

**ASSESSMENT OF PIGEONPEA (*Cajanus cajan* L.) GENOTYPES
AGAINST *FUSARIUM* WILT**

Submitted by

Mr. Wagh Tushar Vitthal

(Reg. No.018 /040)

A Thesis submitted to the
**MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI – 413 722, DIST- AHMEDNAGAR,
MAHARASHTRA, INDIA.**

In partial fulfilment of the requirements for the degree
of

**MASTER OF SCIENCE (AGRICULTURE)
in
AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**



DEPARTMENT OF AGRICULTURAL BOTANY

**POST GRADUATE INSTITUTE
MAHATMA PHULE KRISHI VIDYAPEETH
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2021

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
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by me or other person to
other University or Institute
for a Degree or
Diploma

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Date : / /2021

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This is to certify that the thesis entitled. “**ASSESSMENT OF PIGEONPEA (*Cajanus cajan* L.) GENOTYPES AGAINST *FUSARIUM WILT*”** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra) in partial fulfilment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the result of a piece of bonafide research work carried out by **Mr. WAGH TUSHAR VITTHAL** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been duly acknowledged.

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LIST OF ABBREVIATIONS AND SYMBOLS

%	: Per cent
/	: Per
Σ	: Summation of
σ^2	: Variance
b.s.	: Broad sence
cm	: Centimeter(s)
C.D.	: Critical difference
Cov.	: Covariance
C.V.	: Coefficient of variation
D.F.	: Degrees of freedom
EC	: Exotic collection
EMP	: Error Mean Sum of Product
<i>et al.</i>	: <i>et allia</i> (And other)
Fig.	: Figure
g	: Gram(s)
GA	: Genetic advance
GAM	: Genetic advance as per cent of mean
GMP	: Genotypic mean sum of products
h^2	: Heritability
i.e.	: <i>id est</i> (that is)
IC	: Indigenous collection
kg	: Kilogram (s)
M.S.S.	: Mean sum of squares
m	: Meter(s)

No.	: Number(s)
PCV	: Phenotypic coefficient of variation
R.B.D.	: Randomized Block Design
r	: Correlation coefficient
S.E.	: Standard Error
S.S.	: Sum of Squares
<i>Via.</i>	: By way of, by means of
<i>Viz.</i>	: Videlicet (Namely)
Vs.	: Versus

ABSTRACT

ASSESSMENT OF PIGEONPEA (*Cajanus cajan* L.) GENOTYPES AGAINST *FUSARIUM* WILT

by

Mr. WAGH TUSHAR VITTHAL

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In

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(GENETICS AND PLANT BREEDING)**

**POST GRADUATE INSTITUTE,
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2021

Research Guide	:	Dr. S.S. Patil
Department	:	Agricultural Botany

The investigation on “**Assessment of pigeonpea (*Cajanus cajan* L.) genotypes against *Fusarium* wilt**” was conducted on twenty-eight genotypes of pigeonpea including three checks BDN-711, Rajeshwari and ICP2376 with objectives- viz., to identify the resistant genotypes against *Fusarium* wilt, to study the correlation and path analysis between yield and yield contributing characters in pigeonpea.

Observations were recorded for days to 50 per cent flowering, days to maturity, plant height (cm), plant spread (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and wilt incidence (%).

Number of pods per plant exhibited highest range of variability followed by plant height, seed yield per plant, plant spread, days to 50% flowering and 100 seed weight shows considerable amount of variability. The lowest variability was observed for number of seeds per pod.

Genotypic and phenotypic coefficients of variation were highest for seed yield per plant followed by number of pods per plant, number of secondary branches per plant. Maximum heritability was observed for days to 50 percent flowering and days to maturity. The highest genetic advance as percent of mean was observed for seed yield per plant followed by days to 50 per cent flowering. This suggest that desired improvement of these traits would be effective by simple selection.

The significant positive correlation was reported between seed yield per plant with days to 50 percent flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant spread, number of pods per plant at both genotypic and phenotypic level. This indicates the simultaneous improvement of these characters through selection will be rewarding. It also showed significant negative correlation with plant height, Number of seeds per pod and 100 seed weight at both levels.

Path coefficient analysis revealed that the characters number of pods per plant, plant spread, number of primary branches per plant and days to 50% flowering show direct effect on seed yield per plant. Considering the correlation coefficient and path analysis simultaneously, number of pods per plant, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, and plant spread found to be true components of seed yield. So, these were the important yield components suggesting direct selection and can be given importance during selection.

Out of twenty-eight genotypes four genotypes *viz.*, RPS-2007-105-1, TTO-704-1-2, RVSA-1510, and BDN-711 exhibited resistant reaction for *Fusarium* wilt. Therefore, these four genotypes can be used in resistant breeding programme as a source of resistance parents for developing resistant cultivar.

1. INTRODUCTION

Pigeonpea (*Cajanus cajan* (L.) Millsp.) popularly known as redgram, tur and arhar belongs to family Fabaceae is one of the important grain legume crops of rainfed agriculture in the tropics and sub tropics. Pigeonpea is an often cross pollinated (20-70 %) crop with (2n=2x=22) diploid chromosome number. The origin of pigeonpea is not known with certainty. Presently, peninsular India is considered as the centre of origin of pigeonpea. From here it is supposed to have moved to East-Africa and further to the Nile and West Africa (Jeswani and Baldev, 1997). The major pigeonpea growing regions are south Asia, eastern and southern Africa, latin America and Australia.

It finds an important place in the farming systems adopted by small and marginal farmers in a large number of developing countries. Redgram is cultivated in wide range of soil textures, from clayee to sandy soil. However, pigeonpea is very sensitive to waterlogged conditions but tolerates low fertility soils. Being a drought resistant crop, it is suitable for dry land farming and predominantly used as an intercrop with other crops like cotton, sorghum, ground nut, black gram etc. to increase the yield and maintain soil fertility. It has an ability to fix the atmospheric nitrogen in soil at the rate of 20 kg per ha in symbiotic association with rhizobium under favourable conditions (Reddy *et al.*, 1990).

Pigeonpea ranks sixth among pulses in the world. India is the largest producer and constitutes 75% of world production. Other major growing countries are Myanmar, Kenya, Uganda and Malawi. India is also major consuming country and constitutes 90% of global consumption. Out of the total production of the pulse (239.5 lakh tonnes), 16.78 per cent share (40.2 lakh tonnes) is from pigeonpea (Directorate of Economics and Statistics, 2017 a 2nd advance estimate) and productivity of 711 kg/ha. In Maharashtra, it is grown in an area of 12.13 lakh ha with an annual production of 9.15 lakh tonnes and productivity of 850 kg/ha.

Pigeonpea is a protein rich staple food primarily used as a dhal, its green pods are used as vegetables. The woody stems of pigeonpea can also be used as firewood, fencing and thatch and the leaves and husks provide livestock feed and is an abundant source of minerals and vitamins (Saxena *et al.*, 2002). They contain high levels of protein and the rich source of lysine but usually deficit in sulphur containing amino acids.

Pigeonpea is a hardy, widely adopted and drought tolerant crop. The main constraints in boosting the yield of the crop are its susceptibility to diseases, insects and other physiological stress. Pigeonpea is known to be affected by more than hundred pathogens (Nene *et al.*, 1989). Some of the important diseases are *Fusarium* wilt (*Fusarium udum* Butler), *Phytophthora* blight (*Phytophthora drechsleri* Tucker), *Cercospora* leaf spot (*Cercospora cajani*), collar rot (*Sclerotium rolfsii* Sacc.), and dry root rot (*Rhizoctonia bataticola* (Taub.) Butler), *Alternaria* leaf spot (*Alternaria tenuissima* Wiltshire), powdery mildew (*Oidiopsis taurica* Salmon), sterility mosaic, phyllody and nematodes which includes *Heterodera cajani* (cyst nematode), *Rotylenchulus reniformis* (reniform nematode), *Meloidogyne incognita* (root-knot nematode). Only a few of them cause economic losses (Kannaiyan *et al.*, 1984) and the distribution of the most important diseases are geographically restricted.

Pigeonpea wilt caused by *Fusarium udum* is the most important soil borne disease and was first described in 1906 from Bihar State (Butler, 1906). It is also found to occur in Africa and several other countries in Asia and Australia (Nene *et al.*, 1989). The yield loss of the crop depends on the stage at which the wilt disease appears, the disease can cause yield loss up to 100, 67 and 30 per cent when wilt occurs at pre-pod, maturity and pre-harvest stages, respectively (Kannaiyan and Nene., 1981). The annual crop loss due to wilt alone in India has been estimated as Rs. 37 crores (Kannaiyan *et al.*, 1984).

The pathogen is primarily a soil inhabitant. Hence, controlling the disease is very difficult as no effective chemicals are available at present, even though application of carbendazim has been successful in controlling the disease, but to a limited extent. Secondly the development of wilt resistant varieties is the effective way of managing the wilt disease in farmer's field. However, developing resistant varieties is a tedious and time-consuming procedure. Several attempts have been made to develop resistant varieties and ICRISAT identified a wilt resistant variety "ICP 8863" and released by the name "Maruthi". Recently, disease incidence of more than 10 per cent has been recorded on ICP 8863 in some locations which may be due to the breakdown of resistance caused by the evolving new races of the pathogen. To develop resistant varieties, screening of genotypes is a continuous process to develop integrated management of pigeon pea wilt disease.

Host plant resistance, cultural methods and chemical control individually have limited value in solving the problems on long term basis. Therefore, present studies were undertaken to know the incidence of pigeon pea wilt disease, to search for effective resistance varieties for management of *Fusarium* wilt disease of Pigeon pea and to know the nature of resistance.

The seed and pod husks make a quality feed, whereas dry branches and stems serve as domestic fuel. Fallen leaves from the plant provide vital nutrients to the soil and the plant also enriches soil through symbiotic nitrogen fixation (Varshney, 2010). Productivity of pigeonpea worldwide in comparison to cereals is very low and stagnant due to several biotic and abiotic stresses. This low productivity is attributed to its low harvest index because of limited man-made selections (Varshney *et al.*, 2010, Ajay *et al.*, 2011). To overcome such situation, genetically stable genotypes having high yield potential are required straightaway. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genetic coefficient of variability (GCV), heritability estimates (H) and genetic advance (GA).

The main purpose of correlation in crop plants has been detail understanding of complex characters. The interaction of characters among themselves and with the environment is of great use in plant breeding. Correlation studies provides information on the nature and extent of association between any two pair of metric characters. It also determines the direction and number of characters to be consider for improvement. Hence it would be possible to bring genetic up gradation in one character by selection of other a pair. Grafius (1959) opined that there may not be any gene for yield as such but operates only through its component. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the components on which selection could be made for improvement (Galton, 1889). The basic concept of correlation was elaborated and discussed by Fischer (1918) and Wright (1921) for plant breeding programmes.

Knowledge on correlation would facilitate proper interpretation of results and provide a basis for planning more efficient selection programme. The extent of observed relationship between two characters is known as phenotypic correlation, while

genotypic correlation on the other hand is the inherent association excluding environmental factors. The information on nature and magnitude of correlation coefficient helps breeders to determine the selection criteria for simultaneous improvement of various characters along with seed yield. A study on correlation alone is not enough to give an exact picture of relative importance of direct and indirect influence of each of component characters on seed yield. In this context, path coefficient analysis is an important tool for plant breeder in partitioning the correlation coefficients into direct and indirect effects of independent variables on dependent variable i.e., seed yield. As emphasized by Pandey *et al.*, (2015) the optimum combination of yield contributing traits can be accumulated in a particular genotype only by understanding the inter relationships of various traits using correlation and path coefficients. Seed yield is a dependant character and whenever plant breeder goes for selection for yield it always misleads because it depends on various characters and to some extent to the environmental conditions (Bal Chinmayee, 2016). An attempt has been made in this study to know the relationship between yield and different yield attributing characters and their direct and indirect effects on yield in pigeonpea.

The present investigation was undertaken in pigeonpea with the following objectives

1. To identify the resistance genotypes against *Fusarium* wilt in pigeonpea.
2. To study the correlation and path analysis between yield and yield contributing characters in pigeonpea.

2. REVIEW OF LITERATURE

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is an important pulse crop of India particularly in Maharashtra. It is affected by many diseases. Among the diseases, wilt disease caused by *Fusarium udum* Butler, is the most destructive one causing considerable yield loss. The present investigations included the performance of pigeon pea genotypes against wilt disease and correlation and path analysis between yield and yield contributing characters in pigeon pea. The literature pertaining to studies on these aspects are reviewed and presented here under.

- 2.1 Variability, Heritability and Genetic Advance
- 2.2 Correlation
- 2.3 Path coefficient analysis
- 2.4 Screening of pigeonpea genotypes against *Fusarium* wilt disease

2.1 Variability, Heritability and Genetic Advance

The success of any breeding programme depends on the amount of variability present for different characters in a population and its efficient management. The genetic coefficient of variation is a useful measure of the magnitude of genetic variance present in the population. Estimation of genetic variability alone cannot indicate the possible improvement achieved through selection, but it should be used in conjunction with heritability. The degree of success depends on the magnitude of heritability as it measures the relative amount of the heritable portion of variability. Genetic advance (GA) under selection gives an idea about how much of genetic gain could be obtained due to selection. Hence, the estimates of genetic variability, heritability and genetic advance had an immense value in identifying the superior genotypes.

