# GENETIC DIVERGENCE STUDIES IN PIGEONPEA [*Cajanus cajan* (L.) Millsp.]

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**UNIVERSITY OF AGRICULTURAL SCIENCES**
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# GENETIC DIVERGENCE STUDIES IN PIGEONPEA [*Cajanus cajan* (L.) Millsp.]

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AFFECTIONATELY DEDICATED

TO MY BELOVED PARENTS, BROTHER

AND SISTERS

**DEPARTMENT OF GENETICS AND PLANT BREEDING**
**UNIVERSITY OF AGRICULTURAL SCIENCES**
**BANGALORE**

## CERTIFICATE

This is to certify that the thesis entitled **"GENETIC DIVERGENCE STUDIES IN PIGEONPEA [Cajanus cajan (L.) Millsp.]"** submitted in partial fulfilment of the requirement for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, is a record of research work done by **Mr. BASAVARAJAIAH, D.** during the period of his study in the University under my guidance and supervision and the thesis has not previously formed the basis of the award of a degree, diploma, associateship, fellowship or other similar titles.

BANGALORE
January 10, 1997

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# INTRODUCTION

# I. INTRODUCTION

Pigeonpea [Cajanus cajan (L.) Millsp] is a native of Hindustan centre, belongs to family Leguminoceae and one of the protein rich legume of the semi-arid tropics grown predominantly under rainfed conditions. Pigeonpea is the most important pulse crop next to chickpea covering an area of about 3.63 million hectares producing 2.55 million tonnes with an average productivity of 867 kg per hectare. The major states in terms of area and production are Maharashtra, Uttar Pradesh, Madhya Pradesh, Karnataka, Gujarat and Andhra Pradesh together account for 87 per cent of the area and 83.8 per cent of the production of pigeonpea (Shankarlal, 1996). In Karnataka, it occupies an area of 3.02 lakh hectares with annual production of 1.19 lakh tonnes with an average productivity of 394 kg per hectare. Pigeonpea is cultivated in multitude of production system for diverse uses viz., vegetable, grain, forage, green manure and fuel.

For any crop improvement, basic information on the variability present in the crop is essential. Yield being a complex trait is collectively influenced by various component characters which are polygenically inherited and highly influenced by environmental variations. Further, partitioning the variability into heritable and non-heritable components with suitable genetic parameters such as, genotypic and phenotypic coefficient of variation, heritability estimates

and genetic advance, cause and effect relations through phenotypic and genotypic correlations and path coefficient analysis helps a great deal to formulate selection strategies to develop suitable genotypes. An investigation into the nature and degree of divergence enables to identify genetically diverse genotypes for hybridization, which would result in inducing broad spectrum of variability and incorporation of desirable genes in the recombinant types, aimed to develop suitable ideotypes in pigeonpea, . Mahalanobis $D^2$ analysis and canonical analysis are useful tools in studying the nature and cause for diversity prevalent in the material. Therefore, an investigation to examine genetic variability and diversity is of considerable importance.

The present study was carried out with the following four fold objectives.

1. To study the variability in pigeonpea genotypes for different characters,

2. To estimate the association between yield and yield contributing characters,

3. To assess the relative contribution of yield attributes for seed yield, and

4. To classify the entries on the basis of diversity.

# REVIEW OF LITERATURE

# II. REVIEW OF LITERATURE

Pigeonpea is the second most important grain legume in common use in India. It belongs to the family Leguminocae, subfamily Papilionaceae and group Phaseoleae. The generic name Cajanus is derived from the Malayan name `Katjang'. Watts (1908) reported that, no Indian botanist has recorded the plant in the wild or in the naturalized state and hence, he concluded, it might have been introduced into India from Africa. Numerous types of pigeonpea are known, differing in height, maturity, colour, size and shape of pod and seeds. Shaw et al. (1933) distinguished 86 different types from collections all over India. Mehta and Dave (1931) recognized 36 types from Madhya Pradesh alone. These types can be grouped broadly under two varieties, Cajanus cajan var. bicolor and Cajanus cajan var. flavus. Cajanus flavus is described as a relatively small plant having only 2-3 seeds in a pod which are more spotted, while Cajanus bicolor is a large plant with 4-5 seeds in the pods which are marked with dark streaks. Currently, according to International Rules of Botanical Nomenclature, it is referred to Cajanus cajan Millsp.

The assessment of quantitative variables for genotypic variance, estimates of heritability and genetic advance and the associations of yield contributing characters are important for successful hybridization programme to evolve

new cultivars. This can be achieved by knowing the distantly related parental lines which can be selected based on the information obtained by clustering the genotypes using the techniques of non-hierarchial cluster analysis. This method gives the considerable amount of genetic and geographical diversity of the genotypes. Breeders can make the choice of parent with knowledge of clusters, so that the successful breeding programme can be achieved. The review of literature in pigeonpea related to the present investigation is presented under three sub heads viz.,

1. Genetic variability, heritability and genetic advance studies,
2. Correlation and path coefficient analysis, and
3. Genetic divergence studies.

## 2.1 STUDIES ON GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The progress in improving a plant type by the plant breeder is determined in the initial step by the variability existing between the populations. Thus, for effective selection and utilization of genotypes in breeding programmes, a thorough study of genetic variability, heritability and genetic advance is essential. Genotypic coefficient of variation indicates the relative magnitude of genetic diversity present in the material and helps to compare the genetic variability present for different characters.

The apparent variability in a crop can be divided into:

1. Variability due to genotypes
2. Variability due to the environment and
3. Their interactions

The genotypic variability is the actual heritable component of the apparent variability and is expressed as heritability. Therefore, heritability can be defined as the proportion of the phenotypic (apparent) variability that is due to genotype. The genotypic variability is the result of additive and non-additive gene effects.

Lush (1949) has proposed heritability as the ratio of additive variance to total variance in a narrow sense. The heritability in broadsense was proposed by Hansen et al. (1956) as the ratio of genotypic variance to the total variance.

Heritability influences the selection programme to a large extent. According to Allard (1960), heritability of yield alone is less and that of yield components is more. However, the gain from a selection for a particular character is the function of its heritability, selection pressure and the variance existing in the basal population. Thus, the genetic gain was expressed by Burton and Dewane (1953) as the product of heritability, phenotypic standard deviation and selection differential.

According to Johnson et al. (1955a) genetic advance is more useful in predicting the actual value of selection than heritability, although later value indicates the relative effectiveness of selection based on phenotypic expression of the character.

The contribution of genetic and environmental components to the variance was studied by Johanssen (1909). He attributed that the variation in a segregating population is due to both heritable and non-heritable components and the variation in a pureline due to only environmental factors. Later his works were confirmed by Nilson-Ehle (1909) and East (1916) and they showed that the continuous variation also confirmed to mendelian segregation.

Charles and Smith (1939), Power (1942) and Power et al. (1950) separated genetic variance from the total variance, using estimates of environmental variance in non-segregating populations. Since then, the studies on heritability, genetic advance and their variance component have been estimated for most of the yield contributing characters in several crops.

Rathnaswamy et al. (1973) noted high genotypic coefficient of variation for cluster per plant, seeds per pod, pods per plant, pod weight and days to flowering. High heritability values were reported for plant height, branches

per plant, cluster per plant, pods per plant and days to flower.

In a study of 23 pigeonpea strains, Chandra et al. (1975) reported high genetic variation for yield, primary and secondary branches and days to flowering, of which days to flowering and number of primary and secondary branches showed high heritability. Number of primary and secondary branches were associated with high genetic gain. Similar results observed by Singh et al. (1977).

Ram et al. (1976) reported high GCV and heritability for cluster per plant followed by grain yield, whereas highest genetic advance was observed for cluster per plant followed by harvest index. The grain yield, primary branches and pods per cluster exhibited low values of genetic advance.

High genetic variation for branches per plant, grain yield and pod number was reported by Malhotra and Sodhi (1977). They also observed that high heritability for grain yield and branches per plant was accompanied by high genetic advance. Average heritability was observed for pod number and cluster number.

High value of heritability and genetic gain for days to flowering followed by days to maturity, harvest index, seed yield per plant have been observed in 12 varieties of pigeonpea by Singh et al. (1978).

Bashiruddin and Sreeramulu (1981) observed high genotypic coefficient of variation for 100-seed weight, cluster per plant, pods per plant and branches per plant.

Jagshoran (1983) studied one hundred genotypes of pigeonpea under five environments in two years. The magnitude of phenotypic variability was high for all the characters studied except for 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 flowering across the environments.

Premsagar and Jatasra (1984) reported highest gcv for fruiting height of the lower branches, followed by pods per plant. Very high heritability was observed for the characters days to maturity, seed yield and pods per plant whereas, high heritability was obtained for days to 50 per cent flowering and plant height. The genetic advance was highest for pods per plant, followed by seed yield, fruiting length of lower branch and plant spread.

In a study of traits in 29 genotypes, Balyan and Sudhakar (1985a) reported high estimates of phenotypic and genotypic coefficient of variation, heritability and expected genetic advance for primary and secondary branches, pods per plant, 100-seed weight and yield per plot.

Sindhu et al. (1985) found that variability was highest for pods per plant. Heritability estimates were high for all the traits studied except for seed size and seeds per pod. Genetic advance was greatest for pods per plant.

Kanwan and Hazarika (1988) revealed high heritability with high genetic advance for days to maturity, days to flowering and plant height. Further, cluster analysis revealed moderate to high performance for various yield components of the high yielding genotypes.

Estimates of variability, heritability and genetic advance were carried out in pigeonpea for seven characters by Natarajan et al. (1990). The highest genotypic coefficient of variation was observed for pod numbers followed by cluster number and seed yield, while it was lowest for seeds per pod. High heritability and genetic advance were observed for pod number, cluster number and seed yield.

Twenty seven pigeonpea genotypes were evaluated by Sunil-Holkar et al. (1991). They reported that high GCV and PCV estimates were observed for pest damage, pods per plant and seed yield, high heritability and genetic advance for days to flowering, maturity and pods per plant.

The genetic variability and nature of association for 14 traits studied in a 7 x 7 diallel of pigeonpea under three different cropping system indicates high genetic

variability and genetic advance for grain yield per plant under intercrop system with sorghum, whereas, estimates of heritability were high for all the traits with exception of primary branches under sole crop (Khapre and Nerkar, 1992).

Ghodke et al. (1994) grown ten genotypes of pigeonpea under three cropping systems. The genotypic variability was high under intercropping system compared to sole crop. The estimates of heritability was high for number of pods, days to 50 per cent flowering and days to maturity in pigeonpea as sole crop and for number of primary branches, secondary branches, pods per plant and days to maturity in pigeonpea intercropped with sorghum. The estimates of genetic advance was high for secondary branches and number of pods in all the cropping system.

## 2.2 CORRELATION STUDIES AND PATH COEFFICIENT ANALYSIS

### 2.2.1 Association of characters

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association. Knowledge on phenotypic and genotypic correlations between important characters are of immense help in the selection of suitable plant types.

The details of the associations in pigeonpea among different characters on yield from the earlier studies are presented hereunder.

Pankaja Reddy et al. (1975) reported that duration, seed size and pod number were positively correlated with grain yield.

Veeraswamy et al. (1975) observed positive correlation of grain yield with number of branches, number of clusters and number of pods. Correlation estimated from $F_2$ population by Waknakar and Yadav (1975) revealed positive association of seed yield with stem girth, number of primary and secondary branches and number of pods.

Ram et al. (1976) found positive significant association of grain yield with number of primary branches, cluster per plant, pods per cluster and harvest index.

Singh and Shrivastava (1977) observed positive correlation of grain yield with plant height, plant spread, pod bearing length, pods per plant and 100-seed weight.

Positive association between seed yield and harvest index was observed by Tiwari et al. (1978). They also reported positive correlation for number of pods with number of secondary branches and seed yield.

Strong positive correlation was found between grain yield and number of inflorescence, number of pods and number of seeds per plant in the studies carried out by Raviprakash (1979).

Awatade et al. (1980) recorded positive and highly significant correlations between grain yield and number of pods per plant, number of clusters per plant, plant height, number of secondary branches and days to maturity both at phenotypic and genotypic level.

The grain yield per plant showed significant positive correlations with number of primary branches, 100-grain weight, number of pods per plant and pod length (Godawat, 1980).

A study of correlations involving eight characters in pigeonpea by Asawa et al. (1981) reveled that grain yield was positively correlated with secondary branches, pods per plant, seeds per pod and days to maturity.

Pahuja et al. (1981) observed highly significant correlation of yield with plant height, non-productive as well as productive branches, seed size, pods per plant and days to maturity.

Singh et al. (1981) found highly significant positive correlation of grain yield with number of pods per plant,

plant height, days to 50 per cent flowering, seeds per pod and days to maturity.

Wagh et al. (1983) reported highly significant positive correlation values of grain yield per plant with plant height, number of effective pods per plant and 1000-gra weight both at phenotypic and genotypic level. Number of effective pods and 1000-grain weight however, showed negative phenotypic correlation.

