GENETIC VARIABILITY, CORRELATION AND DIVERSITY ANALYSIS IN PIGEONPEA (Cajanus cajan (L.) Millsp.)

A thesis submitted to the

Mahatma Phule Krishi Vidyapeeth, Rahuri- 413 722,
Dist. Ahmednagar, Maharashtra State, India

By

DEORE SANDIP GANGADHAR
(Reg.No.11/041)

In partial fulfilment of the requirements for the degree
Of
MASTER OF SCIENCE (Agriculture)
In
AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE,
MAHATMA PHULE KRISHI VIDYAPEETH, RAHURI-413 722
MAHARASHTRA (INDIA)
2013

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Approved by

Dr.M.R.Bedis
(Chairman and Research Guide)

Dr.P.N.Harer
(Committee member)

Dr.S.N.Mate
(Committee member)

Dr.C.A.Nimbalkar
(Committee member)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE,
MAHATMA PHULE KRISHI VIDYAPEETH, RAHURI-413 722.
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I hereby declare that this thesis or part there of has not been

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or Diploma

Place : M.P.K.V.Rahuri. (Deore S.G.)
Dated : / /2013.

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Dr.M.R.Bedis,
Senior Scientist (Pigeonpea Breeding),
Pulses Improvement Project,
M.P.K.V. Rahuri,
Maharashtra State (India).

CERTIFICATE

This is to certify that the thesis entitled, GENETIC VARIABILITY, CORRELATION AND DIVERSITY ANALYSIS IN PIGEONPEA (Cajanus cajan (L.) Millsp.) submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra State, India in partial fulfilment of the requirements for the degree of MASTER OF SCIENCE (AGRICULTURE) in GENETICS AND PLANT BREEDING, embodies the results of a piece of bona fide research work carried out by Mr. DEORE SANDIP GANGADHAR under my guidance and supervision and that no part of this thesis has been submitted for any other degree or diploma.

Place : M.P.K.V., Rahuri. (Dr.M.R.Bedis)
Date : / /2013. Research Guide

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Dr. S.G.Borkar,
Associate Dean,
Post Graduate Institute,
MPKV, Rahuri,
Maharashtra State (India).

CERTIFICATE

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Place : Rahuri. (Dr.S.G.Borkar)
Date : / / 2013. Associate Dean

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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 faced both weal and woe, but inspiration and guidance given by my teachers, parents and friends 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.

The words at my command are inadequate to convey the depth of feelings of gratitude and indebtedness to respected Research Guide and Chairman of my Advisory Committee Dr. M.R.Bedis, Senior scientist (Pigeonpea breeding), Pulses Improvement Project, MPKV, Rahuri for suggesting an interesting topic, his scholastic teaching, intellectual guidance with constant encouragement, care for originality and quality work throughout my studies and dissertation writing.

I wish to express my sincere thanks to Dr. T. A. More, Hon. Vice-chancellor, M.P.K.V, Rahuri, Dr. B. R. Ulmek, Dean, Faculty of Agriculture, M.P.K.V, Rahuri, Dr. S. G. Borkar, Associate Dean, Post Graduate Institute, MPKV, Rahuri.

I have immense pleasure in expressing my profound sense of gratitude to Dr. P. N. Harer, Principal Scientist, Pulses Improvement Project, MPKV, Rahuri; Dr. S. N. Mate, Professor of Plant Physiology, MPKV, Rahuri; Dr. C. A. Nimbalkar, Associate Professor of Statistics; for his constant encouragement, valuable suggestions and for being an everlasting source of inspiration to me.

My sincere thanks to Shri. R. S. Chavan, Shri. Y. R. Pawar, Sou. Kambale madam for extending hands of co-operation during the research work.

I would like to take this opportunity to express my deepest and sincere gratitude to my family, Father Shri. Deore Gangadhar Daji,, Mother Sou. Deore Ranjanabai Gangadhar, sister Swati tai, brother Anil and Madhav daji and my relatives kaka, maushi, mama and aatya without their unstinted support and guidance this

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this dissertation would probably be incomplete. Their constant encouragement enabled me to overcome all obstacles to complete my dissertation.

I pleasure to express my heartiest gratitude towards the help rendered by my friends Tushar Kamble, Sunil Jejurkar, Vishal Londhe, Vijay Patil, Swapnil Patil, Rajesh Rathod, Tushar Sonawane, Vivek Suryawanshi, Ganesh Sawant, and all M.Sc. (Agri.) 2011 Batch and my seniors Appa Patil, Satish Raut, Sunil Nehete, Vikas Kalukhe, Jalinder Pangare.

Also, I would like to thanks to my junior friends Vijay Chaure, Ganesh Jadhav, Suraj Murumkar, Pandurang Sable and all KaSaMaDe group member for better co-operation during the course of research work.

Inadvertently I might have forgotten to mention the names of invisible hand for their help, I am thankful to them as well.

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Date : / /2013. (Deore S. G.)

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LIST OF ABBREVIATIONS

B.S.	:	Broad Sense
C.D.	:	Critical difference
cm	:	Centimeter (s)
C.V.	:	Coefficient of variation
Cov.	:	Covariance
d.f.	:	Degrees of freedom
et al.,	:	And others (et alia)
Fig.	:	Figure (s)
g	:	Gramme (s)
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
ha	:	Hectare (s)
h^2	:	Heritability
i.e.	:	That is (id est)
MPKV	:	Mahatma Phule Krishi Vidyapeeth
MSS	:	Mean sum of squares
No.	:	Number (s)
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized Block Design
S.E.	:	Standard Error
S.S.	:	Sum of squares
viz.,	:	Videlicet (namely)
%	:	Per cent
	:	Summation
/	:	Per
	:	Variance
2	:	Standard deviation
Per se	:	Actual
$Ã^2D$	:	Dominance variance
$Ã^2_e$	:	Environmental variance
$Ã^2_g$	:	Genotypic variance
$Ã^2_p$	:	Phenotypic variance
Wt.	:	Weight
Vs	:	Verses
SM	:	Sterility mosaic

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ABSTRACT

GENETIC VARIABILITY, CORRELATION AND DIVERSITY ANALYSIS IN PIGEONPEA (Cajanus cajan (L.) Millsp.)

By

DEORE SANDIP GANGADHAR

A candidate for the degree

Of

MASTER OF SCIENCE (AGRICULTURE)

In

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

Post Graduate Institute,

Mahatma Phule Krishi Vidyapeeth,

Rahuri - 431 722 (M.S.) India.

2013

Research Guide : Dr.M.R.Bedis

Department : Agricultural Botany

Major field : Genetics and Plant Breeding

The present study entitled Genetic variability, correlation and diversity analysis in pigeonpea [Cajanus cajan (L.) Millsp.] was undertaken to study the nature and extent of divergence among the genotypes and to study interrelationships among seed yield and its various components.

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Fifty genotypes of pigeonpea were grown and evaluated at Pulses Improvement Project, MPKV, Rahuri during August 2012 to February 2013, in a Randomized Block Design (RBD) with three replications.

The observations were recorded on the 15 characters viz., days to 50 % flowering, days to maturity, plant height (cm), plant spread (cm), primary and secondary branches per plant, pods per plant, seeds per pod, seed yield per plant (g), 100 seed weight (g), incidence of SM (%), wilt (%), reaction to pod borer (%), harvest index (%) and protein content (%).

The data revealed that, sufficient variability was present among the genotypes under study, PCV estimates were slightly higher than GCV estimates. Very high estimates of heritability (BS) were observed for all the characters studied. High heritability accompanied with high genetic advances, as percentage of mean were observed in case of incidence of sterility mosaic, wilt percentage, secondary branches per plant, seed yield per plant, plant spread, pods per plant and primary branches per plant, suggesting additive genetic control in the inheritance of these characters.

Correlation studies revealed that, genotypic correlation coefficients were higher than the corresponding phenotypic ones. Seed yield showed significant and positive correlation with the plant height (0.323), primary branches per plant (0.266), secondary branches per plant (0.504), pods per plant (0.835), seeds per pod (0.266) and positive correlation with days to 50 % flowering (0.104), days to maturity (0.129), plant spread (0.152) and 100 seed weight (0.105). Whereas, it showed negative and significant correlation with wilt percentage (-0.216), reaction to pod borer (-0.327) and negative correlation with incidence of sterility mosaic (-0.085), harvest index (-0.068) and protein content (-0.147).

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Path analysis revealed that, pods per plant had the highest and positive direct effect (0.773), followed by days to maturity (0.357),seeds per pod (0.172) on seed yield and incidence of sterility mosaic had the highest and negative direct effect (-0.167), followed by reaction to pod borer (-0.150) on seed yield. This suggests the importance of these traits while selecting for improvement in seed yield.

The D^2 statistics showed that, there was considerable divergence among the genotypes with D^2 values ranging from 104.6 to 11047.96. On the basis of D^2 values, 50 genotypes were grouped into 9 clusters. Clustering pattern of these genotypes did not necessarily follow the geographical distribution. Tentative hybridization program is suggested on the basis of the genetic divergence, cluster means and per se performance of genotypes from distantly related clusters to secure yield improvement in pigeonpea involving PT-04-267, PT-04-360-1, ICPL-87, PT-04-343, PT-04-230, PT-03-129-2, PT-04-373, PT-011-6 and PT-011-14 genotypes.

Pages 1 to 106

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1. INTRODUCTION

Pigeonpea is an important legume crop mostly produced in Asia, Africa, Latin America, and the Caribbean region. It belongs to family Leguminoseae, sub family Papilionaceae having chromosome number 2n = 2x = 22 (Roy, 1933).

Pigeonpea is the fourth most important pulse crop after chickpea in the world with almost all production confining to developing countries. In World, total area under pigeonpea cultivation is about 4.58 million ha. with production of 3.27 M.tonnes (Anonymous, 2011).

Pigeonpea is one of the important pulse crops of India and ranks second to chickpea in area and production. India is largest pulses producer and account for 27-28 per cent of global production. In Maharashtra pigeonpea occupies an area of 12.09 lakh ha and has production of 976.00 lakh tons (Anonymous, 2012a.) with average productivity of 750 kg/ha (Anonymous, 2012b). In comparison with area under this crop in India (3.46 million ha), it constitutes approximately 40.02% and also shares equal contribution in total production. Thus, Maharashtra state is a leading producer of pigeonpea at National level.

At present, pigeonpea is classified in tribe Phaseoleae, subtribe Cajaninae, family Leguminosae, sub family Papilionacae genus Cajanus, and species cajan. Keeping in view the wide range of diversity in India, pigeonpea was considered to be of the Indian origin

Pigeonpea is a rich source of proteins, carbohydrates and certain minerals. Protein content of commonly grown pigeonpea cultivars ranges between 17.9 and 24.3 g per 100 g for whole grain samples and split grains. Seed of pigeonpea is a good source of iron and iodine and rich in essential amino acids like lycine, tyrocine, cystine and arginine. Being legume, it has symbiotic association with Rhizobium which play an important role in fixing

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important role in fixing atmospheric nitrogen for which pigeonpea is inevitable part of various cropping system.

Though India ranks first in area and production of pigeonpea, the average productivity of pigeonpea is low at around 655 kg/ha. (Anonymous, 2012c). To break the yield plateau in pigeonpea in India, one of the way is to understand the variability, correlation and diversity among various yield contributing characters in pigeonpea genotypes at commercial level.

Varietal improvement gets top priority in order to increase productivity in research programme of this crop. Since beginning of Agriculture, cultivated crops have been subjected to intense human and natural selection and trends continues. This has resulted in huge collection of different crop species, land races, wild relatives distributed throughout the world, which comprises valuable germplasm collection. For designing an effective breeding programme for improvement of any crop, the information regarding genetic variability and estimates of heritability are pre-requisite. It is therefore necessary to collect, conserve and study genetic diversity among various crops in the form of germplasm.