A brief review of literature on genetic parameters is furnished here under

Bainiwal and Jatasra (1981) studied the nature of genetic variability using 29 genotypes of pigeonpea and noticed that maximum variability for secondary branches followed by primary branches and seed yield. The expected genetic advance was also observed to be high for seed yield, secondary branches, plant height and primary branches.

Jagshoran (1983) evaluated 100 genotypes of pigeonpea and reported that the range for phenotypic variability was high for all the characters except seeds per pod. High estimates of genotypic coefficient of variation and heritability were observed to be accompanied by moderate to high genetic advance for pods per plant, days to maturity, plant height and days to flower across the environments.

Balyan and Sudhakar (1985), in their study on genetic variability noticed that primary branches, secondary branches, pods per plant, 100-seed weight and seed yield per plant exhibited high estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent of mean suggesting predominance of additive gene effects for the characters.

Jagshoran (1985) observed that the characters days to 50 % flowering, days to maturity, plant height, primary branches per plant, pods per plant, 100-seed weight and seed yield per plant had high amount of genotypic and phenotypic coefficients of variation, while it was low for pod length and seeds per pod.

Sidhu *et al.* (1985) observed that genetic variability was highest for pods per plant while it was lowest for seeds per pod.

Bhongale and Raut (1987) screened 80 genotypes of pigeonpea to study the extent of genetic variability for yield and yield contributing characters and highest genotypic coefficient of variation for yield per plant followed by pod number was observed. Days to 50 % flowering, days to maturity and 100-seed weight had high heritability coupled with high genetic advance.

Konwar and Hozarika (1988) studied 16 pigeonpea genotypes for genetic variability and reported high heritability with high genetic advance for days to maturity, days to flowering and plant height.

Patil *et al.* (1989) observed high amount of genotypic coefficient of variation for branches per plant followed by pods per plant, plant height, seed yield per plant and seeds per pod, while low estimates were observed for days to 50 % flowering and days to maturity and high heritability and genetic advance for plant height and 100-seed weight.

Natarajan *et al.* (1990) noticed the highest genotypic coefficient of variation for pods followed by clusters per plant and seed yield, while it was lowest for

seeds per pod. High heritability coupled with high genetic advance was observed for plant height and seed yield per plant, while low heritability with low genetic advance for seeds per pod.

Holker *et al.* (1991) reported high heritability and high genetic advance for days to 50 % flowering, days to maturity and pods per plant.

Khapre and Nerker (1992) observed high amount of genotypic and phenotypic coefficients of variation for plant height, primary branches per plant, pods per plant and seed yield per plant, while low estimates were observed for days to 50 % flowering and days to maturity. High heritability and high genetic advance were observed for days to 50 % flowering, pods per plant and seed yield per plant and high heritability and low genetic advance was reported for days to maturity.

Khapre *et al.* (1993) noticed that plant height, pods per plant, seeds per pod, seed yield per plant and harvest index had high genotypic and phenotypic coefficients of variation, while low estimates of genotypic coefficient of variation were recorded for shelling per cent and seeds per pod.

Ghodke *et al.* (1994) evaluated 10 genotypes under three cropping systems for deciding the selection criteria and noticed that high heritability for pods per plant, days to 50 % flowering and days to maturity and high genetic advance as per cent of mean for secondary branches and pods.

Aher *et al.* (1996) reported that the estimates of genotypic and phenotypic coefficients of variation were highest for plant height, primary branches per plant, secondary branches per plant and pods per plant, while low estimates were observed for days to 50 % flowering, days to maturity, seeds per pod and 100-seed weight. High heritability and low genetic advance were reported for days to 50 % flowering, days to maturity, plant height, primary branches per plant, seeds per pod and protein content.

Dahat *et al.* (1997) noticed that high amount of genotypic and phenotypic coefficients of variation for primary and secondary branches per plant, plant height, pods per plant and seed yield per plant both in sole as well as intercrop situations. High heritability accompanied with high genetic advance was also observed for secondary branches per plant, plant height, pods per plant, seed yield per plant under both the conditions.

Aher *et al.* (1998) reported high magnitude of variability for secondary branches per plant followed by seed yield per plant, days to 50 % flowering and plant height, while low estimates of variability were observed for pods per plant. High heritability accompanied with high genetic advance was observed for primary and secondary branches per plant, followed by seed yield per plant, days to 50 % flowering and plant height.

Pansuriya *et al.* (1998) studied 20 early maturing pigeonpea genotypes and reported that dry matter per plant, plant height and pods per plant showed wide range of phenotypic variation. The genotypic and phenotypic coefficients of variation were highest for dry matter per plant, harvest index, pods per plant and seed yield per plant, high heritability estimates for all the characters and high genetic advance for dry matter per plant followed by pods per plant and plant height.

Patel and Patel (1998) observed high genotypic and phenotypic coefficients of variation for clusters per plant, pods per plant, plant height, primary branches per plant and seed yield in all hybrids.

Takalkar *et al.* (1998) observed maximum variability for pods per plant followed by straw yield per plant. The high heritability estimates were observed for all the characters under study except straw yield per plant. The expected genetic advance was high for pods per plant, plant height, straw yield per plant and days to maturity and low genetic advance was observed for branches per plant, seeds per pod, 100-seed weight and harvest index.

Basavarajaiah *et al.* (1999) noticed high amount of phenotypic and genotypic coefficient of variation for days to 50 % flowering, pods per plant, seed yield per plant and length of pod bearing branches. High heritability and high genetic advance were observed for 100-seed weight and seed yield per plant.

Kingshlin and Subbaraman (1999) reported high heritability and high genetic advance for pod length, seeds per pod and low genetic advance for days to 50 % flowering.

Srinivas *et al.* (1999) carried out studies in a line x tester set with two male sterile lines and 11 pollen parents. They noticed that genetic variability was highest

for pods per plant and lowest for seeds per pod, high heritability for all the characters except seeds per pod and maximum genetic advance for pods per plant.

Deshmukh *et al.* (2000) noticed highest genetic variability for secondary branches per plant under inter crop. Heritability estimates were high for 100- seed weight, primary and secondary branches per plant under sole as well as inter cropping and for plant height and seed yield per plant under sole crop and plant spread under inter crop. High heritability accompanied with high genetic advance was recorded for characters plant height, pods per plant and plant spread.

Venkateswarlu (2001) observed the maximum variability for pods per plant followed by yield per plant and plant height. The high heritability coupled with high genetic advance was observed for seed yield per plant, days to maturity and yield per plant.

Magar (2003) reported that genotypic and phenotypic coefficients of variation were highest for pods per plant, plant spread, seed yield per plant and primary branches per plant and high heritability and genetic advance was observed for pods per plant and seeds per pod.

Gohil (2006) studied 39 genotypes of pigeonpea for 13 characters related to yield and yield contributing characters and noticed high phenotypic coefficients of variation were observed for grain yield per plant, plant height, branches per plant, clusters per plant, pods per plant, pods per cluster and harvest index. Grain yield per plant, days to 50 % flowering, days to maturity, clusters per plant, pods per plant, pods per cluster and harvest index showed high heritability. Considering high genetic advance, percentage of mean was found for grain yield per plant, clusters per plant, pods per plant and harvest index.

Firoz Mahamad *et al.* (2006) studied 49 genotypes of vegetable pigeonpea that high amount of PCV and GCV for branches for per plant, pods per plant, green pod yield and green seed yield per plant. High heritability coupled with high genetic advance was observed for plant height, branches per plant, pods per plant and 100-seed weight.

Anantharaju and Muthiah (2008) reported low amount of PCV and GCV for days to 50 % flowering, days to maturity and pod length, high heritability coupled

with high genetic advance as per cent of mean were observed for seed yield per plant, seeds per pod and 100-seed weight.

Kalaimagal *et al.* (2008) reported high genotypic and phenotypic coefficients of variation and genetic advance for plant height, clusters and pods per plant and low variability, moderate heritability and genetic advance were observed for seed yield per plant.

Singh *et al.* (2008) studied seven genotypes and 10 interspecific crosses and reported high PCV and GCV for all the characters except for days to 50 % flowering and days to maturity. High heritability accompanied with high genetic advance was observed for primary branches per plant, pod length, 100- seed weight and seed yield per plant, whereas days to 50 % flowering showed high heritability and low genetic advance as per cent of mean.

Dodake *et al.* (2009) studied 21 genotypes and observed that the variability in plant spread, 100-seed weight, days to 50 % flowering, days to maturity and seed yield per plant were heritable and additive type of gene action was operative for the characters.

Bhadru (2010) analyzed 27 accessions and recorded moderate to high phenotypic and genotypic coefficient of variation for pods, seed yield per plant, plant height and plant spread. High heritability accompanied with high genetic advance as per cent of mean was observed for pods per plant, primary and secondary branches per plant, test weight, plant height and plant spread.

Patel and Acharya (2011) reported high GCV and PCV for yield per plant, pods per plant and branches per plant. High heritability coupled with moderate to high genetic advance for grain yield per plant, plant height, pods per plant, days to 50 % flowering and days to maturity.

Sreelakshmi *et al.* (2011) studied 36 hybrids and three checks of pigeonpea and noted higher value of PCV over GCV for yield and yield related characters. High heritability coupled with high genetic advance as per cent of mean were observed for seed yield, primary branches per plant and secondary branches per plant.

Jaggal *et al.* (2012) evaluated 135 pigeonpea [*Cajanus cajan* (L.) Millsp.] accessions of mini core collection for 14 characters related to yield and noticed high

genotypic and phenotypic coefficient of variation, genetic advance mean and heritability was recorded for harvest index and seed yield. High heritability and genetic advance mean also found in plant height, days to 50 % flowering, days to maturity and seed protein.

Nagy *et al.* (2013) studied 45 genotypes of pigeonpea and reported pod clusters per plant had the highest magnitude of GCV and PCV followed by seed yield per plant and pods per plant. High heritability coupled with high genetic advance was recorded for pods per plant, pod clusters per plant, seed yield per plant and 100-seed weight.

Rangare *et al.* (2013) evaluated 27 genotypes of pigeonpea for 13 characters related to yield and noticed high heritability coupled with high genetic advance for days to maturity, days to 50 % flowering, plant height, pods per plant, biological yield per plant, seed yield per plant and harvest index.

Prasad *et al.* (2013) studied 11 parents and their 28 hybrids of pigeonpea and reported high magnitude of PCV and GCV was observed for primary and secondary branches per plant, leaf area, pods per plant, harvest index, pollen viability and grain yield. All the characters exhibited low heritability in narrow sense except leaf area and 100-seed weight and low to high genetic advance as per cent of mean.

Saroj *et al.* (2013) evaluated 70 pigeonpea genotypes. Highest GCV was recorded for secondary branches per plant followed by pods per plant. Heritability in broad sense ranged from 61.33 (seeds per pod) to 98.26 (days to 50 % flowering). High genetic advance was observed for primary branches per plant, secondary branches per plant, 100-seed weight, grain yield per plant, pods per plant, plant height and days to 50 % flowering.

Kumar *et al.* (2014) evaluated 38 genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp] for yield and yield contributing characters. Moderate to high PCV and GCV were recorded for 50 % flowering, pods per plant, seed, grain yield and straw yield. High heritability and genetic advance were observed for pods, plant height, test weight, days to maturity and primary and secondary branches per plants, whereas the characters like days to 50 % flowering, test weight, pod length and primary branches showed high heritability along with moderate or low genetic advance.

Ajay *et al.* (2014) evaluated F2 and F3 generations from three crosses of pigeonpea namely BRG-1×ICP-8863, TTB-7 × ICP-8863 and TTB-7 × ICPL-87119 for yield and yield contributing characters. High variance, heritability and genetic advance were recorded for secondary branches per plant, pods per plant and seed yield in F2 and F3 generations.

Vanisree and Sreedhar (2014) evaluated 482 genotypes of pigeonpea and reported that the characters seed yield per plant, pods per plant, plant height, primary branches and days to 50 % flowering showed higher genotypic and phenotypic coefficient of variation. High heritability, high genetic variance and high genetic advance as per cent of mean was recorded for seed yield per plant, pods per plant, plant height, days to 50 % flowering and days to maturity.

Lakhote *et al.* (2015) evaluated 24 vegetable type genotypes of pigeonpea and reported high GCV and PCV for plant height, 100 green pod weight, 100 green seed weight, shelling percentage, TSS (per cent), days to 50 % flowering, pod length, as well as for primary branches. High heritability and genetic advance were reported for 100 green pod weight and days to 50 % flowering.

Pandey *et al.* (2015) reported secondary branches per plant showed highest phenotypic as well as genotypic coefficient of variation followed by seed yield per plant and biological yield. High heritability coupled with high genetic advance as per cent of mean was observed by 100-seed weight, pods per plant, seed yield per plant, biological yield per plant and secondary branches per plant suggesting preponderance of additive gene action in the expression of these characters, while plant height, primary branches per plant, pods per plant, seeds per pod and harvest index showed high heritability with moderate genetic advance as per cent of mean suggesting greater role of non-additive gene action.

Ram *et al.* (2016) reported that phenotypic and genotypic variances, heritability and genetic advances were estimated for yield and yield characters in 30 pigeonpea genotypes. The highest GCV was recorded for secondary branches per plant followed by pods per plant. Heritability in broad sense ranged from 60.31 (seeds per pod) to 96.28 (days to 50 % flowering). High genetic advance was observed for primary branches per plant indicating the prevalence of additive gene action for inheritance.

