

**Study of Genetic Diversity Assessment for Seed  
Yield and its Component Traits in Pigeonpea  
[*Cajanus cajan* (L.) Millsp.]**

**THESIS**



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***By***

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2020**

## CERTIFICATE – I

This is to certify that the thesis entitled “**Study of Genetic Diversity Assessment for Seed Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]**” submitted in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE** in **Plant Breeding and Genetics** of the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafide research work carried out by **Mr. Sumit Kumar Singh, ID No 18131609** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any degree or diploma or has been published. All the assistance and help received during the course of the investigation has been acknowledged by the scholar.

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This is to certify the thesis entitled “**Study of Genetic Diversity Assessment for Seed Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]**” submitted by **Mr. Sumit Kumar Singh**, ID No **18131609** to the Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior in partial fulfillment of the requirements for the degree of Master of Science in **Agriculture (Plant Breeding and Genetics)** has been accepted after evaluation by the External Examiner and approved by the Student’s Advisory Committee after an oral examination on the same.

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## LIST OF SYMBOLS AND ABBREVIATIONS

Symbol	Legend
&	And
@	At the rate of
°C	Degree Celsius
C.D.	Critical Difference
cm	Centimeter
C.V.	Coefficient of Variation
DAS	Days after sowing
D.F.	Degree of Freedom
<i>et al.</i>	And others
etc	and the rest
Fig.	Figure (s)
G	Gram
ha	Hectare
HI	Harvest Index
i.e.	That is
K	Potassium
kg/ha	Kilogramme per hectare
L	Litre
MSS	Mean sum of square
mg	Miligram
m	Meter (s)
N	Nitrogen
No.	Number (s)
NS	Non significant
P	Phosphorus
t	Tonnes
R.V.S.K.V.V.	Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya
R.A.K.	Rafi Ahmed Kidwai
RH	Relative humidity
S.Em.±	Standard error of mean
S.S.	Sum of Square
Viz.	Namely
√	Square root
%	Percent
±	Plus or Minus

## CHAPTER I

### INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.], commonly known as *arhar*, *tur* or *redgram*, belongs to the family Fabaceae, sub family Papilionaceae, tribe Phaseoleae, sub tribe Cajani, genus *Cajanus* and species *cajan*. It has diploid chromosome number  $2n=2x=22$ . It is cultivated in tropical and sub-tropical areas. It is drought tolerant crop and often cross pollinated. After chickpea, it is the second important pulse crop in India eaten in form of *dahl*.

It is an excellent source of protein (20-22%) and supplementing energy rich cereal diets in mainly vegetarian population. The pigeonpea seed contains about 20 to 22 % protein, 57.6 %, carbohydrate, 1.7 % fat, phosphorus 304 mg, calcium 13 mg, iron 5.8 mg, minerals 3.5 % and fiber 1.5 %. The cotyledons, edible portion of pigeon pea, contains 22% protein, however, newly bred pigeonpea lines have protein content between 28-30% (Saxena and Sawargaonkar, 2015). Therefore it can be used as good source of protein.

The plant of pigeonpea is also referred as “biological plough” as it breaks hard pans by its long tap roots, fixes atmospheric nitrogen and add organic matter and micronutrients to the soil (Saxena *et al.* 2010).

Pigeonpea is the fourth most important grain legume crop of the world. Globally pigeonpea is grown on an area spanning 5.40 mha. with grain output of 4.48 million tons and a mean productivity of 829.9 kg/ha in 2017-18. In India it has coverage of around 44 Lha with production of 42 Lt and with aggressive Transfer of Technology (ToT) in various thematic areas, highest ever productivity of 960 kg/ha. was achieved during 2017-18. Major contributing states include Maharashtra, Karnataka, Madhya Pradesh, Telangana, Uttar Pradesh, Andhra Pradesh and Gujarat. In Madhya Pradesh it covers an area of 6.47 lakh ha with production of 8.39 lakh tons with a contribution of 19.72% in total production of Pigeon pea in India (Anonymous, 2018).

This plant has various names in different cultures such as Red gram, Congo pea, Gungo pea, No eye pea etc. and are widely consumed throughout the world. Pigeonpea originated in Asian continent, a native to India, as long as 3000 years ago. It was taken to the eastern African region approximately a thousand years ago from India.

Pigeonpea is best suitable for dry-land farming being a drought resistant crop. It is used as intercrop with cotton, sorghum, black gram, etc. It is mainly cultivated for its dry seeds and green vegetables in dry areas of tropics and subtropics with major producing countries being India, Eastern Africa, Central and South America, the Caribbean, Myanmar and West Indies (Vijayalakshmi *et al.*, 2013).

Yield being an important trait is complex and governed by polygenes and influenced by many physiological processes and highly affected by environment. Yield in pigeonpea is determined by number of pods per plant, seed number per pod, seed weight and influenced by plant height, number of branches, plant resistance to biotic and abiotic stresses etc.

In 1931, pigeonpea varietal improvement programme started in India with selection from landraces and since then over 100 varieties have been released (Saxena and Tikle, 2015) but the yields are leveling off since last many years. The main reason behind plateau formation is narrow genetic base of pigeonpea which is a result of founder effect which occurs when only few individuals are used while domestication of a wild species or when breeders use only a few genotypes for all subsequent crop improvement programme.

The problem of stability of yield which is faced as pigeonpea is grown in rainfed areas can be overcome by more understanding of the component traits that contributes to seed yield. Therefore estimation of genetic parameters like diversity, heritability, genetic advance, genetic divergence etc could be helpful for the study of inheritance.

The biometrical techniques such as simple measures of variability (range, mean, standard deviation, variance, standard error, coefficient of variance component analysis,  $D^2$  statistics etc.) are commonly used for the assessment of variability.

To determine the selection criteria for simultaneous improvement of various characters along with the seed yield, the information on nature and magnitude of correlation coefficient is required. The information on their genetic variability and traits is of considerable importance in selection of elite genotypes as well as exploitation of heterosis breeding programme.

Correlation coefficient analysis is a handy technique that elaborates the degree and extent of relationship among important plant characters and

provides basic criteria for selection and leads to directional model based on yield and its components in the field experiments.

As the study of genetic variability and correlation alone are not enough to study the direct and indirect influence of each of the component rates on grain yield, so in such a case path coefficient analysis is an important technique for partitioning the correlation coefficient in two direct and indirect effects of independent variables on dependent variable. Path coefficient, a standard partial regression coefficient, specifies the cause and effect relationship and also measures the relative importance of each variable (Wright, 1921). Therefore, correlation along with path coefficient analysis is an important tool to quantify the direct and indirect influence of one character upon another.

Genetic divergence is the total amount of genetic variation present in a population. Divergence is very essential to develop improved cultivars with broad genetic base. It is depleted due to genetic erosion and extinction.

The  $D^2$  statistics help in evaluating large number of germplasm lines for genetic diversity and helps in the identification of genetically divergent parents for their exploitation in hybridization programmes. This technique measures the degree of diversification. It provides reliable estimates of genetic divergence. A large number of advance generation lines can be evaluated at a time for genetic diversity by this technique and selection index based on discriminate function analysis is a powerful tool for discriminating the promising genotypes of various characters. It was proposed by Mahalanobis in 1936. This technique measures the forces of differentiation at two levels viz., intra cluster and inter cluster that helps selection of genetically divergent parents for exploitation in hybridization programmes. Three important points should be considered while selecting parents on the basis of  $D^2$  viz., (i) the relative contribution of each character to the total genetic divergence, (ii) the choice of clusters with the maximum statistical distance and (iii) the selection of one or a few genotypes from such clusters. The present study was conducted to find out the degree of genetic divergence in pigeonpea germplasm so that suitable divergent parents may be identified for breeding programme to develop high yielding varieties in pigeonpea.

Therefore, keeping this view in consideration, the present investigation has been proposed with following objectives:-

1. To estimate the genetic variability, heritability and genetic advance for yield and its contributing characters.
2. To estimate correlation and path coefficients among seed yield and its contributing characters.
3. To determine genetic divergence among pigeonpea genotypes for seed yield and its contributing characters.

## CHAPTER-II

### REVIEW OF LITERATURE

The relevant literatures related to various aspects of present study are reviewed under the following heads.

2.1. Genetic variability, Heritability and Genetic advance.

2.2. Path analysis and correlation coefficient.

2.3. Genetic divergence ( $D^2$  analysis).

#### **2.1. Genetic Variability, Heritability and Genetic advance:**

The genetic variability among the genotypes of a species is the backbone for improvement in various yield contributing traits of economic importance. It is pre-requisite in any crop improvement programme. Availability of natural genetic variability, its collection, maintenance, evaluation, preservation is useful for crop breeding programme, as it contributes directly towards the improvement of crop.

The importance of genetic variability in relation to environmental variability was given by Fisher (1918). Later on Wright (1921), Lush (1940), Robinson *et al.* (1949), Warner (1952) and Johnson *et al.* (1955) have suggested the techniques for estimation of components of genetic variation.

Shrivastava *et al.* (1976) observed wide range of variability among the homogenous lines of pigeonpea for protein content and seed density. The mean protein per cent was 17.9. Early, medium and late types had mean protein of 17.76%, 18.06% and 17.92% respectively. The range was much wider in late types with 13.46 to 20.96 per cent, while density was 1.287 with a range of 0.685 to 1.690.

Genetic variability has been critically reviewed in pigeonpea by Raju *et al.* (1972). They studied plant height, plant spread, and number of branches per plant, test weight and yield in 36 varieties of *Cajanus cajan* and reported that all the characters except plant height showed significant variability.

Sidhu *et al.* (1985) observed high genetic variability for number of pods per plant and the lowest for the number of seeds per pod in the complete 8 x 8 diallel set of pigeonpea.

Patel and Patel (1992) observed high genetic advance for the traits such as days to 50% flowering, primary branches, harvest index and seed yield in pigeonpea.

Yadavendra *et al.* (1981) reported maximum heritability for 100-seed weight followed by number of seeds per pod in their evaluation study in pigeonpea for yield contributing characters.

Konwar and Hazarika (1988) analyzed 16 genotypes of *Cajanus cajan* for nine quantitative characters and observed high heritability and high genetic advance for days to flowering and plant height.

Marekar and Nerkar (1988) studied 14 genotypes and their 91 hybrids for 14 yield components in pigeonpea and observed high heritability for pods per plant and days to maturity.

Takalkar *et al.* (1998) estimated variability, heritability and genetic advance using 23 early genotypes of pigeonpea. High variability and genetic advance were observed for pods per plant and dry weight per plant.

Kingshlin *et al.* (1998) studied genetic variance, heritability and genetic advance of yield characters in Pigeonpea (*Cajanus cajan*). High heritability estimate and genetic advance were recorded for number of branches per plant which was positively correlated with yield per plant.

Aher *et al.* (1998) studied genotypic and phenotypic coefficient of variations, heritability, genetic advance and correlation coefficients from the data on 10 yield related traits in 64 genotypes of pigeonpea. Wide genetic variability was observed for plant height, plant spread, number of secondary branches and days to flowering. High heritability accompanied by high genetic advance was observed for number of primary and secondary branches followed by seed yield, days to 50% flowering, plant spread and plant height.

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

Dash and Kole (2000) observed for genetic variability, heritability and genetic advance for 16 characters in 81 genotypes of pigeonpea. High amounts

of phenotypic and genotypic coefficient of variations were observed for days to 50% flowering, straw weight, pods per plant, yield per plant and length of pod bearing branches. High heritability coupled with high genetic advance was observed for days to 50% flowering, straw weight, yield per plant, length of pod bearing branches and 100-seed weight. Based on the mean performance of the genotypes, Japan Super, C-11, KE-71, TTB-7, ICPL-87091, ES-90 and BDN-69 could be chosen for further improvement of grain yield, since they exhibited superiority for most of the characters.

Gohil (2006) studied heritability in 39 Pigeonpea genotypes and observed that grain yield per plant, days to 50% flowering, days to maturity, number of clusters per plant, number of pods per plant, number of pods per clusters and harvest index showed high heritability.

Gupta *et al.* (2007) observed one hundred and seventy seven pigeonpea lines and three checks for grain yield and its component traits, four characters viz. number of branches per plant, number of pods per plant, grain yield per plant and grain yield per plot exhibited high variability. The remaining characters days to 50% flowering, number of grain per pod and 100 grain weight showed relatively low variability.

Bhadru (2008) analyzed 50 pigeonpea genotypes and observed wide range of genetic variation for number of pods, seed yield, plant spread, raceme length and plant height. High heritability accompanied with high genetic advance was observed for number of pods per plant, seed raceme length and plant spread. Major stress should be given for these characters while selecting the superior pigeonpea genotypes.

Sodavadiya *et al.* (2009) reported that estimates of GCV in general were higher than their corresponding PCV indicating strong inherent association among the traits.

Shunyu *et al.* (2013) estimated variability and character association in thirty genotypes of Pigeonpea for grain yield and its attributing characters. The analysis of variance revealed significant differences among the genotypes for all the characters studied, indicating a high degree of variability in the material. The highest PCV and GCV were recorded for number of pods per plant followed by seed yield per plant and number of clusters per plant indicating the presence of ample variation for these traits in the present material. In the

present study high estimates of heritability and genetic advance were obtained for seed yield per plant, days to 50% flowering, plant height, number of pods per cluster, number of clusters per plant, pod length, 100-seed weight, number of primary branches per plant and days to maturity. Thus, selection of these traits is likely to accumulate more additive genes leading to further improvement of their performance and these traits may be used as selection criteria in Pigeonpea breeding program.

Saroj *et al.* (2013) reported that the phenotypic and genotypic variances, correlation and path coefficient, heritability and genetic advances for grain yield and yield traits in 70 Pigeonpea genotypes. The highest GCV was recorded for number of secondary branches/plant (61.81) followed by pods/plant (38.34). Heritability in broad sense ranged from 61.33 (seeds/pod) to 98.26 (days to 50% flowering). High genetic advance were observed for number of primary branches/plant (60.61), number of secondary branches/plant (154.10), 100 seed weight (50.82), grain yield/plant (84.65), pods/plant (92.59), plant height (33.83) and days to 50% flowering (45.05) indicating the prevalence of additive gene action for inheritance of these traits.

Mallesh *et al.* (2017) carried out study for genetic variability, heritability and genetic advance of sixteen characters in twenty eight genotypes including checks. High heritability combined with high genetic advance was recorded for number of pods per plant and seed yield per plant indicating that these characters are controlled by additive gene effect.