Balyan and Sudhakar (1985a) noticed a significant positive correlations between grain yield and seven yield related traits - days to maturity, plant height, number of secondary branches, number of primary branches, pod per plant, seeds per pod and 100-seed weight. A signifiant positive association of grain yield with plant height and pods per plant was reported by Sindhu et al. (1985).

Significant positive correlation of grain yield with plant height, number of branches per plant, number of pods per plant, pod weight and number of seeds per pod was reported by Bhongale et al. (1987).

Merkar and Nerkar (1987a) observed a significant positive correlation of seed yield with plant height, number of secondary branches, number of clusters, pods per plant, biomass and harvest index both at the genotypic and

phenotypic level. Similar results were also obtained by Merkar and Nerkar (1987b).

Angadi et al. (1988) studied eleven hybrids and nine varieties of pigeonpea. Association studies indicated that pod yield, plant height, branches per plant, days to flower and pods per plant were strongly associated with grain yield.

Chaudhary et al. (1988) reported positive correlation of grain yield with plant density, pod number, branches per plant, seeds per pod and smaller seeds. They also revealed that, earliness had negative correlation with plant height, number of branches and cluster per plant.

Patel et al. (1988) reported that yield and other agronomic characters differed significantly among 64 diverse genotypes derived from inter-varietal crosses. Seed yield was strongly correlated with plant height, branches per plant and pods per plant.

Patil et al. (1989) observed a positive correlation of seed yield with number of branches per plant, number of pods per plant and 100-seed weight.

Balakrishnan and Natarajarathnam (1989) while studying pigeonpea genotypes for three growing seasons reported that seed yield per plant was positively correlated with number of pods per plant. The number of pods per plant and 100-seed

weight were negatively correlated with dry matter efficiency and harvest index.

Ganesh Murthy and Stephen Dorairaj (1990) observed significant positive correlation of seed yield with dry matter production, number of pods, number of clusters, number of branches, plant height, leaf area index, seeds per pod, days to flowering, pods per cluster, days to maturity, 100-seed weight, harvest index and pod length.

Studies conducted by Henry and Krishna (1990) on character association revealed that seed yield had highly significant positive association with plant height, number of branches, number of clusters and number of seeds per pod.

Natarajan et al. (1990) reported significant positive correlation of seed yield with pod number, cluster number and plant height.

The correlation coefficients worked out by Holkar et al. (1991) indicated that 100-seed weight and pods per plant had highly positive genotypic correlation with seed yield. On the other hand, days to maturity and days to 50 per cent flowering showed negative correlation with seed yield at both phenotypic and genotypic levels.

Jahargirdar et al. (1991) studied 21 hybrids of pigeonpea in $F_2$ generation along with their seven parents for

eight component characters. Association studies indicated that number of pods, 100-seed weight and plant height were strongly associated with grain yield. High correlation between grain yield and pods per plant was also reported by Paul and Upadhaya (1991).

Khapre and Nerkar (1992) reported that leaf area index, days to maturity, plant height, number of pods per plant and total biomass per plant had highly significant positive association with grain yield under different cropping systems.

Patel et al. (1992) studied 42 pigeonpea genotypes including 30 $F_1$s. The results indicates that grain yield was positively and significantly associated with plant height and pods per plant at both genotypic and phenotpyic level.

Viramgama and Goyal (1994) observed significant positive association of grain yield with number of pods per plant, number of primary branches, plant height, length of secondary branches, 100-seed weight, days to flower and pod length. Number of pods per plant was significantly and positively correlated with all the traits except pod length and number of seeds per pod.

Byre Gowda et al. (1996) reported significant positive association for grain yield with number of pods per plant, plant height, seeds per pod and 100-seed weight.

Significant positive association of grain yield with days to 50 per cent flowering, days to 50 per cent pod set and days to maturity was observed by Gamber et al. (1996).

In study of 28 pigeonpea experimental hybrids by Paul et al. (1996) indicated yield was positively and significantly correlated with number of pods per plant, dry matter and number of secondary branches at phenotypic level, while at genotypic level the association was highest for dry matter at maturity.

### 2.2.2 Path coefficient analysis

Measure of correlation does not consider dependence of one variable over the other. Direct contribution of each component to the yield and the indirect effect through its association with other components cannot be differentiated from mere correlation studies. A statisti al tool called path coefficient analysis suggested by Wright (1921) offers a solution to this problem. It is a tool in genetic analysis which partition the association of the components on yield and indirect effects of the character through other components.

Pankaja Reddy et al. (1975) indicated that the maturity period and pod number had direct effect on seed yield.

The path coefficient analysis by Veeraswamy et al. (1975) revealed that the number of branches had the maximum

influence both directly and indirectly on the seed yield. The number of days to flowering had a direct negative influence on the yield.

Wakankar and Yadav (1975) found that number of pods per plant had high positive direct effect on seed yield followed by number of secondary branches. Plant spread had high negative direct effect on seed yield.

Ram et al. (1976) reported that the primary branches, clusters per plant and pods per cluster contributed directly as well as indirectly to grain yield, plant height and number of pods exerted maximum influence on seed yield as reported by Gunaseelan et al. (1976).

The path analysis in 25 genotypes of pigeonpea by Raviprakash (1979) indicated that the direct contributions from number of inflorescence and number of pods were low and that of the number of seeds per plant alone was high.

Awatade et al. (1980) noticed that the number of clusters per plant and 100-seed weight had direct effect on seed yield at both genotypic and phenotypic levels, whereas days to maturity and seeds per pod had low direct effect on seed yield. Maximum positive direct effect of 100-seed weight on grain yield per plant was also reported by Godawat (1980).

Asawa et al. (1981) reported that most of the yield contributing traits expressed strong indirect effect on yield via secondary branches.

Pahuja et al. (1981) found that pods per plant had high direct positive effect on seed yield while the productive branches had high positive indirect effect through pods per plant.

Singh et al. (1982) observed that maximum direct positive effect on grain yield was shown by the number of pods per plant, followed by 100-seed weight. Days to 50 per cent flowering, however indicated a negative direct effect on yield.

Balyan and Sudhakar (1985b) found that days to maturity, plant height, number of primary and secondary branches, pods per plant, seeds per pod and 100-seed weight had positive direct effect on seed yield.

Sindhu et al. (1985) observed that pods per plant, plant height and seed size were the major contributors to the seed yield.

Path analysis revealed that seed yield was directly and positively influenced by days to first flowering, days to maturity, plant height, pod weight and number of pods per plant (Merkar and Nerkar, 1987a).

Path analysis in 36 $F_1$s hybrids by Merkar and Nerkar (1987b) revealed that biomass and harvest index had the greatest positive direct effect on seed yield.

Angadi et al. (1988) reported that pods per plant, plant height, branches per plant and days to flower influenced seed yield through pod yield which alone had high direct influence on seed yield. Direct effects of branches per plant was of a very low magnitude.

Patel et al. (1988a) reported that plant height, branches per plant and pods per plant had maximum direct effect on seed yield.

Patil et al. (1989) observed that number of seeds per pod, days to flowering, 100-seed weight, number of branches per plant and pods per plant had high direct positive effect on seed yield.

Henry and Krishna (1990) indicated that number of pods per plant had maximum direct effect on seed yield. However, characters like plant height, number of branches per plant, number of clusters per plant and number of seeds per pod affected seed yield via number of pods per plant.

Natarajan et al. (1990) reported cluster number and plant height showed high positive direct effect on seed yield.

Path coefficient analysis by Holkar et al. (1991) revealed that 100-seed weight had the highest direct positive effect on seed yield followed by days to 50 per cent flowering and pods per plant.

Jahargirdar et al. (1991) studied 21 hybrids of pigeonpea in $F_2$ generation along th their seven parents for eight characters. The path coefficient analysis revealed that the number of pods per plant was influencing more on grain yield directly as well as indirectly. Whereas 100-seed weight, plant height, number of branches affected grain yield indirectly.

Paul and Upadhaya (1991) found that pods per plant, pod weight had maximum direct effect on grain yield per plant.

Brar (1993) observed that number of pods per plant, number of clusters per plant and number of secondary branches per plant had high positive direct effect on seed yield. He also reported that, these characters had significant positive association with seed yield.

Viramgama and Goyal (1994) noticed positive direct effects on seed yield by number of pods per plant, pod weight, number of primary branches, plant height and 100-seed weight. However, days to 50 per cent flowering and pod length had high negative direct effects on seed yield.

Byre Gowda et al. (1996) studied 39 genotypes for path coefficient analysis. They observed that number of pods per plant had the maximum direct effect on grain yield followed by 100-seed weight, days to 50 per cent flowering, pod length, number of seeds per pod and plant height.

Gamber et al. (1996) observed that days to 50 per cent seed filling and maturity had high positive direct effects on seed yield.

Paul et al. (1996) reported that number of pods per plant and pod weight had high positive direct effect on seed yield followed by dry matter at maturity and 100-seed weight.

## 2.3 GENETIC DIVERGENCE STUDIES

For the purpose of discriminating any two populations having unknown origin, the anthropologist adopted Karl Pearson's coefficient of Racial Likeness (CRL) (Morant, 1923). But Mahalanobis (1930) after identifying that CRL was a test of divergence between two samples rather than a measure of actual magnitude of divergence between the two groups under comparison. This technique in the form of generalised distance was first used by Mahalanobis et al. (1930, 1949) in an anthropometric survey of the United Provinces of India. The generalised distance was adopted for examining the cases of two sets of measurements of anthropological characters of individual belonging to two

classes of human beings, he introduced the notion of 'group distance'. He also pointed out that $D^2$ would remain reasonably constant when samples were drawn from two different populations irrespective of the size of representative samples which indicated that $D^2$ supplied a measure of the actual magnitude of divergence between the two groups under comparison. Fisher (1938) also believed that for the discrimination between populations when the number of groups was more than two, then Mahalanobis's $D^2$ (1936) would be more useful.

An exact distribution and moments for $D^2$ statistic satisfied some mathematical and logical requirements such as (i) distance between two groups was not less than zero, (ii) sum of distances of a group from two other groups similar to that of differential geometry, (iii) the distance should not decrease when additional characters were considered, and (iv) the increase in distance by the addition of some characters to a suitably chosen set, must be relatively small.

Mahalanobis et al. (1949) used $D^2$ statistic for the analysis of anthropological data of United Provinces and formulated three major clusters of Brahmins, Artisans and Tribal groups.

Nair and Mukherji (1960) were the first to apply the $D^2$ statistics in biological populations. They applied this

method in classifying the natural and plantation teak tree types, based on three important characters such as specific gravity, nodule structure and maximum crushing stress.

The canonical analysis was subsequently used by several others in different crops viz., in Nicotiana rustica (Murthy et al., 1965), in sorghum (Arunachalam and Ram, 1967), in rice (Ram and Panwar, 1970), in groundnut and soybean (Shwe et al., 1972) and in chickpea (Narayan and Macefield, 1976). A brief review in this aspect in pigeonpea and other crops is given below.

Dumbre et al. (1984) measured the genetic divergence by Mahalanobis's $D^2$ statistic in 52 varieties of Cajanus cajan obtained from different parts of India and two varieties from West Indies. The varieties were grouped into 21 clusters. The clustering pattern of the varieties was not related to their geographic distribution.

Analysis of data on seed yield per plant and 11 related traits using the Mahalanobis $D^2$ statistic by Malik et al. (1985). They were able to classify 35 Indian cultivars of pigeonpea into four clusters. Clustering was not related to geographical origin of the clusters.

Analysis of data on seed yield and 10 related characters in 12 parental lines and their 32 hybrids of Cajanus cajan by Hazarika and Singh (1986) revealed that

maximum divergence between the parents Prabhat and Baigani. Fourty four genotypes were grouped into 11 clusters, 16 of hybrids were grouped into different clusters from their parents. Divergence between parents was positively correlated with heterosis in the hybrid for seed yield.

Hazarika et al. (1986) measured the genetic divergence using three statistical techniques for 67 pigeonpea lines evaluated in 3 field environments for 10 traits. The grouping pattern of the lines differed between environments. The metroglyph and index score methods, which are simpler to use than the Mahalanobis $D^2$ statistic, gave the quickest results. The lines ICPL-87, L-3, S-4, BS-1, H-76-20, H-247 and JAM 9-42 were identified as promising for hybridization on the basis of divergence analysis.

Twenty eight genotypes of determinate and non-determinate pigeonpea were clustered after eliminating date of sowing x spacing interaction, using multivariate $D^2$ analysis technique by Singh and Govil (1988). The determinate group showed more diversity than the non-determinate group. Genotype x environment interaction was more predominant in non-determinate group than in determinate one for days to flowering, grain yield and total branches. Plant height, fruiting height, number of fruiting branches, number of pods and total dry matter production were prominent differentiating characters between the two groups.

Patel et al. (1988) have grouped 40 stocks of pigeonpea into 9 clusters on the basis of several yield components using the Mahalanobis $D^2$ statistic. The discriminatory trait between clusters were number of secondary branches, pods per plant, clusters per plant. Genotypes in clusters VII were considered superior for all traits except 100-seed weight.