2.2 Correlation

Genetic improvement of yield is the primary concern to plant breeder as yield is a complex, quantitatively inherited character and is highly influenced by the environment. On the contrary, the yield component characters are not only less complex and relatively simply inherited and are influenced much less due to environmental deviations. Thus, effective improvement in yield may be brought about through selections in yield components (Grafius, 1956 and Srivastava *et al.*, 1972). Yield component characters show associations among themselves and with yield. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, study of associations of component characters with yield enables a plant breeder to know how improvement of one character will bring about simultaneous improvement in other characters and also aid in planning of an effective selection programme. Hence a brief review of literature is presented hereunder.

Asawa *et al.* (1981) noted that yield was positively correlated with secondary branches, pods per plant, seeds per plant and days to maturity and weak correlation among seeds per plant and pods per plant.

Balyan and Sudhakar (1985) reported seed yield per plant had positive and significant association with plant height, days to maturity, primary branches, and secondary branches, pods per plant, seeds per pod and 100-seed weight.

Bhongale and Raut (1987) found that plant height, branches per plant, pod number, pod weight and seeds per pod were positively correlated with each other and also with seedyield.

Angadi *et al.* (1988) noted that pod yield was significantly correlated with seed yield, pods per plant, days to flowering and plant height.

Balakrishnan and Natarajaratnam (1989) revealed that seed yield had a positive correlation with pods per plant and pod setting percentage. Among the yield components, 100-seed weight was positively correlated with pods per plant.

Natarajan *et al.* (1990) observed pod number, cluster number and plant height were positively and significantly correlated with yield. They also reported that plant height, branch number, cluster number, seed number and 100-seed weight were highly correlated.

Paul and Upadhaya (1991) observed positive correlation of yield per hectare with branches per plant, pods per plant, pods per cluster and yield per plant. The correlation between the pods per plant and yield per plant was found to be positively significant and the length of pod was significant but negatively correlated with yield per plant as well as with the pods per plant.

Dhameliya and Pathak (1994) reported significant and positive association of seed yield with plant height and pods per plant, whereas significant and negative association of seed yield with pod length and seeds per pod. They also reported that days to 50 % flowering, days to maturity, plant height, primary branches per plant, pod length, seeds per pod and 100-seed weight were highly correlated.

Salunke *et al.* (1995) observed in a study of 54 diverse genotypes of pigeonpea that seed yield was significantly and positively associated with pods per plant, primary and secondary branches, plant spread, plant height and 100-seed weight. It had a strong negative association with seeds per pod. The yield components like days to 50 % flowering, days to maturity, plant height, plant spread, primary and secondary branches and 100-seed weight were positively associated with each other.

Gumber *et al.* (1996) studied 28 genotypes and noted that the days to flowering and days to maturity showed significant positive association among themselves and with seed yield.

Chandirakala and Raveendran (1998) indicated that seed yield was significantly and positively correlated with branches per plant, pods per plant, clusters per plant, seeds per pod, 100-seed weight.

Srinivas *et al.* (1999) reported that seed yield per plant had significant and positive association with plant height, primary branches, secondary branches and pods per plant.

Basavarajaiah *et al.* (1999) studied 81 genotypes of pigeonpea and indicated significant positive correlation of seed yield observed with pods per plant and branches per plant.

Deshmukh *et al.* (2000) noticed that seed yield was positively and significantly associated with all characters under different cropping systems. Pods per plant exhibited highly significant correlation with seed yield which was also significantly

associated with majority of the characters under sole crop whereas, secondary branches per plant was significantly associated with majority of the characters under intercrop.

Bharadwaj and Gupta (2004) studied 55 diverse genotypes of pigeonpea and reported that the protein content was positively correlated with days to flowering, harvest index and days to maturity, but exhibited negative correlation with plant height, primary and secondary branches, pods per plant, seeds per pod, 100-seed weight and seed yield per plant.

Chattopadhyay and Dhiman (2005) studied 100 accessions of pigeonpea and the reported that plant height, seeds per pod contributed positively and directly, whereas 100-seed weight was negatively correlated with seed yield.

Gangwar and Bajpai (2006) observed negative correlations for protein content with primary branches, pod length, 100-seed weight and seed yield.

Baskaran and Muthiah (2007) assessed 27 genotypes and their correlation studies indicated that seed yield per plant had significant positive relationship with pods per plant, clusters per plant, 100-seed weight and plant height.

Mahajan *et al.* (2007) evaluated nine pigeonpea genotypes to understand the contribution of various characters to the yield and reported that pods per plant, pod length, plant height and days to maturity had significant positive association with yield.

Singh *et al.* (2008) studied 29 genotypes of pigeonpea and reported that seed yield per plant exhibited positive and significant correlation with pods per plant and harvest index, indicating the higher values for these characters contribute towards higher yield potential.

Dodake *et al.* (2009) noticed that the seed yield was positively and significantly correlated with days to 50 % flowering, plant spread and pods per plant.

Sawant *et al.* (2009) studied 46 genotypes and revealed that the genotypic correlation coefficients were higher than corresponding phenotypic correlations. Seed yield showed significant positive correlation with plant spread, secondary branches per plant, pods per plant and days to maturity.

Sodavadiya *et al.* (2009) observed that genotypic correlation coefficients were higher than phenotypic correlation coefficients. Seed yield per plant had significant

and positive association with days to 50 % flowering, days to maturity, branches per plant, pods per plant and 100-seed weight at both genotypic and phenotypic levels.

Bhadru (2010) reported that seed yield was significantly and positively associated with days to 50 % flowering, plant height, primary and secondary branches per plant, pods per plant and raceme length.

Mittal *et al.* (2010) noted that seed yield was positively associated with plant height, branches per plant, pods per plant and harvest index in pigeonpea genotypes.

Linge *et al.* (2010) found that yield was positively and significantly correlated with all characters except for first primary branch from ground level and seeds per pod in 40 inter specific derivatives of pigeonpea.

Thanki and Sawargaonkar (2010) reported significant and positive correlation of pods per plant and harvest index with seed yield per plant in 28 different genotypes of pigeonpea.

Hamid *et al.* (2011) evaluated 100 germplasm lines of pigeonpea and noted high strong and positive correlation of seed yield with pods per plant followed by pod length.

Patel and Acharya (2011) found that yield was significantly and positively correlated with plant height, branches per plant, pods per plant, pod length, seeds per pod and 100-seed weight in 64 F₆ progenies of pigeonpea.

Rathore and Sharma (2011) found that seed yield per plant was positively correlated with seeds per plant in 25 erect groups whereas, pod clusters per plant, pods per plant and 100-seed weight in 25 semi-spreading groups of pigeonpea.

Devi *et al.* (2012) reported significant positive correlation of seed yield with pods per plant in parents (five lines and three testers) and plant height, pods per plant and harvest index in 15 crosses of pigeonpea.

Udensi and Ikpeme (2012) found that there were significant positive correlations between plant height and leaves per plant, leaf area per plant and seeds per plant, leaves per plant and pod length per plant.

Arbad *et al.* (2013) conducted characters association studies for seed yield and its components in pigeonpea and found that pods, secondary branches per plant, plant

height, primary branches per plant showed significantly positive correlation with seed yield at genotypic and phenotypic levels.

Birhan (2013) reported that seed yield had positive and significant phenotypic and genotypic association with plant height, biomass yield per plant, pods per plant, seeds per plant, days to maturity, days to flowering and seeds per pod.

Nagy *et al.* (2013) conducted association studies in 45 pigeonpea germplasm accessions and found that, seed yield per plant showed the highest significant positive correlation with pods per plant followed by pod cluster per plant, primary branches per plant and pod length.

Prasad *et al.* (2013) found that primary branches per plant, secondary branches per plant, pods per plant, pod bearing zone, harvest index and pollen viability exhibited positive and significant correlation with grain yield in pigeonpea.

Singh *et al.* (2013) showed that the seed yield per plant was found to be significant positively associated with seeds per pod, pod length and plant height at genotypic level in pigeonpea.

Rekha *et al.* (2013) reported strong positive association of seed yield with pods per plant, secondary branches per plant, primary branches per plant and plant height.

Saroj *et al.* (2013) revealed that the days to 50 % flowering had significant and strongly positive association with yield per plant, primary branches per plant, pods per plant, days to maturity, 100-seed weight and plant height in both genotypic and phenotypic level.

Kothimbire *et al.* (2015) concluded the correlation analysis for yield per plant recorded highly significant and positive association with days to 50 % flowering, days to maturity, plant height, primary branches, secondary branches and pods per plant.

Pandey *et al.* (2016) found that biological yield per plant, pods per plant, 100-seed weight, harvest index and secondary branches per plant showed positive and highly significant correlation with grain yield per plant to emerge as most important associates of seed yield.

2.3 Path coefficient analysis

Path coefficient analysis which is a standard partial regression coefficient, measures the direct influence of one variable upon another and permits the separation of

correlation coefficient into components of direct and indirect effects (Dewey and Lu, 1959). Direct selection for yield is not a reliable approach since it is highly influenced by the environment. Therefore, it is essential to identify the component characters through which yield can be improved. Thus, correlation in conjunction with path analysis would give better insight into the cause-and-effect relationship between different character pairs. The available literature on path coefficient analysis is furnished here under.

Dumbre *et al.* (1985) revealed that days to flowering had highest positive direct effect on seed yield followed by pods per plant, 100-seed weight and plant height. The indirect effects *via* these characters were also positive for all characters except seeds per pod which had negative indirect effect *via* 100- seed weight.

Marekar and Nerkar (1987) observed biomass and harvest index had largest positive direct effect on seed yield and days to first flowering, days to maturity, plant height, height at first effective branch, primary branches, secondary branches, clusters and 100-seed weight had indirect positive effects on seed yield.

Angadi *et al.* (1988) noticed that pod yield was the only character with a direct effect on seed yield. Pods per plant, plant height, branches per plant and days to flower influenced seed yield through pod yield which alone had direct influence on seed yield.

Balakrishnan and Natarajaratnam (1989) observed that pods per plant had the highest positive direct effect on seed yield followed by harvest index and dry matter efficiency.

Natarajan *et al.* (1990) reported that cluster number followed by pod number showed high positive direct effect on seed yield.

Satpute (1994) revealed that seeds per pod exhibited highest magnitude of positive direct effect on seed yield, followed by dry matter production.

Salunke *et al.* (1995) noticed that pods per plant, seeds per pod, and 100-seed weight had direct positive effects on seed yield. The pods per plant and 100-seed weight also exhibited high positive indirect effects on seed yield through most of the other characters. It was suggested that pods per plant, seeds per pod and 100-seed weight could prove useful as selection criteria for early pigeonpea.

Paul *et al.* (1996) revealed that six independent characters having positive direct effect on seed yield, maximum contribution was of pods per plant, followed by dry matter at maturity and 100-seed weight.

Kingshlin and Subbaraman (1997) assessed that pod length, seeds per pod and 100-seed weight made the greatest contribution towards seed yield, both directly and indirectly.

Musaana and Nahdy (1998) indicated that pod clusters per plant, pods per plant, seeds per pod and seed weight were the main yield components having maximum direct effects on yield.

Chandirakala and Raveendran (1998) revealed from their studies on 13 pigeonpea genotypes that 100-seed weight had the highest positive direct effect on seed yield followed by pods per plant and clusters per plant. Branches per plant, pods per plant, clusters per plant, seeds per pod and 100-seed weight showed high positive indirect effect on seed yield.

Srinivas *et al.* (1999) observed high and positive direct effect of pods per plant, plant height and secondary branches on seed yield.

Basavarajaiah *et al.* (1999) evaluated 81 pigeon pea genotypes and reported that plant height, branches per plant and pods per plant showed maximum direct effects on seed yield.

Bharadwaj and Gupta (2004) reported that protein content showed positive direct effect and negative correlation with yield.

Chattopadhyay and Dhiman (2005) observed that plant height and seeds per pod contributed positive and direct effect on seed yield.

Mittal *et al.* (2006) reported from a study of 21 diverse progenies of pigeonpea that seeds per pod, followed by pods per plant and plant height had high positive direct effect on seed yield.

Baskaran and Muthiah (2007) revealed pods per plant, 100-seed weight and plant height to be the major contributors for seed yield. Selection based on these attributes will be most advantageous in pigeonpea.

Mahajan *et al.* (2007) evaluated nine genotypes, maximum direct positive and negative contribution to yield was observed from pods per plant and days to flower initiation, respectively.

Anuradha *et al.* (2007) studied 30 genotypes of pigeonpea and revealed that the harvest index had a high positive direct effect on seed yield followed by seeds per pod, primary branches per plant.

Jogendra Singh *et al.* (2008) noticed that pods per plant, 100-seed weight and harvest index are main components of seed yield. Hence, more emphasis should be given on these characters in selection programme.

Sawant *et al.* (2009) revealed that pods per plant had the highest positive direct effect on seed yield, followed by plant spread and 100-seed weight.

Sodavadiya *et al.* (2009) reported that 100-seed weight days to maturity and pod length exerted high direct effects on seed yield. 100-seed weight, days to maturity also contributed indirectly towards seed yield per plant through most of the characters.