Pushpavalli *et al.* (2018) evaluated forty nine pigeon pea genotypes and reported broad sense heritability estimates were highest for days to maturity and days to 50% flowering.

## **2.2. Correlation and Path Coefficient Analysis:**

Beohar *et al.* (1980) studied seed yield and five related characters in 18 varieties. Seed yield was highly and positively correlated with number of pods per plant.

Asawa *et al.* (1981), Yadavandra *et al.* (1981) and Shoram (1983) in different studies on yield and yield components of pigeonpea reported that seed yield was positively correlated with pods per plant.

Bhongale and Raut (1986) studied correlation coefficient in 80 genotypes for 12 characters in pigeonpea and observed that plant height,

number of branches per plant, number of pods per plant, pod weight and number of seeds per pod were positively correlated with each other and significantly correlated with yield.

Khapre and Nerkar (1986) studied seed yield per plant, total dry matter and harvest index in seven pigeonpea varieties and found that seed yield was closely associated with harvest index. They concluded that all the aforesaid three characters should be taken into account while breeding for increased yield.

Kingshlin *et al.* (1998) recorded number of branches per plant which was positively correlated with yield per plant.

Shoran *et al.* (1988) observed that seed yield, plant height, branches per plant and days to flower were positively and significantly associated with seed yield in pigeonpea. Significant and positive association was also reported between branch numbers and pod numbers, plant height and seed yield, branch numbers, days to flower, pod length and 100 seed weight, pod length and seeds per pod and 100 seed weight.

Pansuriya *et al.* (1998) studied correlation coefficient derived from data on 10 yield related traits in 20 early maturity pigeonpea. Grain yield was significantly and positively correlated with pods per plant and dry matter per plant indicating that selection on the basis of these traits would be effective for yield improvement.

Basavarajaiah *et al.* (1999) found significant positive correlation of grain yield per plant with pod weight, pods per plant, straw weight, branches per plant and shelling percentage. Path analysis revealed that pod weight had the greatest direct effect on grain yield per plant, followed by plant height, branches per plant and pods per plant. It is suggested that characters such as pod weight, pods per plant, branches per plant and plant height should be given due importance when making selections for increased yield in Pigeonpea.

Bharadwaj (2004) studied to determine the genetic architecture of correlation between yield and other quality, contributing characters. The protein content showed positive correlation with days to flowering, harvest index, days to maturity, while it showed negative association with plant height, number of primary and secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant. The protein content

showed positive direct effect with negative correlation with seed yield in pigeonpea.

Sawant *et al.* (2009) studied correlation, path coefficients analysis and genetic diversity for 11 characters in 56 genotypes of pigeonpea. The correlation studies revealed that the pods per plant and plant spread were positively associated with grain yield. Further pods per plant had the highest positive direct effect on grain yield, followed by plant spread and 1000 grain weight.

Sodavadiya *et al.* (2009) reported that the seed yield per plant had significant and positive association with days to 50 % flowering, days to maturity, number of branches per plant, number of pods per plant and 100 seed weight at both genotypic as well as phenotypic levels. Characters like 100-seed weight, days to maturity and pod length exerted high direct effects on seed yield per plant. 100-seed weight and days to maturity also contributed indirectly towards seed yield per plant through most of the characters. Thus, based on present study days to maturity, numbers of pods per plant and 100 seed weight were emerged as the most important components of seed yield per plant.

Rekha *et al.* (2013) studied correlation and found positive and significant association of seed yield with number of pods per plant, number of secondary branches per plant, number of primary branches per plant and plant height. Path analysis revealed that the number of pods per plant was important in formulating selection criteria for improvement of seed yield in Pigeonpea.

Saroj *et al.* (2013) reported that the phenotypic and genotypic variances, correlation and path coefficient, heritability and genetic advances for grain yield and yield traits in 70 Pigeonpea genotypes. Correlation and Path coefficient analysis (genotypic and phenotypic) revealed that pods/plant (0.858\*\*), 100-seed weight (0.370\*\*), days to 50% flowering (0.458\*\*), primary branches (0.357\*\*) and secondary branches (0.302\*\*) had maximum direct effect resulted significantly positive correlation with grain yield/plant. These traits can be used to improve the grain yield of Pigeonpea.

Ojwang *et al.* (2016) evaluated the yield potential of twelve medium maturity vegetable pigeonpea (*Cajanus cajan*) cultivars two locations in eastern Kenya during 2012 and 2013 cropping years and observed significant ( $P < 0.05$ ) and positive correlation coefficients between grain yield and pods plus grain as

well as shelling percentage were recorded which indicates that this is an important variable for cultivar selection in vegetable pigeonpea.

Kesha *et al.* (2016) studied that correlation and path coefficient analysis (genotypic and phenotypic) revealed that pods per plant, 100 seed weight, days to 50% flowering, primary branches and secondary branches had maximum direct effect resulted significantly positive correlation with grain yield per plant. These traits can be used to improve the grain yield of pigeonpea.

Narayanan *et al.* (2018) used twenty one genotypes of pigeonpea to investigate the nature and magnitude of association of seed yield with major agronomic characters. Correlation studies revealed the positive and significant relationship of number of pods per plant, days to 50 per cent flowering, number of branches per plant with seed yield. The path coefficient analysis indicated that characters viz., plant height, number of pods per plant, days to 50 per cent flowering, and days to maturity should be considered as selection indices in seed yield improvement programme as they recorded high direct effects on seed yield per plant.

Bal *et al.* (2018) conducted studies on correlation between yield and yield components in 34 genotypes of pigeon pea and reported that harvest index, plant height, pod length, pod breadth, number of seeds per pod and number of pods per plant would be more appropriate than any other characters.

Pushpavalli *et al.* (2018) evaluated forty nine pigeonpea genotypes and significant and positive genotypic and phenotypic correlation was observed between seed yield and number of pods/plant and number of secondary branches/plant. Path coefficient analysis revealed that days to maturity exhibited maximum direct effect followed by number of pods/plant.

### **2.3. Genetic Divergence:**

Mahalanobis (1928) proposed  $D^2$  statistics as a measure of group distance on multiple characters.  $D^2$  statistics measures the degree of diversification and determines the relative proportion of each component character to the total divergence. It measures the forces of differentiation at two levels, i.e. intra-cluster and inter-cluster levels.

Mahalanobis (1936) generalized distance ( $D^2$ ) has been very often used by crop breeders to measure the nature and magnitude of diversity. In view of these, 27 genotypes were evaluated in this study to determine the grouping

pattern of genotypes and to identify genetically diverse genotypes for exploitation in a breeding program.

Tocher's method as given by Rao (1952) was used to cluster the genotypes.

Firoz *et al.* (2006) reported forty-nine genotypes of vegetable pigeonpea grown in Bangalore, Karnataka, India, during kharif 2004 for genetic diversity for 14 traits. There was no definite relationship between genetic diversity and geographical origin. Intra cluster  $D^2$  values ranged from 0 (solitary cluster) to 57.08 (cluster II), whereas the inter cluster  $D^2$  values ranged from 34.46 (clusters VI and VII) to 259.13 (clusters IV and XIII). The number of branches per plant, number of pods per plant, seed yield per plant, number of seeds per pod, number of days to 50% flowering, number of days to first picking, and number of days to second pickings and the greatest contribution to the total divergence. The accessions under cluster IV recorded high values for number of branches per plant, green seed yield per plant, 100-green-seed volume, number of seeds per pod, green pod length and green pod width (cluster IV), whereas those under cluster XIII were characterized by early flowering and maturity, dwarf plant types, and early picking. Hybridization between these accessions may yield desirable segregants.

Magar *et al.* (2008) analyzed 40 genotypes of pigeonpea and grouped in to 6 clusters following  $D^2$  analysis. Genetic diversity was found to be unrelated to geographic diversity. Based on genetic divergence and cluster means, crossing programme has been suggested involving Phule T 1037, Phule T 9230, Phule T 11-39, Phule T 8208-1, Pusa 2001-1, NDA 2001-2, MAL-18, BDN-2 and ICPL-87.

Sreelakshmi *et al.* (2011) studied divergence among the 36 hybrids and three checks of Pigeonpea. The hybrids were grouped into nine clusters, where cluster I was the largest containing twenty one hybrids followed by cluster II with seven hybrids. The inter cluster distance was maximum between cluster III and VIII followed by III and VI and seed yield contributed the most (22.2) towards genetic divergence. Seed yield showed positive correlation with all the characters studied except 100-seed weight. Genotypic path analysis revealed that the maximum direct effect on seed yield was exhibited by number of

primary branches per plant, days to 50% flowering and number of pods per plant.

Navneet *et al.* (2017) evaluated 30 pigeonpea genotypes at Gwalior (M.P.) revealing that there were wide range of genetic diversity for all 11 yield and its attributing characters. The contribution of characters towards genetic divergence was highest in seed yield per plant.

Indhu *et al.* (2018) conducted a study to evaluate the genetic divergence among twenty five pigeonpea germplasm using Mahalanobis  $D^2$  statistics for seven different traits and the analysis of variance depicted the significant differences among the traits which indicated the presence of variability in the germplasm. The maximum contribution to genetic divergence was contributed by days to fifty percent flowering and single plant yield followed by number of seeds per pod, plant height and hundred seed weight.

## **CHAPTER III**

### **MATERIAL AND METHODS**

This investigation was performed during the Kharif season of 2019-20 to obtain information on genetic variability, genetic advance, correlation coefficient and path analysis in Pigeonpea [*Cajanus cajan* (L.) Millsp.]. The information of experimental material, applied methods climate and soil of experimental site is also given ahead.

#### **3.1 Experimental site:**

The experimental was conducted in the experimental area of All India Co-Ordinated Research Project on Pigeonpea, R.A.K. College of Agriculture, Sehore (M.P.). The field was fairly uniform with gentle slope, adequate drainage and normal fertility status.

#### **3.2 Experimental soil:**

The soil of the field is clay loam Vertisol with 52% clay, 41.3% silt and 6.6% sand with pH ranging from 7.2 to 7.8. The soil was low in available nitrogen, medium in available phosphorus and high in available potassium.

#### **3.3 Climate and season:**

Sehore is located at the latitude of 23°-12', North longitude of 77°-05' and an altitude of 498.7 meter above the mean sea level. It lies in the western track of Vindhyan plateau agro climatic zone of Madhya Pradesh and enjoy sub tropical climate. The annual rainfall varies from 1000-1250mm with major precipitation in the month of July and August.

Meteorological data recorded during the period of experimentation are given table 3.1

**Table 3.1 Weekly metrological data during the crop season (From June, 2019 to March, 2020).**

Month	Standard week No.	Week	Temperature (C)		Relative humidity (%)	Rainfall (mm)	Rainy days
			Max.	Min.			
June	23	4-10	40.51	28.68	42.64	0.0	0
	24	11-17	38.00	28.42	49.35	0.0	0
	25	18-24	34.37	24.67	63.00	111	2
	26	25-01	32.28	23.95	73.14	117	6
	<b>Average</b>		<b>36.29</b>	<b>21.14</b>	<b>57.03</b>		
July	27	02-08	29.61	24.55	83.57	140	5
	28	09-15	26.85	23.50	84.14	519	4
	29	16-22	29.30	23.64	79.21	82	3
	30	23-29	30.01	23.71	83.42	262	6
	<b>Average</b>		<b>28.94</b>	<b>23.85</b>	<b>82.58</b>		
August	31	30-05	27.78	23.41	84.57	142	5
	32	06-12	27.38	23.01	85.21	235	4
	33	13-19	27.67	22.38	85.57	62	2
	34	20-26	25.45	22.11	84.57	124	2
	35	27-02	27.50	22.31	78.35	41.5	3
	<b>Average</b>		<b>27.15</b>	<b>22.64</b>	<b>83.65</b>		
September	36	03-09	29.40	21.45	75.78	0.0	0
	37	10-16	30.97	21.80	76.14	63	2
	38	17-23	31.84	23.15	74.21	28	4
	39	24-30	31.57	22.12	71.71	7.0	0
	<b>Average</b>		<b>30.94</b>	<b>22.13</b>	<b>74.46</b>		
October	40	01-07	30.45	23.32	73.71	37	2
	41	08-14	32.35	19.01	70.78	2.0	0
	42	15-21	31.62	16.48	53.50	0.0	0
	43	22-28	31.41	15.94	49.28	0.0	0
	44	29-04	31.50	14.30	74.14	32	1
	<b>Average</b>		<b>31.46</b>	<b>17.81</b>	<b>79.72</b>		
November	45	05-11	29.97	18.6	66.78	0	0
	46	12-18	28.2	14.62	58.92	0	0
	47	19-25	27.22	14.52	61.14	0	0
	48	26-02	28.51	15.11	61.78	0	0
	<b>Average</b>		<b>28.47</b>	<b>15.71</b>	<b>62.15</b>		
December	49	03-09	25.01	12.25	63.14	0	0
	50	10-16	21.84	12.91	74.5	19.5	1
	51	17-23	22.11	9.68	78.78	0	0
	52	24-31	21.9	8.76	66.56	0	0
	<b>Average</b>		<b>22.71</b>	<b>10.9</b>	<b>70.74</b>		
January	01	01-07	20.18	9.85	78.64	0	0
	02	08-14	22.54	7.91	67.42	4	1
	03	15-21	20.88	9.4	48.14	0	0
	04	22-28	24.14	10.14	66.57	0	0
	05	29-04	23.15	8.68	62.78	0	0
	<b>Average</b>		<b>22.17</b>	<b>11.96</b>	<b>64.71</b>		
February	06	05-11	23.72	8.85	59.21	0	0
	07	12-18	27.91	9.22	56.21	0	0
	08	19-25	29.04	13.1	53.28	3	1
	09	26-04	29.66	13.81	50.12	1.5	0
	<b>Average</b>		<b>27.58</b>	<b>11.24</b>	<b>54.7</b>		
March	10	05-11	27.61	13.78	47.14	0	0
	11	12-18	28.52	12.71	51.92	0	0
	12	19-25	32.71	18.77	42.35	0	0
	<b>Average</b>		<b>29.61</b>	<b>15.08</b>	<b>47.13</b>	0	0
					<b>G.T.</b>	2032.5	54

Source: Meteorological observatory, R.A.K. College of Agriculture, Sehore (M.P.)