Garlan et al. (1989) assessed the nature of genetic divergence in 58 pigeonpea genotypes of determinate and indeterminate habit. Using Mahalanobis $D^2$ statistic, the genotypes were grouped into 15 clusters.

One hundred genotypes of pigeonpea were evaluated in five trials for 10 characters by Jagshoran (1989). Highly significant differences were found for all characters. The material was grouped into clusters but they differed among the various environments. He concluded that there is no relation between genetic and geographic diversity.

Sandhu et al. (1993) based on their studies grouped 96 genotypes of pigeonpea into 1[illegible] clusters. Cluster means indicated that cluster IX, VII and V had genotypes with high mean values for primary branches, secondary branches, pods per plant, seeds per pod, 100-seed weight, yield per plant and harvest index. The genotypes of cluster XVII were early in maturity. Secondary branches followed by seed yield, pod number and primary branches contributed greatly to genetic divergence.

Sarma and Roy (1994) revealed considerable diversity in 42 genotypes of early pigeonpea genotypes. On the basis of Mahalanobis $D^2$ statistic, they were grouped into eight clusters. Branches per plant, pods per plant, harvest index and yield per plant were contributed maximum to the total genetic divergence.

Santos et al. (1994) obtained inter-relationships between three primary and six secondary yield components in Cajanus cajan genotypes under field condition. Canonical analysis showed a significant correlation between the two groups of characters on the basis of the relationship between pod length and plant height with number of seeds per pod and seed size.

Viramgama and Goyal (1994) employed Mahalanobis $D^2$ statistic to study the genetic divergence in 70 genotypes of pigeonpea. These lines were grouped into 14 clusters. The clustering pattern of the genotypes was independent of their geographical origin. The characters like grain yield per plant, number of pods per plant, plant height and number of primary branches per plant showed high genetic divergence. Based on the inter-cluster distance, cluster XIV showed high genetic divergence with XIII, XII and X.

Singh (1991) studied six agronomically important traits in 48 strains of Dolichos lablab collected from eight Indian

States, using the Mahalanobis $D^2$ statistic. The strains were grouped into 10 clusters. Days to flowering and number of pods per bunch contributing most of the genetic divergence. Canonical analysis confirmed the $D^2$ grouping.

In chickpea, Narayan and Macefield (1976) studied the adaptive responses and genetic divergences in a world germplasm collection of 5477 lines evaluated for eight characters related to fitness and yield at two locations. The $D^2$ analysis was helpful in grouping the collection into six clusters with substantial divergence between them. Plant height was reflected the most important character operating in the genetic divergence between geographical groups, followed by seed colour and flower colour. Further, independent classification using canonical analysis confirmed the results obtained from the $D^2$ analysis.

Salimath (1980) in 80 collections of chickpea, studied the $D^2$ analysis. In all they were grouped into 23 groups. Desi cultivars distinctly formed a different group when compared to Kabuli cultivars.

Genetic diversity assessed by Sarvaliya and Goyal (1994) for 76 genotypes did not reveal any relationship between geographical distribution and genetic diversity. The magnitude of inter-cluster distance was higher than that of intra-cluster distance. The maximum and minimum inter-

cluster distances were between V and IX, and clusters I and VIII, respectively. Whereas the highest and the lowest intra-cluster distances were in cluster II and V, respectively.

Dangaria et al. (1994) reported that 32 genotypes were grouped into five cluster with inter-cluster distance ranging from 7.93 (between I and II) to 17.53 (between IV and V), cultivars K-850 and K-1480 were found to be more divergent with regard to nodulating characters in chickpea.

In cowpea, Mahindritta et al. (1971) studied 40 promising lines using $D^2$ statistic to measure the genetic diversity in respect of grain yield and its components. The varieties were grouped into eight clusters based on the $D^2$ values. Seed size was found to be most important characters contributing towards genetic divergence while the remaining traits made little contribution. It was also observed that wide genetic diversity was present in the material selected from the same geographic regions.

Angadi et al. (1979) used Mahalanobis $D^2$ statistic to study the divergence in 50 types of cowpea. Types studied had not apparent parallellism between genetic and geographical divergence. Maximum divergence was contributed by 100-seed weight. Based on $D^2$ values they were grouped into 15 clusters.

In soybean, Shwe et al. (1972) subjected 16 varieties for 11 characters for measuring the divergence which could be grouped into five clusters. The clustering pattern did not follow their geographic origin. The groupings were confirmed by Canonical analysis.

In soybean, Dobhal (1995) studied genetic divergence among 65 genotypes of soybean using Mahalanobis $D^2$ statistic revealed significant variability among these genotypes for 12 yield and component characters. These genotypes were grouped into 17 clusters. No linear relationship between geographic and genetic divergence was observed. Canonical analysis revealed higher contribution of yield per plant, number of pods per plant, pods per cluster, pod length and seeds per pod towards the total genetic divergence.

In groundnut, Shwe et al. (1972) studied the nature of divergence among 24 elite groundnut varieties consisting of bunch, spreading and semi-spreading types, uisng 17 characters. The 24 varieties were grouped in to three clusters with 7, 13 and 4 varieties respectively. Canonical analysis confirmed the groupings done by Mahalanobis $D^2$ statistic.

In paddy, Ram and Panwar (1970) used the Mahalanobis $D^2$ statistic and Canonical analysis to assess the nature of divergence and its relationship with the components of

genetic variation in rice. The $D^2$ and canonical analysis were potent enough to distinctly discriminate the *indica* and *japonica* races viz., the early, medium and late maturity groups. A brief scheme of the *indica* x *japonica* hybridization programme based on genetic divergence for the maximum exploitation of heterotic effect was also putforth.

Maurya and Singh (1977) assessed the nature and magnitude of genetic divergence in 43 varieties of rice using $D^2$ statistic, the population was grouped into 16 clusters. Maturity time, plant height and tillers contributed most to divergence.

Ziauddin Ahmed *et al*. (1980) measured the genetic divergence by Mahalanobis $D^2$ statistic in 40 strains of Triticales obtained from different parts of India. The strains were grouped into 9 different clusters. The clustering pattern did not follow the geographic origin. Test weight and spike length were the potent variables which could be used as parameters in selecting genetically diverse parents for hybridization programme.

In sorghum, Arunachalam and Jawahar Ram (1967) studied the geographical diversity in relation to genetic divergence in 80 stocks in cultivated sorghum and ten characters were studied. The importance of flowering time in the differentiation of this genus was confirmed by the

divergence in three different physiological groups of sorghum of early (75 days), medium (76-99 days) and late (100 days) in the cultivated varieties of sorghum. This was supported by canonical analysis also.

In finger millet, Hussaini et al. (1977) studied the genetic divergence among 640 entries of cultivated strains using `Principle component analysis' and `Canonical variate analysis'. They observed that congregations were more clearly separated in canonical variate than in principle component analysis. The entries were grouped into 12 clusters.

In Tobacco, Murthy et a' (1965) analysed the sub-specific genetic divergence as measured by $D^2$ statistic, in 15 varieties of Nicotiana rustica. The study revealed the use of leaf size and proportion of panicle height as classification criteria. The canonical analysis confirmed the grouping done by $D^2$ statistic.

# MATERIAL AND METHODS

# III. MATERIALS AND METHODS

The present investigation was undertaken at G.K.V.K. Farm, University of Agricultural Sciences, Bangalore which is located at the latitude of 12°58' North, longitude of 77°35' East and altitude of 930 metres above MSL.

## 3.1 Material

The material for the investigation comprised of 81 pigeonpea genotypes of diverse origin procured from All India Co-ordinated Pulse Improvement Project, U.A.S., G.K.V.K., Bangalore. The list of the pigeonpea genotypes used in the present study is provided in Appendix 1. The crop for the present investigation was raised during kharif, 1995.

## 3.2 Methods

### 3.2.1 Experimental layout

The field experiment was laid out in 9 x 9 simple lattice design with two replications. Each replication consisted of nine sub-blocks with each sub-blocks having nine genotypes. Entries and sub-blocks were randomised. Each genotype was grown in two rows of 3 metre length. A spacing of 60 cm between and 15 cm within rows was adopted.

### 3.2.2 Crop management

The crop was raised providing all necessary agronomic inputs and plant protection measures as per package of practices recommended for pigeonpea.

3.2.3 **Method of sampling and recording observations**

Five plants were selected at random from each replication in each treatment for recording the observations. Each character observed for eliciting the information are described here under.

3.2.3.1 **Days to 50 per cent flowering** : The total number of days taken from the day of sowing to the day on which 50 per cent of the plants showed anthesis.

3.2.3.2 **Days to maturity** : The number of days taken from the date of sowing to physiological maturity of all the pods.

3.2.3.3 **Straw yield (g)** : Weight of the straw per plant after sundrying to a constant weight was recorded in grams.

3.2.3.4 **Plant height (cm)** : The plant height was measured at maturity from the base of the plant to the tip of the main stem.

3.2.3.5 **Branches per plant** : The number of branches per plant were counted at the time of harvest.

3.2.3.6 **Pods per plant** : The number of filled pods per plant were counted at the time of harvest.

3.2.3.7 **Pod weight (g)** : The weight of all the filled pods per plant was measured in grams at harvest.

3.2.3.8 **Pod length (cm)** : The length of ten randomly selected filled pods was recorded in centimeter at the time of harvest.

3.2.3.9 **Pod width (cm)** : Pods which were selected for recording length of pod were also subjected for recording width of pod.

3.2.3.10 **Seeds per pod** : The number of filled seeds were counted from the selected ten pods, averaged to obtain the number of seeds per pod.

3.2.3.11 **Yield per plant (g)** : The total pods of the plant were harvested, cleaned and grains were weighed and expressed as mean yield per plant.

3.2.3.12 **Shelling per cent** : The ratio of yield per plant to the pod weight was worked out and expressed in percentage.

3.2.3.13 **Length of pod bearing branches (cm)** : The distance between the first pod to last pod on the branches was considered as length of pod bearing branches and recorded in centimeters.

3.2.3.14 **100-seed weight (g)** : Weight of the hundred randomly selected seeds was recorded in grams.

3.2.3.15 **Specific gravity** : The ratio of 100-seed weight (test weight) to the volume of 100-seeds (in CC) was worked out and recorded as specific gravity.

3.2.3.16 **Harvest index** : Harvest index was computed as suggested by Donald (1962).

$$\text{Harvest index} = \frac{\text{Grain yield per plant}}{\text{Total dry weight/plant}} \times 100$$

## 3.3 Statistical analysis

### 3.3.1 Analysis of variance

The data of mean values of the 16 characters were analysed for their variances following the simple lattice design suggested by Cochran and Cox (1957), the structure of ANOVA is as follows.

**ANOVA**

| Source of variation | Degrees of freedom | Sum of squares | Mean of squares |
|---|---|---|---|
| Replication | r-1 | $SSQ_r$ | |
| Genotypes (unadj.) | $q^2$-1 | $SSQ_{g(un\ adj.)}$ | |
| Blocks (adj.) | r(q-1) | $SSQ_{(b)}$ | $\frac{SSQ_{b(adj.)}}{r(q-1)} = E_b$ |
| Error (interblock) | (q-1)(rq-q-1) | $SSQ_e$ | $\frac{SSQ_e}{(q-1)(rq-q-1)} = E_e$ |

where, r = Number of replication

$q^2$ = Number of genotypes

The adjusted varietal mean differences were tested for their significance as per the following analysis of variance.

| Source of variation | Degrees of freedom | Sum of squares | Mean of squares | 'F' ratio |
|---|---|---|---|---|
| Genotypes (adj.) | $q^2-1$ | $SSQ_{(adj.)}$ | g | $g/E_e$ |
| Error (interblock) | (q-1)(rq-q-1) | $SSQ_e$ | $E_e$ | |

The computed 'F' ratio was compared with the Table 'F' ratio at ($q^2$-1) and (rq-q-1) degrees of fr dom at five per cent and one per cent level of significance. The average critical difference between any two adjusted genotypic means was worked out by using the formula.

C.D. = S.E. x t at 5 per cent level of significance

### 3.3.2 Estimation of genetic parameters

The coefficient of variability both at phenotypic and genotypic levels for all the characters were computed according to the formula suggested by Burton and Dewane (1953).