Bhadru (2010) noticed that days to 50 % flowering, plant spread, primary and secondary branches per plant, pods and raceme length had moderate to low direct effect on seed yield.

Patel and Acharya (2011) found that pods per plant had the highest positive direct effect on grain yield per plant.

Rathore and Sharma (2011) indicated maximum positive direct effect on seed yield was exhibited by seeds per plant in erect group and days to 50 % flowering in semi-spreading group.

Sreelakshmi *et al.* (2011) in their studies on pigeonpea revealed that maximum direct effect on seed yield was exhibited by primary branches per plant, days to 50 % flowering and pods per plant.

Devi *et al.* (2012) showed that out of 14 characters, pods per plant, days to flowering, plant height and pod length in parents while pods per plant in crosses showed high positive direct effect on seed yield, indicating that these characters should be given due importance while making selection for increased seed yield in pigeonpea.

Nag and Sharma (2012) found that, pod clusters per plant had the highest direct effect on seed yield whereas, pods per plant and days to maturity had the highest indirect effect on seed yield *via* the characters pods per plant and days to 50 % flowering, respectively.

Udensi and Ikpeme (2012) showed that 100-seed weight had the highest positive direct effect on yield. This was followed by the pod length per plant, leaves and leaf area, while plant height had very high negative direct effect.

Arbad *et al.* (2013) reported that, pods, secondary branches per plant, plant height, and primary branches per plant were the most important characters with high direct and positive indirect effect.

Birhan (2013) showed that, days to maturity had the highest positive direct effect on seed yield followed by plant height and seeds per plant whereas, genotypic path analysis revealed that, maximum direct effect on seed yield was exerted by days to flowering and days to maturity followed by seeds per plant and plant height. Thus, seeds per plant and plant height were the potent contributor to seed yield which could be used as indirect selection criteria.

Reddy and Rangare (2013) noticed from their path analysis of 27 genotypes of pigeonpea that harvest index had high positive direct effect on seed yield followed by biological yield per plant and days to 50 % flowering. It also indicated that harvest index, biological yield per plant and days to 50 % flowering are important characters in deciding the grain yield per plant.

Pahwa *et al.* (2013) reported that leaf area, specific leaf weight, pods per plant and plant height had direct positive contribution towards seed yield.

Prasad *et al.* (2013) found that primary branches per plant, secondary branches per plant, pods per plant, harvest index and pollen viability exhibited positive and high direct effects ranged from 0.060 to 0.430.

Rekha *et al.* (2013) showed that pods per plant exerted highest positive direct effect on seed yield whereas, primary branches per plant and 100-seed weight had moderate and low positive direct effects on seed yield, respectively.

Saroj *et al.* (2013) showed that pods per plant, 100-seed weight, days to 50 % flowering, primary branches and secondary branches per plant had maximum direct effect on grain yield per plant.

Singh *et al.* (2013) showed that, seeds per pod exhibited the highest magnitude of direct effects on seed yield, followed by primary branches per plant and pod length. Pod length and seeds per pod showed positive and significant correlation (0.529 and 0.794) with seed yield per plant and also exhibited positive and strong direct effects (0.531 and 0.266) on seed yield per plant.

Arbad *et al.* (2014) reported pods per plant, secondary branches per plant, plant height, and primary branches per plant were the most important character which can be used to improve yield in pigeonpea.

Pandey *et al.* (2016) identified biological yield per plant followed by harvest index, pods per plant, days to maturity, primary branches per plant, 100-seed weight and seeds per pod as most important direct yield contributing characters in pigeonpea.

2.4 Screening of pigeonpea genotypes against *Fusarium* wilt disease

The utilization of resistant sources was a classical approach to prevent the catastrophic losses caused by wilt disease, it decreases the cost of cultivation and increases production.

Nene and Kannaiyan (1982) screened more than 11,000 pigeonpea entries, out of which, 33 were found resistant. Among 33 resistant entries, only one (ICP 8863) was resistant in glass house, lab tests and under field condition. Parameshwarappa *et al.* (1986) reported a pigeonpea wilt resistant variety ICP 8863 from Gulbarga, Karnataka.

Patel *et al.* (1988) tested 61 promising lines against *Fusarium* wilt for two years. Among these two lines *viz.*, GAUT 82-127 and GAUT 82-83 showed less than 10.00 per cent mortality and four showed 11-20 per cent mortality.

Reddy *et al.* (1988) observed 3.50 – 4.61 per cent wilt in short duration cultivars of pigeonpea compared with 81.50 to 88.60 per cent wilt in the medium and long duration cultivars.

Sharma (1988) noticed that the lines Bori, ICP 8863, ICP 9120 and ICP 9144 were resistant to *F. udum* for TAWA command area in Central India.

Parameshwarappa *et al.* (1986) reported a pigeonpea wilt resistant variety ICP 8863 from Gulbarga, Karnataka.

Zote *et al.* (1987) screened a total of seven pigeonpea varieties to control *F. udum* for five years. They found BDN 15-3-3, ICP 7336, ICP 8862 and AWR 74/15 had an average infection of less than 5.00 per cent and were categorized as resistant lines.

Rajkule *et al.* (1989) found pigeonpea variety BP 1809 totally free from *F. udum* infection in both test seasons among 400 local and exotic lines evaluated in wilt sick plot.

Nene *et al.* (1989a) screened 61 pigeonpea lines and cultivars against *F. udum* at 15 wilt endemic locations in India. Lines ICP 4769, ICP 8863, ICPL 9168, ICPL 10958, ICPL 11299 and cultivars C 11, BDN 1 were resistant in all the years of testing at most of the locations, suggesting stability and broad-based resistance. Line ICP 8863 had stable and broad-based resistance to wilt and a good yield potential and released as cultivar Maruthi in Maharashtra.

Pawar *et al.* (1992) screened 160 pigeonpea lines for resistance to *Fusarium udum* strains, out of these, three lines *viz.*, BWR 175, BWR 369 and ICP 8863 showed less than ten per cent wilt incidence and were classified as resistant, whereas six lines *viz.*, BWR 190, BWR 254, BWR 370, ICP 8858, ICP 8859 and ICP 8856 showed less than 20 per cent mortality and were considered as moderately resistant.

The new method was used to evaluate disease resistance in the pigeonpea genotypes ICP 8863, ICP 8518, ICP 12737, ICP 2376 and ICP 6997 under controlled conditions and to demonstrate the pathogenic variability in 1 and 2 *Fusarium udum* isolates, ICP 8863 and ICP 8356 did not show any mortality (Haware and Nene, 1994). In the root dip technique, >90% incidence of wilt was observed within 20-26 days in ICP 2376, ICP 8518 and ICP 6997, and this was 100 % at 30 days after inoculation for both isolates. In comparison, there was a considerable delay of wilt symptoms in the standard pot culture tests.

Reddy *et al.* (1995) found that ICP 8863 and RCP 11292 were resistant to both the *Fusarium* wilt strains identified in India.

Bidzri *et al.* (1996) reported that out of the 90 long duration genotypes tested, DPPA 85-5 showed less than ten per cent disease incidence. Out of 174 medium

duration lines tested, two genotypes *viz.*, BSMR 198 and PRG 100 showed less than ten per cent wilt incidence.

Raguchander and Arjunan (1996) screened several pigeonpea genotypes against *Fusarium* wilt for 5 years, among them five genotypes *viz.*, ICPL 227, DPPA 84-83, ICPL-88046, ICPL-88047 and BWR 254 showed resistant reaction for 2 years.

Bordoloi and Rathaiah (1997) reported that Basant was the best resistant variety among the eight pigeonpea varieties tested against *Fusarium* wilt.

Among the several pigeonpea genotypes screened for multiple disease resistance, seven genotypes *viz.*, ICPL 93001, ICPL 96047, ICPL 96061, ICPL 99046, ICPL 99055, ICPL 87119 and C 11 were found resistance to various diseases during *Kharif*, 2001-02. Three genotypes *viz.*, ICPL 96047, ICPL 96061 and ICPL 99046 were found resistant to *Fusarium* wilt of pigeonpea (Muhammad Saifulla and Byregowda, 2002).

Anjaneya Reddy *et al.* (2003) evaluated fifty-nine pigeonpea genotypes against *Fusarium* wilt. Among the fifty-nine genotypes screened, 14 were found resistant, while rest of the genotypes showed moderately susceptible to susceptible reaction.

Seven promising genotypes and twelve host differentials were evaluated for host plant resistance against *Fusarium udum* under sick plot conditions. Among seven promising genotypes, six were resistant and one was susceptible to wilt disease. Among twelve host differentials, six were resistant, one was susceptible and rest were moderately resistant to pigeonpea wilt disease. (Muhammad Saifulla and Anjaneya Reddy, 2003).

Madhukeshwara *et al.* (2004) screened 226 pigeonpea genotypes to assess their resistance reaction. Out of the 226 genotypes evaluated, 105 genotypes were resistant (0-10% wilt), 33 genotypes were moderately resistant (10-30% wilt) and 88 genotypes were susceptible (>30% wilt) against *Fusarium udum*.

Mahesh *et al.* (2005) evaluated eight pigeonpea wilt promising genotypes *viz.*, ICP8863, ICPL87119, ICPL96047, ICPL99046, ICPL99055, BSMR 853, CORG 9701 and TT 103 along with susceptible check TTB-7 against wilt and evaluated these for their yield performance under sick plot conditions. Among these genotypes, ICP 8863 recorded 2.21 per cent wilt incidence with highest yield of 923 kg/ha, followed by ICPL 96047, which recorded yield of 698 kg/ha with no wilt disease. Six genotypes *viz.*,

ICPL87119, ICPL99046, ICPL99055, BSMR853, CORG 9701 and TT1 recorded wilt incidence of 1.42, 0.00, 3.42, 3.81, 19.13 and 3.45 per cent.

Muhammad Saifulla *et al.* (2005) evaluated eight pigeonpea wilt promising genotypes *viz.*, ICPL 87119, ICPL 93001, ICPL 96047, ICPL 99055, ICPL 99046, ICPL 96061, C-11 and TTB-7 during the period of 2000-01 to 2004-05. Among these, six genotypes *viz.*, ICPL 87119, ICPL 93001, ICPL 96047, ICPL 99055, ICPL 99046, and C-11 showed resistant reaction for all the five years screening, except ICPL 96061 which showed resistant reaction for four years and moderately resistant reaction during 2003-04, whereas TTB-7 showed susceptible reaction for three years and it was found moderately susceptible to wilt for two years.

Shashi Mishra Vishwa Dhar (2010) evaluated twenty-one elite genotypes of pigeonpea against three variants (Vr 2, Vr 4 and Vr 5) of *F. udum* under artificial inoculations. Among these three genotypes *viz.*, ICP 8860, ICP 8863 and ICP 14722 were uniformly resistant to all the three variants revealing their high and broad-based resistance to *Fusarium* wilt. Three other genotypes *viz.*, KPBR 80-2-1, PI 397430 and DPPA 85- 14 showed moderate resistance against all the three variants.

Four long duration pigeonpea genotypes, *viz.*, IPA 16 F, IPA 8 F, IPA 9 F and IPA 12 F possessing acceptable yield levels were evaluated for their reaction to wilt disease in wilt sick plots continuously for three to five years at hot spots in north east plain zone, central zone and south zone (Farindra Singh *et al.*, 2011). All the four genotypes showed resistant to moderately resistant reaction to wilt over the years at all the hot spots. The consistency in the reaction to wilt disease indicated that genotypes IPA 16 F, IPA 8 F, IPA 9 F and IPA 12 F were very good source of resistance to all the variants of *Fusarium udum* prevalent in India.

3. MATERIAL AND METHODS

The present field experiment entitled “Assessment of pigeonpea genotypes against *Fusarium* wilt” was carried out in 28 pigeonpea genotypes including two checks viz., BDN-711 and Phule Rajeshwari for studying genetic variability and assessing this germplasm resistance against *Fusarium* wilt. The germplasm material was obtained from Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri. The first experiment was conducted in plot having normal soil and second experiment was conducted on wilt sick plot, at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, during kharif season of 2019-20. The account of the key materials used, methods adopted and statistical analysis followed, during the investigations, are described below.

3.1 Experimental Material Used

3.1.1 For Diversity Analysis:

The experimental material used for the study of genetic diversity consisted of 28 genotypes including two checks (BDN-711 and Rajeshwari) are listed in Table 1.

3.1.2 For *Fusarium* Wilt Screening

The experimental material used for the study of screening of *Fusarium* wilt consisted of 28 genotypes including two checks (BDN-711 and Rajeshwari) along with *Fusarium* wilt susceptible check.

3.2 Experimental Details:

a) For diversity analysis

- | | | |
|----------------------------|---|---|
| i) Number of genotypes | : | 28 (Including check viz., BDN-711 and Rajeshwari) |
| ii) Season | : | Kharif 2019-2020 |
| iii) Experimental design | : | Randomized Block Design |
| iv) Number of Replications | : | Two |
| v) Plot size | : | Single row of 4 m length |
| vi) Spacing | : | 60 cm x 15 cm |
| vii) Fertilizer Dose | : | 25:50:00 NPK (kg/ha) |

b) For recording of wilt incidence

- i) Number of genotypes : 28 (Including check *viz.*,BDN-711 and Rajeshwari), susceptible check ICP-2376
- ii) Season : Kharif 2019-2020
- iii) Experimental design : Randomized Block Design
- iv) Number of Replications : Two
- v) Plot size : Single row of 4 m length
- vi) Spacing : 45 cm x 15 cm
- vii) Fertilizer Dose : 25:50:00 NPK (kg/ha)

Table 1. List of twenty-eight genotypes of pigeonpea.