### 3.4 Experimental material:

The experimental material consisted of 50 germplasm of Pigeonpea; all genotypes were obtained from All India Coordinated Research Project on Pigeonpea at R.A.K. College of Agriculture, Sehore.

**Table 3.2 List of Pigeonpea genotypes included in the studies.**

Sr. No.	Genotypes	Sr. No	Genotypes	Sr. No.	Genotypes	Sr. No	Genotypes	Sr. No	Genotypes
1	ICPL 20096	11	BDN 2014-1	21	IBT DRG 4	31	GRG 333	41	RVSA 16-4
2	ICPL 20103	12	BDN 2011-1	22	IBT DRG 6	32	AGL 1603-4	42	RVSA 28-1
3	ICPL 20108	13	BDN 2013-41	23	TDRG 60	33	BDN 711	43	PUSA 16
4	ICPL 99050	14	BDN 20142-02	24	TDRG 58	34	JKM 189	44	PUSA 992
5	ICPL 20116	15	BDN 2013-45	25	IBTT DRG 5	35	TDRG 4	45	AISHWARYA
6	ICPH 2871	16	RVSA 15-5	26	LRG 41	36	LRG 52	46	UPAS 120
7	ICPH 2740	17	RVSA 15-6	27	LRG 105	37	TS 3 R	47	MLTP 1-0012
8	ICPH 3933	18	RVSA 1510	28	LRG 160	38	MARUTI	48	ICP-88039
9	ICPH 3762	19	TJT 501	29	GRG 177	39	ASHA	49	ICPL -87
10	LAXMI	20	IBT RG 3	30	GRG 152	40	RVSA 16-1	50	PUSA 991

### 3.5 Experimental details:

Number of Genotypes : 50  
Design : Randomized Block Design  
Replications : 03  
No. of Row : 01  
Plot size : 12 m<sup>2</sup> (4.00 m × 3.00 m)  
Spacing : 75 cm x 25 cm

#### 3.5.1 Observations recoded:

A random selection of five plants in each row was made and the observations were recorded on each selected plant. The mean values of each character under study were computed on the basis of five plants for each genotype in each replication.

#### Days to 50% flowering:

The number of days from date of sowing to the appearance of flowers on fifty percent plants in a row was counted and recorded.

#### Days to maturity:

The number of days from date of sowing to the maturity of plants was counted and recorded.

**Plant height (cm):**

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

**Number of branches per plant:**

The total number of branches were counted and recorded at maturity.

**Number of pods per plant:**

The number of effective pods per plant was counted at the time of maturity for each selected plant.

**Number of seeds per pod:**

This was arrived at counting the seeds from five randomly selected pods in each of five plants and then by calculating the mean.

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

One hundred seeds from each individual genotype were taken at random, after threshing and proper drying, than weighed and measured in grams.

**Biological yield per plant (g):**

The dry weight of selected plant (grain yield+dry matter) from each genotype was recorded and measured in grams per plant.

**Seed yield per plant (g):**

The weight of total seeds collected from each plant was recorded in gram.

**Harvest index (%):**

The value of harvest index was obtained by dividing the total seed yield by biological yield and expressed in percentage.

$$\text{Harvest index} = \frac{\text{Seed yield (g)}}{\text{Biological yield (g)}} \times 100$$

**3.6 Statistical analysis:**

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

The model for experimental design used in randomized block design can be expressed as follows:

$$P_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,  $P_{ij}$  = Phenotypic effect of  $i$ th genotype in the  $j$ th replication.

$\mu$  = General population mean.

gi=Effect of ith genotype.  
 rj=Effect of jth replication.  
 eij=Error associated with the experiment.

### 3.6.1 Analysis of variance (ANOVA):

The data available on individual plant characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1985). The analysis of variance was done as given below.

Source	d.f.	M.S.	Expected M.S.
Replication	(r-1)	RMS	$\sigma^2e + g \sigma^2r$
Genotypes	(g-1)	GMS	$\sigma^2e + r \sigma^2g$
Error	(r-1) (g-1)	EMS	$\sigma^2e$
Total	(rt-1)		

Where, r = Number of replications  
 g = Number of genotypes  
 MS = Mean square

The genotypes mean sum of square (GMS) was tested against error mean sum of square (EMS) by 'F' test for n1= (g-1) and n2= (r-1) (g-1) degrees of freedom.

### 3.6.2 Estimation of mean and range:

The mean value for each character was worked out by dividing the sum of all observations by corresponding number of observations:

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n xi$$

Where,  $\bar{x}$  = Mean of the character  
 $\sum xi$  = Total of all observations  
 n = Number of observation

Range is difference between the lowest and the highest value for each character. The genotypic, phenotypic and environmental components were estimated as explained by Johnson *et al.* (1955).

### 3.6.3 Variance components:

The mean squares due to genotypes and error were used for calculation of variance components by manipulation of expected mean squares as shown below.

### 3.6.3.1 Estimates of genotypic, phenotypic and environmental variances

Genotypic, phenotypic and environmental variances were calculated as suggested by Johnson et al. (1955).

(a) Environmental variance ( $\sigma^2_e$ ) =  $\frac{M_e}{M_g - M_e}$

(b) Genotypic variance ( $\sigma^2_g$ ) =  $\frac{r}{r^2}$

(c) Phenotypic variance ( $\sigma^2_p$ ) =  $\sigma^2_g + \sigma^2_e$

### 3.6.3.2 Estimation of coefficient of variation

Burton and De Vane (1953) have given the formula for calculation of phenotypic and genotypic coefficient of variation.

#### 3.6.3.2.1 Genotypic Coefficient of Variation (GCV)

It was estimated by the formula suggested by Burton (1952).

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

Where,  $\sigma^2_g = V_g$  = Genotypic variance

$\bar{x}$  = General mean of the character

#### 3.6.3.2.2 Phenotypic Coefficient of Variation (PCV)

It was estimated by the formula suggested by Burton (1952).

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

Where,  $\sigma^2_p = V_p$  = Phenotypic variance

$\bar{x}$  = General mean of the character

Categorization of range of variation as proposed by Sivasubramanian and Menon (1973).

Low : < 10 (%)

Moderate : 10 – 20 (%)

High : > 20 (%)

### 3.6.4 Heritability (broad-sense) $h^2$ (b):

It is the proportion of phenotypic variability that is due to genetic reasons. Heritability in broad sense was calculated by using the formula proposed by Allard (1960):

$$h^2(b) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,  $h^2$  (b) = Heritability (broad-sense)

$\sigma^2g$  = Genotypic variance

$\sigma^2p$  = Phenotypic variance

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949).

0-30% - Low

30-60% - Moderate

60% and above - High

### 3.6.5 Estimation of genetic advance (GA):

The genetic advance was calculated in per cent by the formula suggested by Johnson *et al.* (1955).

a)  $GA = \frac{\sigma^2g}{\sigma^2p} \times \sigma p \times k$

b) GA as percentage of mean (GAM) =  $\frac{GA}{\bar{x}} \times 100$

Where,  $\sigma^2g$  = Genotypic variance

$\sigma^2p$  = Phenotypic variance

$\sigma p$  = Phenotypic standard deviation

K = Selection differential at 5 per cent selection intensity (2.06)

$\bar{x}$  = Mean of the character

The range of genetic advance as percent of mean was classified as method suggested by Johnson *et al.* (1955).

Low : < 10 (%)

Moderate : 10 – 20 (%)

High : > 20 (%)

### 3.6.7 Estimation of correlation coefficient:

Analysis of co-variance was carried out by taking two characters at a time and plot error was used as environmental co-variance. The phenotypic and genotypic co-variances were derived as detailed below.

#### ANCOVA for phenotypic and genotypic co-variance

Source	d.f	Mean products
Replication	(r-1)	-
Genotypes	(t-1)	GMP
Error	(r-1)(t-1)	EMP
Total	(rt-1)	-

Where, r = Number of replications

t = Number of treatments

GMP = Genotypic mean sum of products

EMP = Error mean sum of products

The genotypic and phenotypic co-variances were worked out as per the formulae given by Singh and Chaudhary (1977).

Environmental co-variance =  $C_0 V_e x_1 x_2 = EMP$

Genotypic co-variance =  $C_0 V_g x_1 x_2 = \frac{GMP - EMP}{r}$

Phenotypic co-variance =  $C_0 V_P x_1 x_2 = C_0 V_e x_1 x_2 + C_0 V_g x_1 x_2$

The appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson et al., 1955).

**a) Phenotypic correlation coefficients (rp) were derived as:**

$$rpx_1x_2 = \frac{C_0 V_P x_1 x_2}{\sqrt{(\sigma^2 p_1)(\sigma^2 p_2)}}$$

Where,

$rpx_1x_2$  = Phenotypic correlation between character x1 and x2

$C_0 V_P x_1 x_2$  = Phenotypic co-variance between character x1 and x2

$(\sigma^2 p_1)(\sigma^2 p_2)$  = Phenotypic variance of character x1 and x2, respectively

**b) Genotypic correlation coefficients (rg) were derived as:**

$$rgx_1x_2 = \frac{C_0 V_g x_1 x_2}{\sqrt{(\sigma^2 g_1)(\sigma^2 g_2)}}$$

Where

$rgx_1x_2$  = Genotypic correlation between character x1 and x2

$C_0 V_g x_1 x_2$  = Genotypic co-variance between character x1 and x2

$(\sigma^2 g_1) and (\sigma^2 g_2)$  = Genotypic variance of character x1 and x2, respectively.

The significance of phenotypic and genotypic correlation coefficients were tested by using 't' test.

$$T = r \frac{\sqrt{n-2}}{1-r^2}$$

Where, r = Correlation coefficients

n = Total number of observations

The calculated 't' value is tested with table 't' value for respective (n-2) degrees of freedom for significance.

### 3.6.8 Path analysis:

Path coefficient analysis was done according to procedure suggested by Dewey and Lu (1959). If 'y' is the effect 'x1' is the cause, path coefficient for the path from cause x1 to the effect y is  $\delta x_1 / \delta y$ . Direct and indirect effects were worked out by using genotypic correlation as below:

$$\text{Direct effect of } x_1 \text{ on } y = P_{x_1.y}$$

Where,

$P_{x_1.y}$  = Path coefficient of  $x_1$  on  $y$ . Similarly, direct effects of other attributes on yield were calculated.

$$\text{Indirect effect of } x_1 \text{ via } x_2 \text{ on } y = p_{x_2.y} \times r_{x_1.x_2}$$

Where,

$p_{x_2.y}$  = Path coefficient of the component character  $x_2$  on  $y$ .

$r_{x_1.x_2}$  = Genotypic correlation between  $x_1$  and  $x_2$

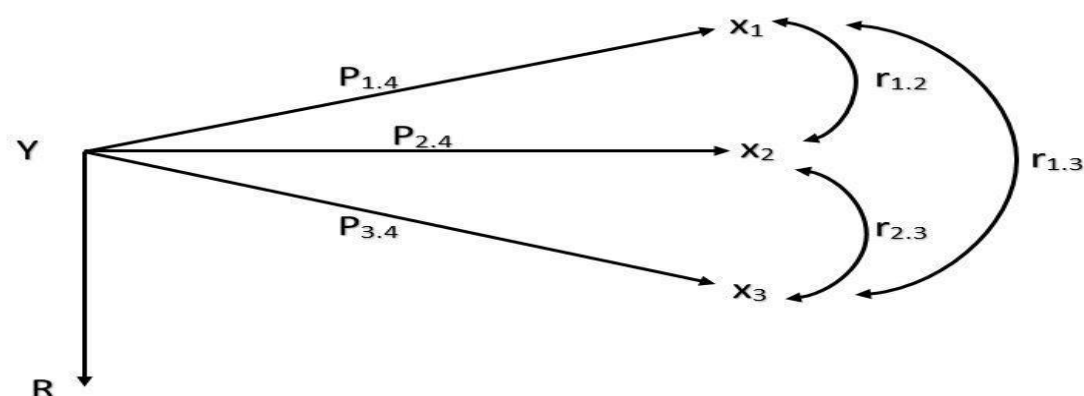
Similarly, indirect effects in all possible combinations were calculated for all component characters. The residual effect (R) was calculated below

$$R = [1 - (P_{x_1.y} \cdot r_{x_1.y}) - (P_{x_2.y} \cdot r_{x_2.y}) - \dots - (P_{x_n.y} \cdot r_{x_n.y})]^{1/2}$$

Where,

$P_{x_1.y}, P_{x_2.y} \dots P_{x_n.y}$  = Direct effects of respective character on seed yield.

$r_{x_2.y} \dots r_{x_n.y}$  = Correlation coefficient between respective characters and seed yield.



### 3.6.9 Mahalanobis generalized distance ( $D^2$ ):

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

$$D^2 = \sum \sum \lambda_{i.j} \cdot d_i \cdot d_j$$

Where,

$\lambda_{i.j}$  = Reciprocal matrix to the common dispersion matrix

$d_i$  = Difference between the mean values of two populations for  $i^{\text{th}}$  character  
 $d_j$  = Difference between the mean values of two populations for  $j^{\text{th}}$  character.

Estimation of  $D^2$  value from the above formula is very complicated in the present study. Since, it requires the inversion of thirteen order determinants and then the evaluation of  $B(BH) / 2$  terms whose sum is  $D^2$ . It was found convenient to work with a set of uncorrelated characters constructed from the original measurements.  $D^2$  with such transformed variables reduces to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation elements.

#### **3.6.9.1 Average intra and inter cluster $D^2$ and D value**

#### **3.6.9.2 Average intra cluster $D^2$**

$$D^2 = \sum D_i / n$$

Where,

$D_i$  is the sum of distance between all possible combinations ( $n$ ) of the population included in a cluster.

#### **3.6.9.3 Average inter cluster $D^2$ :**

$$D^2 = \sum \text{Distance between the population of cluster 1 and } j/n_i \cdot n_j$$

Where,

$n_i$  = Number of population in cluster  $i$

$n_j$  = Number of population in cluster  $j$

#### **3.6.10.4 Average intra and inter cluster distance:**

$$D^2 = \sqrt{D^2}$$

#### **3.6.11 Cluster means:**

Cluster mean were calculated for individual characters on the basis of mean performance of the genotypes included in that cluster.