Knowledge of variability in terms of genotypic and phenotypic coefficients of variation, genetic advance and heritability is of immense importance in evolvement of superior varieties. Also, it can be used for desired improvement in existing varieties.

Yield is main objective of any breeding programme. The yield is result of interactions of number of factors, present both in plant as well as in an environment. It is difficult to evaluate or select for this complex character directly. More efforts should be made towards indirect selection such as determination of the association existing between other less variable plant characters and yield. Selection pressure may

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Selection pressure may then be easily exerted on those variables, which show close association with yield.

Wright (1921) suggested the method of partitioning the correlation into direct and indirect effect by path coefficient analysis. It provides useful information on the relative merits of the traits in selection criteria.

Genetic diversity, which is heritable is a pre-requisite for successful breeding programme. Proper choice of parents in the breeding programme is of paramount importance. Genetic divergence among the parents play vital role in cultivar improvement because a cross involving genetically diverse parents is likely to produce high heterotic effect and more variability in segregating generations, which can be used for the desired improvement. Generally plant breeder select the parents on the basis of phenotypic diversity. The knowledge of genetic diversity among the parents with respect to characters, which are to be improved is must.

The D^2 statistics is a powerful tool for quantifying the genetic divergence. Thus, it gives better idea about the magnitude of the divergence and is independent of the size of the sample and provides the basis for the selection of parental lines for future breeding programme.

Use of advanced novel techniques of plants improvement will be inevitable for twenty-first century, however traditional plant breeding tools such as genetic variability, path analysis, genetic diversity studies will also play important role in plant breeding.

The present study was therefore undertaken with the following objectives:

1. To study the nature and extent of divergence among the genotypes.
2. To study interrelationships among various seed yield and its components.

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2. REVIEW OF LITERATURE

Success of any breeding program depends on the diversity and variability present in population selection of elite genotypes. Though not much work has been found on this crop, an attempt has been made to review the published literature on variability, path analysis and genetic diversity in pigeonpea.

2.1 Origin, cytological studies and types of pigeonpea:

2.1.1 Origin of pigeonpea

Origin of pigeonpea was studied by Van Der Maesen (1980).

The floristic, linguistic and cytological evidences revealed an Indian origin of pigeonpea, from India, it was most probably distributed to Africa at least two millennia B.C. And Africa was definitely a centre of diversity. It was imported to the Eastward America from Africa. Then the crop reached to Indonesia which helped its introduction into Madagascar.

2.1.2 Cytological studies

Roy (1933) reported for the first time, the somatic chromosome number in pigeonpea to be 2n = 22.

Krishnaswami et al. (1935) observed the haploid chromosome number n = 11 in pigeonpea.

Further, Kajjari (1956), Joglekar and Deshmukh (1958); Deshmukh and Phirke (1962) also reported the haploid chromosome number in pigeonpea to be n = 11 in various mutants.

Akinola et al. (1972), D Cruz and Jadhav (1972) reported pigeonpea chromosome complement to be 2n = 22.

2.1.3 Types of pigeonpea

Number and types of pigeonpea have been noticed differing in height, time of maturity, colour, size and shape of flowers, seeds and pods by following workers:

From Madhya Pradesh alone, 36 types of pigeonpea were identified by Mehta and Dave (1931).

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Shaw et al. (1933) have distinguished 86 different types from the germplasm collection all over India. These types are being grouped broadly under two varieties viz., arhar (Cajanus cajan var. bicolor DC) tur (Cajanus cajan var. flavus DC). The arhar variety comprises mostly the perennial types which are the late maturing, large bushy plants streaked yellow flowers and dark coloured pods each with 4-5 seeds. tur variety includes early maturing, small plants bearing yellow flowers and plain pods each with 2-3 seeds.

In peninsular India, tur varieties are cultivated on large scale, while the late maturing types that of arhar are being grown in Uttar Pradesh, Bihar, Bengal and Assam. In Madhya Pradesh both the types viz., tur and arhar are cultivated.

2.2 Correlation and genetic variability

2.2.1 Correlation

Joshi (1973) noticed that, the seed yield in pigeonpea was positively correlated with number of pods and number of branches per plant.

Singh and Malhotra (1973) observed significant and positive association of yield with clusters per plant in pigeonpea.

Gupta et al. (1975) reported that, in pigeonpea traits viz., pods per plant, pod cluster per plant, pod cluster per five branches and number of branches were the major yield contributing components suggesting that selection should be based on more number of branches, the highest cluster per five branches along with higher number of pods per plant.

Wagh (1976) reported that, grain yield per plant in pigeonpea was highly and significantly associated with days to 50% flowering, plant height, number of secondary branches, number of seeds per pod and 100 grain weight.

Singh and Shrivastava (1977) reported the positive significant association of grain yield per plant with plant height, pod length and 100 grain weight in pigeonpea.

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Awatade et al. (1980a) observed that, seed yield is positively and significantly associated with plant height, number of branches, number of clusters per plant, number of pods per plant and days to maturity in pigeonpea. The weight of 100 grain was positively significantly associated with seeds per pod but plant height had negatively correlated with number per plant.

Singh et al. (1982) studied correlation in F_4 progenies of pigeonpea. They found that, seed yield per plant was positively and significantly associated with plant height, number of pods per plant, days to 50% flowering, seeds per pod and days to maturity.

Balyan and Sudhakar (1985) observed that, plant height, primary and secondary branches, pods per plant, seeds per pod, weight of 100 grain had positive and significant association with seed yield in pigeonpea.

Sidhu et al. (1985) observed positive and significant association with seed yield with plant height, pods per plant, seed size and seeds per pod in pigeonpea.

Bhongale and Raut (1987) showed that, grain yield in pigeonpea was found to be significantly correlated with important yield contributing characters viz., plant height, branches per plant, pod number, pod weight and stated that the selection based on these traits would be effective in breeding for high yielding pigeonpea types.

Marekar and Nerkar (1987) noticed that, seed yield of tur was positively and significantly associated with plant height, number of secondary branches, clusters and pods per plant, plant biomass and harvest index both at the genotypic and phenotypic level.

Patil et al. (1989) observed that, seed yield in pigeonpea was positively correlated with number of branches per plant, number of pods per plant and 100 seed weight.

Theyalsonoticedthat, the days to first flowering had a direct negative influence on seed yield. The number of clusters and

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Natarajan et al. (1990) noticed that, number of pods, number of clusters and plant height were positively and significantly associated with seed yield in pigeonpea.

Khapre and Nerkar (1992) observed that, traits like leaf area index, days to maturity, plant height, number of pods per plant and total biomass per plant had positive significant correlation with grain yield in pigeonpea.

Khapre et al. (1993) noticed that, grain yield in pigeonpea had positive and significant association with pods per plant, days to 50% flowering, grain to shell ratio and harvest index, however, it had low positive association with plant height, days to maturity and 100 seed weight.

Dhameliya and Pathak (1994) reported that, plant height and no. of primary branches showed positive significant genotypic and phenotypic correlation with no. of pods per plant, no. of primary and secondary branches, while percent pod damage showed negative and significant genotypic and phenotypic correlation with plant height.

Dhameliya and Pathak (1995) reported that, 100 seed weight showed positive significant genotypic and phenotypic correlation with pod length and seeds per pod.

Salunke (1994) reported that, grain yield per plant in pigeonpea had highly significant and positive correlation with number of pods, number of secondary branches, plant spread, number of primary branches, plant height and 100 grain weight. However, it had strong negative correlation with number of seeds per pod.

Salunke et al. (1995) revealed that, the yield components viz., days to 50 % flowering, days to maturity, plant height, plant spread, primary branches per plant, secondary branches per plant and 100 grain weight were positively and significantly associated among themselves. Pods per plant were positively and significantly associated with primary branches, secondary branches, plant height and plant spread.

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Singh and Gumber (1995) showed that the magnitude of genotypic correlation in general was higher than the phenotypic correlations. Days to maturity was positively correlated with plant height in parental, F_2 and back cross generations and with seed yield in parental and F_1 generation.

Mahajan et al. (1995) studied genotypic correlation in 23 pigeonpea genotypes grown in 3 environments. They observed that, pods per plant were significantly and positively correlated with yield in all the 3 environments.

Paul et al. (1996) reported in pigeonpea that, at phenotypic level, yield was significantly and positively correlated with number of pods per plant, dry matter at maturity and number of secondary branches. At genotypic level, the association was highest for dry matter at maturity.

Thombare (1997) observed that, grain yield per plant in pigeonpea has significant and positive correlation with plant height, plant spread, days to 50% flowering, 100 grain weight, days to maturity, number of primary and secondary branches per plant, number of seeds per pod and number of pods per plant.

Khandwe et al. (1998) observed that, negative and significant genotypic and phenotypic correlation was present between percent pod damage and pods per plant.

Srinivas et al. (1999) observed that, seed yield showed significant and positive correlation with plant height, number of primary and secondary branches per plant, number of pods per plant in pigeonpea.

Sawant (2001) showed that, plant spread, number of secondary branches per plant and days to maturity had strong positive genotypic correlations with grain yield per plant.

Pandey and Singh (2002) showed that, percent pod damage had negative but significant genotypic correlation days to 50 % flowering and days to maturity.

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Chandirakala and Subbaraman (2010) estimated nature and magnitude of association of seed yield with other components and their direct effects on seed yield were studied in pigeonpea. Character association studies indicated that branches per plant, clusters per plant, pods per plant, pod length, seeds per pod and 100 seed weight were strongly associated with seed yield. Path coefficient analysis revealed that 100 seed weight, days to maturity, days to 50 per cent flowering, pod length and seeds per pod had high positive direct effect on seed yield. It is inferred that for improving seed yield in pigeonpea, due emphasis should be given on characters viz., branches per plant, clusters per plant, pods per plant, seeds per plant and 100 seed weight.

Linge et al. (2010) studied that grain yield was found to be positively and significantly correlated with all characters except for percent pod damage where the association was negative and significant. It indicated that these characters are useful for taking them as the basis of selection for high yield.

2.2.2 Genetic variability

Joshi (1973) noticed a wide range of variability in seed yield per plant, seeds per pod, pod length and plant height.

Rathnaswamy et al. (1973) noticed significant varietal differences in pigeonpea for all the traits studied. They found a wide range of variation for the different plant characters viz., plant height, branches per plant, weight of pods, seeds per pod and days to flowering. The GCV estimates were high for clusters, seeds weight of pods, branches per plant, plant height and days to flower, however, the estimates were low for days to maturity.

Chandra et al. (1975) also reported sufficient genetic variation for yield and other characters. Highest phenotypic variability was noticed for clusters per five branches followed by pods per plant and yield per plant.

Wagh (1976) have studied 79 genotypes and noticed sufficient variation for various characters. He reported

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that, higher heritable variation for days to 50% flowering, number of secondary branches, leaf area and 100 grain weight.

Malhotra and Sodhi (1977) observed significant differences among the genotypes for all characters under study. GCV was highest for branches per plant followed by grain yield, cluster number and pod number per plant.

Singh and Srivastav (1977) noticed that, maximum GCV for number of secondary branches followed by yield and 100 grain weight.

Sheldrake and Narayanan (1979) reported that, harvest index of pigeonpea was low and ranges between 25-30 %.

Awatade et al. (1980b) reported significant variation for 7 yield components among F_2 and F_3 progenies of 12 crosses involving pigeonpea. They also observed that phenotypic coefficient of variation was generally greater than genotypic coefficient of variation for the characters studied.

Bainiwal et al. (1981) reported the maximum variability for secondary branches followed by primary branches and seed yield in pigeonpea.

Shoran (1983) noticed higher phenotypic variability for all the characters except seeds per pod. High estimates of GCV were obtained for pods per plant, days to maturity, plant height and days to flowering.

Dumbre and Deshmukh (1983) also reported that estimates of GCV were high for grain yield, number of primary branches and pods per plant.