Sr. No.	Genotype	Sr. No.	Genotype
1	BDN-711	2	RVKT-314(733)
3	RKPV-911(732)	4	RKPV-912(732)
5	RPS-2007-105-1(730)	6	AKTE-1202-724
7	CRJ-1608	8	LPG-229
9	BRGL-18-1(728)	10	BAUUP-15-19
11	RRG-300	12	RVSA-157
13	ICPL-15048	14	IBTO-RG-7
15	RPS-2007-109-001	16	BRGL-18-2
17	TTO-704-1-2	18	TDRG-59
19	WRG-353	20	KRG-224
21	CRG-16-008	22	RVSA-1510
23	SKNP-1413	24	PTO-705-4-1-2
25	GGP-1721	26	GGP-1715
27	LRG-134	28	Rajeshwari

3.3. Experimental Design

a. For diversity analysis

Twenty-eight genotypes along with two check *viz.* BDN-711 and Rajeshwari evaluated in a Randomized Block Design (RBD) with two replications during Kharif 2019-2020. Each genotype was sown in single row of 4 m length with spacing 60 cm between row and 15 cm within row.

b. For recording of wilt incidence

Twenty-eight genotypes along with *Fusarium* wilt susceptible check were planted in artificial epiphytotic created wilt sick plot at Pulses Improvement Project, M.P.K.V, Rahuri. Sowing was done on 22nd July 2019. Each genotype was planted on a 4 m row length and row to row and plant-to-plant distances were maintained at 45 cm and 15 cm respectively. A highly wilt susceptible check *i.e.*, ICP-2376, was planted after every two test entries.

3.4 Observations Recorded

Five plants per genotype were selected randomly for recording observations on following characters in each replication and averages were calculated.

3.4.1 Days to 50 % Flowering

Number of days from sowing to the date when 50 per cent plants in each plot initiate flowering was recorded and the average number of days for 50 per cent flowering was calculated.

3.4.2 Days to Maturity

Number of days required from the date of sowing to the maturity of crop was recorded as day to maturity.

3.4.3 Plant Height (cm)

Plant height was recorded in centimetre at the time of harvesting by measuring the height of a plant from ground level to the top of the main axis.

3.4.4 Plant Spread (cm)

Plant spread was recorded at the time of harvesting by measuring maximum spread of plant.

3.4.5 Number of Primary Branches per Plant

Branches arising from main stem were considered as basal or primary branches which were counted and recorded at the time of harvest.

3.4.6 Number of Secondary Branches per Plant

Branches arising from primary branches were recorded as secondary branches at the time of harvest.

3.4.7 Number of Pods per Plant

The total numbers of pods were counted from five plants at maturity and the average was worked out.

3.4.8 Number of Seeds per Pod

This observation was recorded by taking the seeds of randomly selected five pods from observation plants and the average was estimated.

3.4.9 100 Seed Weight (g)

It was recorded by weighing randomly selected 100 seeds.

3.4.10 Seed Yield per Plant (g)

The weight of seeds obtained as a mean of five observational plants represented the yield of seed yield per plant, which was recorded in gram.

3.4.11 Wilt Incidence as Percentage

The observation was recorded on germination percentages of all genotypes. The disease data were recorded at 15, 30, 45, 60, 75, 90, 105, 120, 135, 150, 165, 180 days after sowing.

3.5 Statistical Methodology

3.5.1 Assessment of Variability

a. Analysis of variance

The analysis of variance is the procedure of splitting the overall variation into different components (sources). Each component is attributed to an identifiable cause or source of variation. For this analysis data collected from first year trial on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1985)

$$Y_{ij} = \mu + G_k + R_j + E_{ij}$$

Where,

- i = 1, 2, g
 j = 1, 2 r
 y_{ij} = Observation on i^{th} genotype in j^{th} replication
 μ = General mean
 G_i = Effect of i^{th} genotype
 R_j = Effect of j^{th} replication
 E_{ij} = Random error associated with y_{ij} observation

ANOVA Table:

Sources	d.f.	M.S. S	Expected M.S. S
Replications	r-1	RMS	$\sigma_e^2 + \sigma_r^2$
Genotypes	g-1	GMS	$\sigma e^2 + \sigma g^2$
Error	(r-1)(g-1)	EMS	σe^2

Where,

- r = Number of replications
 g = Number of genotypes
 σ_r^2 = Variance due to replications
 σ_g^2 = Variance due to genotypes and
 σ_e^2 = Variance due to error

The genotype mean square (**GMS**) was tested against error mean square (**EMS**) by 'F' test for $n_1 = (g-1)$ and $n_2 = (r-1)(g-1)$ degrees of freedom. The characters showing significant differences were subjected to further analysis.

Estimation of S.E. and C. D.

$$\text{S.E. of mean (S.E.m)} = \sqrt{\sigma_e^2 / r}$$

$$\text{C.D.} = t \text{ at error d.f.} \times \text{S.E.m} \times \sqrt{2}$$

b. Estimation of mean and range

The mean values for each character were worked out by dividing the total by corresponding number of observations:

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

Where,

\bar{X} = Mean of character

$\sum X_i$ = Total of all the observations for character

N = Number of observations

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

c. Estimation of components of variation

The phenotypic and genotypic variances were calculated using the respective mean squares from variance Table (Johnson *et al.*, 1955) as below.

Environmental variance (σ^2_e) = EMS

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{GMS} - \text{EMS}}{r}$$

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated as per Burton, (1952).

i. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sigma^2_g}{\bar{X}} \times 100$$

Where,

σ^2_g = Genotypic variance and,

\bar{X} = Mean of character

ii. Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sigma^2_p}{\bar{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance and,

\bar{X} = Mean of character

The high, medium and low GCV and PCV estimates were classified as:

Low : 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

e. Estimation of heritability (b.s.)

Heritability in broad sense was estimated as suggested by Hanson *et al.* (1956).

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

Where,

h^2 = Heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Johnson *et al.*, (1955).

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

f. Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1960)

i. Genetic advance (G.A.)

$$\text{G.A.} = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

$\sqrt{\sigma_p^2}$ = Phenotypic standard deviation

ii. G.A. as percentage of means (GAM)

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

G. A. = Genetic advance

\bar{X} = Character mean

GA (As percentage of mean) was classified as

Low : 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

3.5.2 Correlation

Analysis of covariance was carried out by taking two characters at a time.

The genotypic co-variance was calculated as per Johnson *et al.*, (1955) as below:

Sources	d.f.	Sum of product	Mean sum of product	Expectation of mean sum of product
Replications	(r-1)	RP	RMP	$\text{COV}_{e_{1.2}+g} \text{COV}_{r_{1.2}}$
Genotypes	(g-1)	GP	GMP	$\text{COV}_{e_{1.2}+r} \text{COV}_{g_{1.2}}$
Error	(r-1) (g-1)	EP	EMP	$\text{COV}_{e_{1.2}}$

Environmental covariance (COV. $e_{1.2}$) = EMP

Genotypic covariance (COV. $g_{1.2}$) = $\frac{\text{GMP} - \text{EMP}}{r}$

Phenotypic covariance (COV. $p_{1.2}$) = (COV. $g_{1.2}$) + (COV. $e_{1.2}$)

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

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

The phenotypic correlation coefficient (r_p) was calculated as:

$$r_{p1.2} = \frac{COV_{.p1.2}}{\sqrt{(\sigma_{p1}^2)(\sigma_{p2}^2)}}$$

Where,

$r_{p1.2}$ = Phenotypic correlation coefficient between character 1 and 2

$COV_{.p1.2}$ = Phenotypic covariance between character 1 and 2.

$\sigma_{p1}^2, \sigma_{p2}^2$ = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by referring to formula given by Fisher and Yates (1943). The genotypic correlation coefficient (r_g) was calculated as:

$$r_{g1.2} = \frac{COV_{.g1.2}}{\sqrt{(\sigma_{g1}^2)(\sigma_{g2}^2)}}$$

Where,

$r_{g1.2}$ = Genotypic correlation coefficient between character 1 and 2

$COV_{.g1.2}$ = Genotypic covariance between character 1 and 2

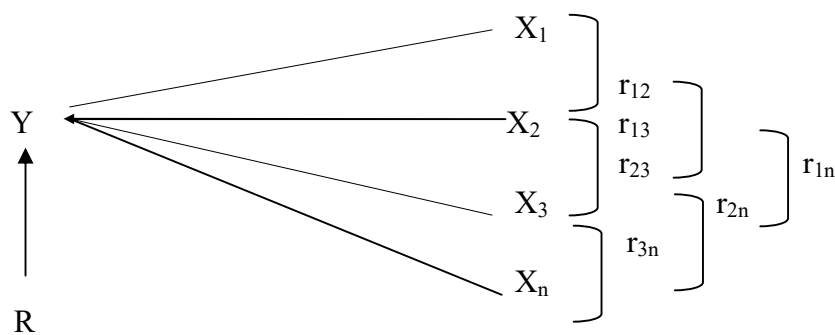
$\sigma_{g1}^2, \sigma_{g2}^2$ = Genotypic variance of character 1 and 2 respectively.

The significance of correlation coefficients was tested from the statistical Table of correlation coefficient at 1 and 5 per cent level of significance (Snedcor and Cochran, 1967).

3.5.3 Path coefficient analysis

To establish a cause and effect relationship the first step used was to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

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



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

Path coefficients were obtained by solving a set of simultaneous equation of the form as per Dewey and Lu (1959).

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

Where,

- r_{ny} = represents the correlation between one component and yield
- P_{ny} = represents path coefficient between that character and yield
- r_{n2} = represents correlation between that character and each of the other components in turn.

Matrix A	Matrix B	C
$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{pmatrix}$	$= \begin{pmatrix} r_{11} & r_{12} & r_{13} & \dots & r_{1n} \\ r_{21} & r_{22} & r_{23} & \dots & r_{2n} \\ r_{n1} & r_{n2} & r_{n3} & \dots & 1 \end{pmatrix}$	$\begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{ny} \end{pmatrix}$

Where,

- $r_{12} = r_{21}$ and so on
- r_{1y} = Correlation between one component character and seed yield

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

i.e. $P_{ij} = (B)^{-1} \cdot A$

The indirect effects of a particular character through other characters were obtained by multiplication of direct paths and particular correlation between these characters separately.

$$\text{Indirect effects} = r_{ij} \times p_{iy}$$

Where,

$$i = 1 \text{ to } 9$$

$$j = 1 \text{ to } 9$$

$$P_{iy} = P_{1y}, P_{2y}, \dots, P_{ny}$$

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

$$\text{Residual factor (R)} = (1 - R^2)$$

Where,

$$R^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \dots + P_{ny} r_{ny}$$

$$P_{1y}, P_{2y}, \dots, P_{ny} = \text{Direct path values}$$

$$r_{1y}, r_{2y}, r_{ny} = \text{Correlation coefficient}$$

3.5.4 Wilt incidence percentage

Wilt incidence recorded as percentage. The wilt incidence of each entry was calculated by the following formula:

$$\text{Wilt incidence} = \frac{\text{Number of plants wilted}}{\text{Total number of plants}}$$

The level of resistance and susceptibility of each test entry was determined by using five-point scales. The disease rating scale were put in Table NO. 2, according to this rating scale twenty-eight pigeonpea genotypes along with three check were grouped into resistant, moderately resistant, susceptible and highly susceptible category.

Table 2. Disease rating scale

Asy	0 %	Asymptomatic
R	0.0 to 10 %	Resistant
MR	10.1 to 20 %	Moderately Resistant
S	20.1 to 40 %	Susceptible
HS	Above 40 %	Highly Susceptible

4. RESULTS AND DISCUSSION

Plant breeding deals with management and utilization of genetic variability. Hence, assessment of genetic variability, study of character association and genetic diversity in the available germplasm is of immense value to design a selection programme and to identify the superior, genetically diverse genotypes to be used as parents in future hybridization programme. In extreme cases, low genetic diversity may lead to complete elimination of some plant species resulting in loss of overall biological diversity. It is, therefore necessary to classify and utilize this variability systematically for genetic up gradation of biological population. Similarly, the assessment of the magnitude and direction of association between different yield contributing characters especially with yield is useful in selecting desired genotypes on the basis of their phenotypic values. Simple correlation coefficients in this direction are of limiting value. Hence, it is important to study the cause-and-effect relationship between yield and its component characters through correlation and path analysis studies.

Among various diseases in pigeonpea *Fusarium* wilt is a major problem in most of the growing areas of this crop, not only in India but also countries like Pakistan, Bangladesh, African countries and Syria etc. Hence, it is not only to select diverse parent but also to select disease resistant diverse parent which can be used in the development of resistant variety.

In this investigation correlation and path analysis were worked out to study the associations between component characters and the direct and indirect path coefficients of the component characters on yield. The results obtained on genetic aspects are discussed in this chapter along with disease reaction of (*Cajanus cajan* L.) 28 accessions under appropriate headings.