#### (i) Genotypic and phenotypic variability (GCV and PCV)

$$GCV\ (\%) = \frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

$$PCV\ (\%) = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973) and are given below.

| | | |
|---|---|---|
| 0-10% | : | Low |
| 10-20% | : | Moderate |
| 20% and above | : | High |

**(ii) Heritability (Broadsense)**

Heritability in broadsense (H) estimates were computed by the formula suggested by Hansen et al. (1956).

$$H = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

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

$\sigma^2 p$ = Phenotypoic variance

The heritability percentage was categorised as suggested by Robinson et al. (1949) as mentioned below.

| | | |
|---|---|---|
| 0-30% | : | Low |
| 30-60% | : | Moderate |
| 60% and above | : | High |

(iii) **Genetic advance (GA)**

The extent of genetic advance expected through selection for each of the character was calculated as per the formula suggested by Johnson et al. (1955b).

$$GA = H.\sigma p.K$$

where, H = Heritability (broadsense)

$\sigma p$ = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5 per cent intensity of selection (Lush, 1949)

$$GA \text{ as per cent mean} = \frac{GA}{\bar{X}} \times 100$$

where, GA = Genetic advance

$\bar{X}$ = General mean

The genetic advance as per cent of mean was categorised as suggested by Johnson et al. (1955b) and the same is given below.

| | | |
|---|---|---|
| 0-10% | : | Low |
| 10-20% | : | Moderate |
| 20% and above | : | High |

### 3.3.3 Estimation of correlation coefficients

The phenotypic and genotypic correlation coefficients were estimated among all possible combination of characters in each population as suggested by Al.Jibouri et al. (1958).

$$r_{12} = \frac{Cov_{12}}{\sqrt{V_1 \times V_2}}$$

where = $r_{12}$ = Correlation coefficient between characters 1 and 2

$Cov_{12}$ = Covariance between character 1 and 2

$V_1$ = Variance of character 1

$V_2$ = Variance of character 2

The significance of correlation coefficients was tested using `t' values of Fisher and Yates (1963).

### 3.3.4 Path coefficient analysis

To estimate the direct and indirect contribution of various yield components to the yield, path coefficient analysis was followed as suggested by Wright (1921). Direct and indirect effects of different traits were calculated by solving the sets of simultaneous equations by the abbreviated Doo-little technique as described by Goulden (1959) and illustrated by Dewey and Lu (1959).

### 3.3.5 Mahalanobis $D^2$ analysis

The square of the Mahalanobis generalised distance between any two populations is given by the formula.

$$\Delta^2 = \Sigma \, ó_i \, ó_j \, \lambda_{ij}$$

$\Delta^2$ = Square of generalised distance

$\lambda_{ij}$ = Reciprocal of the Canmen dispersion matrix ij

$\acute{o}_i = (u_{i1} - u_{i2})$

$\acute{o}_j = (u_{j1} - u_{j2})$

where, u = vector of mean values for all the characters.

The formula for the estimation of distance D for the samples:

$$D^2_P = \underset{\sim}{d}^1 S^{-1} \underset{\sim}{d}$$

where, $D^2_P$ = Square of the distance considering P variables

$\underset{\sim}{d}$ = Vector of observed differences of the mean values of all the characters - $(X_{i1} - X_{i2})$

$X_i$ = Vector of the mean values of all the characters

$S^{-1}$ = Inverse of variance and covariance matrix

Since inverting the matrix is complicated, the original correlated variables ($X_i$) were transferred to non-correlated variables ($Y_i$). So the computation of $D^2$ values reduces to single summation of the squares of the difference between the values of transformed variables of the two populations.

This transformation is done by pivotal condensation method. These newly transformed uncorrelated variables were used to calculate the square of distance using the formula.

$$D^2 = (\underset{\sim}{Y}_{i1} - Y_{i2})$$

where, Y = Vector of transformed mean values.

The square root of the $D^2$ values gives the general distance between the two populations. The $D^2$ values were arranged in a matrix form. The significance of the $D^2$ values between any two populations is tested using the following formula.

$$T^2 = \frac{N_1 N_2}{N_1 + N_2} \times D^2$$

using $T^2$, the F value was calculated using the formula.

$$F = \frac{N_1 + N_2 - P - 1}{(N_1 + N_2 - 2)\, P} \times T^2$$

This computed F value was compared with the table 'F' value at 5 per cent and 1 per cent level of significance at P and $(N_1 + N_2 - P - 1)$ degrees of freedom.

### 3.3.6 Clustering of the $D^2$ value

All the $\frac{n(n-1)}{2}$ $D^2$ values were clustered using Tocher's method (Rao, 1952). But before this, preliminary grouping was done through canonical variate analysis (Ramanujam et al., 1974).

The $D^2$ values of all the 80 combinations for each entry were aranged in the descending order. The two genotypes having the lowest $D^2$ values between them were selected and a third genotype which had on an average smallest $D^2$ value from the first two was added. Similarly, a

fourth entry was picked which showed a least average $D^2$ from the first three. This was continued till when a genotype if added increased the average $D^2$ value more than the average of those included. That genotype was taken out The genotype already included in that group were considered as the first cluster. The procedure was repeated for other genotypes, omitting those that are already included in the earlier cluster.

The inter and intra cluster distances were also calculated following the method of Singh and Chaudhary (1977).

### 3.3.7 Canonical variate analysis

This analysis is done to represent a number of uncorrelated variables by lesser number of canonical variates, which were obtained as linear combinations of a number of uncorrelated variables. The coefficients ($l_1$, $l_2$, ... $l_n$) are got by solving the equation.

$$I\ (A - \lambda_I) = 0$$

where, I is the coefficient vector

$\lambda$ is the characteristic root of matrix `A'

The method follows, the construction of the matrix of sum of squares and sum of products for the transformed mean values. The suitable power of the original matrix and

canonical vectors were obtained by iteration, starting from a trial vector (1, 1, 1 ... 1).

The canonical roots were also obtained by substracting the product of $\lambda_i$) ($i^{th}$ element $Y_j^{th}$ element) of the first vector from the power matrix. Then this process of iteration was repeated to get subsequent roots ($\lambda_2$) and vector ($i_2$). The roots are obtained in the decreasing order of magnitude. The Z values were calculated from the mean values of ($Y_i$) transformed variables using the formula.

$$Z = (I)(Y)$$

where, I is the canonical vector

Y is the transformed variables in a vector

The Z values were computed for every genotype corresponding to $\lambda_1$, $\lambda_2$ and $\lambda_3$ respectively using their corresponding vectors. These values are plotted on a three dimensional graph taking $\lambda_1$, $\lambda_2$ and $\lambda_3$. The clusters were made arbitrarily. The percentage contribution for each of the canonical roots was calculated using the formula.

$$\text{The percentage contribution for each canonical vector} = \frac{\lambda}{\text{Trace in the dispersion matrix}} \times 100$$

where, $\lambda$ is the root.

# EXPERIMENTAL RESULTS

# IV. EXPERIMENTAL RESULTS

The results obtained from the present investigation are presented under the following heads.

1. Variability and genetic parameters
2. Association of characters
3. Path coefficient analysis
4. Divergence studies

The mean values of all the germplasm lines for 16 characters are presented in Appendix 1. Analysis of variance is presented in Table 1. As evident from the table, the `F' test indicated highly significant differences among the genotypes for all the 16 characters.

## 4.1 Variability and genetic parameters

The variability for yield and other axillary characters were computed like: mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broadsense and genetic advance are furnished in Table 2. The graphical representation of the PCV with GCV and heritability with genetic advance are given in Fig.1 and Fig.2, respectively.

### 4.1.1 Days to 50 per cent flowering

The overall mean days taken to 50 per cent flowering among the lines was 75.09 days. Range of variation for this

Table 1. Mean sum of squares for 16 quantitative characters in pigeonpea.

| Source | D.F. | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 1 | 0.64 | 0.82 | 5.05 | 1.02 | 1.28 | 200.19 | 12.64 | 0.02 | 0.001 | 0.01 | 17.11 | 12.93 | 26.01 | 0.01 | 0.0001 | 10.66 |
| Genotypes | 80 | 495.80** | 569.70** | 255.71** | 1146.00** | 5.02** | 785.02** | 116.60** | 0.43** | 0.020** | 0.12** | 67.05** | 39.62** | 66.40** | 4.46** | 0.0004** | 15.77** |
| Block (A) | 16 | 522.20 | 171.70 | 1376.60 | 2871.00 | 10.92 | 1471.30 | 504.00 | 0.36 | 0.011 | 0.20 | 202.26 | 98.26 | 86.00 | 1.82 | 0.0006 | 14.61 |
| Error | 64 | 17.51 | 65.09 | 59.53 | 323.60 | 1.51 | 166.86 | 39.60 | 0.13 | 0.004 | 0.01 | 14.64 | 20.71 | 9.09 | 0.35 | 0.0002 | 6.51 |
| C.V. (%) | | 5.57 | 5.36 | 19.05 | 15.27 | 13.88 | 16.96 | 19.20 | 6.09 | 8.020 | 2.64 | 19.76 | 7.86 | 12.73 | 6.18 | 1.5600 | 9.30 |

* = Significant at 5 per cent level; ** = Significant at 1 per cent level

$X_1$ = Days to 50 per cent flowering
$X_2$ = Days to maturity
$X_3$ = Straw weight (g)
$X_4$ = Plant height (cm)
$X_5$ = Branches per plant
$X_6$ = Pods per plant
$X_7$ = Pod weight (g)
$X_8$ = Pod length (cm)
$X_9$ = Pod width (cm)
$X_{10}$ = Seeds per pod
$X_{11}$ = Yield per plant (g)
$X_{12}$ = Shelling per cent
$X_{13}$ = Length of pod bearing branches (cm)
$X_{14}$ = 100-seed weight (g)
$X_{15}$ = Specific gravity (g/ml)
$X_{16}$ = Harvest index

Table 2. Range, mean, PCV (%), GCV (%), heritablity (%) and genetic advance for 16 traits in pigeonpea.

| Sl. No. | Characters | Range | | Mean | PCV (%) | GCV (%) | Herita-bility (%) | GA (% of mean) | C.D. at 5% |
|---|---|---|---|---|---|---|---|---|---|
| | | Minimum | Maximum | | | | | | |
| 1. | Days to 50% flowering | 51.00 | 102.50 | 75.09 | 21.34 | 20.59 | 93.18 | 40.95 | 19.25 |
| 2. | Days to maturity | 109.50 | 170.00 | 150.31 | 11.85 | 10.57 | 79.49 | 19.41 | 15.25 |
| 3. | Straw weight (g) | 5.76 | 76.51 | 40.57 | 30.95 | 24.41 | 62.23 | 39.67 | 18.46 |
| 4. | Plant height (cm) | 28.90 | 177.30 | 117.83 | 23.01 | 17.21 | 55.96 | 26.52 | 31.79 |
| 5. | Branches per plant | 5.20 | 13.50 | 8.85 | 20.42 | 14.97 | 53.75 | 22.61 | 2.58 |
| 6. | Pods per plant | 43.00 | 122.10 | 76.12 | 30.83 | 25.74 | 69.71 | 44.28 | 27.98 |
| 7. | Pod weight (g) | 14.65 | 50.50 | 32.77 | 26.96 | 18.92 | 49.28 | 27.37 | 13.44 |
| 8. | Pod length (cm) | 4.50 | 6.50 | 5.21 | 10.16 | 7.43 | 53.57 | 11.21 | 0.69 |
| 9. | Pod width (cm) | 0.62 | 0.91 | 0.74 | 14.66 | 12.26 | 69.99 | 21.13 | 0.09 |
| 10. | Seeds per pod | 3.40 | 4.35 | 3.79 | 6.72 | 6.18 | 84.62 | 11.73 | 0.46 |
| 11. | Yield per plant (g) | 6.54 | 38.40 | 19.36 | 33.00 | 26.44 | 64.16 | 43.63 | 9.19 |
| 12. | Shelling per cent | 41.93 | 64.60 | 57.88 | 9.48 | 5.31 | 31.34 | 6.13 | 6.65 |
| 13. | Length of pod bearing branches (cm) | 4.60 | 38.36 | 23.69 | 25.93 | 22.59 | 75.92 | 40.56 | 8.53 |
| 14. | 100-seed weight (g) | 7.10 | 12.70 | 9.57 | 16.21 | 14.98 | 85.45 | 28.52 | 2.04 |
| 15. | Specific gravity (g/ml) | 0.75 | 0.84 | 0.80 | 2.03 | 1.31 | 41.18 | 1.73 | 0.02 |
| 16. | Harvest index (%) | 18.76 | 32.76 | 26.66 | 12.42 | 8.23 | 43.89 | 11.23 | 3.62 |