Balyan and Sudhakar (1985) studied the nature of genetic variability and noticed that primary and secondary branches, pods per plant, 100 seed weight and yield per plot exhibited high estimates of GCV and PCV.

Sidhu et al. (1985) showed that, genetic variability was highest for number of pods per plant and the lowest for number of seeds per pod.

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Bhongale and Raut (1987) reported highest GCV for yield per plant followed by number of pods.

Natarajan et al. (1990) noticed the highest GCV for number of pods followed by number of clusters and seed yield, while it was the lowest for seeds per pod.

Khapre et al. (1993) noticed that, traits like height, pods per plant, grain yield per plant and harvest index had high GCV and PCV estimates.

Salunke (1994) observed sufficient variability among 54 genotypes of early pigeonpea. He observed that, estimates of GCV were low as compared to PC.

Singh and Gumber (1996) reported that, the analysis of variance showed significant differences for all the traits studied in each generation viz., parental, F_1, F_2 and back cross generations in pigeonpea.

Thombare (1997) noticed that, GCV as well as PCV were the highest for the number of secondary branches per plant followed by 100 grain weight, number of primary branches per plant, days to 50% flowering and plant spread and were the lowest for number of seeds per pod. The values of GCV and PCV were also higher for plant height and number of pods per plant.

Pande et al. (2006) observed and categorized the improved pigeonpea genotypes on the basis of incidence of diseases (SM and Phytopthora blight) as resistant (=10% incidence), moderately resistant (10.1 20.0%), moderately susceptible (20.1-40.0%), and susceptible (40.1 100%). Also reported the reaction of pigeonpea genotypes to Phytophthora blight (PB), wilt and sterility mosaic (SM).

Sreelakshmi et al. (2010) studied for genetic divergence using Mahalanobis D^2 statistic indicated wider genetic diversity. Considerable variability was observed for days to 50% flowering, days to maturity, plant height, number of pods per plant and seed yield due to non-linear pooled deviation.

2.3 Path analysis

Veerswamy et al. (1973) observed the maximum influence of number of branches on the seed yield directly.

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that, the days to first flowering had a direct negative influence on seed yield. The number of clusters and pods per plant did not have much direct influence on the yield but they had indirect influence.

Pokale and Mohatkar (1975) observed that, pod number had a higher direct effect on grain yield that its correlation with yield and it was the major yield determining in pigeonpea. It also directly affected through plant height, 100 seed weight and number of primary branches per plant.

Ram et al. (1976) revealed that, number of primary branches, clusters per plant and pods per cluster had both direct and indirect effects on grain yield in pigeonpea. Plant height contributed indirectly to the yield as its direct effect was negative.

Pods per plant were given maximum weightage in selection of high yielding genotypes in pigeonpea by Sharma and Asawa (1977). The study revealed that, the characters like days to flowering, primary and secondary branches did not have effects independently but mainly through pods per plant.

Awatade et al. (1980b) reported that, the number of clusters per plant and 100 seed weight did have direct effects on yield in pigeonpea both at genotypic and phenotypic levels. However, days to maturity and seeds per pod had a slight direct effect on yield.

Ahuja et al. (1981) observed that, significant positive correlation of plant height with yield in pigeonpea was mainly due to indirect effects via number of pods per plant. Pods per plant were the most important character followed by seed size. Seeds per pod were observed to have a direct high negative effect on yield which was countered by indirect effect via seed size. Plant height and days to maturity had positive correlation with yield due to the indirect effects of pods per plant through productive branches. Malik et al. (1981) reported that, the characters like days to maturity, plant spread, clusters per plant and pods

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per plant as the major factors contributing towards seed yield in pigeonpea. They have stated that, the selection based on these attributes would be most advantageous in pigeonpea.

High direct and indirect effects of days to maturity, pods per plant, seeds per pod and 100 seed weight on the yield per plot of pigeonpea were observed by Balyan and Sudhakar (1985). They observed that, plant height, primary and secondary branches had high direct and indirect contributions to pods per plant. This revealed that these traits may be used for yield improvement in pigeonpea.

Dumbre and Deshmukh (1985) reported that, characters viz., pods per plant and 100 grain weight were the only direct components and days to flowering and plant height were the developmental components in pigeonpea.

Malik *et al.* (1987) observed that, the days to flowering had a high and positive direct effect on grain yield of pigeonpea. They observed that, the pods per plant had a low direct but high indirect effect on yield which revealed a high positive genotypic correlation with yield.

Marekar and Nerkar (1987) reported that, the grain yield in pigeonpea was positively and directly affected by the traits like days to first flowering, days to maturity, plant height and pods per plant. Biomass and harvest index were having the greatest positive direct effect.

Patel *et al.* (1988) observed that, the seed yield in pigeonpea was strongly associated with plant height, branches and pods per plant at genotypic level. These characters were reported to have the greatest direct effect on seed yield. Days to maturity were observed to be moderately associated with seed yield and hence, these characters were emphasized for inclusion in yield improvement programme.

Raut and Bhongale (1988) reported that, the characters like days to 50% flowering, pod weight, pod length had direct effect on seed yield in pigeonpea.

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Patil et al. (1989) conducted a path analysis study in pigeonpea and concluded that the characters like seeds per pod, days to flower, 100 seed weight, number of branches per plant and pods per plant should be given greater emphasis while selecting high yielding genotypes.

Khapre et al. (1993) observed that, the harvest index had the highest direct effect on yield of pigeonpea followed by pods per plant, plant height and days to 50% flowering. These characters therefore, should be given weightage while selecting for high yielding strains.

Salunke (1994) observed that, the characters like days to 50% flowering, days to maturity, plant height, number of pods per plant and 100 grain weight had positive direct effects on grain yield in pigeonpea.

Dahat et al. (1995) reported the direct contribution of number of primary and secondary branches and number of pods per plant to the yield both in sole crops as well as in intercrop of pigeonpea. In addition to these characters, days 50% flowering in sole crop and plant height and number of seeds per pod in intercrop showed direct contribution towards grain yield.

Paul et al. (1996) noticed that, pods per plant had highest direct effect on seed yield, followed by dry matter at maturity and 100 seed weight in pigeonpea.

Aher et al. (1997) based on path analysis in pigeonpea concluded that, the characters like viz., days to maturity, plant spread, number of pods per plant, number of seeds per pod and 100 grain weight may be of merit while making selection for developing high yielding genotypes in pigeonpea.

Thombare (1997) observed that, the characters such as plant spread, days to 50% flowering, days to maturity, number of sees per pod, 100 seed weight and number of secondary branches per plant had positive direct effects on grain yield in pigeonpea.

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Through the path analysis studies in pigeonpea Srinivas et al. (1999) concluded that, pods per plant, plant height and secondary branches per plant to be the major contributors for seed yield.

Singh et al. (1999) carried out path coefficient analysis in pigeonpea and reported that, pods per plant had the highest positive direct effect on grain yield followed by 100 grain weight, number of grains per pod and days to 50% flowering. The direct effects of the remaining characters on grain yield were negative and of low magnitudes. 100 grain weight and number of grains per pod had no correlation with grain yield per plant.

Sawant (2001) reported that, number of pods per plant, plant spread, 100 grain weight and days to 50% flowering had high direct effect on grain yield. So these are the most important yield contributing characters as revealed by path analysis.

Thanki and Sawargaonkar (2010) studied path coefficient analysis which revealed that number of pods per plant, 100-seed weight and harvest index made maximum direct contribution towards seed yield per plant. Correlations of number of pods per plant and harvest index were also significant and positive which were reflected in path analysis as high direct effects. In addition to this, number of branches per plant and plant height contributed indirectly via number of pods per plant towards seed yield per plant.

2.4 Genetic diversity in pigeonpea

Bainiwal and Jatasra (1980) reported a quantitative assessment of genetic diversity in pigeonpea for 10 characters in relation to productivity and survival. They found that maximum divergence was due to the plant height followed by pod length and days to flowering and also concluded that geographic diversity did not seem to have direct association with genetic diversity.

Asawa et al. (1981) observed a considerable amount of genotypic diversity in pigeonpea due to seeds per pod.

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Dumbre (1981) grouped 54 genotypes of pigeonpea into 21 clusters. He concluded that, there was no direct relationship between genetic and geographic diversity.

Mane (1986) observed that, genetic diversity was not necessarily related to geographic distribution. He suggested crossing programme involving distantly related clusters to seed yield improvement in pigeonpea.

Patel et al. (1988) grouped 40 strains of pigeonpea into 9 clusters by using Mahalanobis D^2 statistics. Number of secondary branches per plant, pods and clusters per plant were the main discriminatory traits between clusters.

Garten et al. (1989) grouped 58 genotypes of pigeonpea into 15 clusters. They observed no relationship between genetic diversity and geographic diversity. Henry and Krishna (1992) and Sandhu et al. (1993) also revealed that genetic diversity was not always related to geographical diversity.

Salunke (1994) grouped 54 genotypes of early pigeonpea into 12 clusters and suggested to undertake hybridization programme.

Sarma and Roy (1994) groped 42 genotypes into 8 clusters. They noticed that, the inter cluster distances were greater than intra cluster distances, revealing a considerable amount of genetic diversity among the genotypes studied. Branches per plant, harvest index and yield per plant contributed most to total genetic divergence.

Singh and Gumber (1996) reported that, the parents which were not diverse, failed to produce genetic diversity when crossed with each other. Genetically diverse genotypes fell into different clusters. When indeterminate or semi determinant parents were involved in a cross, sufficient amount of genetic diversity was produced as the F_1s, F_2s and BCs groped into different clusters.

Aher et al. (1998) observed that, the cluster means showed appreciable differences for various characters among single as well as multiple genotypic clusters. While

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selecting genotypes for hybridization from a particular cluster, the inter cluster distance, cluster mean and per se performance should be taken into consideration.

Wide range of genetic diversity was observed by Thombare (1997) among the 64 genotypes studied. They were grouped into 15 clusters. He observed that, clustering pattern did not necessarily follow geographic distribution.

Murugan et al. (2000) groped 37 genotypes of pigeonpea into 5 clusters. They observed significant difference among 37 genotypes for all the characters under study.

Sawant (2001) grouped 56 genotypes into 13 clusters. He observed substantial genetic diversity among the genotypes studied.

Sreelakshmi et al. (2010) studied for genetic divergence using Mahalanobis D^2 statistic indicated wider genetic diversity. Considerable variability was observed for days to 50% flowering, days to maturity, plant height, number of pods per plant and seed yield due to non-linear pooled deviation. The variability was low for number of primary branches per plant and test weight. Among the 7 characters studied, seed yield contributed the most (89.49%) towards the divergence of genotypes followed by number of pods per plant, days to 50% flowering and plant height. The genotypes were grouped into 8 clusters, maximum inter cluster distance being observed between the clusters III and VII (725.69). Hence, crossing of parents from these clusters would be desirable for combining earliness, short plant height, more primary branches per plant with more pod number coupled with high seed yield. The genotypes ICPL 98008, ICPHAL 4979-2 and ICP 77303 were identified as desirable and stable for days to maturity. Stability parameters along with per se performance across three kharif seasons revealed that ICPL 20036 and ICPL 20058 were stable genotypes for seed yield and were found to be suitable for low input cultivation while, ICPL 13198 was found suitable for input rich cultivation.

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3. MATERIAL AND METHODS

The present investigation entitled, Genetic variability, correlation and diversity analysis in pigeonpea [Cajanus cajan (L.) Millsp.] was conducted at Pulses Improvement Project, MPKV, Rahuri during August 2012 to February 2013, envisaged the studies on:

i) Genetic variability

ii) Correlation and

iii) Genetic diversity by D^2 statistics.

The details of the material used, method adopted and statistical analysis followed during investigation are described below:

3.1. Experimental Material:

The experimental material use for the study consisted of 50 genotypes of pigeonpea [Cajanus cajan (L.) Millsp.] from different geographic origins and showing phenotypic variability for agronomic and yield characters. Seeds of these genotypes were received from Pulses Improvement Project, MPKV, Rahuri-413 722 (M.S.)

