the good general combiners for number pods per plant and grain yield per plant. The line BSMR 853, BDN 711 and the tester LRG-41 have registered significant negative GCA effects for days to 50 per cent flowering and for days to maturity. The crosses BSMR 853 x AL882, BSMR 853 x TJT-501, BSMR 736 x TJT-501, BSMR 736 x LRG-41, BDN 711 x TJT-501, and BDN 708 x TJT-501 had high *per se* performance and desirable significant SCA effects for grain yield and other components. The cross BDN 716 x LRG-41 had manifested significant positive standard heterosis over the checks Vipula and Asha for yield and yield contributing characters *viz.*, seed yield per plant and number of pods per plant.

These promising crosses can be further handled by pedigree method and the stability can be studied across the environments.

VITA

Mr. JAYBHAYE DNYANESHWAR BHAGWAN

A candidate for the degree of

MASTER OF SCIENCE (AGRICULTURE)

in

GENETICS AND PLANT BREEDING

2020

Title of Thesis	**"Studies of Heterosis and Combining Ability in Pigeonpea (*Cajanus cajan (L.) Millsp.*)"**
Major field	Genetics and Plant Breeding
Biographical information	
Personal	Born at Village Kankarwadi, Tq-Risod, Dist- Washim on 4thJuly, 1993. Son of Shri Bhagwan Kundlik Jaybhaye and Sau. Mahananda Bhagwan Jaybhaye.
Educational	Passed S.S.C. in 2010 with first class from Bhavana Public School, Degaon. Dist-Washim.
	Passed H.S.C. in 2012 with First Class from Sudhakar Rao Naik Umakhetan jr College, Akola.
	Received Bachelor of Science (Agriculture) degree in 2018 with First Division from College of Agriculture, Nagpur. University: PDKV Akola.

Address	_	AtKankarwadi, Post-Chinchamba bhar, Tq-Risod, Dist- Washim
E-mail Id	-	dnyaneshwarjaybhaye008@gmail.com
Mobile No.	-	9923932644