- 4.1 Analysis of variance
- 4.2 Mean performance
- 4.3 Components of genetic variability
- 4.4 Correlation studies
- 4.5 Path coefficient analysis
- 4.6 Wilt incidence percentage

4.1 Analysis of variance

Analysis of variance revealed highly significant difference among genotypes for all the ten characters, *i.e.* days to 50 per cent flowering, days to maturity, plant height, plant spread, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant indicating wide spectrum of variation among the genotypes.

Table 3. Analysis of variance for ten different characters in pigeonpea

Sr. No.	Name of characters	Mean Sum of Squares		
		Replications (d.f. 1)	Genotypes (d.f. 27)	Error (d.f. 27)
1.	Days to 50 per cent flowering	84.84	261.44**	7.22
2.	Days to maturity	98.60	310.92**	9.41
3.	Number of primary branches plant ⁻¹	9.44	3.58*	1.28
4.	Number of secondary branches plant ⁻¹	9.01	25.48**	12.15
5.	Plant height (cm)	12.74	404.29**	143.52
6.	Plant spread (cm)	54.01	131.13**	55.79
7.	Number of pods plant ⁻¹	229.13**	632.01**	197.64
8.	Number of seeds pod ⁻¹	0.04	0.56*	0.018
9.	100 seed weight (g)	0.11	0.73*	0.13
10.	Seed yield plant ⁻¹ (g)	46.57	199.20**	52.83

*, ** indicate significant at 5 and 1 per cent level, respectively.

Note: Figure in the parenthesis indicates the degrees of freedom.

4.2 Mean performance and the range of variability

The genotypes mean values for different characters studied are presented in Table 4.

4.2.1 Days to 50 per cent Flowering

The variation in days to 50 per cent flowering ranged between 81.6 and 127.65 days. Genotype CRJ-1608 took significantly least 81.6 days while significantly highest 127.65 days were taken by WRG-353. The mean value for days to 50 per cent flowering was 109.10 days and fifteen genotypes had days for 50 per cent flowering higher than mean value (109.10).

4.2.2 Days to Maturity

The variation in days to maturity ranged between 133.1 and 183.8 days. Genotype CRJ-1608 matured in significantly least numbers of (133.1) days while PTO-705-4-12 matured late (183.8) days. The mean number of days for maturity was 161.53 days and fifteen genotypes had days to maturity higher than mean value (161.53).

4.2.3 Number of Primary Branches per Plant

Number of primary branches per plant ranged from 7.75 to 13.35. Genotype RVKT-314-733 recorded lowest, while RKPV-912-735 had maximum number of primary branches per plant. Eleven genotypes recorded higher number of primary branches than the mean value (9.54).

4.2.4 Number of Secondary Branches per Plant

Number of secondary branches per plant ranged from 16.15 to 31.95. Genotype CRJ-1608 recorded lowest, while RKPV-911-732 had maximum number of secondary branches per plant. Thirteen genotypes were recorded having a greater number of secondary branches than the mean (24.02).

4.2.5 Plant Height (cm)

The variation for plant height ranged between 158.35 cm to 212.82 cm. Genotype WRG-353 recorded lowest, while the genotype GGP-1721 highest plant height. Sixteen genotypes were found taller when compared to mean (194.72 cm).

4.2.6 Plant Spread (cm)

The variation for plant spread ranged between 87.8 cm to 132.63 cm. Genotype CRJ-1608 had minimum while RKPV-912-735 had maximum plant spread and the mean value for plant spread was 112.5 cm. Thirteen genotypes recorded higher plant spread than mean value (112.5).

4.2.7 Number of Pods per Plant

Number of pods per plant ranged from 121.5 to 206.63. Genotype CRJ-1608 recorded lowest while RKPV-912-735 had maximum number of pods per plant. The mean for this character was 153.81 thirteen genotypes recorded highly significant number of pods per plant.

Table 4. Mean performance of twenty-eight pigeonpea genotypes for ten characters

Sr. No.	Genotype	Days to 50 % flowering	Days to maturity	Number of primary branches plant ⁻¹	Number of secondary branches plant ⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
1	BDN-711	100.15	157.80	10.45	25.50	179.10	114.25	168.26	3.85	10.65	66.45
2	RVKT-314-733	116.45	160.25	7.75	19.85	184.15	117.75	132.86	3.88	9.75	48.75
3	RKPV-911-732	120.70	172.66	10.35	31.95	175.50	118.65	176.69	3.72	9.75	71.86
4	RKPV-912-735	117.75	171.35	13.35	30.55	176.75	132.63	206.63	3.64	9.65	85.39
5	RPS-2007-105-1	118.80	166.25	9.75	24.50	197.10	106.80	159.52	3.71	9.55	61.40
6	AKTE-12-02-724	114.00	163.50	9.05	23.35	191.05	113.20	150.94	3.83	10.60	57.135
7	CRJ-1608	81.60	133.10	8.45	16.15	200.05	87.80	121.05	3.82	10.45	39.25
8	LPG-229	111.90	143.65	9.10	21.85	201.45	104.5	135.55	3.63	9.40	52.25
9	BRGL-18-1-728	110.80	167.00	9.05	23.35	206.50	116.6	150.50	3.30	9.55	57.90
10	BAUUP-15-19	108.65	174.66	9.65	23.25	188.55	121.68	167.95	3.72	10.6	67.86
11	RRG-300	114.75	162.60	8.20	23.05	208.20	107.5	155.05	3.68	9.60	62.50
12	RVSA-157	123.30	181.15	12.00	28.865	177.44	126.15	182.03	3.71	9.45	74.23
13	ICPL-15048	112.30	152.10	8.45	21.435	195.55	107.1	143.15	3.83	10.85	52.25
14	IBTO-RG-7	105.95	156.80	8.55	23.215	207.80	114.30	148.93	3.69	11.00	55.43
15	RPS-2007-109	101.15	146.65	9.00	24.50	205.40	110.80	138.75	3.62	9.80	51.82
16	BRGL-18-2	106.66	169.25	10.05	26.55	185.35	117.10	158.70	3.31	9.80	66.40
17	TTO-704-1-2	93.65	141.25	9.55	23.95	202.20	105.80	150.95	3.76	9.69	50.60
18	TDRG-59	95.30	151.50	8.95	23.50	210.55	107.00	149.55	3.39	8.85	53.85
19	WRG-353	127.65	168.83	11.80	27.70	158.35	116.15	165.25	3.91	10.15	68.00
20	KRG-224	93.65	164.00	7.80	17.70	198.20	104.90	132.45	3.64	10.25	44.95
21	CRG-16-008	123.5	181.00	9.25	23.65	211.6	110.5	159.35	3.83	9.35	64.55
22	RVSA-1510	98.80	148.75	8.20	19.05	201.70	115.60	136.10	3.93	11.00	51.55
23	SKNP-1413	118.80	168.00	11.65	26.65	181.20	112.38	152.30	3.83	9.80	60.30

Table 4 contd....

Sr. No.	Genotype	Days to 50 % flowering	Days to maturity	Number of primary branches plant ⁻¹	Number of secondary branches plant ⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
24	PTO-705-4-12	125.55	183.83	8.30	20.00	213.00	107.75	137.50	3.91	11.20	53.90
25	GGP-1721	109.90	169.50	9.35	25.75	212.85	110.48	158.55	3.82	10.40	61.85
26	GGP-1715	95.50	153.50	9.45	25.50	211.1	115.55	155.75	3.72	10.05	63.60
27	LRG-134	99.00	155.50	9.60	25.35	181.40	110.20	141.05	3.86	10.70	49.20
28	Rajeshwari	108.65	158.50	10.10	25.90	190.25	116.90	171.43	3.92	10.65	70.10
	Mean	109.10	161.53	9.54	24.02	194.72	112.50	153.81	3.73	10.08	59.40
	S.E.	1.90	2.16	0.80	2.46	8.47	5.28	9.94	0.09	0.20	5.10
	C.D. at 5 %	5.51	6.29	2.32	7.15	24.58	15.32	28.84	0.28	0.76	14.91
	C.D. 1 %	7.44	8.50	3.13	9.65	33.19	20.69	38.95	0.37	1.02	20.13
	C.V.	2.46	1.89	11.87	14.51	6.1	6.63	9.14	3.66	3.68	12.23

4.2.8 Number of Seeds per Pod

Number of seeds per pod ranged from 3.31 to 3.93. Number of seeds per pod was lowest in case of BRGL-18-2 while RVSA-1510 maximum number of seeds per pod recorded in. The general mean for this character was 3.73. Fourteen number of genotypes were recorded highly significant number of seeds per pod.

4.2.9 100 Seed Weight (g)

The variation in 100 seed weight ranged between 8.85 g to 11.2 g. Genotype TDRG-59 was with lowest while PTO-705-4-12 with highest 100 seed weight and the mean for this character was 10.08 g. Twelve genotypes recorded highly significant 100 seed weight.

4.2.10 Seed Yield per Plant (g)

The variation for seed yield per plant ranged between 29.25 g and 85.39 g. The genotype CRJ-1608 recorded minimum seed yield per plant (29.25 g), while RKPV-912-735 recorded maximum seed yield per plant (85.39 g). Out of twenty-eight genotypes, thirteen genotypes recorded higher seed yield per plant than the mean (59.40 g).

4.3. Estimates of Components of Variation

The estimates of GCV, PCV, heritability (b. s.) and genetic advance as per cent of mean for the different characters studied are presented in Table 5.

4.3.1. Genotypic and Phenotypic Coefficients of Variation

Genotypic coefficient of variation (GCV) was moderate for grain yield per plant (14.40 %) followed by number of primary branches (11.24 %), number of secondary branches per plant (10.74 %) and days to 50 % flowering (10.33 %). The moderate phenotypic coefficient of variation (PCV) was recorded for seed yield per plant (18.79 %) followed by number of secondary branches per plant (18.05 %), number of primary branches per plant (16.35 %), number of pods per plant (13.24 %) and days to 50 % flowering (10.65 %).

Genetic variability is the basis for any heritable improvement in the crop plants. The estimates of GCV and PCV for all the characters studied showed little difference the latter being slightly greater than the former, thus indicating that the variability existing in these characters was not only due to genetic factors but also due to

environmental factors. These observations were conformity with the findings of Bhadru (2011) and Hari Kesh *et al.* (2014). Moderate GCV and PCV were found for number of branches per plant, seed yield per plant and days to 50 per cent flowering. Birhan *et al.* (2013) and Hari Kesh *et al.* (2014) reported high GCV and PCV value for number of branches per plant and seed yield per plant. Lowest GCV and PCV estimates were obtained for plant height, 100 seed weight and days to maturity indicating the presence of comparatively low variability. Lower estimates of GCV and PCV for days to maturity were also reported by Satish Kumar *et al.* (2006), Bhadru (2011) and Hari Kesh *et al.* (2014). The analysis of genotypic and phenotypic coefficient of variation showed that GCV estimates were closer to the PCV estimates for days to 50 per cent flowering, days to maturity and 100 seed weight, indicating lesser influence of environment in the expression of the characters.

This seems to be valid as the heritability estimates of these characters are high. On the other hand, the characters number of pods per plant, plant height, number of primary branches per plant, number of secondary branches per plant, no. of seeds per pod, plant spread and yield per plant, PCV was of much higher magnitude than the GCV, indicating the characters are much prone to environmental fluctuation. Meena *et al.* (2017) also reported that magnitude of PCV was higher than GCV for the same characters. Thus, from the present study, it can be suggested that a magnitude of variability is present in these genotypes, which can be exploited in genetic improvement.

4.3.2 Heritability and Genetic Advance as percentage of mean

High heritability was observed for days to maturity and days to 50 % flowering (94 %). Moderate heritability observed for the character 100 seed weight (68 %). Low heritability (<60 %) was observed for seven characters viz, number of primary branches per plant, number of secondary branches per plant, plant height, plant spread, number of pods per plant, number of seeds per pod and seed yield plant. These results are in agreement with Rangare *et al.* (2013), Kumar *et al.* (2013), Kumara *et al.* (2014) and Chethana *et al.* (2015). High heritability indicates the scope of improvement of these characters through selection. Similar type of heritability was recorded by Patel and Patel (1998) and Linge *et al.* (2010).

Table 5. Estimates of variability parameters for ten different characters in pigeonpea

Sr. No.	Characters	Mean	Range	GCV %	PCV %	h²% (b.s)	GA	GA as % mean
1	Days to 50 per cent flowering	109.10	81.6-127.65	10.33	10.62	94	22.59	20.70
2	Days to maturity	161.53	133.1-183.83	7.60	7.83	94	24.53	15.19
3	Number of primary branches plant ⁻¹	9.54	7.75-13.35	11.24	16.35	47	1.51	15.92
4	Number of secondary branches plant ⁻¹	24.02	16.15-31.95	10.74	18.05	35	3.16	13.17
5	Plant height (cm)	194.72	158.35-212.85	5.86	8.94	47	16.22	8.33
6	Plant spread (cm)	112.50	87.8-132.63	5.45	8.59	40	8.02	7.13
7	Number of pods plant ⁻¹	153.81	121.5-206.63	9.58	13.24	52	21.96	14.28
8	Number of seeds pod ⁻¹	3.73	3.31-3.93	3.68	5.20	50	0.20	5.38
9	100 seed weight (g)	10.08	8.85-11.20	5.42	6.55	68	0.93	9.25
10	Seed yield plant ⁻¹ (g)	59.40	39.25-85.39	14.40	18.79	58	13.43	22.60

Whereas high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals. According to Johnson *et al.* (1995) heritability estimates along with genetic gain are usually more useful.