Table 3.1 : Pigeonpea genotypes included in the study were as below:

Sr. No.	Genotype	Origin
1	PT-04-78	MPKV, Rahuri
2	PT-04-138	MPKV, Rahuri
3	PT-04-164	MPKV, Rahuri
4	PT-04-175	MPKV, Rahuri
5	PT-04-267	MPKV, Rahuri
6	PT-04-360-1	MPKV, Rahuri
7	PT-04-365	MPKV, Rahuri
8	PT-03-62	MPKV, Rahuri
9	PT-03-124	MPKV, Rahuri
10	PT-04-169	MPKV, Rahuri
11	PT-04-194	MPKV, Rahuri
12	PT-04-217	MPKV, Rahuri

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13	PT-04-221	MPKV, Rahuri
14	PT-04-230	MPKV, Rahuri
15	PT-04-259	MPKV, Rahuri
16	PT-04-261	MPKV, Rahuri
17	PT-04-264	MPKV, Rahuri
18	PT-04-292	MPKV, Rahuri
19	PT-04-312	MPKV, Rahuri
20	PT-04-316	MPKV, Rahuri
21	PT-04-321	MPKV, Rahuri
22	PT-04-329	MPKV, Rahuri
23	PT-04-336	MPKV, Rahuri
24	PT-04-356	MPKV, Rahuri
25	PT-04-373	MPKV, Rahuri
26	PT-04-378	MPKV, Rahuri
27	PT-04-382	MPKV, Rahuri
28	PT-04-386	MPKV, Rahuri
29	PT-04-391	MPKV, Rahuri
30	PT-04-257-1	MPKV, Rahuri
31	PT-04-281	MPKV, Rahuri
32	PT-04-348-2	MPKV, Rahuri
33	PT-04-415-1	MPKV, Rahuri
34	Khirpuri Local	Akola
35	PT-011-6	Nandurbar
36	PT-011-14	Navapur
37	PT-011-15	Navapur
38	PT-011-16	Navapur
39	PT-011-18	Navapur
40	PT-011-21	Nandurbar
41	PT-011-23	Navapur
42	PT-011-34	Navapur
43	PT-04-212	MPKV, Rahuri
44	PT-04-343	MPKV, Rahuri
45	PT-03-129-2	MPKV, Rahuri
46	PT-04-273	MPKV, Rahuri

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47	PT-03-148	MPKV, Rahuri
48	PT-04-31	MPKV, Rahuri
49	ICPL-87(Ch.)	MPKV, Rahuri
50	PT-0012(Ch.)	MPKV, Rahuri

3.2. Experimental design:

Fifty genotypes were evaluated in a Randomized Block Design with three replications at Pulses Improvement Project, MPKV, Rahuri-413 722 (M.S.), during August 2012 to February 2013. Each genotype was sown in single row of 3.0 m length in each replication. Spacing of 45 cm between rows and 20 cm within rows was maintained.

3.3. Cultural practices:

Land selected for experiment was medium black. The crop was fertilized at the rate of 25 kg N and 50 kg P_2O_5 per hectare as a basal dose. One irrigation was given immediately after sowing in order to ensure better germination and subsequent irrigations were given at an interval of 20-30 days.

Other cultural practices like weeding were done manually on regular basis.

3.4. Observations recorded:

3.4.1. Days to 50% flowering:

The date on which 50 per cent of the plants in a treatment flowered was recorded and the number of days from actual germination to 50% flowering were calculated.

3.4.2. Days to maturity:

The stage when maximum pods of plants in a line per plot matured was recorded and the numbers of days from actual germination to physiological maturity were calculated.

3.4.3. Plant height (cm):

Plant height at maturity was recorded from ground level to the growing tip of the main shoot in centimeters.

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3.4.4. Plant spread (cm):

Maximum spread of the plant was measured at maturity.

3.4.5. Primary branches per plant:

Total number of primary branches borne on the main shoot of the plant were recorded at maturity.

3.4.6. Secondary branches per plant:

Total numbers of fruiting branches on the primary branches of the plant were recorded at maturity.

3.4.7. Pods/plant:

Total numbers of matured pods on the plant were recorded at maturity.

3.4.8. Seeds/pod:

The total numbers of filled seeds from five randomly selected fully developed pods from the observational plants were counted to work out the number of seeds per pod at maturity.

3.4.9. 100 seed weight (g):

Weight of 100 seed from random individual plant was recorded.

3.4.10. Seed Yield/plant (g):

Weight of seeds harvested from individual plant was recorded in gm.

3.4.11. Harvest index (%):

Harvest index was estimated by calculating ratio of economic yield to the biomass of plant.

3.4.12. Incidence of SM (sterility mosaic) (%):

Incidence of SM was recorded at flowering stage.

3.4.13. Reaction to pod borer (%):

It was recorded at harvesting by calculating pod damage percentage.

3.4.14. Wilt (%):

Incidence of wilt was recorded during every growth stages.

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3.4.15. Protein content (%):

Protein content of seed was estimated by taking 100 gm seed in spectrometer protein analyser.

3.5. Statistical analysis:

The mean values of five randomly selected plants for fifteen different characters were used for statistical analysis. The following statistical parameters were calculated for presentation of data on different quantitative attributes.

3.5.1. Analysis of variance:

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1967). Mean values of the plants selected in each replication were used for statistical analysis. The analysis of variance is set out under ANOVA.

Table 3.2 : ANOVA:

Sr. No.	Source of variation	d. f.	MSS	F ratio	Table value t at 5% or 1% level
1	Replications	(r-1)	Mr	Mr / E	
2	Treatments	(t-1)	Ms	Ms / E	
3	Error	(r-1)(t-1)	E	-	
4	Total	(rt-1)	-	-	

Where,

r : Number of replications

t : Number of treatments

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3.5.2. Estimation of components of variability:

a) Mean:

The mean value for each character was worked out by using following formula:

$$\bar{X} = (1/n)\left(\sum_{i=1}^{n} Xi\right)$$

Where,

Xi : Sum total of the character

n : Number of observations

b) Range:

The lowest and the highest values of mean for each character represented the range.

3.5.2.1 Estimation of standard error of mean, standard error of difference and critical difference:

The SE of mean difference was calculated as follows:

i) SE of mean [SE(m)] = $\sqrt{\sigma^2 e / r}$

ii) The standard error of difference between two means was calculated as:
SE difference =SE (m) x $\sqrt{2}$

iii) The critical difference between only two means was calculated as:
CD = SE (d) x t 5% (at error d.f.)

3.5.2.2 Estimation of components of variation:

The phenotypic and genotypic variances were calculated by utilizing the respective mean square values (Johnson et al. 1955).

i) Environmental Variance ($\sigma^2 e$) = MSe

ii) Genotypic Variance ($\sigma^2 g$) = (MSg - MSe)/r

iii) Phenotypic Variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where,

MSg : Genotypic mean sum of square

MSe : Error mean sum of square

r : Number of replications

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3.5.2.3 Estimation of coefficients of variation:

The genotypic and phenotypic coefficients of variation were calculated by following Burton and Devane (1953).

i) Genotypic coefficient of variation (GCV):

$$GCV = \sqrt{{}^2g / \bar{X} \times 100}$$

Where,

^2g : Genotypic variance

$\bar{X}$: General mean of the characters

ii) Phenotypic coefficient of variation (PCV):

$$PCV = \sqrt{{}^2p / \bar{X} \times 100}$$

Where,

^2p : Phenotypic variance

$\bar{X}$: General mean of the characters

3.5.2.4 Estimation of Heritability (Per cent):

Heritability (broad sense) was calculated according to the method suggested by Hanson et al., (1956) for each character as:

$$\text{Heritability (b. s.)} = \frac{\tilde{A}^2g}{\tilde{A}^2p} \times 100$$

Where,

$\tilde{A}^2g$: Genotypic variance

$\tilde{A}^2p$: Phenotypic variance

3.5.2.5 Genetic advance:

Genetic advance was calculated by the formula suggested by Johnson et al. (1955).

$$G.A. = ({}^2g / {}^2p) \times p \times K \text{ or}$$

$$G.A. = K \times h^2 \text{ (b. s.)} \times p$$

$$\text{G.A. as percentage of mean} = \frac{GA}{\bar{X}} \times 100$$

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Where,

^2g : Genotypic variance

^2p : Phenotypic variance

p : Phenotypic standard deviation

K : Selection differential at 5 per cent selection intensity (i.e. 2.06)

h^2 (bs) : Heritability broad sense

$\bar{X}$: Mean of the character.

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

Less than 10% : Low

10 20% : Moderate

More than 20% : High

3.5.3 Correlations:

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by following Singh and Chaudhari (1977).

3.5.3.1 Phenotypic correlation coefficient (r_p):

It is derived by

$$r_{p\,1.2} = \frac{\text{Covariance } (X.Y)_p}{\sqrt{\text{Variance } X_p \times \text{Variance } Y_p}}$$

Where,

$r_{p1.2}$: Phenotypic correlation between character X and Y,

p : Phenotypic

3.5.3.2 Genotypic correlation coefficient (r_g):

It is derived by as follows:

$$r_{g\,1.2} = \frac{\text{Cov } (X.Y)_g}{\sqrt{\text{Variance } X_g \times \text{Variance } Y_g}}$$

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Where,

$r_{g.1.2}$: Genotypic correlation between character X and Y

g : Genotypic

The significance of the phenotypic and genotypic correlation coefficients were tested by t test (Panse and Sukhatme, 1985)

$$t = r \sqrt{(n - 2) / 1 - r^2}$$

Where,

r : Correlation coefficient

n : Total number of observations

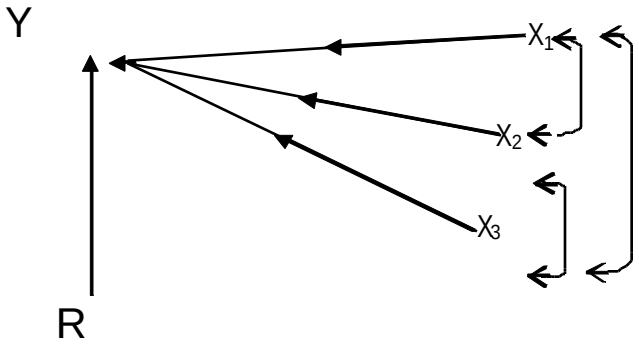
The calculated t value was tested with table t value for respective (n-2) degrees of freedom for significance.

Significance of various correlation coefficient at 1 and 5 per cent level of significance were tested by Fisher and Yates (1963) table.

3.5.4 Path coefficient analysis

To establish cause and effect relationship, the genotypic and phenotypic correlation coefficients were partitioned in to direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

The second step in the path analysis is to prepare the path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as the effect and various yield contributing characters like X_1, X_2, X_3 as casual factors. These components showed following type of association with each other.



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In path diagram yield is the result of X_1, X_2, X_3 and some other undefined factors designated by R. The double arrow lines indicated natural association as measured by correlation and the single arrows represents direct influence as measured by path coefficient P_{ij}.

Path coefficients were obtained by solving a set of simultaneous equations:

$r_{ny} = P_{ny} + r_{n2}P_{2y} + r_{n3}P_{3y} + \& \& \& \& \& \& \& \& ..$

Where,

r_{ny} : represents the correlation between n^{th} character and yield.

P_{ny} : represents the path coefficient between the n^{th} character and yield,

r_{n2} : represents correlation between n^{th} character and second character.

Matrix A Matrix B

$$r_{1y} \qquad r_{11}\, r_{12}\, r_{13} \ldots r_{1n}$$
$$r_{2y} \qquad r_{21}\, r_{22}\, r_{23} \ldots r_{2n}$$
$$r_{r3y} \qquad r_{n1}\, r_{n2}\, r_{n3} \ldots 1$$

Where,

$r_{12} = r_{21}$ and so on and r_{1y} represents correlation between one component character and yield.