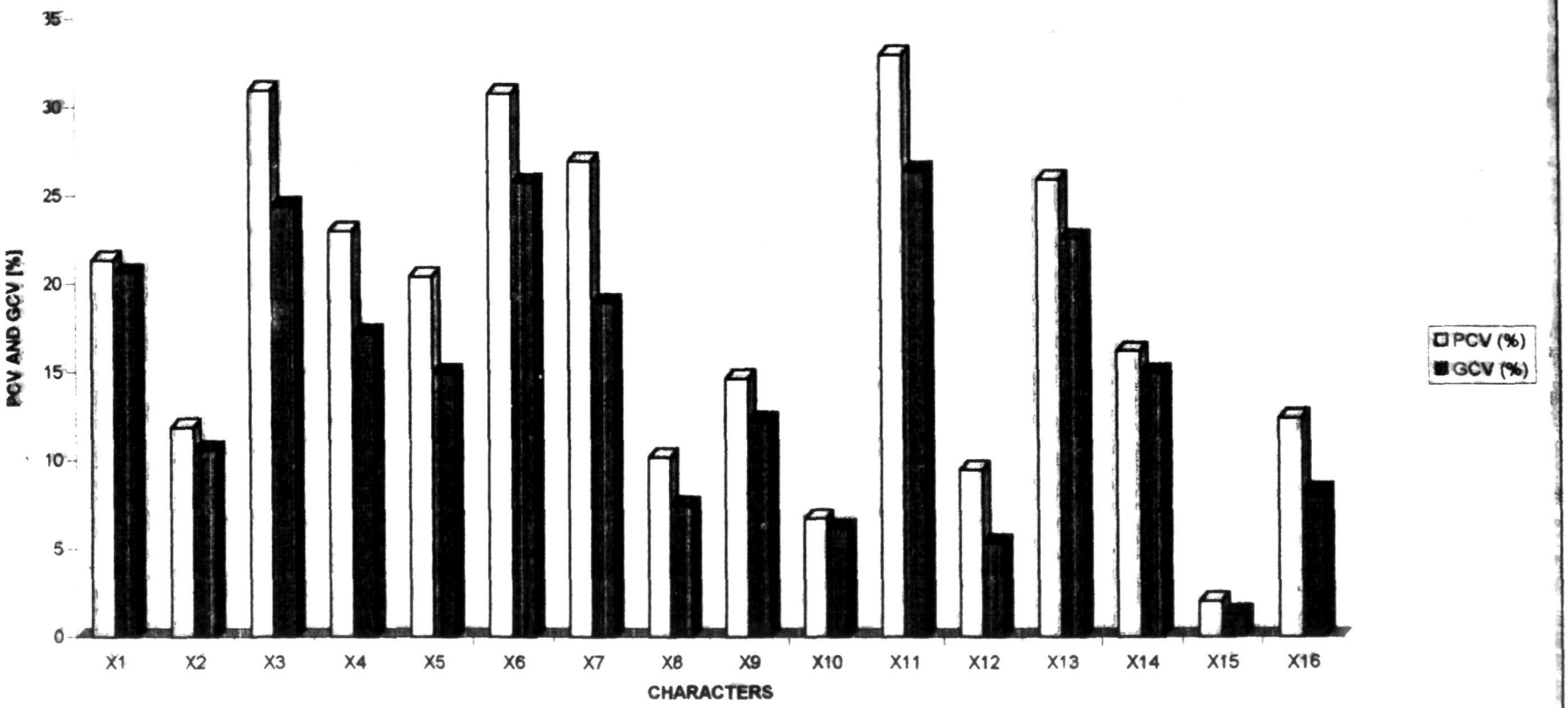


**FIG1: PHENOTYPIC AND GENOTYPIC COEFFICIENTS OF VARIABILITY FOR 16 CHARACTERS IN PIGEONPEA.**

*X1=DAYS TO 50% FLOWERING*
*X2= DAYS TO MATURITY*
*X3=STRAW WEIGHT [g]*
*X4=PLANT HEIGHT [cm]*
*X5=BRANCHES PER PLANT*
*X6=PODS PER PLANT*
*X7=POD WEIGHT [g]*
*X8=POD LENGTH [cm]*
*X9=POD WIDTH [cm]*
*X10=SEEDS PER POD*
*X11=YIELD PER PLANT [g]*
*X12=SHELLING PERCENT*
*X13=LENGHT OF POD BEARING BRANCHES [cm]*
*X14=100 SEED WEIGHT [g]*
*X15=SPECIFIC GRAVITY [gm/ml]*
*X16=HARVEST INDEX [%]*

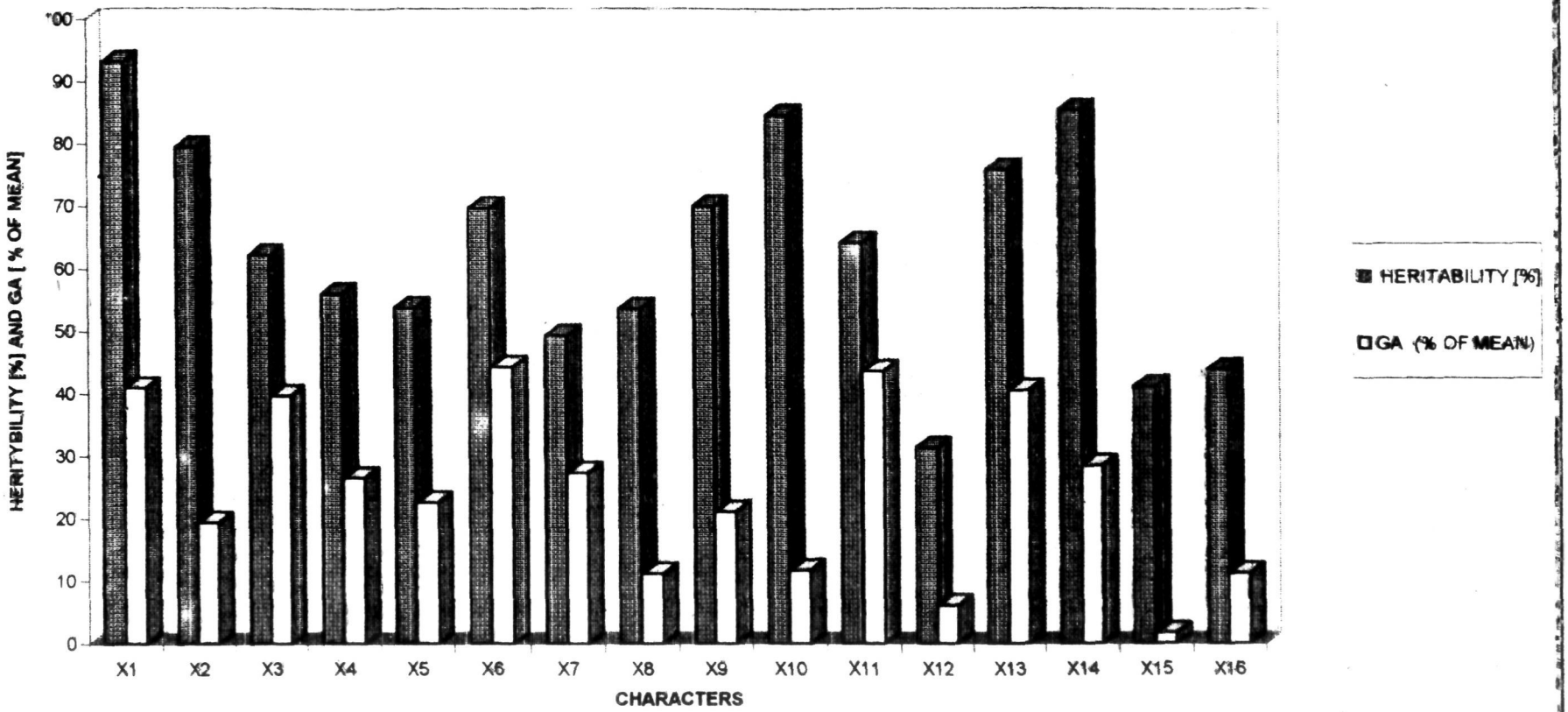


**FIG 2: HERITABILITY ESTIMATES AND GENETIC ADVANCE AS % OF MEAN FOR 16 CHARACTERS IN PIGEONPEA.**

*X1=DAYS TO 50% FLOWERING*
*X2= DAYS TO MATURITY*
*X3=STRAW WEIGHT [g]*
*X4=PLANT HEIGHT [cm]*
*X5=BRANCHES PER PLANT*
*X6=PODS PER PLANT*
*X7=POD WEIGHT [g]*
*X8=POD LENGTH [cm]*
*X9=POD WIDTH [cm]*
*X10=SEEDS PER POD*
*X11=YIELD PER PLANT [g]*
*X12=SHELLING PERCENT*
*X13=LENGHT OF POD BEARING BRANCHES [cm]*
*X14=100 SEED WEIGHT [g]*
*X15=SPECIFIC GRAVITY [gm/ml]*
*X16=HARVEST INDEX [%]*

character was from 51 (ICPL-85010) to 102.5 days (Japan Super and C-11).

The phenotypic and genotypic coefficient of variability for this character was high with values of 21.34 per cent and 20.59 per cent, respectively. The estimates of heritability was found to be very high (93.18%). Genetic advance of 40.95 per cent was observed for this character.

### 4.1.2 Days to maturity

Days taken to maturity ranged from 109.5 in ICPL-85010 to 170 days in Japan Super with a mean value of 150.31 days.

Coefficient of variability was moderate with values of 11.85 and 10.57 per cent at phenotypic and genotypic levels, respectively. A high heritability estimate of 79.49 per cent was recorded for this character, while the genetic advance was moderate (19.41%).

### 4.1.3 Straw weight (g)

The straw weight ranged from 5.76 g (ICPL-85010) to 76.51 g (KE-71) with an average straw weight of 40.57 g.

The phenotypic and genotypic coefficients of variability was 30.95 to 24.41 per cent, respectively. High estimates of heritability (62.23%) and genetic advance (39.67%) was observed for this character.

### 4.1.4 Plant height (cm)

A wide variation was observed for plant height with the mean values for this character ranged from 28.9 cm to 177.3 cm with a overal mean of 117.83 cm. Among the 81 accessions KM-84 was the tallest with a plant height of 177.3 cm and the shortest one being ICPL-85010 with a height of 28.9 cm.

The phenotypic and genotypic coefficient of variability for this character was 23.01 and 17.21 per cent, respectively. Moderate estimates of heritability (55.96%) and high genetic advance (26.52%) were registered for this attribute.

### 4.1.5 Branches per plant

This character ranged from 5.2 (ICPL-85010) to 13.5 (EC-90) with overall mean of 8.85 branches.

A wide difference between phenotypic coefficient of variability (20.42%) and genotypic coefficient of variability (14.97%) was observed. The character showed moderate heritability estimate 53.75 per cent and high genetic advance as per cent mean was 22.61 per cent.

### 4.1.6 Pods per plant

This character had a mean of 76.12 pods with a wide range of variation from 43.0 to 122.1 pods. The minimum

number of pods was recorded in the genotype BWR-23 (43.0) and maximum in the genotype ICP-4595 (122.1).

The phenotypic and genotypic coefficient of variation was 30.83 per cent and 25.74 per cent respectively. Fairly high estimates of heritability (69.71%) and genetic advance (44.28%) were observed for this character.

4.1.7 Pod weight (g)

A wide variability for this character was observed with the genotype KE-71 recording the highest pod weight (50.5 g), while, the genotype ICP-8752 recorded the lowest pod weight (14.65 g). The overall mean for this character was 76.12 g.

The phenotypic and genotypic coefficient of variability values were 26.96 and 18.92 per cent, respectively. Moderate estimates of heritability (49.28%) and high genetic advance (27.37%) were observed for pod weight.

4.1.8 Pod length (cm)

This character exhibited a moderate range of variation, ranging from 4.5 cm (JJAL-15) to 6.5 cm (ICPL-87091) with an overall mean of 5.21 cm.

The phenotypic and genotypic coefficient of variability for this character were 10.16 and 7.43 per cent, respectively. This character had a moderate estimates of heritability (53.57%) and genetic advance (11.21%).

4.1.9 Pod width (cm)

The genotypes ICPL-87091, C-11 and BDN-699 had the maximum pod width of 0.91 cm and the genotypes JJAL-15, KM-29, ICP-9238 and PA-116 exhibited the minimum pod width of 0.62 cm with an overall mean of 0.74 cm.

The phenotypic and genotypic coefficient of variability for this character were 14.66 and 12.26 per cent, respectively. Heritability (69.99%) value was relatively high for this character. Moderate genetic advance of 21.13 per cent was observed.

4.1.10 Seeds per pod

A narrow variation was observed for this character with an overall mean of 3.79 seeds. Maximum number of seeds per pod were recorded in the genotype BDN-699 (4.35) while, the genotypes BDN-1 and ICP-8755 had 3.4 seeds per pod.

The phenotypic and genotypic coefficient of variation were 6.72 and 6.18 per cent, respectively. A high estimates of heritability (84.62%) and moderate value of genetic advance (11.73%) were observed for this character.

4.1.11 Yield per plant (g)

Marked variability was observed for this trait with an overall mean of 19.36 g. The genotype KE-71 was observed to

possess highest grain yield of 38.4 g, while the genotype ICPL-85010 had lowest grain yield of 6.54 g.

The phenotypic and genotypic coefficient of variations were 33 and 26.44 per cent, respectively. This trait showed a fairly high heritability estimate of 64.16 per cent and a high genetic advance of 43.63 per cent.

### 4.1.12 Shelling per cent

The shelling per cent ranged from 41.93 to 64.6 per cent with a mean of 57.88 per cent. The genotype MRG-66 had the highest shelling per cent (64.6%) and the genotype ICPL-85010 had the lowest shelling per cent (41.93%).

The phenotypic and genotypic coefficient of variability were low with values of 9.48 and 5.31 per cent, respectively. A moderate heritability estimate of 31.34 per cent and low genetic advance of 6.13 per cent of mean was observed.

### 4.1.13 Length of pod bearing branches (cm)

The length of pod bearing branches ranged from 4.6 (ICPL-85010) to 38.36 cm (T-21). The overall mean recorded for this trait was 23.69 cm.