#### **3.6.10.5 Genetic diversity as an index for selecting desirable parents for hybridization:**

Bhatt (1970) advocated the use of multivariate analysis for the selection of parents. He also stated that statistical distance of all possible cluster combination may be considered arbitrarily as guideline and suggested that it would be logical to affect crosses between genotypes belonging to the clusters separated by high estimated statistical distance.

## CHAPTER IV

### RESULTS

The experimental findings of the present investigation have been mentioned in this chapter under following heads.

- 4.1 Analysis of variance.
- 4.2 Mean performance.
- 4.3 Estimation of Variance Components.
- 4.4 Phenotypic and Genotypic coefficients of variation.
- 4.5 Estimation of heritability, genetic advance and genetic advance expressed as percentage of mean.
- 4.6 Correlation coefficients.
- 4.7 Path coefficient analysis.
- 4.8 Genetic divergence ( $D^2$  analysis).

#### **4.1 Analysis of variance**

The analysis of variance for ten different characters studied in the present investigation is given in table 4.1. The analysis revealed that genotypes exhibited highly significant differences for all of the characters under study. It showed that all these characters have significant variation.

#### **4.2 Mean performance**

The mean performance of 50 genotypes of pigeonpea for 10 different characters along with the, range, general mean, standard error of mean (S.Em.), critical difference and coefficient of variation (CV %) are presented in Table 4.2.

##### **Days to 50 % flowering**

The fifty genotypes varied significantly for this character and it ranged from 85.00 to 117.30. The general mean for days to 50 per cent flowering was 103.24 days. Genotype AISHWARYA (85.00) recorded minimum number of days to 50% flowering while the maximum number of days to 50% flowering was recorded by the genotype TS 3 R (117.30). All genotypes were statistically significant superior over population mean.

##### **Days to maturity**

The fifty genotypes varied significantly for this character and it ranged from 116.70 to 154. The general mean for days to maturity was 137.56 days. Genotype GRG 177 (116.70) recorded minimum number of days to maturity while the maximum number of days to maturity was recorded by the genotype

LAXMI (154.0). All genotypes were statistically significant superior over population mean.

#### **Plant height (cm)**

The fifty genotypes varied significantly for this character and it ranged from 150.7 to 178.7 cms. The general mean for plant height was 165.8. Genotype TJT 501 (150.7) was dwarf genotype for plant height while the tallest genotype for plant height was recorded by the genotype BDN 2013-41 (178.7). All genotypes were statistically significant superior over population mean.

#### **Number of branches per plant:**

The fifty genotypes varied significantly for this character and it ranged from 18.6 to 26.30. The general mean for number of branches per plant was 23.30. Genotype IBT DRG-4 (26.30) recorded maximum number of branches while the minimum number of branches was recorded by the genotype TDRG 4(18.60). All genotypes were statistically significant superior over population mean.

**Table 4.1 Analysis of variance for ten different characters studied in pigeonpea**

Sr.no.	Source	Mean Squares		
		Replication	Genotypes	Error
	Degree of freedom	2	49	98
1.	Days to 50% flowering	11.12	292.26**	17.58
2.	Days to maturity	22.02	312.97**	17.79
3.	Plant height (cm)	43.28	151.04**	84.59
4.	Number of branches/ plant	0.04	12.51**	1.10
5.	Number of pods/plant	98.33	1231.36**	180.37
6.	Number of Seeds/pod	0.07	0.75**	0.07
7.	Biological yield/ plant(g)	7.09	625.53**	36.09
8.	Seed yield per plant (g)	135.95	748.10**	72.26
9.	100 seed weight (g)	0.09	2.75**	0.11
10.	Harvest index (%)	36.70	207.14**	21.87

\* Significant at 5 level of probability

\*\* Significant at 1% level of probability

#### **Number of pods per plant:**

The fifty genotypes varied significantly for this character and it ranged from 164.0 to 237.7. The general mean for number of pods per plant was 208.1. Genotype ICPL 20103 (237.70) recorded maximum number of pods per plant while the minimum number of pods per plant was recorded by the genotype BDN 2013-41 (164.0). All genotypes were statistically significant superior over population mean.

**Table 4.2 Mean performance of fifty Pigeonpea genotypes studied for ten different quantitative characters.**

Sr. no.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches /plant	Pods /plant	Seed /pod	Biological yield / plant(g)	Seed yield per plant (g)	100 seed weight (g)	Harvest index (%)
		1	2	3	4	5	6	7	8	9	10
1	ICPL 20096	98	148.3	171.3	22.9	234	3.7	187.9	88.5	10.3	47
2	ICPL 20103	98	147	156	24.6	<b>237.7</b>	4.2	179.8	107.6	10.7	<b>59.8</b>
3	ICPL 20108	105.7	146.7	152.3	24.9	231.7	4.4	184	95.9	9.4	52.3
4	ICPL 99050	108.3	149	168	25.9	224.3	4.2	197	95.6	10.2	48.7
5	ICPL 20116	93	138	162.3	24.6	191.7	4.4	203	88.3	10.5	43.6
6	ICPH 2871	87	131	165	24.4	195	3.7	205.1	83.7	11.5	40.9
7	ICPH 2740	107	141.7	171	25.1	195	3.3	206.7	70.1	11	34
8	ICPH 3933	108	141	176.7	24.5	207	4.5	200.7	110.5	11.9	55
9	ICPH 3762	107.3	149.7	174.3	23.6	216.7	3.4	178.4	90.3	12.1	50.7
10	LAXMI	111.3	<b>154</b>	165	22.8	221.7	3.5	163.6	81.8	10.6	50.1
11	BDN 2014-1	92.7	135.3	166	25.3	184.3	3.5	164.7	67.2	10.5	41
12	BDN 2011-1	91.3	128.7	168.7	24.2	177.3	4	173.3	70.2	9.9	40.5
13	BDN 2013-41	91	145	<b>178.7</b>	24	<b>164</b>	4	185.6	67.7	10.3	36.5
14	BDN 20142-02	95.3	150.3	172	24.7	190	3.7	199.1	80.8	11.4	40.6
15	BDN 2013-45	105.7	137	175.7	25.4	215.7	4.5	210.9	100.9	10.4	47.8
16	RVSA 15-5	114.7	146.3	174	23.8	226.3	3.8	175.7	94.3	11	53.7
17	RVSA 15-6	108.7	143	169.7	24.3	206.7	3.4	181.2	77.5	11.2	42.8
18	RVSA 15-10	112.3	147.7	158.7	23.5	236.3	3.4	192	77.4	9.6	40.3
19	TJT 501	115	147.7	<b>150.7</b>	25.5	166	<b>4.7</b>	<b>162.1</b>	82.1	10.5	50.7
20	IBT RG 3	112.7	146	157	25.7	185.7	3.7	172.7	65.2	9.5	37.8
21	IBT DRG 4	92.3	129	155.7	<b>26.3</b>	188.7	3.2	178.8	53.2	8.8	29.7
22	IBT DRG 6	113	134.3	169.3	25.4	224	3.3	188.2	70.1	9.5	37.2
23	TDRG 60	102	120	165	24.8	232.3	3.6	205.8	87.4	10.4	42.5
24	TDRG 58	101.7	128	168.7	24.3	223.3	4.5	209.5	104.4	10.4	50
25	IBTT DRG 5	114.3	137.3	170.3	25.4	227	3.4	212.5	79.2	10.1	37.4
26	LRG 41	108	142.3	162	24.3	188.7	<b>2.6</b>	195.4	<b>45.1</b>	9.2	<b>23</b>
27	LRG 105	88.7	142.7	166	24.6	175.7	3.6	191.3	61.9	9.8	32.4

28	LRG 160	94.7	119	155	25	215.7	4	182.4	90.8	10.5	49.8
29	GRG 177	85.3	116.7	157	23.4	228	2.7	200.8	63.3	10.1	31.6
30	GRG 152	108	137.7	163	24.4	229.7	3.5	210	82	10.3	39
31	GRG 333	112.3	141.3	167.7	24.3	224.7	3.5	207.1	67.7	8.5	32.7
32	AGL 1603-4	117	148.3	172	21.2	223	4.2	200.7	87.4	9.4	43.6
33	BDN 711	96.7	128.3	170	19.7	195.3	3.6	201.5	65.4	9.4	32.5
34	JKM 189	114.3	137	160	22.8	222.7	4.3	201.6	118	12.3	58.6
35	TDRG 4	116	142.3	158.3	18.6	229.7	4.4	209.9	114.7	11.5	54.7
36	LRG 52	113.7	147.3	175.3	19.5	186.7	3.7	198.5	87.5	12.8	44.1
37	TS 3 R	117.3	147.7	154.7	20.1	178.7	3.8	217	85.5	12.5	39.4
38	MARUTI	113.3	141.3	161	22.3	191.3	4.5	211.9	91.5	10.6	43.1
39	ASHA	94	124.7	168.3	24.5	211	3.5	202.9	67.4	9.1	33.2
40	RVSA 16-1	89.3	123.7	171.7	19.4	214.3	4.3	201.6	93.9	10.1	46.6
41	RVSA 16-4	88.3	118.7	173.7	20.7	229	3.6	191.8	93.8	11.4	49
42	RVSA 28-1	104	123.3	165.3	20.4	218	3.3	178.9	82.9	11.4	46.5
43	PUSA 16	106.3	142.7	173.3	23	219.7	4.3	168.8	96.2	10.3	56.9
44	PUSA 992	95.7	119	158.7	23.2	214.7	3.6	212.3	73.4	9.6	34.6
45	AISHWARYA	85	127.7	172	24.5	220.3	4.2	209.5	96.7	10.5	46.3
46	UPAS 120	95	134	153.7	21.6	211	3.2	188	63.1	9.4	33.6
47	MLTP 1-0012	101	128	163.7	19.7	214	3.1	201.3	62.4	9.6	31
48	ICP-88039	101.7	128.3	166	21.1	191	4.3	192.9	91.1	10.9	47.1
49	ICPL -87	115.7	147.7	169	20.4	194.3	3.8	190.3	69.3	9.5	36.4
50	PUSA 991	114.3	146.3	169.7	20.9	175	4.6	203	80.5	10	39.6
	Mean	103.24	137.56	165.8	23.3	208.1	3.8	193.8	82.4	10.4	42.7
	Range	Max.	117.3	154	178.7	26.3	237.7	4.7	217	118	59.8
		Min.	85	116.7	150.7	18.6	164	2.6	162.1	45.1	23
	S.Em.	2.42	2.44	5.31	0.61	7.75	0.15	3.47	4.91	0.19	2.70
	C.D. 5%	6.79	6.83	14.90	1.70	21.76	0.43	9.73	13.77	0.54	7.58
	C.V.%	4.06	3.07	5.55	4.50	6.45	6.92	3.10	10.31	3.21	10.95

**Number of seeds per pod:**

The fifty genotypes varied significantly for this character and it ranged from 2.60 to 4.70. The general mean for number of seeds per pod was 3.80. The genotypes TJT 501 (4.70) showed highest number of seeds per pod where the genotype LRG 41 (2.60) showed lowest number of seeds per pod. All genotypes were statistically significant superior over population mean.

**Biological yield/ plant (gm):**

The fifty genotypes varied significantly for this character and it ranged from 162.10 gm to 217.00 gm. The general mean for biological yield per plant was 193.8 gm. The genotypes TS-3-R recorded highest (210.0 gm) Biological yield per plant while the genotype TJT-501 (162.1 gm) showed lowest biological yield per plant. All genotypes were statistically significant superior over population mean.

**Seed yield per plant (gm):**

The fifty genotypes varied significantly for this character and it ranged from 45.10 gm to 118.0 gm. The general mean for seeds yield per plant was 82.40 gm. The genotypes JKM-189 recorded highest (118.0 gm) seed yield per plant while the genotype LRG-41 (45.10 gm) showed lowest seed yield per plant. All genotypes were statistically significant superior over population mean.

**100 seed weight (gm):**

The fifty genotypes varied significantly for this character and it ranged from 8.5 gm to 12.8 gm. The general mean for 100 seed weight was 10.4. The genotype LRG 52 (12.8 gm) showed highest 100 seed weight while the genotype GRG 333 (8.5 gm) showed lowest 100 seed weight. All genotypes were statistically significant superior over population mean.

**Harvest Index (%):**

The fifty genotypes varied significantly for this character and it ranged from 23.0% to 59.80%. The general mean for harvest index was 42.70%. The genotypes ICPL 20103 recorded highest (59.80%) harvest index while the genotype LRG 41 (23.0%) showed lowest harvest index. All genotypes were statistically significant superior over population mean.

### **4.3 Estimation of Variance Components**

The phenotypic and genotypic variances calculated for all the ten characters under study are presented in table 4.3. The results revealed that magnitude of phenotypic variance was higher than respective genotypic variance for all the characters. Genotypic and phenotypic variances were close to each other for days to 50% flowering, number of branches per plant, number of seeds per pod and 100-seed weight (gm).

### **4.4. Phenotypic and Genotypic Coefficient of Variation:**

It was observed that the estimates for genotypic coefficient of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the ten characters.

The highest GCV was recorded for Harvest Index (18.356) followed by seed yield per plant (18.205), Number of seeds per pod (12.556), days to 50% flowering (9.268), 100 seed weight (9.009), number of pods per plant (8.995), number of branches per plant (8.365), biological yield (7.235), days to maturity (7.211) and the character plant height (2.839) was recorded lowest GCV.

The highest PCV was recorded for Harvest Index (21.334) followed by seed yield per plant (20.926), number of seeds per pod (14.335), number of pods per plant (11.071), days to 50% flowering (10.119), 100 seed weight (9.562), number of branches per plant (9.5), biological yield per plant (7.871), days to maturity (7.836) and the character plant height (6.232) was recorded lowest PCV.

However, looking to the magnitudinal differences between GCV and PCV estimates, the maximum differences between PCV and GCV values was observed for Plant height. The GCV and PCV difference was of lowest of magnitude for days to maturity.

### **4.5 Estimation of heritability and genetic advance:**

Heritability in broad sense ranged from 20.751 to 88.756 percent. Highest heritability was exhibited for the character 100 seed weight (88.756%) followed by days to maturity (84.689%) and biological yield per plant (84.483%). The lowest heritability estimate recorded in plant height (20.751%) followed by number of pods per plant (66.012%). Other characters had

heritability at the tune of 74.026 per cent for harvest index, 75.684 per cent for seed yield per plant, 76.724 per cent for number of seeds per pod and 77.524 per cent for number of branches per plant.