The B matrix was inverted $[B]^{-1}$ and path coefficients (P_{ij}) were obtained as:

$(P_{ij}) = A \times [B]^{-1}$

The indirect effect of a particular character through other characters was obtained by multiplication of direct paths and particular correlation coefficient between the characters separately.

Indirect effect = $r_{ij} \times P_{ij}$

Where,

i : 1 to 9

j : 1 to 10

P_{ij} : $P_{1y}.P_{2y}\& \& . P_{ny}$

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Path coefficients (P_{ij}), correlation coefficient (r_{ij}) and residual factors (R) were diagrammatically presented. The residual factor, i.e. variation in yield uncounted for by these associations, was calculated from the following formula.

Residual factor (R) = $\sqrt{(1 \quad R^2)}$

Where,

$R^2 = P_{1y}.r_{1y} + P_{2y}.r_{2y} + P_{3y}.r_{3y} + \& \& .. + P_{ny}.r_{ny}$

Where,

P_{1y}, P_{2y} & & & & & & . P_{ny} = Path values

r_{1y}, r_{2y} & & & & & & . r_{ny} = Correlation coefficients.

3.5.5 Genetic diversity

D^2 analysis

The analysis of divergence was carried out by D^2 statistics of Mahalanobis (1928, 1936) as described by Rao (1952). Analysis of variance for individual characters studied was worked out as per Random Block Design to test the significance among genotypes. The characters exhibiting significant differences were only used for further analysis of D^2 statistic. The analysis of covariance for character pairs, based on plot averages was carried out (Cochran and Cox, 1957).

a) Wilk s criteria

After testing for differences from population, a simultaneous test of significance of difference in the mean values of a number of correlated variables with regard to the pooled effect of fifteen characters considered together was carried out using Wilks criteria (Wilk, 1932) which was estimated using the relationship.

$$= \frac{|E|}{|E+V|}$$

Where, |E| is the determinant of experimental error sum of squares and sum of products matrix and |E+V| the determinant

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of experimental error sum of squares and sum of products plus the population sum of squares and product matrix significance of was estimated by X^2 as:

$$X^2_{pq} = V = -m.\log_e$$

Where,

$$m = n - \frac{(p+q+1)}{2}$$

Where,

n : N_1 + & & & &+NK-1 = Total number of observations-1

p : Number of characters

q : K-1

K : Number of varieties

b) Mahalanobis generalized distance:

The generalized distance between two populations is defined by Mahalanobis (1936) as:

$$D^2 = D^2 = ?? \text{ » } i.j.\ di.\ dj.$$

Where,

» i.j : Reciprocal matrix to the common dispersion matrix

di : Difference between the mean values of two population for i^{th} character

dj : Difference between the mean values of the two populations for the j^{th} character.

c) Computation of D^2 values

For each combination, mean deviation i.e. $\bar{Y}_i^1 \quad \bar{Y}_i^2$ with i=1, 2, & & p, was computed and the D^2 was calculated as sum of the squares of these deviations i.e. $(\bar{Y}_i^1 \quad \bar{Y}_i^2)^2$.

d) Determination of population constellations

No rules can be laid down for finding the clusters because cluster is not a well defined term. The only criteria appears to be that, any two genotypes belonging to the same clusters should be

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same clusters should be at least, on an average show a smaller D^2 values than those belonging to two different clusters.

A simple method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related genotypes and find a third genotype which had the smaller average D^2 value from the first two. Similarly the fourth genotype is chosen to have the smaller average D^2 value from the first three and so on. While proceeding further for the cluster formation, if at any stage, the average D^2 value of a genotype appears to be high than those already listed, then this genotype does not fit in that former group and taken to be outside of that cluster. The varieties included in the first cluster are then omitted and the rests are treated similarly to form next cluster.

e) Average intra cluster distances

The intra cluster distances were calculated as:

$$D^2_i / n$$

Where, D^2_i : sum of distance between all possible combinations of (n) genotype included in cluster.

n : number of genotypes included in a cluster.

f) Average inter cluster distance

The procedure followed for calculating the inter cluster distances was first to measure the distance between cluster I and II, between I and III, between I and IV and so on, likewise the clusters were one by one and the distance from other clusters were calculated. The average inter cluster distances were then calculated as:

$$D^2_i / (n_i n_j)$$

Where,

n_i : Number of genotypes in cluster i and

n_j : Number of populations in cluster j

The intra and inter cluster distances (D) values were obtained by taking square root of average D^2 values of the respective genotypes.

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g) Cluster diagram

With the help of D values between the clusters, a diagram showing the relationships between different genotypes was drawn.

3.5.5.1 Genetic diversity as an index for selecting desirable parents for hybridization

The possible limits to parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandiopadhyay (1984). They advised to delineate the divergence among parents into four divergence classes. To take into account the variable magnitude of variation in parental divergence, the mean (m) and standard deviation (s) of the values of divergence were calculated. The divergence classes were defined as follows:

DC_1 = D > or = m+s

DC_2 = D < (m+s) and > or = m

DC_3 = D > or = (m-s) and < m

DC_4 = D > (m-s)

They postulated that two parents whose genetic divergence falls between (m-s) and (m+s) i.e. in the classes DC_2 and DC_3 when crossed have higher chances of producing high frequency and magnitude of heterosis when compared to a cross whose parental divergence fall outside the limits [(m-s), (m+s)].

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5. DISCUSSION

Plant breeding deals with the management of genetic variability. Hence, the assessment of genetic variability in the available germplasm is of immense value to design a selection procedure and to identify the superior genotypes. It is, therefore, necessary to classify and utilize this variability systematically for genetic upgradation of biological population. Similarly, the assessment of magnitude and direction of association between different yield contributing characters especially with yield, is also useful in selecting desired genotype on the basis of their genotypic values. Simple correlation coefficients in the direction, are of limited value. Hence, it is important to study the cause and effect relationship between yield and its component characters.

In plant breeding, genetic diversity plays an important role because, hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related patterns. D^2 statistics is one of the potent techniques of measuring genetic divergence.

In the present investigation, 50 genotypes of pigeonpea were assessed to know the correlation among 15 characters and also the nature and extent of genetic divergence among the genotypes as well as the interrelationships among various seed yield components. The results obtained are presented in chapter 4 and discussed in this chapter.

5.1 Variability and genetic parameters

There can be little doubt that the existence of genetic variability is advantageous to evolutionary survival of a species. Yield improvement in any crop can be brought through plant breeding but necessarily variability upon which selection is to be practiced must be available in the genetic material. Therefore, before embarking on any plant breeding, a plant breeder must survey and assess

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survey and assess variability present, with respect to yield and its attributes. The variability for a given characters can be estimated through variance, coefficients of variability (GCV, PCV), heritability and genetic advance.

5.1.1 Range of variability

A wide range of variability was observed almost for all characters studied (Table 4.3). A wide range of variability was also observed by Rathnaswamy *et al.* (1973), Chandra *et al.* (1975), Shoran (1983), Thombare (1997) and Sreelakshmi *et al.* (2010). Presence of high variation for all the important yield contributing characters studied, indicating great scope to selections of desirable types.

5.1.2 Genotypic and phenotypic coefficients of variation

The estimates of GCV and PCV for all the characters studied showed little differences, the later being slightly greater than the former, thus indicating that, the variability existing in these characters was mainly due to genetic factors (Table 4.3).

The estimates of genotypic as well as phenotypic coefficients of variation in the present study were highest for the incidence of sterility mosaic, followed by wilt percentage, secondary branches per plant and seed yield per plant, while GCV and PCV values were lowest for the protein content, followed by days to maturity. Rathnaswamy *et al.* (1973) observed high estimates of GCV for the characters like clusters per plant, number of pods per plant and plant height, while it was lowest for days to maturity. Malhotra and Sodhi (1977) observed highest GCV for branches per plant followed by grain yield, cluster number and pod number per plant. Singh and Srivastav (1977) observed maximum GCV for number of secondary branches followed by yield and 100

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and 100 grain weight. Bainiwal et al. (1981) observed maximum variability for secondary branches followed by primary branches and seed yield in pigeonpea.

5.1.3 Heritability (broad sense) and genetic advance

Genetic coefficient of variation alone would not indicate proportion of total heritable variation. However, the heritability estimates were better indication of heritable portions of the variation. The heritability (bs) percentage includes the contribution of additive gene effects, allelic interactions due to dominance and non allelic due to epistasis.

Very high estimates of variability were obtained for almost all characters studied in the present investigation. Rathnaswamy et al. (1973), Awatade et al. (1980), Sidhu et al. (1985), Salunke (1994) and Thombare (1997) also reported high estimates of heritability in almost all characters, confirming the present results.

The character with high heritability associated with high genetic gain may be attributed to the additive gene effects and can easily be improved by selection (Panse, 1967). On the other hand, the traits exhibiting high heritability and low genetic gain may be governed by non additive gene effects (dominance and epistasis). The characters showing such inheritance can be improved through hybridization. The low heritability estimates suggest that the selection for such characters will not be much effective.

In the present investigation, incidence of sterility mosaic, wilt percentage, secondary branches per plant, seed yield per plant, plant spread, pods per plant, primary branches per plant and reaction to pod borer expressed high estimates of heritability (bs) accompanied by high genetic advance as a percentage of mean (Table 4.3) indicating that these traits were predominantly governed by additive gene action and selection of these traits would be more

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traits would be more effective for desired genetic improvement. This confirming the results of Balyan and Sudhakar (1985), Khapre et al. (1993), Salunke (1994), Thombare (1997) and Chandirakala and Subbaraman (2010). However, days to 50 % flowering, days to maturity, plant height, seeds per pod, 100 seed weight, harvest index and protein content exhibited high heritability accompanied by lower genetic advance as a percentage of mean which suggest that, variability for these traits was probably due to non additive gene action indicating limited scope for improving these characters through phenotypic selection. Thombare (1997) reported high heritability and low genetic advance for number of seeds per pod, 100 seed weight, days to maturity and number of pods per plant.

Thus, considering the estimates of genetic parameters like GCV, heritability and genetic advance as a percentage of mean together, incidence of sterility mosaic, wilt percentage, secondary branches per plant, seed yield per plant, plant spread, pods per plant are the important characters showing the additive gene action. Selection for these traits in segregating generations would be more effective for improvement of seed yield per plant.

5.2 Correlation studies

Correlated characters are of interest for three chief reasons, firstly, in connection with genetic cause of correlation through the pleiotrophic action of the genes, secondly, in connection with the change brought by selection. It is important to know how the improvement of one character will cause simultaneous changes in other character and thirdly in connection with natural selection.

The value of correlation coefficients cannot be constant. It varies considerably according to kind of material handled and environmental conditions in which material

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material grown even though the material used is the same, the environmental conditions including fertilization, plant population and cultural practices changes the values of correlation coefficients considerably. All correlations are depends upon poor soil and increased fertility stands to decrease variability.

In the improvement of any crop, yield is the most important character that has to be taken into consideration. The knowledge of inter relationships among the characters especially with yield is therefore, useful to the plant breeder for improving the efficiency of selection program. The phenotypic correlation indicates the extent of the observed relationship between two characters. This does not give a true genetic picture of the relationship, because it indicates the effects of both heredity as well as environmental influences. Genotypic correlations provide us the estimates of an inherent association between genes controlling two characters. Hence, it is of greater significance and can effectively be utilized in formulating an effective selection theme. The estimates of correlation coefficients may also help to identify the characters that prove to be of little or no importance in the selection program.

In the present studies, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients (Table 4.3) among all the characters studied. This indicates that, there was a strong inherent association between the various characters studied and the same was less influenced by environmental variations.