The phenotypic and genotypic coefficient of variability for the character were 25.93 and 22.59 per cent, respectively. A high heritability (75.92%) and genetic advance as per cent of mean (40.50%) were registered.

4.1.14 100-seed weight (g)

Maximum 100-seed weight was observed in the genotype ICPL-87091 (12.7 g), whereas, minimum was showed by the genotype PA-116 (7.1 g) with an overall mean of 9.57 g.

The estimated values of phenotypic and genotypic coefficient of variation were 16.21 and 14.98 per cent, respectively. High estimates of heritability (85.45%) and genetic advance as per cent of mean (28.52%) were recorded for this character.

4.1.15 Specific gravity (g/ml)

This character had a mean specific gravity of 0.8 g per ml with a narrow range of variability from 0.75 (BDN-627) to 0.83 g per ml (AL-604).

Very low phenotypic and genotypic coefficient of variability of 2.03 and 1.31 per cent, respectively, were observed with relatively moderate value of heritability (41.18%). Very low genetic advance of 1.73 per cent was observed for this character.

4.1.16 Harvest index (%)

Highest harvest index was observed in the genotype Pusa-952 (32.76%) whereas, the genotype GAUT 86-30 exhibited lowest harvest index of 18.76 per cent with an overall mean of 26.66 per cent.

The phenotypic and genotypic coefficient of variability were found to be 12.42 and 8.23 per cent, respectively. High heritability estimate of 43.89 per cent and a moderate genetic advance of 11.23 per cent were observed for this character.

## 4.2 Association of characters

The genotypic and phenotypic correlation coefficients for all the 16 characters are presented in Table 3 and 4, respectively. The graphical representation of the same have been depicted in Figs. 3 and 4, respectively. In general, the genotypic correlation coefficients were found to be higher than the respective phenotypic correlation coefficients.

Highly significant association of grain yield was observed with days to 50 per cent flowering, days to maturity, straw weight, plant height, branches per plant, pods per plant, pod weight, pod width, seeds per pod, shelling per cent and 100-seed weight both at phenotypic and genotypic level.

Non-significant negative correlation of grain yield was observed with specific gravity. Whereas, the associations of grain yield with pod length, length of pod bearing branches, and harvest index were positive but non-significant. The trends were similar both at phenotypic and genotypic levels.

Table 3. Genotypic correlation co-efficients of 16 characters in pigeonpea.

| Sl. No. | Characters | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. | Days to 50% flowering | 1.0000 | 0.7782** | 0.7439** | 0.6653** | 0.4759** | 0.4066** | 0.5965** | -0.0916 | 0.2970** | 0.2753* | 0.6446** | 0.7509** | 0.1308 | 0.4738** | -0.1255 | -0.2674* |
| 2. | Days to maturity | | 1.0000 | 0.7036** | 0.7527** | 0.4230** | 0.3884** | 0.5645** | -0.0395 | 0.2927** | 0.3096** | 0.6046** | 0.7660** | 0.3815** | 0.5631** | -0.1933 | -0.2715* |
| 3. | Straw weight (g) | | | 1.0000 | 0.7409** | 0.7326** | 0.6488** | 0.8660** | 0.1042 | 0.4138** | 0.4177** | 0.8881** | 0.7635** | 0.2670* | 0.4747** | -0.0958 | -0.3619** |
| 4. | Plant height (cm) | | | | 1.0000 | 0.6655** | 0.5351** | 0.6512** | -0.1945 | 0.2044 | 0.1649 | 0.7010** | 0.8627** | 0.5964** | 0.4150** | -0.2512* | -0.1189 |
| 5. | Branches per plant | | | | | 1.0000 | 0.6805** | 0.7829** | 0.1293 | 0.3324** | 0.3623** | 0.7981** | 0.6680** | 0.1597 | 0.3118** | -0.0679 | 0.0097 |
| 6. | Pods per plant | | | | | | 1.0000 | 0.8384** | -0.1700 | 0.0388 | 0.1973 | 0.8352** | 0.5691** | 0.3170** | -0.0189 | -0.1238 | 0.2126 |
| 7. | Pod weight (g) | | | | | | | 1.0000 | 0.1782 | 0.4498** | 0.5107** | 0.9933** | 0.6637** | 0.1915 | 0.3957** | -0.1377 | 0.0782 |
| 8. | Pod length (cm) | | | | | | | | 1.0000 | 0.6665** | 0.7115** | 0.1255 | -0.1674 | -0.3851** | 0.4733** | 0.1229 | 0.0648 |
| 9. | Pod width (cm) | | | | | | | | | 1.0000 | 0.6344** | 0.4337** | 0.2315* | -0.2486* | 0.6563** | 0.0517 | 0.0089 |
| 10. | Seeds per pod | | | | | | | | | | 1.0000 | 0.5988** | 0.2763* | -0.2585* | 0.4406** | 0.0891 | 0.1297 |
| 11. | Yield per plant (g) | | | | | | | | | | | 1.0000 | 0.7365** | 0.2131 | 0.3950** | -0.1400 | 0.0604 |
| 12. | Shelling per cent | | | | | | | | | | | | 1.0000 | 0.4487** | 0.[illegible]06** | -0.1422 | -0.0765 |
| 13. | Length of pod bearing branches (cm) | | | | | | | | | | | | | 1.0000 | 0.0005 | -0.2529* | -0.0797 |
| 14. | 100-seed weight (g) | | | | | | | | | | | | | | 1.0000 | -0.1682 | -0.2417* |
| 15. | Specific gravity (g/ml) | | | | | | | | | | | | | | | 1.000 | -0.0277 |
| 16. | Harvest index (%) | | | | | | | | | | | | | | | | 1.0000 |

** = Significant both at 5 and 1 per cent level of signifience for n-2 degrees of freedom
* = Significant at 5 per cent level of signifience for n-2 degrees of freedom

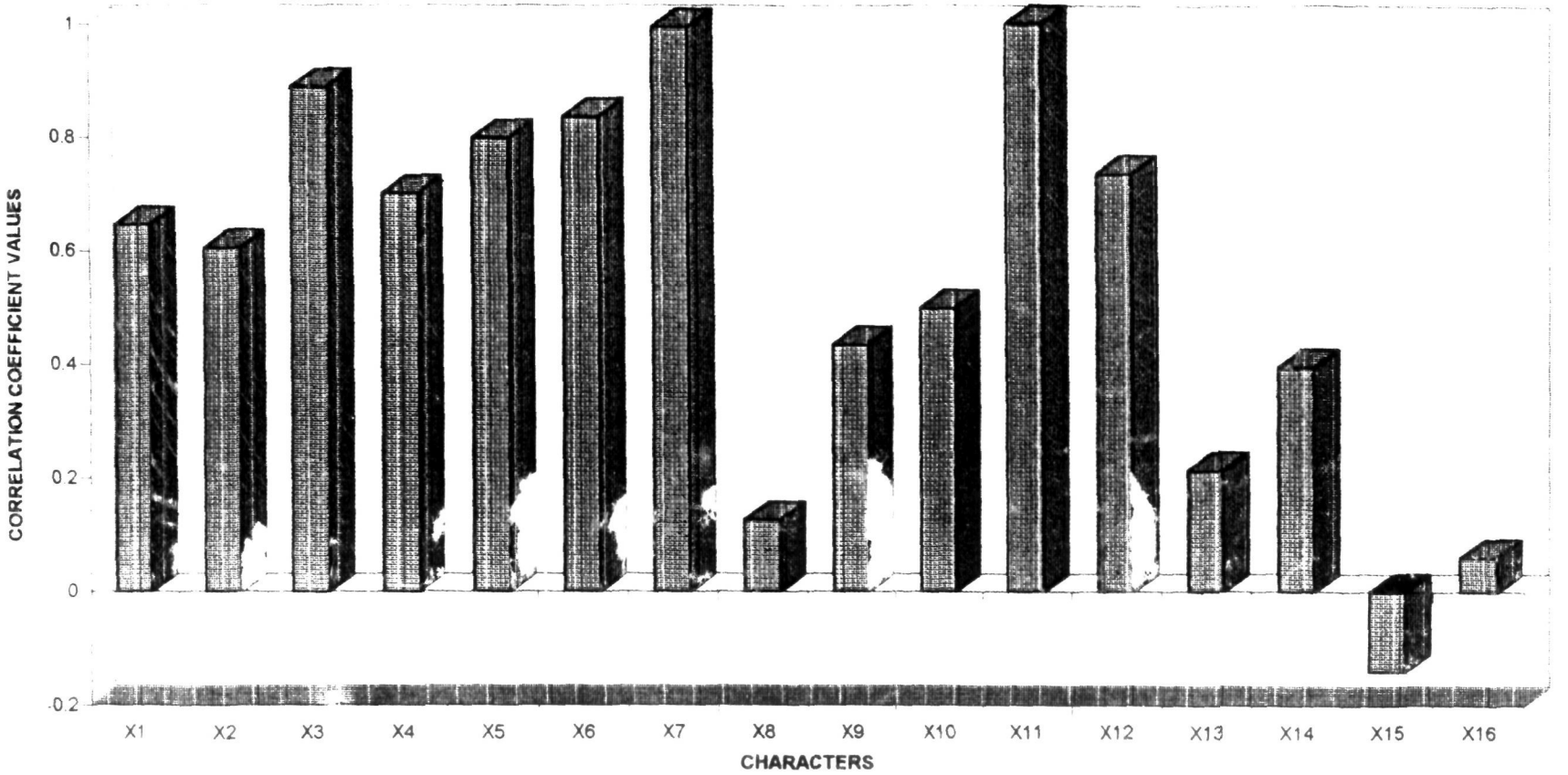


**FIG 3: GENOTYPIC CORRELATION COEFFICIENTS OF 16 CHARACTERS WITH SEED YIELD IN PIGEONPEA**

X1=DAYS TO 50% FLOWERING
X2= DAYS TO MATURITY
X3=STRAW WEIGHT (g)
X4=PLANT HEIGHT [cm]
X5=BRANCHES PER PLANT
X6=PODS PER PLANT
X7=POD WEIGHT [g]
X8=POD LENGTH [cm]
X9=POD WIDTH [cm]
X10=SEEDS PER POD
X11=YIELD PER PLANT [g]
X12=SHELLING PERCENT
X13=LENGHT OF POD BEARING BRANCHES [cm]
X14=100 SEED WEIGHT [g]
X15=SPECIFIC GRAVITY [gm/ml]
X16=HARVEST INDEX [%]

Table 4. Phenotypic correlation coefficients of 16 characters in pigeonpea.

| Sl. No. | Characters | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. | Days to 50% flowering | 1.0000 | 0.7667** | 0.7286** | 0.6579** | 0.3629** | 0.3959** | 0.5884** | -0.0841 | 0.2863** | 0.2589* | 0.6317** | 0.6832** | 0.1309 | 0.4575** | -0.0907 | -0.2436* |
| 2. | Days to maturity | | 1.0000 | 0.6810** | 0.7365** | 0.3140** | 0.3733** | 0.5550** | -0.0343 | 0.2835* | 0.2861** | 0.5904** | 0.6936** | 0.3749** | 0.5401** | -0.1374 | -0.2312* |
| 3. | Straw weight (g) | | | 1.0000 | 0.7219** | 0.5596** | 0.6248** | 0.8504** | 0.0932 | 0.3802** | 0.3843** | 0.8686** | 0.7030** | 0.2590* | 0.4513** | -0.0527 | -0.3320** |
| 4. | Plant height (cm) | | | | 1.0000 | 0.5210** | 0.5222** | 0.6432** | -0.1840 | 0.2053 | 0.1477 | 0.6895** | 0.7939** | 0.5867** | 0.4032** | -0.1769 | -0.0893 |
| 5. | Branches per plant | | | | | 1.0000 | 0.5394** | 0.6264** | 0.0565 | 0.2924** | 0.2415* | 0.6453** | 0.5308** | 0.1250 | 0.2509* | -0.0138 | 0.0850 |
| 6. | Pods per plant | | | | | | 1.0000 | 0.8188** | -0.1601 | 0.0433 | 0.1794 | 0.8161** | 0.5251** | 0.3123** | -0.0147 | -0.0770 | 0.1207 |
| 7. | Pod weight (g) | | | | | | | 1.0000 | 0.1763 | 0.4323** | 0.4722** | 0.9894** | 0.6199** | 0.1912 | 0.3791** | -0.0939 | 0.1081 |
| 8. | Pod length (cm) | | | | | | | | 1.0000 | 0.6149** | 0.6543** | 0.1246 | -0.1451 | -0.3616** | 0.4397** | 0.0511 | 0.0803 |
| 9. | Pod width (cm) | | | | | | | | | 1.0000 | 0.5760** | 0.4106** | 0.1884 | -0.2283* | 0.6141** | 0.0212 | 0.0184 |
| 10. | Seeds per pod | | | | | | | | | | 1.0000 | 0.4509** | 0.2130 | -0.2527* | 0.4004** | 0.0141 | 0.0900 |
| 11. | Yield per plant (g) | | | | | | | | | | | 1.0000 | 0.7128** | 0.2126 | 0.3825** | -0.1036 | 0.1123 |
| 12. | Shelling per cent | | | | | | | | | | | | 1.0000 | 0.4151** | 0.3480** | -0.1282 | -0.0495 |
| 13. | Length of pod bearing branches (cm) | | | | | | | | | | | | | 1.0000 | 0.0003 | -0.1929 | -0.0583 |
| 14. | 100-seed weight (g) | | | | | | | | | | | | | | 1.0000 | -0.1201 | -0.2016 |
| 15. | Specific gravity (g/ml) | | | | | | | | | | | | | | | 1.000 | -0.0449 |
| 16. | Harvest index (%) | | | | | | | | | | | | | | | | 1.0000 |