The range of genetic advance was ranged from 0.861 to 31.327. The highest estimates of genetic advance were noticed in number of pods per plant (31.327), seed yield per plant (26.895) followed by biological yield per plant (26.541), where as lowest estimates of genetic advance was recorded in number of seeds per pod (0.861). Other characters had genetic advance at the tune of 1.819 for 100 seed weight, 3.536 for number of branches per plant, 4.416 for plant height, 13.907 for harvest index, and 18.055 for days to 50% flowering, 18.805 for days to maturity, 26.541 for biological yield per plant and 26.895 for seed yield per plant.

**Table 4.3 Estimates of genetic parameters for ten different characters of pigeonpea genotypes.**

Character	Mean	Range		$\sigma^2_g$	$\sigma^2_p$	SEm ±	GCV	PCV	H <sup>2</sup> b (%)	GA	GA as % of mean
		Min.	Max.								
<b>Days to 50% flowering</b>	<b>103.24</b>	85	117.3	91.56109	109.1369	2.42	9.268	10.119	83.896	18.055	17.488
<b>Days to maturity</b>	<b>137.56</b>	116.7	154	98.39442	116.1831	2.44	7.211	7.836	84.689	18.805	13.67
<b>Plant height (cm)</b>	<b>165.8</b>	150.7	178.7	22.1498	106.7427	5.31	2.839	6.232	20.751	4.416	2.664
<b>Number of branches /plant</b>	<b>23.3</b>	18.6	26.3	3.801472	4.903592	0.61	8.365	9.5	77.524	3.536	15.172
<b>Number of pods/plant</b>	<b>208.1</b>	164	237.7	350.3279	530.7022	7.75	8.995	11.071	66.012	31.327	15.055
<b>Number of Seeds/pod</b>	<b>3.8</b>	2.6	4.7	0.227902	0.297041	0.15	12.556	14.335	76.724	0.861	22.657
<b>Biological yield/ plant(gm)</b>	<b>193.8</b>	162.1	217	196.4808	232.5683	3.47	7.235	7.871	84.483	26.541	13.698
<b>Seed yield per plant (gm)</b>	<b>82.4</b>	45.1	118	225.2787	297.539	4.91	18.205	20.926	75.684	26.895	32.625
<b>100 Seed weight (gm)</b>	<b>10.4</b>	8.5	12.8	0.878795	0.990124	0.19	9.009	9.562	88.756	1.819	17.483
<b>Harvest index (%)</b>	<b>42.7</b>	23	59.8	61.75916	83.62439	2.70	18.356	21.334	74.026	13.907	32.533

## 4.6 Correlation

The correlation coefficients were estimated for all the combinations of ten characters under study at genotypic (rg) and phenotypic (rp) levels. The seed yield is a complex character which depends on different independent characters and hence, it is essential to know the relationship between the yield and its component characters. Correlation analysis is very useful in finding out the mutual association between yield and its component characters. The estimates of phenotypic and genotypic correlation provide an effective way of predicting response of selection and isolating desirable individuals from breeding population. The genotypic correlation coefficient is higher in magnitude than the phenotypic correlation. The phenotypic and genotypic correlations between ten characters are given in Table 4.4 and Table 4.5 respectively.

### Phenotypic correlation coefficient

The phenotypic correlation coefficient helps in determining selection index.

Days to 50% flowering exhibited significant positive correlation with days to maturity (0.571), seed yield per plant (0.179) and harvest index (0.161). It had non-significant but positive correlation with number of pods per plant (0.057), number of seeds per pod (0.138), biological yield per plant (0.045) and 100 seed weight (0.147) while non significant and negative correlation with plant height (-0.004) and number of branches per plant (-0.122).

Days to maturity exhibited significant negative correlation with biological yield per plant (-0.210) while significant but positive correlation with number of seeds per pod (0.176) and harvest index (0.178). It had non-significant negative correlation with number of pods per plant (-0.155) while non significant but positive correlation with plant height (0.101), number of branches per plant (0.056), seed yield per plant (0.097) and 100-seed weight (0.153).

Plant height exhibited non significant positive correlation with number of seeds per pod (0.035), biological yield per plant (0.044), seed yield per plant (0.080), 100-seed weight (0.150) and harvest index (0.056). It had non-significant but negative correlation with number of branches per plant (-0.082) and number of pods per plant (-0.024).

Number of branches per plant exhibited significant negative correlation with biological yield per plant (-0.178) and 100 seed weight (-0.197). It had non-significant but positive correlation with number of pods per plant (0.020) while non-significant negative correlation with number of seeds per pod (-0.021), seed yield per plant (-0.085) and harvest index (-0.012).

Number of pods per plant exhibited significant positive correlation with seed yield per plant (0.465) and harvest index (0.429). It had non-significant but positive correlation with biological yield per plant (0.114). It had non-significant but negative correlation with number of seeds per pod (-0.089) and 100 seed weight (-0.038).

Number of seeds per pod exhibited significant positive correlation with seed yield per plant (0.718), 100 seed weight (0.216) and harvest index (0.672). It had non-significant positive correlation with biological yield per plant (0.060).

Biological yield per plant exhibited significant negative correlation with harvest index (-0.247). It had non-significant positive correlation with 100 seed weight (0.086) and seed yield per plant (0.143).

Seed yield per plant exhibited significant positive correlation with 100 seed weight (0.569) and harvest index (0.919).

100 seed weight per plant exhibited significant positive correlation with harvest index (0.512).

**Table 4.4 Estimates of phenotypic correlation coefficient between ten different characters in pigeonpea.**

	Days to 50% flowering	Days to maturity	Plant height (cms)	Branch /plant	Pod /plant	Seed /pod	Biological yield /plant (g)	Seed yield / plant (g)	100 seed weight (g)	Harvest index
<b>Days to 50% flowering</b>	1	0.571**	-0.004 <sup>NS</sup>	-0.122 <sup>NS</sup>	0.057 <sup>NS</sup>	0.138 <sup>NS</sup>	0.045 <sup>NS</sup>	0.179*	0.147 <sup>NS</sup>	0.161*
<b>Days to maturity</b>		1	0.101 <sup>NS</sup>	0.056 <sup>NS</sup>	-0.155 <sup>NS</sup>	0.176*	-0.210*	0.097 <sup>NS</sup>	0.153 <sup>NS</sup>	0.178*
<b>Plant height (cm)</b>			1	-0.082 <sup>NS</sup>	-0.024 <sup>NS</sup>	0.035 <sup>NS</sup>	0.044 <sup>NS</sup>	0.080 <sup>NS</sup>	0.150 <sup>NS</sup>	0.056 <sup>NS</sup>
<b>Branch/plant</b>				1	0.020 <sup>NS</sup>	-0.021 <sup>NS</sup>	-0.178*	-0.085 <sup>NS</sup>	-0.197*	-0.012 <sup>NS</sup>
<b>Pod/plant</b>					1	-0.089 <sup>NS</sup>	0.114 <sup>NS</sup>	0.465**	-0.038 <sup>NS</sup>	0.429**
<b>Seed/pod</b>						1	0.060 <sup>NS</sup>	0.718**	0.216**	0.672**
<b>Biological yield /plant (g)</b>							1	0.143 <sup>NS</sup>	0.086 <sup>NS</sup>	-0.247**
<b>Seed yield / plant (g)</b>								1	0.569**	0.919**
<b>100 seed weight (g)</b>									1	0.512**
<b>Harvest index</b>										1

\* Significant at 5 level of probability

\*\* Significant at 1% level of probability

### **Genotypic correlation coefficient**

Days to 50% flowering exhibited significant positive correlation with days to maturity (0.633), number of seeds per pod (0.184), seed yield per plant (0.235) and harvest index (0.238) while significant but negative correlation with number of branches per plant (-0.166). It had non-significant negative correlation with plant height (-0.087) while non-significant but positive correlation with biological yield per plant (0.016), 100-seed weight (0.150) and number of pods per plant (0.105).

Days to maturity exhibited significant negative correlation with number of pods per plant (-0.176) and biological yield per plant (-0.251) while significant but positive correlation with number of seeds per pods (0.216) and harvest index (0.230). It had non-significant and positive correlation with plant height (0.099), number of branches per plant (0.078), seed yield per plant (0.120) and 100-seed weight (0.156).

Plant height exhibited significant positive correlation with biological yield per plant (0.207), seed yield per plant (0.208) and 100-seed weight (0.293). It had non-significant but positive correlation with number of pods per plant (0.011), number of seeds per pod (0.115) and harvest index (0.123) while non significant negative correlation with number of branches per plant (-0.108).

Number of branches per plant exhibited significant negative correlation with biological yield per plant (-0.245), seed yield per plant (-0.172) and 100-seed weight (-0.271). It had non-significant and negative correlation with number of pods per plant (-0.022), number of seeds per pod (-0.059) and harvest index (-0.073).

Number of pods per plant exhibited significant positive correlation with seed yield per plant (0.407), harvest index (0.338) and biological yield per plant (0.184). It had non-significant but negative correlation with number of seeds per pod (-0.111) and 100-seed weight (-0.052).

Number of seeds per pod exhibited significant positive correlation with seed yield per plant (0.733), 100-seed weight (0.252) and harvest index (0.688). It had non-significant positive correlation with biological yield per plant (0.082).

Biological yield per plant exhibited significant positive correlation with seed yield per plant (0.183) while significant but negative correlation with harvest index (-0.231). It had non-significant positive correlation with 100-seed weight (0.069).

Seed yield per plant exhibited significant positive correlation with 100-seed weight (0.618) and harvest index (0.914).

100-seed weight exhibited significant positive correlation with harvest index (0.582).

**Table 4.5 Estimates of genotypic correlation coefficient between ten different characters in pigeonpea**

	<b>Days to 50% flowering</b>	<b>Days to maturity</b>	<b>Plant height (cm)</b>	<b>Branch /plant</b>	<b>Pod /plant</b>	<b>Seed / pod</b>	<b>Biological yield / plant (g)</b>	<b>Seed yield / plant (g)</b>	<b>100 seed weight (g)</b>	<b>Harvest index</b>
<b>Days to 50% flowering</b>	1	0.633 <sup>**</sup>	-0.087 <sup>NS</sup>	-0.166 <sup>*</sup>	0.105 <sup>NS</sup>	0.184 <sup>*</sup>	0.016 <sup>NS</sup>	0.235 <sup>**</sup>	0.150 <sup>NS</sup>	0.238 <sup>**</sup>
<b>Days to maturity</b>		1	0.099 <sup>NS</sup>	0.078 <sup>NS</sup>	-0.176 <sup>*</sup>	0.216 <sup>**</sup>	-0.251 <sup>**</sup>	0.120 <sup>NS</sup>	0.156 <sup>NS</sup>	0.230 <sup>**</sup>
<b>Plant height (cm)</b>			1	-0.108 <sup>NS</sup>	0.011 <sup>NS</sup>	0.115 <sup>NS</sup>	0.207 <sup>*</sup>	0.208 <sup>*</sup>	0.293 <sup>**</sup>	0.123 <sup>NS</sup>
<b>Branch/plant</b>				1	-0.022 <sup>NS</sup>	-0.059 <sup>NS</sup>	-0.245 <sup>**</sup>	-0.172 <sup>*</sup>	-0.271 <sup>**</sup>	-0.073 <sup>NS</sup>
<b>Pod/plant</b>					1	-0.111 <sup>NS</sup>	0.184 <sup>*</sup>	0.407 <sup>**</sup>	-0.052 <sup>NS</sup>	0.338 <sup>**</sup>
<b>Seed/pod</b>						1	0.082 <sup>NS</sup>	0.733 <sup>**</sup>	0.252 <sup>**</sup>	0.688 <sup>**</sup>
<b>Biological yield /plant (g)</b>							1	0.183 <sup>*</sup>	0.069 <sup>NS</sup>	-0.231 <sup>**</sup>
<b>Seed yield / plant (g)</b>								1	0.618 <sup>**</sup>	0.914 <sup>**</sup>
<b>100 seed weight (g)</b>									1	0.582 <sup>**</sup>
<b>Harvest index</b>										1

\* Significant at 5 level of probability

\*\* Significant at 1% level of probability

#### **4.7 Path coefficient analysis**

In this study, different traits such as the days to flower to 50%, days of maturity, number of branches per plant, plant height, number of pods per plant, number of seeds per pod, biological yield of each plant, 100-seed weight (gm), seed yield per plant and the harvest index are used. The genotypic correlation coefficient between them and the yield of seeds is divided into direct effects and indirect effects. The seed yield is considered as the outcome variable, and the above composition characteristics are considered as the causal variable. Table 4.6 and 4.7 show the direct and indirect effects of these causal variables on seed yield.

##### **Note-**

##### **4.7.1 Genotypic correlation coefficient allocation for path coefficient analysis:**

Table no.4.6 List the phenotypic correlation coefficients divided into direct effects and indirect effects.

##### **Direct effects**

Out of ten characters studied, harvest index (1.48264) recorded high magnitude with direct positive effect on seed yield per plant followed by biological yield per plant (0.61076), plant height (0.00304) and branches per plant (0.00300). The characters viz; number of seeds per pod (-0.30662) showed maximum magnitude but direct negative effect on seed yield per plant followed by number of pods per plant (-0.25337).

##### **Indirect effects**

Days to 50 percent flowering had positive indirect effect for Biological yield per plant (0.00971) and harvest index (0.35285). It had negative indirect effect via days to maturity (-0.00622), plant height (-0.00026), number of branches per plant (-0.00050), number of pods per plant (-0.02669), number of seeds per pod (-0.05636) and 100 seed weight (-0.03306). This character had positive significant correlation (0.23474) with seed yield per plant.

Days to maturity had positive indirect effect via plant height (0.00030), number of branches per plant (0.00023), number of pods per plant (0.04470) and harvest index (0.34173). It had negative indirect effect via days to 50% flowering (-0.00299), number of seeds per pod (-0.06619), biological yield per

plant (-0.0164) and 100-seed weight (-0.03436). This character had non-significant positive correlation (0.12037) with seed yield per plant.

Plant height had positive indirect effect via days to 50% flowering (0.00041), biological yield per plant (0.12668) and harvest index (0.18199). It had negative indirect effect via days to maturity (-0.00097), number of branches per plant (-0.00032), number of pods per plant (-0.00275), number of seeds per pods (-0.03530) and 100 seed weight (-0.06455). This character had positive significant correlation (0.20823) with seed yield.