A strong significant positive association was observed between the seed yield per plant with plant height, plant spread, primary branches per plant, secondary branches per plant, pods per plant and seeds per pod at genotypic and phenotypic levels. Similar results were also observed

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results were also observed by Joshi (1973), Awatade et al. (1980), Singh et al. (1981), Sidhu et al.(1985), Bhongale and Raut (1987), Khapre and Nerkar (1992), Singh and Gumber (1995), Salunke et al. (1995), Srinivas et al. (1999), Sawant (2001) and Chandirakala and Subbaraman (2010).

A strong positive but non significant association was observed between the seed yield per plant with days to 50 % flowering, days to maturity and 100 seed weight at genotypic and phenotypic levels. Similar results were also observed by Wagh (1976), Srinivas et al. (1999).

A strong negative and significant correlation was found between the seed yield per plant with wilt percentage, reaction to pod borer and negative correlation with incidence of sterility, harvest index and protein content both at genotypic and phenotypic levels. Similar results were also observed by Pandey and Singh (2002) and Linge et al. (2010).

Days to 50 % flowering showed significant and positive correlation with days to maturity, plant height, plant spread, secondary branches per plant genotypic and phenotypic levels, indicating that there was certain inherent relationship between these characters, while positive correlation with pods per plant and incidence of sterility mosaic. Salunke et al. (1995), similarly reported that, the yield components viz., days to 50 % flowering, days to maturity, plant height, plant spread, primary branches per plant, secondary branches per plant and 100 grain weight were positively and significantly associated among themselves.

A strong negative but significant correlation was found between the days to 50 % flowering with protein content and negative correlation with primary branches per plant, seeds per pod, 100 seed weight, wilt percentage, reaction

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percentage, reaction to pod borer and harvest index at both levels. Similar results were also observed by Pandey and Singh (2002) and Linge et al. (2010).

Days to maturity had shown highly significant and positive genotypic and phenotypic correlation with plant height, plant spread, secondary branches per plant, while positive correlation with pods per plant, incidence of sterility mosaic and reaction to pod borer. Salunke et al. (1995), similarly reported that, the yield components viz., days to 50 % flowering, days to maturity, plant height, plant spread, primary branches per plant, secondary branches per plant and 100 grain weight were positively and significantly associated among themselves.

A strong negative but significant correlation was found between the days to maturity with seeds per pod, harvest index and protein content, while negative correlation with primary branches per plant, 100 seed weight, wilt percentage at both levels. Such type of correlation was found for the first time.

Plant height had positive and significant genotypic and phenotypic correlation with plant spread, secondary branches per plant, pods per plant, 100 seed wt., while positive correlation with primary branches per plant, seeds per pod. Similar results were also observed by Pandey and Singh (2002) and Linge et al. (2010).

A strong negative but significant correlation was found between the plant height with harvest index and protein content, while negative correlation with incidence of sterility mosaic, wilt percentage and reaction to pod borer. Similar observations were recorded by Dhameliya and Pathak (1994) and Linge et al. (2010).

Plant spread showed positive genotypic and phenotypic correlation with secondary branches per plant, pods per plant, 100 seed weight, while positive correlation with incidence of sterility mosaic and reaction to pod borer at

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to pod borer at both levels. Salunke et al. (1995), similarly reported that, the yield components viz., days to 50 % flowering, days to maturity, plant height, plant spread, primary branches per plant, secondary branches per plant and 100 grain weight were positively and significantly associated among themselves.

A strong negative but significant correlation was found between the plant spread harvest index, protein content and negative correlation with primary branches per plant, wilt percentage at both levels. Such type of correlation was found for the first time.

Primary branches per plant showed positive and significant genotypic and phenotypic correlation with secondary branches per plant, pods per plant, incidence of sterility mosaic, while positive correlation with 100 seed weight, wilt percentage and protein content. Similar results were obtained by Linge et al. (2010).

A strong negative correlation was found between the primary branches per plant with seeds per pod, reaction to pod borer and harvest index both at genotypic and phenotypic level. Such type of correlation was found for the first time.

Secondary branches per plant showed positive and significant genotypic and phenotypic correlation with pods per plant and seeds per pod, while positive correlation with incidence of sterility mosaic and wilt percentage. Similar results were obtained by Linge et al. (2010).

A strong negative and significant correlation was found between the secondary branches per plant with protein content and negative correlation with 100 seed weight, reaction to pod borer and harvest index both at genotypic and phenotypic level. Such type of correlation was found for the first time.

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Pods per plant showed positive and significant genotypic and phenotypic correlation with incidence of sterility mosaic, wilt percentage, while positive correlation with 100 seed weight. Such type of correlation was found for the first time.

A strong negative and significant correlation was found between the pods per plant with reaction to pod borer, protein content and negative correlation with harvest index. Similar results were obtained by Khandwe et al. (1998) and Linge et al. (2010).

Seeds per pod showed positive genotypic and phenotypic correlation with 100 seed weight, incidence of sterility mosaic and harvest index. Such type of correlation was found for the first time.

A strong negative and significant correlation was found between the seeds per pod with wilt percentage and negative correlation with reaction to pod borer, protein content at both levels. Such type of correlation was found for the first time.

100 seed weight showed positive and significant genotypic and phenotypic correlation with incidence of sterility mosaic. Similar results were obtained by Linge et al. (2010), while it had negative but significant correlation with harvest index, protein content and negative correlation with wilt percentage and reaction to pod borer at both levels. Such type of correlation was found for the first time.

Incidence of sterility mosaic showed negative genotypic and phenotypic correlation with wilt percentage, reaction to pod borer, harvest index and protein content. Such type of correlation was found for the first time.

Wilt percentage showed positive and significant genotypic and phenotypic correlation with protein content and positive correlation with harvest index, while negative

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index, while negative correlation with reaction to pod borer at both levels. Such type of correlation was found for the first time.

Reaction to pod borer showed positive correlation with protein content, while it was negatively correlated with harvest index both at genotypic and phenotypic levels. Such type of correlation was found for the first time.

Harvest index showed positive correlation with protein content both at genotypic and phenotypic levels. Such type of correlation was found for the first time.

Thus, to summarize, the characters viz., plant height, plant spread, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, days to 50 % flowering, days to maturity and 100 seed weight were significantly and positively correlated with seed yield per plant and with each other except few which could be due to modifying effects of the environment. However, the characters like wilt percentage, reaction to pod borer, incidence of sterility mosaic, harvest index and protein content were significantly and negatively correlated with seed yield per plant and with each other except few which could be due to modifying effects of the environment. Therefore, the desirable plant type in pigeonpea with high seed yield potential should have more height, more plant spread, more number of primary branches per plant, more number of secondary branches per plant, more number of pods per plant, more number of seeds per pod, more days to 50 % flowering, more days to maturity and high 100 seed weight, but simultaneously it should have resistance to pod borer, wilt, incidence of sterility mosaic and high harvest index, protein content. Similar types of results were reported by Aher et al. (1997), he proposed that characters viz., days to maturity, plant spread, number of pods per plant, number of seeds per pod and

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number of pods per plant, number of seeds per pod and 100 grain weight should be considered while making selection for developing high yielding genotypes in pigeonpea.

5.3 Path coefficient analysis

Genotypic path coefficient analysis outlined by Dewey and Lu (1959) was carried out to find out the direct and indirect effects of yield components on grain yield.

Direct effect of any component character on seed yield gives an idea about the reliability of indirect selection to be made through that characters to bring about improvement in seed yield. If the correlation coefficient between a causal factor and the effect is equal to its direct effect, then correlation explains the true relationship and a selection for that trait will be effective. If the final correlation coefficient is positive, but the direct effect is negative or negligible, in such relation the indirect causal factors are to be considered simultaneously for selection. When correlation coefficient is negative but the direct effect is positive and high, a restricted simultaneous selection model is to be followed i.e. restriction are to be imposed to emulsify the undesirable indirect effects in order to make use of direct effects. The residual effect determines how best the causal factors accounts for the variability of the dependent factor, the seed yield per plant in this case.

In the present investigation, days to maturity, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, 100 seed weight, harvest index and protein content had positive direct effects, while days to 50 % flowering, plant height, plant spread, incidence of sterility mosaic, wilt percentage and reaction to pod borer had negative direct effects on seed yield per plant.

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Days to maturity had high positive direct effect on seed yield. Its association with seed yield was positive and highly significant. Its positive indirect effects via secondary branches per plant, pods per plant were also observed. Malik et al. (1981) observed similar results and Thanki et al. (2010) observed similar results at phenotypic level.

Primary branches per plant had high positive direct effect on seed yield. Its association with seed yield was positive and highly significant. Its positive indirect effects via days to 50 % flowering, plant spread, secondary branches per plant, pods per plant, 100 seed weight, wilt percentage, reaction to pod borer and protein content were also observed. Ram et al. (1976) observed similar results.

Secondary branches per plant had high positive direct effect on seed yield. Its association with seed yield was positive and highly significant. Its positive indirect effects through days to maturity, primary branches per plant, pods per plant, seeds per pod, wilt percentage, reaction to pod borer were also observed. Veerswamy et al. (1973) observed similar results.

Pods per plant had high positive direct effect on seed yield. Its association with seed yield was positive and highly significant. Its positive indirect effects through days to maturity, primary branches per plant, secondary branches per plant, seeds per pod, 100 seed weight, wilt percentage, reaction to pod borer were also observed. Pokale and Mohatkar (1975), Sharma and Asawa (1977) and Thanki et al. (2010) observed similar results.

Seeds per pod had high positive direct effect on seed yield. Its association with seed yield was positive and highly significant. Its positive indirect effects through days to 50 % flowering, plant spread, secondary branches

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per plant, pods per plant, 100 seed weight, reaction to pod borer, harvest index were also observed. Chandirakala and Subbaraman (2010) and Thanki *et al.* (2010) observed similar results.

100 seed weight had positive direct effect on seed yield. Its association with seed yield was positive. Its positive indirect effects through days to 50 % flowering, primary branches per plant, pods per plant, seeds per pod and reaction to pod borer were also observed. Balyan and Sudhakar (1985) and Thanki *et al.* (2010) observed similar results.

Harvest index had positive direct effect on seed yield. Its association with seed yield was negative. Its positive indirect effects through days to 50 % flowering, plant height, plant spread, seeds per pod, incidence of sterility mosaic, wilt percentage, reaction to pod borer and protein content were also observed. Khapre *et al.* (1993) and Thanki *et al.* (2010) observed similar results.

Protein content had positive direct effect on seed yield. Its association with seed yield was negative. Its positive indirect effects through days to 50 % flowering, plant height, plant spread, primary branches per plant, incidence of sterility mosaic, wilt percentage, and harvest index were also observed.

Days to 50 % flowering had negative direct effect on seed yield. Its association with seed yield was positive. This may be due to its positive indirect contribution to seed yield through days to maturity, secondary branches per plant, pods per plant and reaction to pod borer. Thanki *et al.* (2010) observed similar results at phenotypic level.

Plant height had negative direct effect on seed yield. Its association with seed yield was positive and highly significant. This may be due to its positive indirect contribution to seed yield through days to maturity,

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primary and secondary branches per plant, pods per plant, seeds per pod, 100 seed weight, incidence of sterility mosaic and reaction to pod borer. Ram et al. (1976) observed that plant height contributed indirectly to the yield as its direct effect was negative. Sawant (2001) and Thanki et al. (2010) observed negative direct effect of plant height on seed yield.

Plant spread had negative direct effect on seed yield. Its association with seed yield was positive. This may be due to its positive indirect contribution to seed yield through days to maturity, primary and secondary branches per plant, pods per plant, seeds per pod and 100 seed weight.

Incidence of sterility mosaic had negative direct effect on seed yield. Its association with seed yield was negative. This may be due to its negative indirect contribution to seed yield through days to 50 % flowering, plant spread, wilt percentage, harvest index and protein content.

Wilt percentage had negative direct effect on seed yield. Its association with seed yield was negative and significant. This may be due to its negative indirect contribution to seed yield through days to maturity, plant spread, primary and secondary branches per plant, pods per plant, seeds per pod and 100 seed weight.