** = Significant both at 5 and 1 per cent level of signifience for n-2 degrees of freedom
* = Significant at 5 per cent level of signifience for n-2 degrees of freedom

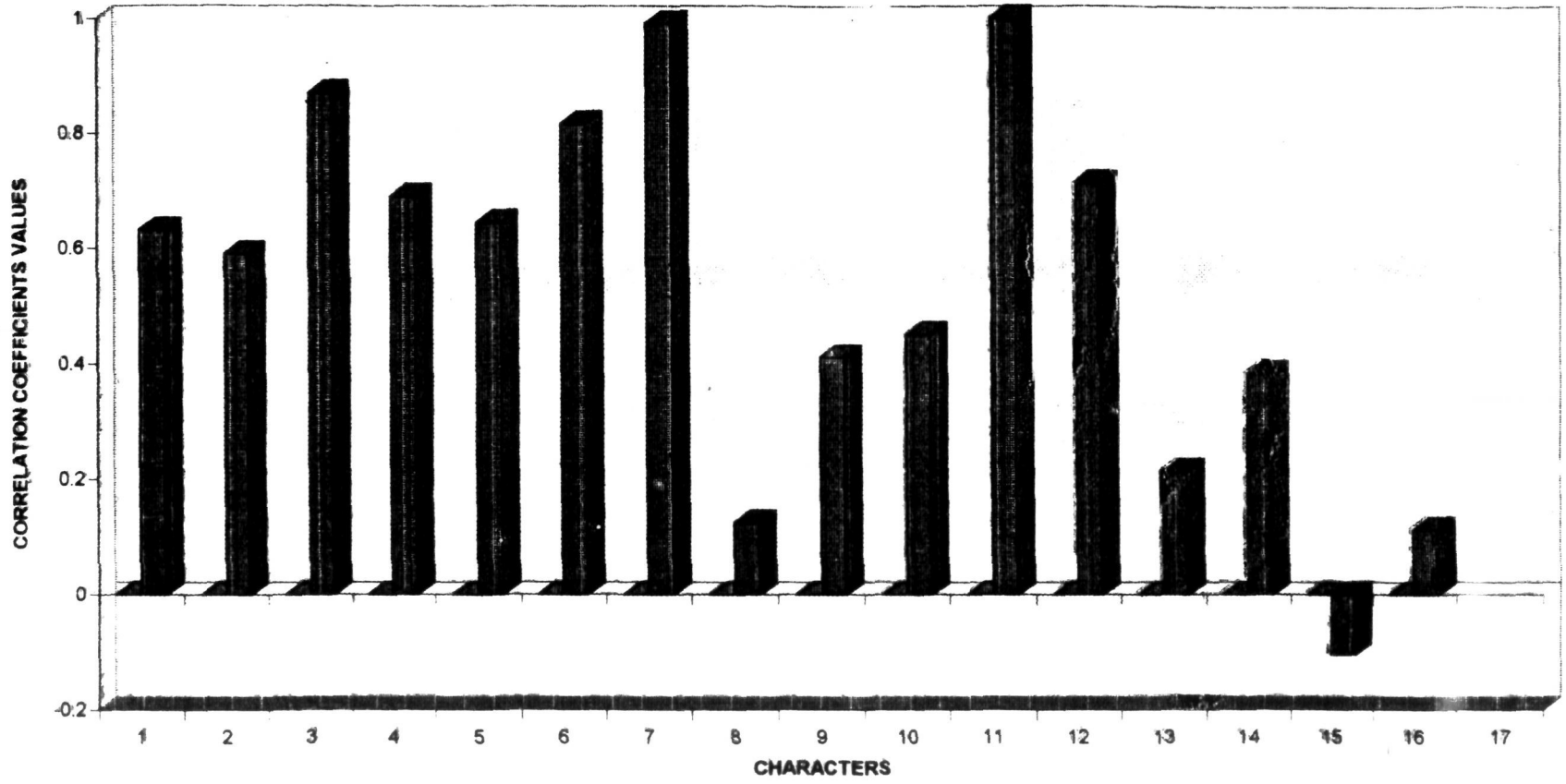


**FIG 4: PHENOTYPIC CORRELATION COEFFICIENTS OF 16 CHARACTERS WITH SEED YIELD IN PIGEONPEA**

*X1=DAYS TO 50% FLOWERING*
*X2= DAYS TO MATURITY*
*X3=STRAW WEIGHT (g)*
*X4=PLANT HEIGHT [cm]*
*X5=BRANCHES PER PLANT*
*X6=PODS PER PLANT*
*X7=POD WEIGHT [g]*
*X8=POD LENGTH [cm]*
*X9=POD WIDTH [cm]*
*X10=SEEDS PER POD*
*X11=YIELD PER PLANT [g]*
*X12=SHELLING PERCENT*
*X13=LENGHT OF POD BEARING BRANCHES [cm]*
*X14=100 SEED WEIGHT [g]*
*X15=SPECIFIC GRAVITY [gm/ml]*
*X16=HARVEST INDEX [%]*

Days to 50 per cent flowering showed positively significant association with days to maturity, straw weight, plant height, branches per plant, pods per plant, pod weight, pod width, seeds per pod, yield per plant, shelling per cent and 100-seed weight. The same trend was observed both at phenotypic and genotypic levels. Significantly negative relationship was observed between days to 50 per cent flowering and harvest index. Days to 50 per cent flowering showed non-significant but positive relationship with length of pod bearing branches.

The association of days to maturity with days to 50 per cent flowering, straw weight, plant height, branches per plant, pods per plant, pod weight, pod width, seeds per pod, yield per plant, shelling per cent, length of pod bearing branches and 100-seed weight were found to be positive and highly significant both at genotypic and phenotypic levels. The association of days to maturity was negative and significant with harvest index both at phenotypic and genotypic levels.

Both at genotypic and phenotypic levels straw weight possessed significant and positive association with days to 50 per cent flowering, days to maturity, plant height, branches per plant, pods per plant, pod weight, pod width, seeds per pod, yield per plant, shelling per cent, length of pod bearing branches and 100-seed weight. Thus character

showed highly significant and negative association with harvest index.

Plant height showed highly significant positive association with days to 50 per cent flowering, days to maturity, straw weight, branches per plant, pods per plant, pod weight, yield per plant, shelling per cent, length of pod bearing branches, and 100-seed weight. It had a significantly negative association with specific gravity only at genotypic level.

Both at genotypic and phenotypic levels branches per plant showed positive and highly significant correlation with days to 50 per cent flowering, days to maturity, straw weight, plant height, pods per plant, pod weight, pod width, yield per plant and shelling per cent. It showed positively significant association with seeds per pod and 100-seed weight only at phenotypic level.

Pods per plant exhibited strong positive association with days to 50 per cent flowering, days to maturity, straw weight, plant height, branches per plant, pod weight, yield per plant, shelling per cent and length of the pod bearing branches both at phenotypic and genotypic levels.

Pod weight registered highly significant and positive association with days to 50 per cent flowering, days to maturity, straw weight, plant height, branches per plant,

pods per plant, pod width, seed per pod, yield per plant, shelling per cent and 100-seed weight both at phenotypic and genotypic levels.

Highly significant and positive correlation was observed between pod length and pod width, seeds per pod and 100-seed weight both at genotypic and phenotypic levels. It had negative and significant association with length of pod bearing branches.

Pod width had highly significant positive correlation with days to 50 per cent flowering, straw weight, branches per plant, pod weight, pod length, seeds per pod, yield per plant and 100-seed weight both at phenotypic and genotypic levels. Association with days to maturity and shelling per cent was highly significant at genotypic level.

The association of seeds per pod was positive and highly significant with days to 50 per cent flowering, days to maturity, straw weight, pod weight, pod length, pod width, yield per plant and 100-seed weight. It showed significant positive association with shelling per cent and significant negative association with length of pod bearing branches at genotypic level.

Both at genotypic and phenotypic levels, shelling per cent had highly significant positive association with days to 50 per cent flowering, days to maturity, straw weight, plant

height, branches per plant, pods per plant, pod weight, yield per plant, length of pod bearing branches and 100-seed weight. It showed signifi-cantly positive association with pod width and seeds per pod at genotypic level.

Length of pod bearing branches showed highly significant positive association with days to maturity, plant height, pods per plant and shelling per cent. It had significant positive association with straw weight both at genotypic and phenotypic level. This character showed significant negative association with pod length, pod width and seeds per pod both at genotypic and phenotypic levels and negative and significant relation with specific gravity at genotypic level.

Hundred seed weight showed strong significant positive association with days to 50 per cent flowering, days to maturity, straw weight, plant height, pod weight, pod length, pod width, seeds per pod, yield per plant and shelling per cent both at genotypic and phenotypic level. Hundred seed weight had significant and negative association with harvest index at genotypic level.

Harvest index showed negative and significant association with days to 50 per cent flowering, days to maturity and straw weight both at genotypic and phenotypic levels, while, the association was non-significant negative

association with plant height, shelling per cent, length of pod bearing branches and specific gravity.

### 4.3 Path coefficient analysis

The phenotypic path cofficients of grain yield with days to 50 per cent flowering, days to maturity, plant height, branches per plant, pods per plant, pod weight, seeds per pod and 100-seed weight are presented in Table 5. The graphical representation of the same is depicted in Fig. 5.

Pod weight exhibited the highest positive direct effect of 0.881 on grain yield, while plant height (0.0629), days to 50 per cent flowering (0.0579), branches per plant (0.0298), seeds per pod (0.0045) and pods per plant (0.0223) had low positive direct effects. The direct effect of days to maturity (-0.0026) and 100-seed weight (-0.0106) on grain yield were low and negative.

Days to 50 per cent flowering exhibited a low positive direct effect (0.0579) on grain yield. Its positive indirect effect through pod weight (0.518) alone was substantial. The indirect effects of days to 50 per cent flowering through plant height (0.0414), branches per plant (0.0108), pods per plant (0.0092) and seeds per pod (0.0012) were found to be very low. It had a low negative indirect influence through days to maturity (-0.0019) and 100-seed weight (-0.0049).

Table 5. Direct (diagonal) and indirect (above and below diagnoal) effects of quantitative characters on seed yield in pigeonpea at phenotypic level.

| Sl. No. | Characters | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | Correlation coefficients with yield |
|---|---|---|---|---|---|---|---|---|---|---|
| 1. | Days to 50% flowering | 0.0579 | -0.0019 | 0.0414 | 0.0108 | 0.0092 | 0.5180 | 0.0012 | -0.0049 | **0.6317** |
| 2. | Days to maturity | 0.0444 | -0.0026 | 0.0464 | 0.0094 | 0.0087 | 0.4890 | 0.0013 | -0.0058 | **0.5904** |
| 3. | Plant height (cm) | 0.0382 | -0.0019 | 0.0629 | 0.0155 | 0.0122 | 0.5660 | 0.0062 | -0.0040 | **0.6895** |
| 4. | Branches per plant | 0.0210 | -0.0008 | 0.0323 | 0.0298 | 0.0126 | 0.5510 | 0.0011 | -0.0027 | **0.6453** |
| 5. | Pods per plant | 0.0229 | -0.0009 | 0.0329 | 0.0161 | 0.0233 | 0.7210 | 0.0008 | 0.0002 | **0.8161** |
| 6. | Pod weight (g) | 0.0341 | -0.0014 | 0.0405 | 0.0187 | 0.0191 | 0.8810 | 0.0021 | -0.0041 | **0.9894** |
| 7. | Seeds per pod | 0.0149 | -0.0007 | 0.0093 | 0.0072 | 0.0042 | 0.4160 | 0.0045 | -0.0042 | **0.4509** |
| 8. | 100-seed weight (g) | 0.0265 | -0.0014 | 0.0254 | 0.0075 | -0.0004 | 0.3340 | 0.0018 | -0.0106 | **0.3825** |