The estimates of genetic advance ranged from 0.20 to 24.53 with the highest estimate in case of days to maturity (24.53) followed by days to 50 per cent flowering (22.59) and number of pods plant (21.96). The high genetic advance as per cent of mean was observed for seed yield per plant (22.60 %) followed by days to 50 % flowering (20.70 %). It is moderate for number of primary branches per plant (15.92 %), days to maturity (15.19) number of pods plant (14.28) and number of secondary branches per plant (13.17).

High heritability with high genetic advance as per cent of the mean in case of days to 50 per cent flowering and moderate heritability with high genetic advance as per cent of mean for seed yield per plant indicate that these are simply inherited traits and most likely the heritability is due to additive gene action and selection based on phenotypic characters is effective for these traits in early generation. Saroj *et al.* (2015) reported similar result for primary and secondary branches per plant. However, days to maturity had high heritability associated with low genetic advance indicates non-additive gene effect and these characters were under control of complex nature of inheritance. Similar findings were reported by Gowda *et al.* (2003) and Arshad *et al.* (2003).

4.4 Correlation coefficient analysis

Correlation measures the degree and direction of association between two or more variables. Correlated characters are of interest for three chief reasons, firstly, in connection with the genetic cause of correlation through the linkage and pleiotropic action of genes, secondly it is important to know how the improvement of one character causes simultaneous changes in other characters and thirdly in connection with natural selection (Falconer, 1960). The value of correlation coefficient cannot be constant everywhere. It varies considerably according with kind of material handled, mode of observations taken, cultural practices followed and environmental conditions in which material is grown. In the present investigation genotypic correlation coefficients were higher than their corresponding phenotypic correlations. For ten different characters in

pigeonpea the genotypic and phenotypic correlations were studied and presented in Table 6.

4.4.1 Association of seed yield with its components

It is revealed from Table 6 that seed yield per plant show highly significant positive correlation with days to 50 per cent flowering ($r_g=0.599$, $r_p=0.545$), days to maturity ($r_g=0.658$, $r_p=0.616$), number of primary branches per plant ($r_g=0.762$, $r_p=0.804$), number of secondary branches per plant ($r_g=0.878$, $r_p=0.824$), plant spread ($r_g=0.944$, $r_p=0.724$), number of pods per plant ($r_g=0.966$, $r_p=0.968$) at both genotypic and phenotypic levels. It also showed highly significant negative correlation with plant height ($r_g=-0.746$, $r_p=-0.297$), and 100 seed weight ($r_g=-0.378$, $r_p=-0.310$) at genotypic levels, and non-significant negative correlation with number of seeds per pod ($r_g=-0.123$, $r_p=-0.068$) at both levels.

Highly positive and significant correlation observed for number of pods per plant ($r_g=0.968$, $r_p=0.966$). Prasad *et al.* (2013), Pushpavalli *et al.* (2017) Pal *et al.* (2018) reported the similar results for the trait number of pods per plant. Sarsamkar *et al.* (2008), Thanki and Sawargaonkar (2010) and Narayanan *et al.* (2018) corroborated similar findings. Days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant and plant spread had positive and significant association with seed yield per plant. The same result was corroborated by Katiyar *et al.* (2004), Mahajan *et al.* (2007), Sodavadiya *et al.* (2009), Mahendran (2011), Saroj *et al.* (2013), Vanisree and Sreedhar (2014) and Kesh Ram *et al.* (2016). This indicates the simultaneous improvement of these characters through selection will be rewarding.

Highly significant negative correlation was reported between seed yield per plant with plant height, 100 seed weight. Similar results were obtained by Chandirakala and Subbaraman (2010) and Padmavathi *et al.* (2013) for plant height.

4.4.2 Interrelationship of Yield Components

4.4.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed highly significant positive correlations with days to maturity ($r_g=0.766$, $r_p=0.774$), number of pods per plant ($r_g=0.486$, $r_p=0.453$), number of primary branches per plant ($r_g=0.415$, $r_p=0.399$),

Table 6 Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients in pigeonpea

Sr. No.	Characters	Days to 50 % flowering	Days to maturity	Number of primary branches plant ⁻¹	Number of secondary branches plant ⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
1.	Days to 50 % flowering	1.000	0.766**	0.415**	0.529**	-0.456**	0.579**	0.486**	0.196	-0.194	0.599**
2.	Days to maturity	0.774**	1.000	0.378**	0.485**	-0.332*	0.674**	0.575**	-0.012	-0.084	0.658**
3.	Number of primary branches per plant	0.399**	0.383**	1.000	0.787**	-0.957**	0.604**	0.794**	-0.036	-0.510**	0.762**
4.	Number of secondary branches per plant	0.444**	0.429**	0.835**	1.000	-0.947**	0.723**	0.889**	-0.219	-0.637**	0.878**
5.	Plant height (cm)	-0.264*	-0.177	-0.497**	-0.310*	1.000	-0.719**	-0.784**	-0.464**	0.026	-0.746**
6.	Plant spread (cm)	0.451**	0.526**	0.613**	0.661**	-0.373**	1.000	0.850**	-0.074	-0.223	0.944**
7.	Number of pods per plant	0.453**	0.536**	0.834**	0.836**	-0.316*	0.735**	1.000	-0.139	-0.445**	0.966**
8.	Number of seeds per Pod	0.138	-0.013	-0.033	-0.101	-0.704**	-0.109	-0.069	1.000	0.717**	-0.123
9.	100 seed weight (g)	-0.107	-0.024	-0.120	-0.169	-0.029	-0.023	-0.114	0.489**	1.000	-0.378**
10.	Seed yield per plant	0.545**	0.606**	0.804**	0.824**	-0.297*	0.726**	0.968**	-0.068	-0.310*	1.000

*,** indicate significant at 5 and 1 per cent level, respectively.

Note : Figure in the parenthesis indicates the degrees of freedom

number of secondary branches per plant ($r_g=0.539$, $r_p=0.444$), plant spread ($r_g=0.579$, $r_p=0.453$) at both genotypic and phenotypic levels. It shows significant negative correlation with plant height ($r_g=-0.456$, $r_p=-0.264$) at both genotypic and phenotypic level also shows non-significant positive correlation with seed per pod ($r_g=0.196$, $r_p=0.138$) at both genotypic and phenotypic level and highly significant negative correlation with 100 seed weight ($r_g=-0.310$) at phenotypic level only.

4.4.2.2 Days to maturity

Days to maturity highly significant positively correlated with primary branches per plant ($r_g=0.378$, $r_p=0.38$), number of secondary branches per plant ($r_g=0.4854$, $r_p=0.429$), plant spread ($r_g=0.674$, $r_p=0.526$), number of pods per plant ($r_g=0.575$, $r_p=0.535$), also with seed yield ($r_g=0.658$, $r_p=0.606$) at both genotypic and phenotypic level. It is significantly negatively correlated with plant height ($r_g=-0.332$, $r_p=-0.177$) at both genotypic and phenotypic level. It is non significantly negative correlated with number of seed per pod ($r_g=-0.012$, $r_p=-0.013$), 100 seed weight ($r_g=-0.084$, $r_p=-0.024$) at both phenotypic level and genotypic level.

4.4.2.3 Number of primary branches per plant

The number of primary branches per plant highly significant positively with number of pods per plant ($r_g=0.794$, $r_p=0.834$), seed yield per plant ($r_g=0.762$, $r_p=0.804$), plant spread ($r_g=0.604$, $r_p=0.613$), number of secondary branches per plant ($r_g=0.787$, $r_p=0.835$) at both phenotypic and genotypic level. It is negatively significant with plant height ($r_g=-0.957$, $r_p=-0.497$) at both genotypic and phenotypic level and 100 seed weight ($r_g=-0.510$) at genotypic level only. It is negatively non significant with number of seed per pod ($r_g=-0.036$, $r_p=-0.033$) at genotypic and phenotypic level.

4.4.2.4 Number of secondary branches per plant

The number of secondary branches per plant showed significant positive correlation at plant spread ($r_g=0.723$, $r_p=0.661$), number of pods per plant ($r_g=0.889$, $r_p=0.836$), seed yield per plant ($r_g=0.878$, $r_p=0.824$) at both genotypic and phenotypic level only, it had significant negative correlation with plant height ($r_g=-0.947$, $r_p=-0.310$) at both level and 100 seed weight ($r_g=-0.637$, $r_p=-0.169$) at genotypic level only, and had non-significant negative correlation with number of seeds per pod ($r_g=-0.219$, $r_p=0.101$) at both genotypic level and phenotypic level.

4.4.2.5 Plant height

Plant height showed highly significant negative association with plant spread ($rg=-0.719, rp=-0.373$), number of pods plant ($rg=-0.784, rp=-0.316$), seed yield per plant ($rg=-0.746, rp=-0.297$) and number of seed per pod ($rg=-0.464, rp=-0.704$) at both genotypic and phenotypic level only. It also showed non-significant negative relation with 100 seed weight ($rg=-0.269, rp=-0.029$) at both levels.

4.4.2.6 Plant spread

Plant spread showed positive significant correlation with seed yield per plant ($rg=0.944, rp=0.726$) and number of pods per plant ($rg=0.374, rp=0.735$) at both genotypic and phenotypic level only. It also showed non-significant negative correlation with number of seeds per pod ($rg=-0.074, rp=0.109$) and 100 seed weight ($rg=-0.223, rp=-0.023$) at genotypic and phenotypic level.

4.4.2.7 Number of pods per plant

The number of pods per plant showed significant positive correlation with seed yield per plant ($rg=0.966, rp=0.968$) at both genotypic and phenotypic level. It shows non-significant negative correlation with number of seeds per pod ($rg=0.105, rp=0.083$) and 100 seed weight ($rg=0.078, rp=0.090$) at both level.

4.4.2.8 Number of seeds per pod

Number of seeds per pod showed non-significant negative correlation with seed yield per plant ($rg=-0.683, rp=-0.123$) at both genotypic and phenotypic level. It shows positive significant correlation with number of seed per pod ($rg=0.717, rp=-0.489$) at both level.

4.4.2.9 100 seed weight

100 seed weight showed significant negative correlation with seed yield per plant ($rg=-0.378, rp=-0.310$) at both genotypic and phenotypic level.

4.5. Genotypic Path Coefficient Analysis

To find out the direct and indirect contribution from each of the characters towards seed yield per plant, path coefficient analysis was carried out. The genotypic correlation coefficients being more important were only partitioned into direct and indirect effects which were presented in Table 7.

Genotypic Path

4.5.1 Direct effect

Residual effect was found to be 0.076 which indicate that the characters under study contributed to 92.4 per cent of total variation.

In the present investigation, path coefficient analysis revealed that the character's number of pods per plant (0.663), plant spread (0.304), days to 50 % flowering (0.241) number of primary branches per plant (0.022), and 100 seed weight (0.150) had direct positive effect on seed yield per plant. Whereas the characters plant height (-0.086), number of secondary branches per plant (-0.066), days to maturity (-0.107) and number of seeds per pod (-0.218) had direct negative effect on seed yield per plant.

4.5.2 Indirect effect of different independent trait on grain yield

4.5.2.1 Days to 50 % flowering

Days to 50 per cent flowering showed positive direct effect (0.241) on seed yield. It was highly significant and positively associated with seed yield (0.599**). It was due to positive indirect effects through number of pods per plant (0.323), plant spread (0.176), plant height (0.040), and number of primary branches per plant (0.009), whereas negative indirect effect through days to maturity (-0.082), number of secondary branches per plant (-0.035), number of seeds per pod (-0.043) and 100 seed weight (-0.029).

4.5.2.2 Days to Maturity

Days to maturity showed negative direct effect (-0.107). The indirect effects of it were positive through days to 50 per cent flowering (0.185), number of primary branches per plant (0.008), plant height (0.029), plant spread (0.205), number of pods per plant (0.381) and number of seed per pod (0.003), whereas it had negative indirect effect number of secondary branches per plant (-0.032), 100 seed weight (-0.013). Thus, leads to significant positive correlation with seed yield per plant (0.65).

4.5.2.3 Number of Primary Branches per Plant

The primary branches per plant showed positive direct effect (0.022). It had indirect positive effect through days to 50 per cent flowering (0.100), number of primary branches per plant (0.022), plant height (0.091), plant spread (0.183), number of

Table 7 Estimate of genotypic direct (diagonal) and indirect effect (above and below diagonal) of component characters on seed yield in pigeonpea

Sr. No.	Characters	Days to 50 % flowering	Days to maturity	Number of primary branches plant ⁻¹	Number of secondary branches plant ⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Total genotypic correlation with seed yield per plant
1.	Days to 50 % flowering	0.240	-0.082	0.009	-0.035	0.040	0.176	0.323	-0.043	-0.029	0.599**
2.	Days to maturity	0.185	-0.107	0.008	-0.032	0.029	0.205	0.381	0.003	-0.013	0.659**
3.	Number of primary branches per plant	0.100	-0.040	0.022	-0.052	0.091	0.183	0.527	0.008	-0.076	0.762**
4.	Number of secondary branches per plant	0.127	-0.052	0.017	-0.066	0.091	0.220	0.590	0.048	-0.095	0.879**
5.	Plant height (cm)	-0.110	0.035	-0.023	0.069	-0.086	-0.218	-0.520	0.101	0.004	-0.747**
6.	Plant spread (cm)	0.140	-0.072	0.013	-0.048	0.062	0.304	0.564	0.016	-0.034	0.945**
7.	Number of pods per plant	0.117	-0.061	0.017	-0.059	0.068	0.258	0.663	-0.030	-0.067	0.966**
8.	Number of seeds per pod	0.047	0.001	-0.001	0.015	0.040	-0.023	-0.092	-0.218	0.107	-0.123
9.	100 seed weight (g)	-0.046	0.009	-0.011	0.042	-0.002	-0.068	-0.295	-0.157	0.150	-0.378**

Residual effect (R) = 0.076 Bold figure indicate direct effect

*,** = significant at 5 per cent and 1 per cent respectively

pods per plant (0.527) and number of seed per pod (0.008). The indirect effects of it were negative through days to maturity (-0.04), number of secondary branches (-0.05) and 100 seed weight (-0.07). Thus, leads to significant positive correlation with seed yield per plant (0.762).