Reaction to pod borer had negative direct effect on seed yield. Its association with seed yield was negative and significant. This may be due to its negative indirect contribution to seed yield through plant spread, primary and secondary branches per plant, pods per plant, seeds per pod, 100 seed weight, wilt percentage and harvest index.

Considering both, the correlation coefficients and path coefficients, it can be concluded that, plant height, plant spread, days to maturity, primary branches per plant,

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per plant, secondary branches per plant, pods per plant, seeds per pod and days to 50 % flowering, wilt percentage and reaction to pod borer are the important yield contributing characters and should be given due importance during selection as they were correlated significantly with seed yield per plant and also themselves.

5.4 Genetic divergence

When genetically diverse parents are crossed, they known to produce heterotic F_1 and also yield a spectrum of transgressive segregates in segregating generations. A set of 50 genotypes of pigeonpea under study therefore, assessed for genetic diversity for 15 different growth and yield contributing characters.

5.4.1 Diversity based on set of fifteen characters

Analysis of variance (Table 4.2) revealed highly significant differences among the genotypes for all the characters under study. Hence the D^2 values were estimated as per Mahalanobis (1928) and (1936) and described by Rao (1952), based on 15 characters. The minimum and maximum D^2 values were observed between the pair of genotypes, PT-04-415-1 and PT-04-382 (104.6) and ICPL-87 and PT-04-360-1 (11047.96), respectively. It showed the adequate diversity between the genotypes.

5.4.2 Cluster formation

The aim of cluster formation and estimation of intra and inter cluster divergence is to provide the basis for selecting better parents for the hybridization program. The theoretical concept behind such grouping is that, the genotypes grouped into same cluster presumably are less diverse from each other than those belonging to different clusters (Rao, 1952). The crossing between the genotypes belonging to the same clusters is not expected to give desired heterotic response. Consequently the parents

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Consequently the parents selected for crossing should belong to different clusters. Greater is the inter cluster differences, wider is the genetic diversity in the genotypes included in those clusters. Thus, while selecting the parents for hybridization, consideration must be given on genetic diversity, *per se* performance of parents and the cluster mean for the character for which genetic improvement is sought.

50 genotypes included in the present investigation were grouped into 9 clusters (Table 4.8). 40 genotypes of pigeonpea studied by Patel *et al.* (1988) were grouped into 9 clusters, while 54 genotypes of early pigeonpea studied by Salunke (1994) were grouped in 12 clusters. Murugan *et al.* (2000) groped 37 genotypes of pigeonpea into 5 clusters. 56 genotypes of pigeonpea studied by Sawant (2001) were grouped into 13 clusters and 30 genotypes of pigeonpea were grouped into 8 clusters by Sreelakshmi *et al.* (2010).

In the present studies, cluster number I was the largest cluster comprising of 27 genotypes, followed by cluster number II (9 genotypes), cluster number VI (4 genotypes), cluster number III and VIII (3 genotypes in each) and cluster number IV, V, VII and IX (1 genotype in each).

The clustering pattern obtained in the present study, confirmed that the genetic diversity is not necessarily parallel to the geographic diversity. In the present investigation, the genotypes originating from different geographical areas were sometimes included in the same cluster, whereas different genotypes collected from the same area were grouped into different clusters. Bainiwal and Jatasra (1980), Asawa *et al.* (1981), Mane (1986), Patel *et al.* (1988), Henry and Krishna (1992), Sandhu *et al.* (1993), Sawant (2001) and Sreelakshmi *et al.* (2010) reported the similar results.

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The maximum inter cluster distance was observed between cluster VI and IX (D = 94.91), followed by cluster V and IX (D = 92.37) and cluster IV and IX (D = 84. 38) and cluster VIII and IX (D = 78.33). This shows that, these genotypes are having the maximum genotypic variation. Highest cluster distance between cluster VI and IX is 94.91, hence, the genotypes under cluster VI and IX will be utilized for further hybridization program in diallel or L x T mating system.

The cluster means are presented in Table 4.9, considering the cluster means or the various clusters which can provide the desired parents for hybridization programs for improvement in the characters are shown against them and are listed below:

Table 5.1 : Clusters with best parents for hybridization:

Sr. No.	Characters	Source clusters
1	Days to 50 % flowering (Early)	IX, III
2	Days to maturity (Early)	IX, III
3	Plant height (Tall)	V, VI
4	Plant spread (Maximum)	IV, VI
5	Primary branches per plant (Maximum)	VIII, VI
6	Secondary branches per plant (Maximum)	VII, VIII
7	Pods per plant (Maximum)	III, VIII
8	Seeds per pod (Maximum)	V, IV, IX
9	Seed yield per plant (Maximum)	III, VIII
10	100 grain weight (high)	VIII, VI
11	Incidence of SM (Minimum)	I , III, IV, V, VII, IX
12	Wilt (Minimum)	IV, IX
13	Reaction to pod borer (Minimum)	III, VIII
14	Harvest index (Maximum)	VII, IX
15	Protein content (Maximum)	IX, II

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On the basis of inter cluster distance, cluster means and per se performance observed in the present study, the tentative hybridization program (Table 5.2) is suggested, which involving the genotypes so that the better recombinants may be obtained in the segregating generations and as the most of the characters are showing the additive gene action, selection for these characters will be more effective.

Table 5.2 : Suggested future hybridization programme on the basis of cluster means and per se performance

Sr. No.	Characters to be improved	Cluster combinations with inter cluster distance	Possible crosses
1	Earliness	IX x VI (94.91)	ICPL-87 x PT-04-267 ICPL-87 x PT-04-360-1
		III x I (43.4)	PT-04-78 x PT-04-138 PT-04-78 x PT-04-164
2	Plant height (cm)	V x IX (92.37)	PT-04-343 x ICPL-87
		VI x IX (94.91)	PT-04-267 x ICPL-87
3	Plant spread (cm)	IV x IX (84.88)	PT-04-230 x ICPL-87
		VI x IX (94.91)	PT-04-360-1 x ICPL-87
4	Primary branches per plant	VIII x IX (78.33)	PT-03-62 x ICPL-87
		VI x IX (94.91)	PT-04-221 x ICPL-87
5	Secondary branches per plant	VII x IX (64.45)	PT-03-129-2 x ICPL-87
		VIII x IX (78.33)	PT-04-261 x ICPL-87

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6	Pods per plant	III x I (43.4)	PT-04-264 x PT-04-365 PT-04-264 x PT-011-21
		VIII x IX (78.33)	PT-04-386 x ICPL-87
7	Seeds per pod	V x IX (92.37)	PT-04-343 x ICPL-87
		IV x IX (84.88)	PT-04-230 x ICPL-87
		IX x VI (94.91)	ICPL-87 x PT-04-267 ICPL-87 x PT-04-360-1
8	Seed yield per plant	III x I (43.4)	PT-04-329 x PT-04-169 PT-04-329 x PT-04-217
		VIII x IX (78.33)	PT-03-62 x ICPL-87
9	100 grain weight (high)	VIII x IX (78.33)	PT-04-261 x ICPL-87
		VI x IX (94.91)	PT-04-348-2 x ICPL-87
10	Resistance to SM	I x VIII (50.48)	PT-04-138 x PT-03-62 PT-04-138 x PT-04-261
		III x VI (66.25)	PT-04-78 x PT-04-221 PT-04-78 x PT-04-348-2
		IV x II (57.81)	PT-04-230 x PT-04-373 PT-04-230 x PT-04-391
		V x II (63.94)	PT-04-343 x PT-04-281 PT-04-343 x PT-011-6
		VII x VIII (54.02)	PT-03-129-2 x PT-04-386
		IX x VI (94.91)	ICPL-87 x PT-04-267 ICPL-87 x PT-04-360-1
11	Resistance to Wilt	IV x III (61.37)	PT-04-230 x PT-04-78 PT-04-230 x PT-04-264
		IX x VI (94.91)	ICPL-87 x PT-04-221 ICPL-87 x PT-04-348-2
12	Resistance to pod borer	III x VI (66.25)	PT-04-264 x PT-04-267 PT-04-264 x PT-04-360-1
		VIII x IX (78.33)	PT-04-386 x ICPL-87

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13	Harvest index	VII x IX (64.45)	PT-03-129-2 x ICPL-87
		IX x VI (94.91)	ICPL-87 x PT-04-221 ICPL-87 x PT-04-348-2
14	Protein content	IX x VI (94.91)	ICPL-87 x PT-04-267 ICPL-87 x PT-04-221
		II x VI (66.83)	PT-011-14 x PT-04-360-1 PT-011-14 x PT-04-348-2

The D^2 analysis, thus proved to be a very useful technique in isolating diverse groups from the germplasm under study.

5.4.3 Proposed tentative crossing programme

Being a numerical estimate, D^2 statistics has the added advantage over other criteria of permitting precise comparison among the possible pairs of populations in any given group. Since the estimates are obtained from a study of potential parents themselves, the required information is available before attempting any crosses and thus the D^2 cluster means and inter-cluster coverage divergence can be utilized for the choice of parents to decide the cross combinations which are likely to produce high heterotic effects for various economic and qualitatively important characters. It is suggested that diverse genotypes with maximum inter cluster distance and having high yield potential with more height, more plant spread, more number of primary branches, more fruit length and diameter, more fresh fruit weight and number of fruits per plant and good qualitative characters might be very useful suggesting a suitable breeding programme. Such crosses are expected to throw superior transgressive segregants in advanced generations. The biotypes originating in a particular habitat have ability only for certain traits for which selection has been practiced. Therefore, the varieties

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Likewise, certain types may possess similar characteristics though they have their origins are different. The varieties grouped under the same cluster was presumed very little diverse from each other and thus crossing between them is not expected to produce the desirable heterotic response. Thus, the selection of parents from distant diverse groups is useful in hybridization programme, Such crosses are expected to throw superior segregants in advanced generations.

Hence, on the basis of above assumptions a tentative crossing programme is suggested as below for obtaining high yielding with pest and disease resistant in pigeonpea.

1) Earliness

The lowest cluster means for days to 50% flowering was 65.1 shown by cluster IX, followed by cluster III (71.9) and II (75.37). Inter cluster distance between cluster IX and cluster VI was (94.91), followed by cluster IX and V (92.37) and cluster IX and IV (84.88). It is suggested that genotypes from more diverse groups and having high yield potential coupled with quality attributes selected for breeding programme.

Cluster IX x cluster VI : ICPL-87 x PT-04-267

Cluster III x cluster I : PT-04-78 x PT-04-138.

2) Plant height (Maximum)

The highest cluster means for plant height was 182.3 shown by cluster V, followed by cluster VI (181.9) and cluster IV (171.63). The inter cluster distance was maximum between cluster VI and IX (94.91), followed by cluster V and IX (92.37) and cluster IV and IX (84.88). It is suggested that genotypes from more diverse groups and having high plant height coupled with quality attributes selected for breeding programme.

Cluster V x Cluster IX : PT-04-343 x ICPL-87

Cluster VI x Cluster IX : PT-04-267 x ICPL-87.

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3) Plant spread (Maximum)

The highest cluster means for plant spread was 60.3 shown by cluster IV, followed by cluster VI (55.56) and cluster V (48.57). The inter cluster distance was maximum between cluster VI and IX (94.91), followed by cluster V and IX (92.37) and cluster IV and IX (84.88). It is suggested that genotypes from more diverse groups and having more plant spread coupled with quality attributes selected for breeding programme.

Cluster IV x Cluster IX : PT-04-230 x ICPL-87

Cluster VI x Cluster IX : PT-04-360-1 x ICPL-87.

4) Primary branches per plant (Maximum)

The highest cluster means for primary branches per plant was 12.73 shown by cluster VIII, followed by cluster VI (10.48). The inter cluster distance was maximum between cluster VI and IX (94.91), followed by cluster VIII and IX (78.33). It is suggested that genotypes from more diverse groups and more primary branches coupled with quality attributes selected for breeding programme.