Number of branches per plant had positive indirect effect via days to 50% flowering (0.00078), number of pods per plant (0.00562), and number of seeds per pod (0.01817) and 100 seed weight (0.05959). It had negative indirect effect via days to maturity (-0.00076), plant height (-0.00033), harvest index (-0.10856) and biological yield per plant (-0.14956). This character had significant negative correlation (-0.1721) with grain yield per plant.

Number of pods per plant had positive indirect effect via harvest index (0.50065), biological yield per plant (0.11264), days to maturity (0.00173), plant height (0.00003), 100 seed weight (0.01151) and number of seeds per pod (0.03395). It had negative indirect effect via days to 50% flowering (-0.00050) and number of branches per plant (-0.00007). This character had highly significant positive correlation (0.40657) with seed yield per plant.

Number of seeds per pod had positive indirect effect via harvest index (1.02030), biological yield per plant (0.04985), plant height (0.00035) and number of pods per plant (0.02805). It had negative indirect effect via 100 seed weight (-0.05561), days to 50% flowering (-0.00087), days to maturity (-0.00212) and number of branches per plant (-0.05561). This character had highly significant positive correlation (0.73315) with seed yield per plant.

Biological yield per plant had positive indirect effect via plant height (0.00063) and days to maturity (0.00246). It had negative indirect effect via days to 50% flowering (-0.00008), number of branches per plant (-0.00073), number of pods per plant (-0.04673), 100 seed weight (-0.01524), number of seeds per pod (-0.02503) and harvest index (-0.34268). This character had highly significant positive correlation (0.18336) with seed yield per plant.

**Table-4.6 Direct and indirect effect of ten causal variables on seed yield of Pigeonpea at genotypic level (Residual - 0.00038)**

Characters	Days to 50% flowering	Days to maturity	Plant Height (cm)	Branch / plant	Pod / plant	Seeds / pod	Biological yield/plant	100 Seed wt	Harvest Index	Correlation of seed yield
<b>Days to 50% flowering</b>	<b>-0.00473</b>	-0.00622	-0.00026	-0.00050	-0.02669	-0.05636	0.00971	-0.03306	0.35285	0.23474**
<b>Days to maturity</b>	-0.00299	<b>-0.00982</b>	0.00030	0.00023	0.04470	-0.06619	-0.15323	-0.03436	0.34173	0.12037 <sup>NS</sup>
<b>Plant Height(cm)</b>	0.00041	-0.00097	<b>0.00304</b>	-0.00032	-0.00275	-0.03530	0.12668	-0.06455	0.18199	0.20823*
<b>Branch / plant</b>	0.00078	-0.00076	-0.00033	<b>0.00300</b>	0.00562	0.01817	-0.14956	0.05959	-0.10856	-0.1721*
<b>Pods/plant</b>	-0.00050	0.00173	0.00003	-0.00007	<b>-0.25337</b>	0.03395	0.11264	0.01151	0.50065	0.40657**
<b>Seeds/pod</b>	-0.00087	-0.00212	0.00035	-0.00018	0.02805	<b>-0.30662</b>	0.04985	-0.05561	1.02030	0.73315**
<b>Biological yield/ plant</b>	-0.00008	0.00246	0.00063	-0.00073	-0.04673	-0.02503	<b>0.61076</b>	-0.01524	-0.34268	0.18336*
<b>100 Seed wt</b>	-0.00071	-0.00153	0.00089	-0.00081	0.01324	-0.07742	0.04227	<b>-0.22023</b>	0.86242	0.61812**
<b>Harvest Index</b>	-0.00113	-0.00226	0.00037	-0.00022	-0.08556	-0.21100	-0.14116	-0.12810	<b>1.48264</b>	0.91358**

100 seed weight had positive indirect effect via harvest index (0.86242), biological yield per plant (0.04227), number of pods per plant (0.01324) and plant height (0.00089). It had negative indirect effect via number of seeds per pod (-0.07742), days to maturity (-0.00153), number of branches per plant (-0.00081) and days to 50% flowering (-0.00071). This character had highly significant positive correlation (0.61812) with seed yield per plant.

Harvest index had positive indirect effect via plant height (0.00037). It had negative indirect effect via days to maturity (-0.00226), days to 50% flowering (-0.00113), number of branches per plant (-0.00022), biological yield per plant (-0.14116), number of pods per plant (-0.08556), 100 seed weight (-0.12810) and number of seeds per pod (-0.21100). This character had highly significant positive correlation (0.91358) with seed yield per plant.

**Table 4.7 Direct and indirect effect of ten causal variables on seed yield of Pigeonpea at phenotypic level**

Characters	Days to 50% flowering	Days to maturity	Plant Height (cm)	Branch/ plant	Pod /plant	Seeds /pod	Biological yield/plant	100 Seed wt	Harvest Index	Correlation of seed Yield
<b>Days to 50% flowering</b>	<b>-0.0033</b>	-0.00297	-0.00001	-0.00035	0.01168	0.03721	0.01071	0.02711	0.09932	0.17943*
<b>Days to maturity</b>	-0.00187	<b>-0.0052</b>	0.00027	0.00016	-0.03171	0.04749	-0.04997	0.02816	0.10983	0.09716 <sup>NS</sup>
<b>Plant Height (cm)</b>	0.00001	-0.00052	<b>0.00272</b>	-0.00024	-0.00489	0.00938	0.01057	0.02771	0.03476	0.0795 <sup>NS</sup>
<b>Branch / plant</b>	0.0004	-0.00029	-0.00022	<b>0.00288</b>	0.00403	-0.00554	-0.04243	-0.03628	-0.0076	-0.0851 <sup>NS</sup>
<b>Pods/plant</b>	-0.00019	0.0008	-0.00006	0.00006	<b>0.20497</b>	-0.02413	0.0272	-0.00701	0.26381	0.46545**
<b>Seeds/pod</b>	-0.00045	-0.00091	0.00009	-0.00006	-0.01832	<b>0.27005</b>	0.01439	0.03975	0.41368	0.71822**
<b>Biological yield / plant</b>	-0.00015	0.00109	0.00012	-0.00051	0.0234	0.01631	<b>0.23825</b>	0.01579	-0.15177	0.14253 <sup>NS</sup>
<b>100 Seed wt</b>	-0.00048	-0.0008	0.00041	-0.00057	-0.0078	0.05828	0.02042	<b>0.18422</b>	0.31491	0.56859**
<b>Harvest Index</b>	-0.00053	-0.00093	0.00015	-0.00004	0.08787	0.18152	-0.05876	0.09427	<b>0.6154</b>	0.91895**

Residual are 0.00752

\* Significant at 5 level of probability

\*\* Significant at 1% level of probability

**4.7.2 Phenotypic correlation coefficient allocation for path coefficient analysis:** Table 4.7. List the phenotypic correlation coefficients divided into direct effects and indirect effects.

**Direct effects**

Among the 10 characters studied, harvest index (0.6154) recorded the highest direct positive direct effect on seed yield per plant followed by number of seeds per pod (0.27005), biological yield per plant (0.23825), number of pods per plant (0.20497), 100 seed weight (0.18422), number of branches per plant (0.00288) and plant height (0.00272). Rest of the characters like days to maturity (-0.0052) and days to 50% flowering (-0.0033) showed negative direct effects of high magnitude.

The characters days to 50% flowering, number of pods per plant, number of seeds per pod, 100 seed weight and harvest index recorded high magnitude with significant positive association with seed yield while the characters days to maturity, plant height and biological yield per plant had high magnitude of positive direct effects but non-significant association with grain yield per plant. The character branches per plant showed negative non-significant association with seed yield per plant.

**Indirect effect**

The character days to 50 percent flowering had positive indirect effects via number of pods per plant (0.01168), biological yield per plant (0.01071), number of seeds per pod (0.03721), 100 seed weight (0.02711) and harvest index (0.09932) while negative indirect effects via days to maturity (-0.00297), plant height (-0.00001) and number of branches per plant (-0.00035). It had positive significant correlation (0.17943) with seed yield per plant.

The character days to maturity had positive indirect effects via number of seeds per pod (0.04749), number of branches per plant (0.00016), plant height (0.00027), 100 seed weight (0.02816), harvest index (0.10983) while negative indirect effects via days to 50 % flowering (-0.00187), number of pods per plant (-0.03171), biological yield per plant (-0.04997). It had positive non-significant correlation (0.09716) with seed yield per plant.

Plant height had positive indirect effect via harvest index (0.03476), number of seeds per pod (0.00938), biological yield per plant (0.01057), 100 seed weight (0.02771) and days to 50 percent flowering (0.00001). It had

negative indirect effect via days to maturity (-0.00052), number of branches per plant (-0.00024) and days to maturity (-0.00052). This character had positive but non-significant correlation (0.0795) with seed yield per plant.

Number of branches per plant had positive indirect effect via number of pods per plant (0.00403), days to 50 percent flowering (0.0004). It had negative indirect effect via harvest index (-0.0076), days to maturity (-0.00029), plant height (-0.00022), number of seeds per pod (-0.00554), biological yield per plant (-0.04243), 100 seed weight (-0.03628). This character had negative non-significant correlation (-0.0851) with seed yield per plant.

Number of pods per plant had positive indirect effect via harvest index (0.26381), biological yield per plant (0.0272), number of branches per plant (0.00006) and days to maturity (0.0008). It had negative indirect effect via 100-seed weight (-0.00701), number of seeds per pod (-0.02413) and days to 50 percent flowering (-0.00019) and plant height (-0.00006). This character had positive significant correlation (0.46545) with seed yield per plant.

Number of seeds per pod had positive indirect effect via harvest index (0.41368), biological yield per plant (0.01439), 100 seed weight (0.03975) and plant height (0.00009). It had negative indirect effect via days to 50% flowering (-0.00045), days to maturity (-0.00091), number of branches per plant (-0.00006) and number of pods per plant (-0.01832). This character had positive significant correlation (0.71822) with seed yield per plant.

Biological yield per plant had positive indirect effect via number of pods per plant (0.0234), Number of seeds per pod (0.01631), 100-seed weight (0.01579), days to maturity (0.00109) and plant height (0.00012). It had negative indirect effect via days to 50% flowering (-0.00015), number of branches per plant (-0.00051) and harvest index (-0.15177). This character had positive non-significant correlation (0.14253) with seed yield per plant.

100-seed weight had positive indirect effect via harvest index (0.31491), biological yield per plant (0.02042), number of seeds per pod (0.05828) and plant height (0.00041). It had negative indirect effect via number of pods per plant (-0.0078), number of branches per plant (-0.00057), days to maturity (-0.0008) and days to 50% flowering (-0.00048). This character had positive significant correlation (0.56859) with seed yield per plant.

Harvest index had positive indirect effect via number of pods per plant (0.08787), 100-seed weight (0.09427), number of seeds per pod (0.18152) and plant height (0.00015). It had negative indirect effect via days to 50 percent flowering (-0.00053), days to maturity (-0.00093), number of branches per plant (-0.00004) and biological yield per plant (-0.05876). This character had positive significant correlation (0.91895) with seed yield per plant.

#### 4.8 Genetic divergence ( $D^2$ analysis)

The genetic divergence or  $D^2$  values calculated by Mahalanobis  $D^2$  statistics, between all possible traits of fifty genotypes.

##### 4.8.1 Clustering pattern of genotypes

By using the Tocher method suggested by Rao (1952) the cluster was formed. The distribution of fifty genotypes in different clusters was presented in Table 4.8.

**Table 4.8 Grouping of Pigeonpea genotypes into different clusters by Tocher method.**

Cluster number	Number of Genotypes	Genotypes
I.	11	IBTT DRG 5, GRG 152, BDN 2013-45, IBT DRG 6, ICPH 2740, TDRG 60, ICPL 99050, GRG 333, RVSA 1510, TDRG 58AGL 1603-4
II.	6	BDN 711, MLTP 1-0012, PUSA 992, UPAS 120, RVSA16-1, ASHA
III.	5	MARUTI, PUSA 991, ICP-88039, ICPH 3933, ICPL 20116
IV.	7	RVSA15-5, PUSA16, RVSA15-6, LAXMI, ICPH3762, ICPL 20103, ICPL 20096
V.	3	ICPL 20108, IBT RG 3, ICPL -87
VI.	2	LRG 52, TS 3 R
VII.	5	BDN 2014-1, BDN 2011-1, BDN 2013-41, LRG 105, LRG 160
VIII.	2	JKM 189, TDRG 4
IX.	4	AISHWARYA, ICPH 2871, GRG 177, RVSA 16-4
X.	1	BDN 20142-02
XI.	1	RVSA 28-1
XII.	2	IBT DRG 4, LRG 41
XIII.	1	TJT 501

On the basis of magnitude of  $D^2$  values, the fifty genotypes were grouped into thirteen clusters. Cluster I is the largest cluster with 11 genotypes followed by cluster IV with 7 genotypes whereas the cluster X, XI and XIII were solitary.

#### 4.8.2 Intra and Inter cluster divergence

Table number 4.9 represented the average intra and inter cluster  $D^2$  values whereas the Table number 4.10 represented the average intra and inter cluster distances  $(D) = (\sqrt{D^2})$ .

The highest intra cluster distance was observed for cluster IX ( $D=6.48$ ) followed by cluster XII ( $D=6.463$ ), cluster V ( $D=6.390$ ), cluster I ( $D=6.182$ ), cluster III ( $D=6.033$ ), cluster VII ( $D=5.950$ ), cluster IV ( $D=5.581$ ), cluster VIII ( $D=5.518$ ), cluster II ( $D=5.437$ ) and cluster VI ( $D=4.00$ ) while cluster X, XI and XIII showed no intra cluster distance.

The maximum inter cluster distance was observed between cluster XII and VI ( $D=18.322$ ) followed by cluster XIII and XII ( $D=15.424$ ), cluster XII and VIII ( $D=15.227$ ), cluster XIII and IX ( $D=14.869$ ), cluster XIII and II ( $D=14.357$ ), cluster XII and XI ( $D=14.351$ ), cluster VII and VI ( $D=13.600$ ), cluster VI and V ( $D=13.528$ ) while inter cluster distance between cluster X and IV ( $D=7.139$ ), cluster X and III ( $D=7.211$ ), cluster X and VII ( $D=7.318$ ), cluster V and I ( $D=7.520$ ) and cluster II and I ( $D=7.590$ ) recorded low inter cluster distance among themselves and others.