4.5.2.4 Number of Secondary Branches per Plant

It showed negative direct effect on seed yield (-0.066). It showed positive effect through days to 50 per cent flowering (0.127), number of primary branches per plant (0.017), plant height (0.091), plant spread (0.220), number of pods per plant (0.590) and number of seeds per pod (0.048). The indirect effects of it were negative through days to maturity (-0.052), and 100 seed weight (-0.095). Thus, leads to significant positive correlation with seed yield per plant (0.87).

4.5.2.5 Plant Height

The plant height showed negative direct effect (-0.218). The indirect effects of it were negative through days to 50 per cent flowering (-0.110), number of primary branches per plant (-0.023), spread (-0.218) and number of pods per plant (-0.520). The indirect effects of it were positive through days to maturity (0.03), number of secondary branches per plant (0.06), number of pods per plant (0.29) and number of seeds per pod (0.10), 100 seed weight (0.004). Thus, leads to significant negative correlation with seed yield per plant (-0.747).

4.5.2.6 Plant Spread

The plant spread showed positive direct effect (0.304) on seed yield. The indirect effects of it were positive through days to 50 per cent flowering (0.014), number of primary branches per plant (0.013), plant height (0.062), number of pods per plant (0.564) and number of seeds per pod (0.016). The indirect effects of it were negative through days to maturity (-0.072), number of secondary branches per plant (-0.048) and 100 seed weight (-0.034). Thus, leads to significant positive correlation with seed yield per plant (0.945).

4.5.2.7 Number of Pods per Plant

The number of pods per plant showed positive direct effect (0.966) on seed yield. The indirect effects of it were positive through days to 50 per cent flowering (0.117), number of primary branches per plant (0.017) and plant height (0.068), plant

spread (0.258), number of seed per pod (0.030). The indirect effects of it were negative through, days to maturity (-0.061), number of secondary branches per plant (-0.059) and 100 seed weight (-0.067). Thus, leads to significant positive correlation with seed yield per plant (0.966).

4.5.2.8 Number of Seeds per Pod.

The number of seeds per pod showed negative direct effect (-0.218) on seed yield. The indirect effects of it were negative through number of primary branches per plant (-0.001), plant spread (-0.023), number of pods per plant (-0.092). The indirect effects of it were positive through days to 50 % flowering (0.047), days to maturity (0.001), number of secondary branches per plant (0.015), plant height (0.040), and 100 seed weight (0.107). Thus, leads to negative correlation with seed yield per plant (-0.123).

4.5.2.9 100 Seed Weight

The 100 seed weight showed positive direct effect (0.150) on seed yield. The indirect effects of it were positive through days to maturity (0.009), number of secondary branches (0.042). It shows negative indirect effect through days to 50 % flowering (-0.046), number of primary branches (-0.011), plant height (-0.002), plant spread (-0.068), number of pods per plant (-0.295), number of seeds per pod (-0.157). Thus, leads to significant negative correlation with seed yield per plant (-0.378).

Varma (2018) reported that number of pods per plant had positive direct effect on single plant yield. Similar results were reported by Nethravati and Patil (2014), Puhpavalli *et al.* (2017), Pal *et al.* (2018) and Narayanan *et al.* (2018). High direct positive effect of number of primary branches per plant on seed yield per plant was reported by Prasad *et al.* (2013), Pandey *et al.* (2016) and Kesh *et al.* (2017). Negative and negligible direct effect on seed yield per plant observed for the trait's days to maturity, 100 seed weight and number of seed per pod Krishna Chaitanya *et al.* (2014) and Pandey *et al.* (2016). Singh *et al.* (2013) reported similar research proof for days to maturity and plant height.

Based on findings of the present investigations it could be enforced that the most desirable plant type in pigeonpea should possess a greater number of pods per

plant, higher number of primary branches, plant spread, and more days to 50 per cent flowering.

4.6 Wilt Incidence

Fusarium wilt incidence in 28 pigeonpea genotypes lines ranged from 0 to 100 per cent. Based on the mean disease incidence of both the replications during kharif-2019, three genotypes in present investigation *viz.*, RPS-2007-105-1, TTO-704-1-2 and RVSA-1510 exhibited resistant reaction for *Fusarium* wilt. However, eight genotypes *viz.*, RKPV-911-732, RKPV-912-335, RVSA-157, RPS-2007-109, WRG-353, SKNP-1413, GGP-1715 and LRG-134 found to be moderately resistant towards *Fusarium* wilt. Moreover, four genotypes *viz.*, CRJ-1608, TDRG-59, GGP-1721, BRGL-18-2 exhibited susceptible reaction, while remaining ten genotypes *viz.* LPG-229, AKTE-12-02-724, IBTO-RG-7, BRGL-18-1-728, KRG-224, PTO-705-4-12, RVKT-314-733, RRG-300, BAUUP-15-19, ICPL-15048 showed highly susceptible reaction for wilt pathogen. One genotype CRG-16-008 shows asymptomatic respond. The check varieties BDN-711 showed resistance reaction while Rajeshwari shows moderate resistance towards wilt disease.

Choudhary (2010) found that IPA 204 entry was resistant to wilt line of long-duration pigeonpea. Similarly, Choudhary and Nadarajan (2011) recorded that BDN 1, BDN 2, C 11, ICPL 87119, BSMR 736, TS 3, WRP 1 and DA 11 entries were resistant to wilt disease. Singh *et al.* (2011) also reported that IPA 16F, IPA 8F, IPA 9F and IPA 12F were resistant to wilt disease. Sharma *et al.* (2012) noticed that ICP 6739, ICP 8860, ICP 11015, ICP 13304, ICP 14638 and ICP 14819 were wilt resistant accessions after screening a pigeonpea mini-core collection. Jaggal *et al.* (2014) observed that 39 accessions were resistant to wilt disease. Pawar *et al.* (2015) reported that two germplasm lines *viz.*, ICP-7088 and ICP-8863 were only wilt resistant.

Table 12. Evaluation of pigeonpea genotypes against *Fusarium* wilt disease

Sr. No.	Genotype	Wilt incidence (%)	Disease reaction
1	RVKT-314-733	69.72	HS
2	RKPV-911-732	15.00	MR
3	RKPV-912-735	19.33	MR
4	RPS-2007-105-1	3.70	R
5	AKTE-12-02-724	40.56	HS
6	CRJ-1608	25.27	S
7	LPG-229	41.43	HS
8	BRGL-18-1-728	89.33	HS
9	BAUUP-15-19	80.60	HS
10	RRG-300	85.97	HS
11	RVSA-157	12.18	MR
12	ICPL-15048	64.00	HS
13	IBTO-RG-7	87.85	HS
14	RPS-2007-109	14.99	MR
15	BRGL-18-2	25.48	S
16	TTO-704-1-2	5.39	R
17	TDRG-59	21.96	S
18	WRG-353	11.87	MR
19	KRG-224	44.23	HS
20	CRG-16-008	0.00	ASY
21	RVSA-1510	2.70	R
22	SKNP-1413	13.23	MR
23	PTO-705-4-12	73.00	HS
24	GGP-1721	34.10	S
25	GGP-1715	11	MR
26	LRG-134	10.60	MR
27	BDN-711	8.33	R
28	Rajeshwari	16.30	MR
29	ICP-2376 (Check)	93.33	HS

5. SUMMARY AND CONCLUSION

The present experiment entitled “Assessment of pigeonpea (*Cajanus cajan* L.) genotypes against *Fusarium* wilt” was conducted during *Kharif*-2019 season with objectives *viz.*, to assess the pigeonpea genotypes against *Fusarium* wilt resistance and to study the correlation and path analysis between yield and yield contributing characters in pigeonpea.

Twenty eight genotypes of pigeonpea were evaluated in a randomized block design with two replications in one season. Eleven characters were studied *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), plant spread (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g), and wilt incidence. The results obtained are summarized and concluded as below.

5.1 Summary

5.1.1 Genetic Variability and Heritability

The range of variability, genotypic and phenotypic coefficient of variation, heritability percentage and genetic advance as per cent of mean were worked out. The characters days to maturity exhibited highest range of variability followed by number of pods per plant, plant height, plant spread, days to 50 per cent flowering, number of primary branches per plant, number of secondary branches per plant. The variability was lowest for number of seeds per pod followed by 100 seed weight. The estimates of genotypic as well as phenotypic coefficient of variation were highest for number of pods per plant and genotypic coefficient of variation was lowest in number of seeds per pod as well as phenotypic coefficient of variation lowest in days to 50 % flowering. High heritability estimates associated with high genetic advance as per cent of mean were observed for number of pods per plant, plant spread and seed yield per plant. Characters *viz.*, days to 50 per cent flowering and 100 seed weight showed high heritability accompanied with low genetic advance.

5.1.2 Correlation Studies

Correlation studies at both genotypic and phenotypic levels were made to resolve the direction and magnitude of association among characters. The highly significant positive correlation was reported between seed yield per plant with days to 50

% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant spread, number of pods per plant at both genotypic and phenotypic level. It also shows non-significant negative correlation with height of plant and 100 seed weight at both levels.

5.1.3 Path Coefficient Analysis

Path coefficient analysis is important to obtain information about how the component characters influence the seed yield through each other. In the present investigation, path coefficient analysis revealed that character's number of pods per plant, plant spread, days to 50 % flowering and number of primary branches per plant had direct effect on seed yield per plant. Whereas the characters number of secondary branches per plant and days to maturity had indirect effect on seed yield per plant. The characters plant height, 100 seed weight had direct negative effect on seed yield per plant. Genotypic correlation coefficients were higher than corresponding phenotypic correlations coefficients.

5.1.4 Wilt Incidence

Out of 28 pigeonpea genotypes three genotypes *viz.*, RPS-2007-105-1, TTO-704-1-2 and RVSA-1510 exhibited resistant reaction for *Fusarium* wilt. Eight genotypes *viz.*, RKPV-911-732, RKPV-912-335, RVSA-157, RPS-2007-109, WRG-353, SKNP-1413, GGP-1715 and LRG-134 found to be moderately resistant. Four genotypes *viz.*, CRJ-1608, TDRG-59, GGP-1721, BRGL-18-2 were susceptible, ten genotypes *viz.*, LPG-229, AKTE-12-02-724, IBTO-RG-7, BRGL-18-1-728, KRG-224, PTO-705-4-12, RVKT-314-733, RRG-300, BAUUP-15-19, ICPL-15048 showed highly susceptible reaction for wilt pathogen. The check varieties BDN-711 showed resistance reaction while Rajeshwari shows moderate resistance towards wilt disease. One genotype CRG-16-008 shows asymptomatic respond.

5.2 Conclusion

5.2.1 Genetic Variability and Heritability

Moderate genotypic coefficients of variation were observed for seed yield per plant followed by number of pods per plant, number of primary branches per plant and number of secondary branches per plant suggested presence of more variability and can be improved by simple selection.

Characters *viz.*, days to maturity, days to 50 per cent flowering, 100 seed weight showed high heritability accompanied with high genetic advance as per cent of mean. It is indicative of additive gene action which indicated scope for selection for improvement of these characters.

5.2.2 Correlation Studies

Number of pods per plant, days to 50 % flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant spread, had strong positive correlation with seed yield per plant. These indicate the simultaneous improvement of these characters through selection.

5.2.3 Path Coefficient Analysis

Number of pods per plant followed by number of primary branches per plant, days to 50 % flowering, plant spread and 100 seed weight showed positive direct effects on seed yield. Considering the correlation coefficient and path analysis simultaneously, number of pods per plant, days to 50 % flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, and plant spread found to be true components of seed yield. So, these were the important yield components suggesting direct selection and can be given importance during selection.

5.2.4 Wilt Incidence

Out of twenty-eight genotypes studied four genotypes including checks *viz.*, RPS-2007-105-1, TTO-704-1-2, RVSA-1510 and BDN-711 show resistant reaction for *Fusarium* wilt. So, by using these genotypes resistant varieties could be developed for *Fusarium* wilt.

Based on the screening and yield performance of data the genotype RKPV 912-735 showed moderately resistant reaction to *Fusarium* wilt disease with high single plant yield. Hence, this genotype may be used as parent for *Fusarium* wilt disease resistant breeding programme. Highly resistant lines RPS-2007-105-1, TTO-704-1-2, and RVSA-1510 may also be used as donor parent for introgression of resistance to high yielding varieties.

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7. VITAE

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in

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