Cluster VIII x Cluster IX : PT-03-62 x ICPL-87

Cluster VI x Cluster IX : PT-04-267 x ICPL-87.

5) Secondary branches per plant (Maximum)

The highest cluster means for secondary branches per plant was shown by cluster VII (18), followed by cluster VIII (13.99). The inter cluster distance was maximum between cluster VIII and IX (78.33), followed by cluster VII and IX (64.45). It is suggested that genotypes from more diverse groups and having more secondary branches coupled with quality attributes selected for breeding programme.

Cluster VII x Cluster IX : PT-03-129-2 x ICPL-87

Cluster VIII x Cluster IX : PT-04-261 x ICPL-87.

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6) Pods per plant (Maximum)

The highest cluster means for pods per plant was 194.17 shown by cluster III, followed by cluster VIII (193.36). The inter cluster distance was maximum between cluster VIII and IX (78.33), followed by cluster III and I (43.4). It is suggested that genotypes from more diverse groups and having more number of pods per plant coupled with quality attributes selected for breeding programme.

Cluster III x Cluster I : PT-04-264 x PT-04-365

Cluster VIII x Cluster IX : PT-04-386 x ICPL-87.

7) Seeds per pod (Maximum)

The highest cluster means for seeds per pod was 4.23 shown by cluster V, followed by cluster IV and IX (4.07). The inter cluster distance was maximum between cluster VI and IX (94.91), followed by cluster V and IX (92.37). It is suggested that genotypes from more diverse groups and having more number of seeds per pod coupled with quality attributes selected for breeding programme.

Cluster V x Cluster IX : PT-04-343 x ICPL-87

Cluster IV x Cluster IX : PT-04-230 x ICPL-87.

8) Seed yield per plant (Maximum)

The highest cluster means for seed yield per plant was 44.06 shown by cluster III, followed by cluster VIII (35.33). The inter cluster distance was maximum between cluster VIII and IX (78.33), followed by cluster III and I (43.4). It is suggested that genotypes from more diverse groups and having high seed yield coupled with quality attributes selected for breeding programme.

Cluster III x Cluster I : PT-04-329 x PT-04-169

Cluster VIII x Cluster IX : PT-03-62 x ICPL-87.

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9) 100 seed weight (Maximum)

The highest cluster means for 100 seed weight was 11.36 shown by cluster VIII, followed by cluster VI (10.9). The inter cluster distance was maximum between cluster VI and IX (94.91), followed by cluster VIII and IX (78.33). It is suggested that genotypes from more diverse groups and having more 100 seed weight coupled with quality attributes selected for breeding programme.

Cluster VIII x Cluster IX : PT-04-261 x ICPL-87

Cluster VI x Cluster IX : PT-04-348-2 x ICPL-87.

10) Incidence of sterility mosaic (SM) (Minimum)

The lowest cluster means for incidence of sterility mosaic was 0.00shown by cluster I, III, IV, V, VII and IX, followed by cluster II (0.34). The inter cluster distance was maximum between cluster I and VIII (50.48), followed by cluster III and VI (66.25). It is suggested that genotypes from more diverse groups and having low incidence of SM coupled with quality attributes selected for breeding programme.

Cluster I x Cluster VIII : PT-04-138 x PT-03-62

Cluster III x Cluster VI : PT-04-78 x PT-04-221.

11) Wilt (%) (Minimum)

The lowest cluster means for wilt percentage was 0.00 shown by cluster IV and IX, followed by cluster VII (7.27). The inter cluster distance was maximum between cluster IX and VI (94.91), followed by cluster IV and III (61.37). It is suggested that genotypes from more diverse groups and having low wilt incidence coupled with quality attributes selected for breeding programme.

Cluster IV x Cluster III : PT-04-230 x PT-04-78

Cluster IX x Cluster VI : ICPL-87 x PT-04-221.

12) Reaction to pod borer (Minimum)

The lowest cluster means for reaction to pod borer was 10.54 shown by cluster III, followed by cluster VIII (12.38). The inter cluster distance was maximum

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between cluster VIII and IX (78.33), followed by cluster III and VI (66.25). It is suggested that genotypes from more diverse groups and having low pod borer infestation coupled with quality attributes selected for breeding programme.

Cluster III x Cluster VI : PT-04-264 x PT-04-267

Cluster VIII x Cluster IX : PT-04-386 x ICPL-87.

13) Harvest index (Maximum)

The highest cluster means for harvest index was 34.37 shown by cluster VII, followed by cluster IX (32.97). The inter cluster distance was maximum between cluster VI and IX (94.91), followed by cluster VII and IX (64.45). It is suggested that genotypes from more diverse groups and having high harvest index coupled with quality attributes selected for breeding programme.

Cluster VII x Cluster IX : PT-03-129-2 x ICPL-87

Cluster IX x Cluster VI : ICPL-87 x PT-04-221.

14) Protein content (Maximum)

The highest cluster means for protein content was 19.43 shown by cluster IX, followed by cluster II (19.05). The inter cluster distance was maximum between cluster IX and VI (94.91), followed by cluster II and VI (66.83). It is suggested that genotypes from more diverse groups and having high protein content coupled with quality attributes selected for breeding programme.

Cluster IX x Cluster VI : ICPL-87 x PT-04-267

Cluster II x Cluster VI : PT-011-14 x PT-04-360-1.

Considering the intra cluster and inter cluster distances the following genotypes may be more effective for improvement of seed yield per plant and yield contributing characters. These are PT-04-267, PT-04-360-1, ICPL-87, PT-04-343, PT-04-230, PT-03-129-2, PT-04-373, PT-011-6 and PT-011-14.

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6. SUMMARY AND CONCLUSION

Fifty genotypes of pigeonpea from different eco-geographic regions, maintained at Pulses Improvement Project, MPKV, Rahuri (M.S.) were evaluated in the present investigation Genetic variability, correlation and diversity analysis in pigeonpea [Cajanus cajan (L.) Millsp] during Kharif, 2012.

The observations were recorded on the 15 characters viz., days to 50 % flowering, days to maturity, plant height, plant spread, primary and secondary branches per plant, pods per plant, seeds per pod, seed yield per plant, 100 seed weight, incidence of SM, wilt, reaction to pod borer, harvest index and protein content.

6.1 Summary

6.1.1 Variability and genetic parameters

Sufficient variability was present in the genotypes studied. The high ranges were observed for days to 50 % flowering, days to maturity, plant height, plant spread, secondary branches per plant, pods per plant, seed yield per plant, 100 seed weight and wilt, while it was low for primary branches per plant, seeds per pod, 100 seed weight, incidence of SM, reaction to pod borer, harvest index and protein content.

Genotypic and phenotypic coefficients of variation were the highest for pods per plant, plant height, days to maturity, plant spread, seed yield per plant, days to 50 % flowering and wilt and the values were least for the remaining characters.

High heritability was observed for all the characters. High heritability associated with high genetic advance as a percentage of mean were observed for incidence of sterility mosaic, wilt percentage, secondary branches per plant, seed yield per plant, plant spread, pods per plant and primary branches per plant, indicating

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additive genetic control in their inheritance and thus scope for selection for improving these characters.

6.1.2 Correlations

In the present study, values of genotypic correlation were higher than the corresponding phenotypic correlation. Seed yield per plant was significantly and positively correlated with the plant height (0.323), primary branches per plant (0.266), secondary branches per plant (0.504), pods per plant (0.835), seeds per pod (0.266) and positively correlated with days to 50 % flowering (0.104), days to maturity (0.129), plant spread (0.152) and 100 seed weight (0.105). Whereas, it was negatively and significantly correlated with wilt percentage (-0.216), reaction to pod borer (-0.327) and negatively correlated with incidence of sterility mosaic (-0.085), harvest index (-0.068) and protein content (-0.147) both at genotypic and phenotypic levels.

6.1.3 Path analysis

Path analysis revealed that, pods per plant had the highest and positive direct effect (0.773), followed by days to maturity (0.357), and seeds per pod (0.172). They exhibited positive and significant correlation with seed yield per plant indicating their true and perfect association with seed yield.

While, incidence of sterility mosaic had highest and negative direct effect (-0.167), followed by reaction to pod borer (-0.150). They exhibited negative and significant correlation with seed yield per plant indicating their true but negative association with seed yield.

In addition to these, days to 50 % flowering, plant height, plant spread had negative direct effects but their total contribution to seed yield was positive and significant as their indirect effects through days to maturity, secondary branches per plant, pods per plant were positive.

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6.1.4 Genetic divergence

The D^2 values ranging from 104.6 to 11047.96 showed adequate diversity between the genotypes. On the basis of D^2 values, all these genotypes were grouped into 9 clusters with substantial genetic divergence between them. Cluster I included the highest number of genotypes (27 genotypes) followed by cluster number II (9 genotypes), cluster number VI (4 genotypes), cluster number III and VIII (3 genotypes in each) and cluster number IV, V, VII and IX (1 genotype in each). The maximum intercluster distance was found between cluster VI and IX (94.91). Whereas, minimum inter cluster distance was found between cluster number IV and V (19.86). Clustering pattern of these genotypes did not necessarily follow the geographical distribution and genotypes included in the same cluster may have the same genetic architecture.

6.2 Conclusions

6.2.1 Variability

High genotypic coefficients among the genotypes indicates more variability for the characters viz.,incidence of sterility mosaic, wilt, secondary branches per plant, seed yield per plant, plant spread, pods per plant and primary branches per plant.

High heritability with genetic advance as a percentage of mean suggest additive genetic control in the inheritance of characters viz., incidence of sterility mosaic, wilt percentage, secondary branches per plant, seed yield per plant, plant spread,pods per plant, primary branches per plant and reaction to pod borer indicating scope for selection in these characters.

6.2.2 Correlations

Plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod were positively and significantly, while days to 50 % flowering, days to maturity, plant spread and 100 seed weight were

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weight were positively correlated with seed yield and had strong positive genotypic correlations with seed yield per plant. Whereas, it was negatively and significantly correlated with wilt percentage, reaction to pod borer and negatively correlated with incidence of sterility mosaic, harvest index and protein content and had negative genotypic correlations with seed yield per plant.

6.2.3 Path analysis

Pods per plant, days to maturity, seeds per pod, primary and secondary branches per plant, 100 seed weight, harvest index and protein content had direct positive effect on seed yield, while incidence of sterility mosaic, wilt and reaction to pod borer had direct negative effect on seed yield. So these are the most important characters as revealed by path analysis.

6.2.4 Genetic divergence

1. There is substantial genetic diversity among the genotypes studied.
2. The 50 genotypes grouped into 9 clusters.
3. The pair of genotypes viz., PT-04-415-1 and PT-04-382 was most divergent from one another (11047.96).
4. On the basis of intercluster distances , cluster means and per se performance for the hybridization program may involving the following genotypes PT-04-267, PT-04-360-1, ICPL-87, PT-04-343, PT-04-230, PT-03-129-2, PT-04-373, PT-011-6 and PT-011-14.

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8. VITA

DEORE SANDIP GANGADHAR

A Candidate for the degree

Of

MASTER OF SCIENCE (AGRICULTURE)

In

Agricultural Botany

(GENETICS AND PLANT BREEDING)

2013

Title of thesis : Genetic variability, correlation and diversity analysis in pigeonpea [Cajanus cajan (L.) Millsp.]

Major field : Genetics and Plant Breeding.

Biographical Information

Personal : Born on 27th March,1989. Son of Shri. Deore Gangadhar Daji and Sou. Deore Ranjanabai Gangadhar.

Educational : Received Bachelor of Science (Agriculture) degree from Dr.Ulhas Patil College of Agriculture, Jalgaon.

Permanent Add.: A/P : Dahiwad,
Tal. : Deola,
Dist : Nashik.
(M.S.), Pin: 423102.

Email-id : sdipdeo11@gmail.com

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