**Table no 4.9 Average intra (bold) and inter cluster values in 13 clusters (D<sup>2</sup>) in Pigeonpea.**

[illegible]

**Table no 4.10 Average intra (bold) and inter cluster values in 13 clusters (D) = ( $\sqrt{D^2}$ ) in Pigeonpea.**

[illegible]

#### **4.8.3 Cluster means**

The cluster means for ten characters among fifty genotypes are presented in Table 4.11.

##### **Days to 50% flowering**

The genotypes in the cluster IX (86.417 days) were early for the days to 50% flowering followed by cluster VII (91.667 days), cluster II (95.278 days), cluster X (95.333 days), cluster XII (100.167 days), cluster XI (104.00 days), cluster III (106.067 days), cluster IV (106.333 days), cluster I (109.242 days), cluster V (111.333 days), cluster XIII (115.00 days), cluster VIII (115.167 days) and cluster VI (115.500 days).

##### **Days to maturity**

Cluster mean for this character varied between 123.333 days to 150.333 days with population mean of 138.426 days. The genotypes from cluster XI were early for this character and cluster X were late for this character.

##### **Plant height**

The population mean for this character was 164.070 and a wide range was noticed for this character. High cluster mean values were recorded by cluster X (172.00) whereas lowest values were observed for cluster XIII (150.667).

##### **Number of branches per plant**

Cluster mean for this character ranged between 20.400 for cluster XI to 25.500 for cluster XIII. The population mean for this character is 23.081.

##### **Number of pods per plant**

The cluster mean of this character ranged from 182.667 clusters VI to 223.238 clusters IV. The population mean for this character is 201.891.

##### **Number of seed per pod**

The highest cluster mean of this character is recorded by the genotype in cluster XIII (4.733) while lowest by the genotype in cluster XII. The population mean for this character is 3.817.

##### **Biological Yield/Plant (gm)**

The cluster mean of this character is between 162.133 (cluster VIII) to 207.767 (cluster VI). The population mean for this character 191.393.

**Seed Yield/Plant (gm)**

The cluster mean of this character is between 49.117 (cluster XII) to 116.350 (cluster VIII). The population mean for this character is 82.212.

**100 Seed Weight (gm)**

The highest cluster mean of this character is recorded by the genotype in cluster VI (12.633) while the lowest by the genotype in cluster XII (8.983). The population mean for this character is 10.653.

**Harvest Index**

The highest cluster mean of this character is recorded by the genotype in cluster VIII (56.617) while the lowest is recorded by the genotype in cluster XII (26.367). The population mean for this character is 43.124.

**Table 4.11 Cluster means performance for 10 characters in fifty genotypes of Pigeonpea**

Characters	Clusters													Population mean
	I.	II.	III.	IV.	V.	VI.	VII.	VIII.	IX.	X.	XI.	XII.	XIII.	
<b>Days to 50% flowering</b>	109.242	95.278	106.067	106.333	111.333	115.500	91.667	115.167	86.417	95.333	104.000	100.167	115.000	103.962
<b>Days to maturity</b>	138.394	126.278	139.000	147.286	146.778	147.500	134.133	139.667	123.500	150.333	123.333	135.667	147.667	138.426
<b>Plant height (cm)</b>	168.121	164.333	167.133	169.095	159.444	165.000	166.867	159.167	166.917	172.000	165.333	158.833	150.667	164.070
<b>Branch/plant</b>	24.524	21.361	22.660	23.567	23.667	19.800	24.613	20.700	23.250	24.733	20.400	25.283	25.500	23.081
<b>Pod/plant</b>	223.212	210.056	191.200	223.238	203.889	182.667	183.400	226.167	218.083	190.000	218.000	188.667	166.000	201.891
<b>Seed/pod</b>	3.761	3.533	4.467	3.748	3.956	3.750	3.827	4.333	3.550	3.733	3.333	2.900	4.733	3.817
<b>Biological yield/plant (g)</b>	203.670	201.256	202.300	176.491	182.344	207.767	179.433	205.767	201.775	199.133	178.933	187.100	162.133	191.393
<b>Seed yield / plant (g)</b>	83.849	70.933	92.387	90.895	76.778	86.517	71.567	116.350	84.400	80.867	82.933	49.117	82.167	82.212
<b>100 seed weight (g)</b>	9.991	9.533	10.787	10.881	9.456	12.633	10.180	11.900	10.883	11.400	11.400	8.983	10.467	10.653
<b>Harvest index</b>	41.236	35.317	45.740	51.581	42.256	41.750	40.040	56.617	41.975	40.567	46.467	26.367	50.700	43.124

#### 4.8.4 Per cent contribution of various characters for divergence

All ten character study was conducted on fifty genotypes of pigeonpea. The collected data is used to determine the divergence (table no.4.12). Within ten characters studied the character Biological Yield/Plant (gm) (22.12245%) contributed the highest for divergence followed by Seed yield/Plant (gm) (16.16327%), Day to 50% flowering (14.77551%), 100 seed weight (gm) (13.38776%), and days to maturity (13.14286%), number of branches /plant (9.632653%), number of seeds /pod (7.102041%). Number of pods per plant (3.346939%) and harvest index (.3265306%) recorded lowest contribution for divergence. The character plant height contributed zero percent for the divergence.

**Table 4.12 Contribution of various characters towards divergence in pigeonpea genotypes.**

S.No.	Characters	Contribution (%)
1.	<b>Days to 50% flowering</b>	14.77551
2.	<b>Days to maturity</b>	13.14286
3.	<b>Plant height (cm)</b>	0
4.	<b>Number of Branches/plant</b>	9.632653
5.	<b>Number of Pods/plant</b>	3.346939
6.	<b>Number of Seeds/pod</b>	7.102041
7.	<b>Biological yield /plant (g)</b>	22.12245
8.	<b>Seed yield / plant (g)</b>	16.16327
9.	<b>100 seed weight (g)</b>	13.38776
10.	<b>Harvest index</b>	.3265306

## **CHAPTER V**

### **DISCUSSION**

Yield is the ultimate standard that plant breeders must always be complying with but be careful when assessing the genotype of any crop. However, the highest seed yield is a complex feature controlled by multiple genes. It is often difficult to make a choice directly target such a complex character. Therefore, the difference between characters is greater and must have the prerequisites for in-depth research on the association of characters. The results obtained under present investigation of pigeonpea are discussed here in detail in the following heads.

#### **5.1 General performance of genotypes**

##### **5.1.1 Genetic variability**

Genetic variability is prerequisite for any crop breeding programme. Therefore, plant breeders are always interested in collecting or creating variability, exploration and recombination. Moreover, plant breeders should thoroughly understand the nature and expression of different characters and variability range present in a population of crops before accepting the different methods for assessment of variability in the population. The technique to adopt any breeding programme depends upon the nature and magnitude of variability present in the programme.

In the current investigation, it is observed that large range of variation present in the genotypes of all characters in the study. Characters showing highly significant mean sum of squares of all characters indicates the degree of variability in the population.

##### **5.1.2 Range of variability**

The variability of wide range is present for almost all the character. Genotype AISHWARYA (85.00) recorded minimum number of days to 50% flowering while the maximum number of days to 50% flowering was recorded by the genotype TS 3 R (117.30). Genotype GRG 177 (116.70) recorded minimum number of days to maturity while the maximum number of days to maturity was recorded by the genotype LAXMI (154.0). Genotype TJT 501 (150.7) was dwarf genotype for plant height while the tallest genotype for plant height was recorded by the genotype BDN 2013-41 (178.7). Genotype IBT

DRG-4 (26.30) recorded maximum number of branches while the minimum number of branches was recorded by the genotype TDRG 4(18.60). Genotype ICPL 20103 (237.70) recorded maximum number of pods per plant while the minimum number of pods per plant was recorded by the genotype BDN 2013-41 (164.0). The genotypes TJT 501 (4.70) showed highest number of seeds per pod where the genotype LRG 41 (2.60) showed lowest number of seeds per pod. The genotypes TS-3-R recorded highest (210.0 g) Biological yield per plant while the genotype TJT-501 (162.1 g) showed lowest biological yield per plant. The genotypes JKM-189 recorded highest (118.0 g) seed yield per plant while the genotype LRG-41 (45.10 g) showed lowest seed yield per plant. The genotype LRG 52 (12.8 g) showed highest 100 seed weight while the genotype GRG 333 (8.5 g) showed lowest 100 seed weight. The genotypes ICPL 20103 recorded highest (59.80) harvest index while the genotype LRG 41 (23.0) showed lowest harvest index.

### **5.1.3 Genotypic and phenotypic coefficients of variation:**

Phenotype of any individual plant is the result of genotype and its effect with environment. Thus, phenotypic and genotypic coefficient of variation plays an important role in understanding the nature and extent of variability in the population studied. Estimates of GCV and PCV for all characters research shows that the difference is small, with PCV slightly larger than the former indicates that there is variability in these characters mainly due to genetic factors.

It was observed that the estimates for genotypic coefficient of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the ten characters. Sodavadiya *et al.* (2009), Shunyu *et al.* (2013) and Mallesh *et al.* (2017) also observed higher PCV value than GCV value for all the traits.

However, looking to the magnitudinal differences between GCV and PCV estimates, the maximum differences between PCV and GCV values were observed for Plant height. The GCV and PCV difference was of lowest of magnitude for days to maturity. This shows that selection based on these characters would facilitate isolation of desirable genotypes. These findings are in agreement with the results obtained by Bhadru (2008). Similar results were reported by Shrivastava *et al.* (1976).

#### **5.1.4 Heritability (broad sense) and genetic advance:**

The efficacy of selection for any character depends not only on the magnitude of variability present for the character but also on the extent to which it can be transferred to the offspring from parents. Heritability estimates along with genetic advance is more important than heritability alone to predict the resulting effects of selection. Broad sense heritability includes the contribution of additive gene effect. In reality, heritability and genetic advance are two complementary aspects of crop improvement through selection.

Heritability estimates are helpful in predicting the gain under selection. It is the heritable portion of phenotypic variance and a good index of the transmission of character from parents to the offspring. The heritability estimates in broad sense were classified by Robinson et al. (1951) as low (<50%), medium (50-70%) and high (>70%).

Heritability in broad sense ranged from 20.751 to 88.756 per cent. Highest heritability was exhibited for the character 100 seed weight (88.756%) followed by days to maturity (84.689%) and biological yield per plant (84.483%). The lowest heritability estimate recorded in plant height (20.751%) followed by pods per plant (66.012%) showing medium heritability. Other characters had heritability at the tune of 74.026 per cent for harvest index, 75.684 per cent for seed yield per plant, 76.724 per cent for seed per pod and 77.524 per cent for branches per plant showing high heritability. This result indicates that the characters showing high heritability were highly heritable and hence were less affected by the environment. Similar high heritability estimates have been reported by Saroj et al. (2013) and Shunyu et al. (2013).

Heritability estimates alone are useful in predicating the response to selection, if it is accompanied by genetic advance which will provide better picture of gene action of the traits (Johnson et al., 1955).

The range of genetic advance was ranged from 0.861 to 31.327. The highest estimates of genetic advance were noticed in pods per plant (31.327), seed yield per plant (26.895) followed by biological yield per plant (26.541), where as lowest estimates of genetic advance was recorded in seeds per pod (0.861). Similar results were observed by Sidhu *et al.* (1985), Aher et al. (1998), Takalkar *et al.* (1998) and Bhadru (2008). Partially similar results were observed by Patel and Patel (1992).

High estimates of GCV, PCV, heritability and genetic advance as percentage of mean were observed for biological yield per plant and for seed yield per plant. Thus these characters seem to be more promising.

## **5.2 Correlation studies**

Direct improvement in the yield is difficult because it is complex in nature and there is high influence of the environmental factors. A correlation study gives an idea about the degree of association the different components of yield are having. Many plant traits which are highly heritable and they are also associated with the yield provide an opportunity for making direct and effective selection for improvement yield. Thus improvement in the desirable traits can be made with the help of direct selection through associated characters.

It is significant to know how the improvement of one character will cause concurrent changes in other character and thirdly in association with normal determination. The estimation of correlation coefficients cannot be consistent. It changes significantly as per sort of material taken care of and ecological conditions in which material developed despite the fact that the material utilized is the equivalent the natural counting preparation, plant population and the social practices changes the estimations of correlation coefficients significantly. It was revealed from the current investigation, the genotypic correlation coefficients among the vast majorities of the characters were higher than the phenotypic correlation coefficients. The phenotypic correlations are generally of a lower magnitude than genotypic correlation due to the masking effect of environment. This shows that there was a solid inherent relationship between different characters considered and the equivalent were less affected by ecological conditions.

### **5.2.1 Association of seed yield per plant with its components**

It is revealed from the current examination that seed yield per plant is significantly and positively correlated with 100 seed weight, days to 50% flowering, number of pods per plant, number of seeds per pod and harvest index at phenotypic level. While seed yield per plant is significantly and positively correlated with days to 50% flowering, plant height, number of pods per plant, number of seeds per pod, biological yield, 100 seed weight and harvest index at genotypic level.

Sodavadiya *et al.* (2009) reported that the seed yield per plant had significant and positive association with days to 50 % flowering.

Pansurya *et al.* (1998) and Basawarajah *et al.* (1999) obtained similar result for number of pods per plant. Khapre and Nerkar (1986) and Bal *et al.* (2018) for harvest index.

The above results are in agreement with the finding of Beohar *et.al* (1980), Asawa *et al.* (1981), Yadavandra *et al.* (1981), Shoram (1983), Sawant *et al.* (2009), Kesha *et al.* (2016) and Narayanan *et al.* (2018) for number of pods per plant at genotypic level.

Therefore, for high seed yield potential of pigeonpea, the plants should have more number of pods per plant, number of seeds per pods, harvest index, days to 50% flowering and 100 seed weight.

### **5.3 Path coefficient analysis**

Simple correlation coefficient provides the measure of positive and negative association between variables but it does not give the causal basis of such association. Path analysis provides the information on direct and indirect effects of various independent components on the dependent character. The general connection saw between any two characters is a component of a progression of direct as well as indirect connection between those characters. Seed yield is the result of interaction of segment characteristics.

Path coefficient examination plot by Wright (1921) was completed to locate the indirect and direct impacts of yield components on seed yield. Apart from correlation, path analysis is critical to get the data about various manners by which parts characters impact the seed yield. Hence, path investigation gives the base to the breeder for planning to determine the best program in view of hardly any dependable characters. The total phenotypic and genotypic correlation coefficients are further partitioned into direct and indirect effects through path coefficient analysis.

Path analysis revealed that at phenotypic level harvest index recorded the highest direct positive direct effect on seed yield per plant followed number of seeds per pod, biological yield per plant, number of pods per plant, 100 seed weight, number of branches per plant and plant height. Hence direct selection based on these characters will be effective.

The character days to 50% flowering showed negative direct effects but positive correlation which could be due to indirect effects. Indirect contribution of harvest index of plant through biological yield per plant was negative and of moderate magnitude. It clearly indicated that increase in the harvest index resulted in decrease in the biological yield per plant.

Partially similar results laying emphasis on more number of pods per plant and number of seeds per plant in selection programme of pigeonpea were given by Sawant *et al.* (2009), Rekha *et al.* (2013) and Saroj *et al.* (2013).

### **5.5 Genetic divergence:**

$D^2$  statistics helps in the selection of various genetically divergent parents for their exploitation in hybridization programmes. This technique measures the degree of diversification and also determines the relative proportion of each components/characters to the total divergence. It usually measures the forces of differentiation at two levels i.e. intra cluster and inter cluster levels. It provides reliable estimates of genetic divergence and a large number of germplasm lines can also be evaluated at time for genetic diversity. The considerable measure of variability in the quantitative characters shows up to lead the wide scope of genetic diversity among the genotypes under study.

Thus,  $D^2$  examination dependent on Mahalanobis  $D^2$  measurements (Mahalanobis, 1936) was done to evaluate the level of dissimilarity among the 50 pigeon pea genotypes to survey the relative contribution of various parts to the absolute dissimilarity at inter and intra group levels.

On the basis of  $D^2$  statistics values, the fifty genotypes were grouped in 13 clusters. Cluster I is the largest cluster with 11 genotypes followed by cluster IV with 7 genotypes whereas the cluster X, XI and XIII were solitary. Similar results have obtained by Firoz *et al.* (2006).

The cluster I was included of eleven genotypes. These genotypes were better than average for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, biological yield per plant and seed yield per plant.

The cluster II was included six genotypes. These genotypes were better than average for plant height, number of pods per plant and biological yield per plant.

The cluster III was included five genotypes. This genotype had better average for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, biological yield per plant, seed yield per plant, 100 seed weight and harvest.

The cluster IV includes seven genotypes. The average values of genotypes for days to 50% flowering, days to maturity, plant height, number of branches per Plant, number of pods per plant, seed yield per plant, 100 seed weight and harvest index were superior to their respective population means.

The cluster V includes three genotypes, had better average for the characters days to 50% flowering, days to maturity, number of branches per plant, Number of Pod per Plant and number of seeds per pod surpassing their respective population mean.

The cluster VI was included two genotypes, had better average for the characters days to 50% flowering, Days to maturity, plant height (cms), biological yield per plant, seed yield per plant and hundred seed weight. The average value of these characters were exceeded their respective population mean.

The cluster VII includes five genotypes, had better average for the characters plant height, number of branches per plant and number of seed per pods. The average value of these characters exceeding their respective population mean.

The cluster VIII include two genotype, had better average for the characters days to 50% flowering, days to maturity, number of pods per plant, number of seed per pods, biological yield per plant, seed yield per plant, 100 seed weight and harvest index. The average value of these characters were exceeded their respective population mean.

The cluster IX includes four genotypes, had better average for the characters plant height, number of branches per plant, number of pods per plant, biological yield per plant, Seed Yield per Plant(gm) and hundred seed weight. The average value of these characters were exceeded their respective population mean

The cluster X include one genotype, had better average for the characters days to maturity, Plant Height(cm), number of branches per plant,

100 seed weight and biological yield per plant. The average value of these characters were exceeded their respective population mean.

The cluster XI includes one genotype, had better average for the characters days to 50% flowering, plant height (cms), number of pods per plant, seed yield per plant, 100 seed weight and harvest index.

The cluster XII includes two genotypes, had better average for the characters number of branches per plant.

The cluster XIII includes one genotype, had better average for the characters days to 50% flowering, days to maturity, number of branches per plant, number of seeds per pod and harvest index. The average value of these characters were exceeded their respective population mean.

Intra-cluster distance is another boundary, other than cluster mean for specific character, as it demonstrates the degree of inconstancy existed in the genotypes contained in a specific cluster. High intra-cluster distance inside a group showed high extent of changeability inside the cluster offers scope for development by different determination techniques. The highest intra cluster distance was observed for cluster IX followed by cluster XII, cluster V, cluster I, cluster III, cluster VII, cluster IV, cluster VIII, cluster II and cluster VI while cluster X, XI and XIII showed no intra cluster distance. Thereby cluster IX showed highest degree of variability. The single groups demonstrating their autonomous identity and significance due to the one of a kind characters comprised by that genotypes. These genotypes may fill in as expected parents for breeding program.

The inter cluster considers showed extent of genetic divergence between the cluster. It demonstrated that, how much this cluster was hereditarily different from one another. The maximum inter cluster distance was observed between cluster XII and VI followed by cluster XIII and XII, cluster XII and VIII, cluster XIII and IX, cluster XIII and II, cluster XII and XI, cluster VII and VI, cluster VI and V while inter cluster distance between cluster X and IV, cluster X and III, cluster X and VII, cluster V and I and cluster II and I recorded low inter cluster distance among themselves and others. The genotypes grouped in the clusters having high inter cluster distance i.e. cluster XII and VI can be used in breeding programme in order to get a wide spectrum of variability and transgressive segregants. The minimum distance between

clusters II and I indicated that they were genetically closure clusters. Selection of parents from such clusters may be avoided because it may result into a narrow genetic base. The above findings are broadly in agreement with report of Magar *et al.* (2008), Sreelakshmi *et al.* (2011) and Navneet *et al.* (2017).

### **5.6 Contribution of each character towards total divergence**

$D^2$  estimates disclose us the greatness of divergence between two bunches. The question emerges what are those characters which are liable for divergence between the genotypes. By examining the contribution of various characters towards the aggregate divergence, breeder can get a thought regarding the characters, which are principally answerable for the total divergence. This is significant while choosing the parents in breeding program.

All ten characters study was conducted on fifty genotypes of pigeonpea. Within ten characters studied the character biological yield/plant (gm) (22.12245%) contributed the highest for divergence followed by seed yield/plant (gm) (16.16327%), Day to 50% flowering (14.77551%), 100 seed weight (gm) (13.38776%), days to maturity (13.14286%), branches/plant (9.632653%) and number of seeds/pod (7.102041%). Number of pods per plant (3.346939%) and harvest index (.3265306%) recorded lowest contribution for divergence. The character plant height contributed zero percent for the divergence.

In this way, changes in variability in character among genotypes for breeding can't be made uniquely based on yield potential. Thus to improve it, choice must be finished considering biological yield per plant, seed yield per plant, days to 50% flowering, 100 seed weight as their commitment towards absolute uniqueness is more.

## **CHAPTER VI**

### **SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK**

The current investigation named, "Study of genetic diversity assessment for seed yield and its component traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]" will be undertaken with the following objectives:

1. To study the genetic variability, heritability and genetic advance for major quantitative traits.
2. To identify the seed yield contributing traits through association analysis.
3. To estimate the direct and indirect effects through path analysis.
4. To study genetic divergence and classify the genotypes through genetic distance.

The material for the current examination included 50 genotypes of Pigeonpea gathered from various parts of the nation which involved local and improved genotypes. These genotypes were planted in Randomized Block design with three replications during kharif season of 2019-20. Observations were recorded on ten characters viz., Days to 50% flowering, Days to maturity, Plant height (cm), No. of branches per plant, Number of pods per plant, Number of seed per pod, 100 seed weight (g), Biological yield per plant(g), Seed yield per plant (g) and Harvest index (%).

The investigation of variance uncovered significant variation among the genotypes for all the characters examined. The appraisals of mean sum of squares appeared nearly wide scope of variation for the characters number of pods per plant, seed yield per plant, biological yield per plant, days to maturity and days to 50% flowering while the least variation was recorded for 100 seed weight and number of seeds per pod.

The variability of wide range is present for almost all the character. Variation present and observed for seed yield per plant ranged between 45.10 gm to 118.0 gm. The other yield contributing characters also showed wide amount of variability like Days to 50 % flowering (85.00 to 117.30 days), Days to maturity (116.70 to 154 days), Plant height (150.7 to 178.7 cms), number of branches per plant (18.6 to 26.30), Number of pods per plant (164.0 to 237.7), number of seeds per pod (2.60 to 4.70), 100 seed weight (g) (8.5 gm to 12.8

gm), Biological yield/ plant(g) (162.10 gm to 217.00 gm) and Harvest Index (23.0 to 59.80).

The appraisals of phenotypic and genotypic variance uncovered that phenotypic changes are higher than genotypic fluctuations for all the characters examined. Extraordinary characters demonstrated differing percent of coefficient of variance at both phenotypic and genotypic levels. The highest GCV was recorded for harvest yield per plant followed by seed yield per plant and the character plant height was recorded lowest GCV followed by days to maturity. The highest PCV was recorded for harvest index followed by seed yield per plant. The character plant height was recorded lowest PCV.

Appreciable heritability values were observed for the characters under study. Highest heritability was exhibited by the character 100 seed weight followed by days to maturity. The lowest heritability estimate recorded in plant height followed by number of pods per plant.

The highest estimates of genetic advance were noticed in character number of pods per plant followed by seed yield per plant and lowest estimates of genetic advance were noticed in seeds per pod.

High estimates of heritability attached with higher genetic advance as per cent of mean was observed for biological yield per plant and for seed yield per plant, whereas the lowest genetic advance as per cent of mean was recorded in plant height (cm). Thus, it indicates the role of additive gene action in the expression of such characters.

In the current examination, the genotypic correlation coefficients were higher in extent than their phenotypic partners for the majority of the characters. The characters 100 seed weight, days to 50% flowering, number of pods per plant, number of seeds per pod and harvest index profoundly high significant positive correlation with grain yield per plant at both phenotypic and genotypic levels.

Path coefficient analysis revealed that the characters *viz.*, harvest index recorded the highest direct positive direct effect on seed yield per plant followed number of seeds per pod, biological yield per plant, number of pods per plant, 100 seed weight, number of branches per plant and plant height at both phenotypic and genotypic levels. Rest of the characters like days to maturity (-0.0052) and days to 50% flowering (-0.0033) showed negative direct effects of

high magnitude. The character days to 50% flowering showed negative direct effects but positive correlation which could be due to indirect effects.

The elevated level of  $D^2$  estimates demonstrated wide scope of dissimilarity among the population of pigeonpea. On the basis of  $D^2$  statistics values, the fifty genotypes were grouped in 13 clusters. Cluster I is the largest cluster with 11 genotypes followed by cluster IV with 7 genotypes whereas the cluster X, XI and XIII were solitary. The highest intra cluster distance was observed for cluster IX followed by cluster XII, cluster V, cluster I while the maximum inter cluster distance was observed between cluster XII and VI followed by cluster XIII and XII. Within ten characters studied the character biological yield/plant (g) contributed the highest for divergence followed by seed yield/plant (g).

### **Conclusion:**

- The mean sum of squares appeared nearly wide scope of variation for the characters number of pods per plant, seed yield per plant, biological yield per plant, days to maturity and days to 50% flowering while the least variation was recorded for 100 seed weight and number of seeds per pod.
- The variability of wide range is present for almost all the character.
- The highest GCV and PCV was recorded for harvest yield per plant followed by seed yield per plant and the character plant height was recorded lowest GCV followed by days to maturity.
- There exists a magnitudinal differences between GCV and PCV estimates, the maximum differences between PCV and GCV values was observed for Plant height. The GCV and PCV difference was of lowest of magnitude for days to maturity. This shows that selection based on these characters would facilitate isolation of desirable genotypes.
- High heritability was shown by characters 100 seed weight, days to maturity and biological yield per plant. Thus they are less affected by environment and can be improved by direct selection.
- High genetic advance was seen in number of pods per plant, seed yield per plant and biological yield per plant. Considering high GCV, PCV, Heritability and Genetic advance characters i.e. biological yield per plant and seed yield per plant are to be more promising.

- 100 seed weight per plant, days to 50% flowering, number of pods per plant, number of seeds per pod and harvest index showed significant and positive correlation at genotypic and phenotypic level. Therefore, for high seed yield potential of pigeonpea, the plants should have more number of pods per plant, number of seeds per pods, harvest index, days to 50% flowering and 100 seed weight.
- Path analysis revealed that Harvest index recorded the highest direct positive direct effect on seed yield per plant followed number of seeds per pod, biological yield per plant. Hence direct selection based on these characters will be effective.
- On the basis of  $D^2$  statistics values, the fifty genotypes were grouped in 13 clusters. Cluster I is the largest cluster with 11 genotypes. Cluster IX showed high degree of variability as it has highest intra cluster distance. Thus genotypes i.e. AISHWARYA, ICPH 2871, GRG 177 and RVSA 16-4 are promising.
- The maximum inter cluster distance was observed between cluster XII and VI. Thus genotypes IBT-DRG-4, LRG-41, LRG-52 and TS-3-R can be used in breeding programme to get wide variability. However cluster II and I showed minimum inter cluster distance, thus, genotypes from these cluster should be avoided as they have narrow genetic base.

The genotypes JKM 189, TDRG 4, ICPH 3762, ICPL 20103, BDN 2013-45 and TDRG 58 are seen as promising genotypes in the considered genotypes as these performed well for a large portion of the significant quantitative qualities.

#### **Suggestion for further work :**

1. Sufficient genetic variability for different characters is available that can be used in genetic improvement through direct selection and cross breeding programme and where it lacks, we need more germplasm.
2. High heritability in broad sense for 100 seed weight, days to maturity and biological yield per plant suggested that they can be improved by direct selection.

3. The genotypes i.e. AISHWARYA, ICPH 2871, GRG 177 and RVSA 16-4 were found high yielder in this investigation which can also be utilized for development of high yielding varieties and crossing programme.
4. Genotypes used in present investigation should be tested in different agronomic situations and environment.

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