Residual effect = 0.01424

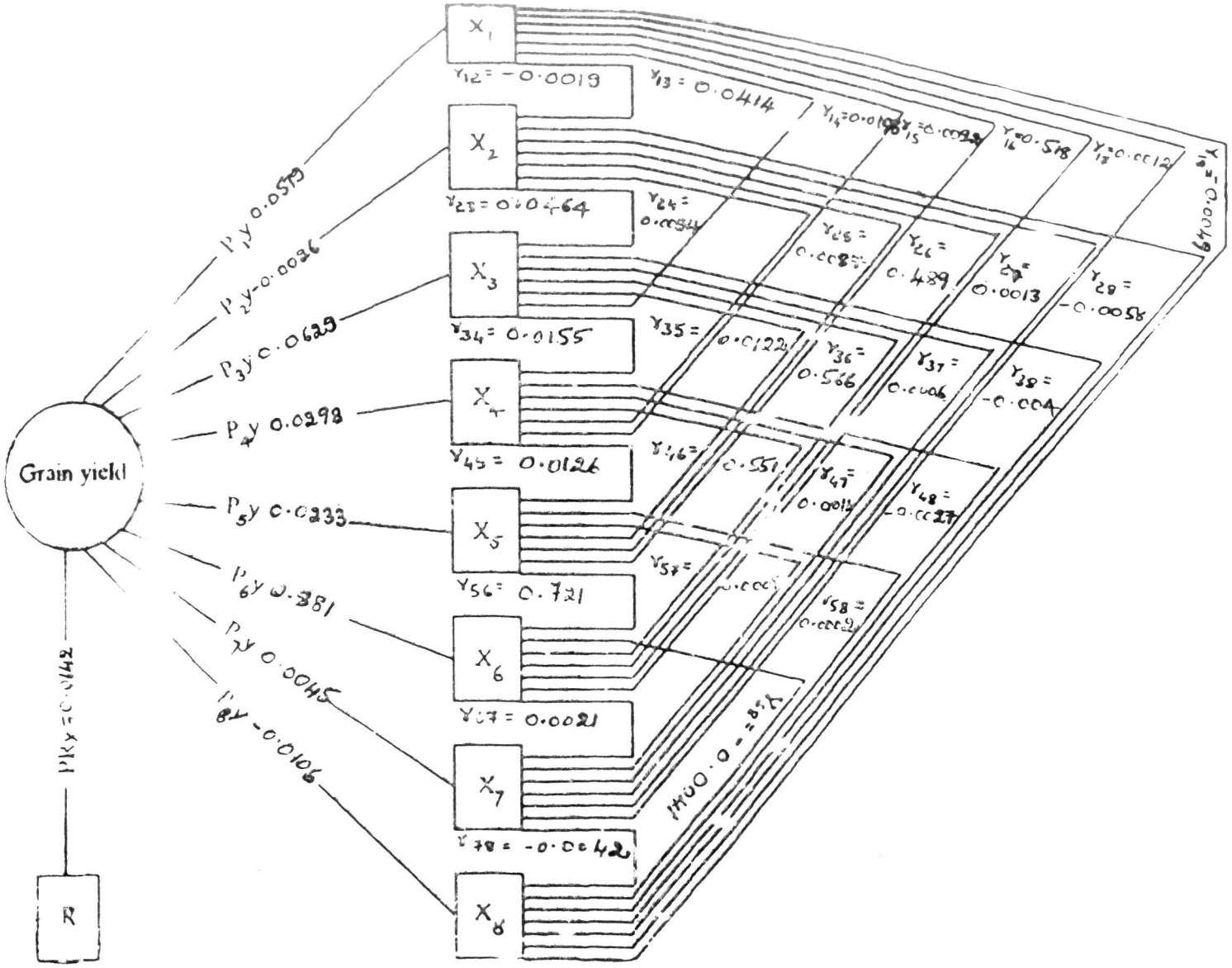


Fig. 5 : Phenotypic path diagram showing the influence of 8 different characters on grain yield.

Days to maturity showed very low negative direct (-0.0026) and its indirect effect via pod weight was maximum (0.489). Low positive indirect effects were observed through days to 50 per cent flowering (0.0444), plant height (0.0464), branches per plant (0.0094), pods per plant (0.0087) and seeds per pod (0.0013). It had low negative indirect effect via 100-seed weight (-0.0058).

Plant height exhibited low positive direct effect of 0.0629 on grain yield. Its indirect influence through pod weight was high and positive (0.566). Plant height showed low positive indirect effects via days to 50 per cent flowering (0.0382), branches per plant (0.0155), pods per plant (0.0122) and seeds per pod (0.0006). It also had low negative indirect effects via days to maturity (-0.0019) and 100-seed weight (-0.004).

Branches per plant had a low positive direct effect of 0.0298 on grain yield, but its positive indirect effect through pod weight (0.551) was very high. It exhibited a low positive indirect effects via plant height (0.0323), days to 50 per cent flowering (0.021), branches per plant (0.0126) and seeds per pod (0.0011) and low negative indirect effects through 100-seed weight (-0.0027) and days to maturity (-0.0008).

Pods per plant exhibited a low positive direct effect of 0.0233 on grain yield per plant and its positive indirect

effect via pod weight (0.721) was very high. Low positive indirect effects via plant height (0.0329), days to maturity (0.0229), branches per plant (0.0161), seeds per pod (0.0008) and 100-seed weight (0.0002) and low negative indirect effect via days to maturity (-0.0009) were observed.

Pod weight exhibited a very high positive direct effect (0.881) on grain yield. But its negative indirect effects through days to maturity (-0.0014) and 100-seed weight (-0.0041) and positive indirect effects via plant height (0.0405), days to maturity (0.0341), pods per plant (0.0191), branches per plant (0.0187) and seeds per pod (0.0021) were negligible.

Seeds per pod showed a very low direct effect of 0.0045 on grain yield. But it had a high positive indirect effect of 0.416 through pod weight. The positive indirect effects through days to 50 per cent flowering (0.0149), plant height (0.0073), branches per plant (0.0072) and pods per plant (0.0042) and negative indirect effects via days to maturity (0.0007) and 100-seed weight (-0.0042) were very low.

Hundred seed weight exhibited very low negative direct effect (-0.0106) on grain yield. It had a high positive indirect effect of 0.334 through pod weight. The indirect effects through days to 50 per cent flowering (0.0265), plant height (0.0254), branches per plant (0.0075),

seeds per pod (0.0018), days to maturity (-0.0014) and pods per plant (-0.0004) were not substantial.

## 4.4 Genetic divergence studies

### 4.4.1 Canonical roots and extent of variability extracted by them

The canonical variate analysis was employed to get the spatial positioning of all the 81 genotypes on a graph. The first two canonical vectors derived are given in the Table 6. It could be seen from the first vector that the variables days to 50 per cent flowering, plant height and harvest index contributed more in discriminating entries as shown in Fig. 6 and through the second vector, the variables plant height, length of pod bearing branches and harvest index were found to contribute for divergence. Hence days to 50 per cent flowering, plant height, length of pod bearing branches and harvest index could be considered as most contributing variables towards divergence.

The amount of variability extracted by each of these first two vectors and subsequent four vectors derived in the decreasing order of magnitude for canonical vectors is presented in Table 7.

It was noticed that the first canonical vector absorbed 70.78 per cent of the total variability and the second vector absorbed 11.74 per cent of variability. The first two

Table 6. The two canonical vectors which supply best linear functions of variates.

| Sl. No. | Characters | Vector-1 | Vector-2 |
|---|---|---|---|
| 1. | Days to 50% flowering | 0.785 | -0.215 |
| 2. | Days to maturity | 0.209 | 0.184 |
| 3. | Straw weight (g) | 0.200 | 0.089 |
| 4. | Plant height (cm) | 0.229 | 0.428 |
| 5. | Branches per plant | 0.027 | 0.057 |
| 6. | Pods per plant | 0.097 | 0.064 |
| 7. | Pod weight (g) | -0.155 | -0.139 |
| 8. | Pod length (cm) | -0.038 | -0.044 |
| 9. | Pod width (cm) | -0.127 | -0.255 |
| 10. | Seeds per pod | 0.144 | -0.002 |
| 11. | Yield per plant (g) | 0.187 | -0.126 |
| 12. | Shelling per cent | -0.060 | 0.024 |
| 13. | Length of pod bearing branches (cm) | -0.153 | 0.730 |
| 14. | 100-seed weight (g) | 0.027 | -0.081 |
| 15. | Specific gravity (g/ml) | -0.132 | -0.058 |
| 16. | Harvest index (%) | -0.309 | -0.275 |

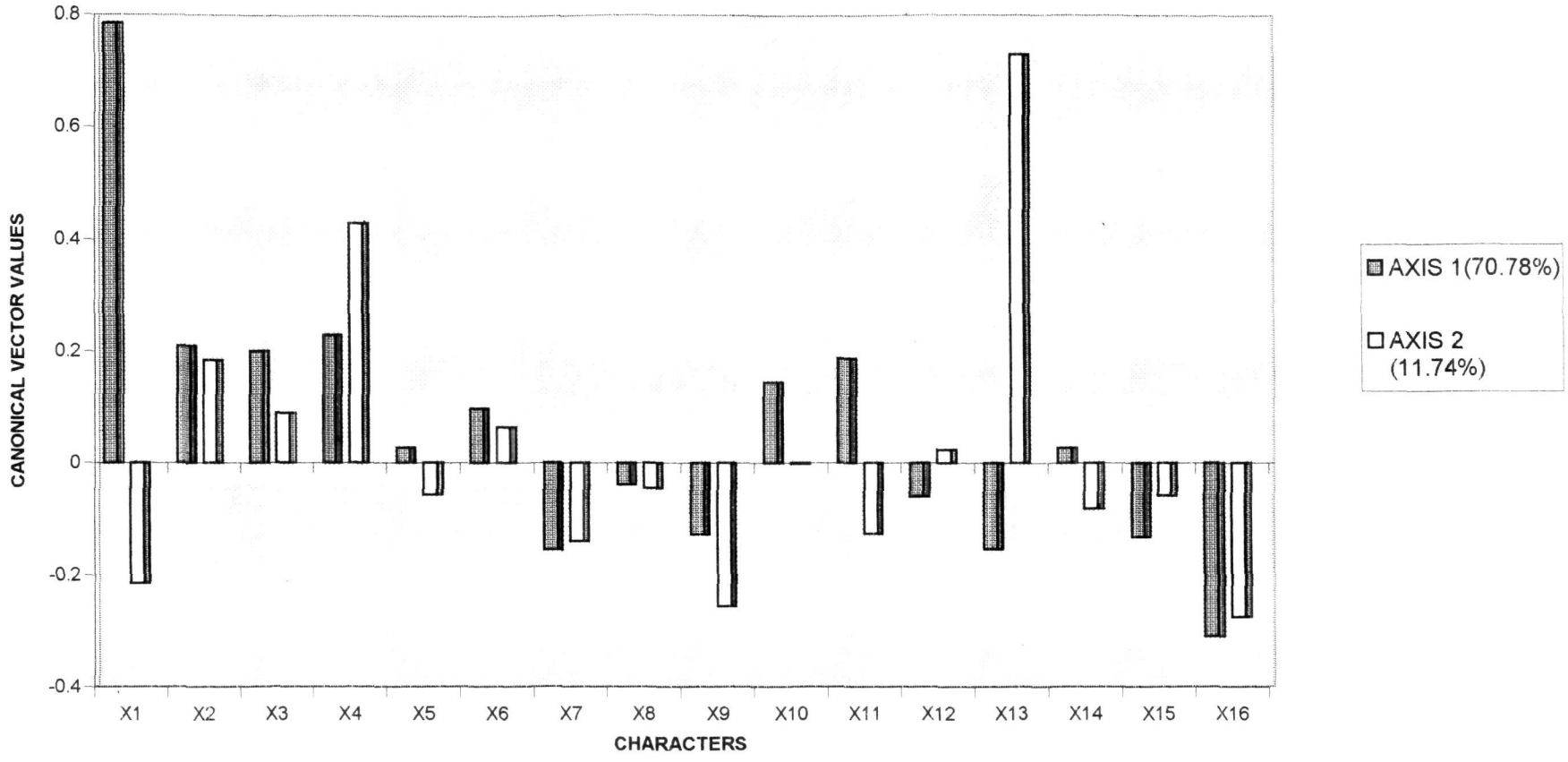


**FIG 6 : GRAPH SHOWING THE EXTENT OF CONTRIBUTION OF 16 CHARACTERS TOWARDS GENETIC DIVERGENCE IN PIGEONPEA.**

*X1=DAYS TO 50% FLOWERING*
*X2= DAYS TO MATURITY*
*X3=STRAW WEIGHT (g)*
*X4=PLANT HEIGHT [cm]*
*X5=BRANCHES PER PLANT*
*X6=PODS PER PLANT*
*X7=POD WEIGHT [g]*
*X8=POD LENGTH [cm]*
*X9=POD WIDTH [cm]*
*X10=SEEDS PER POD*
*X11=YIELD PER PLANT [g]*
*X12=SHELLING PERCENT*
*X13=LENGHT OF POD BEARING BRANCHES [cm]*
*X14=100 SEED WEIGHT [g]*
*X15=SPECIFIC GRAVITY [gm/ml]*
*X16=HARVEST INDEX [%]*

Table 7. Canonical roots and variability extracted by them.

| Canonical roots | Percentage of variability | Cumulative percentage of variability extracted |
|---|---|---|
| 1 | 70.78 | 70.78 |
| 2 | 11.74 | 82.52 |
| 3 | 5.59 | 88.11 |
| 4 | 4.06 | 92.17 |
| 5 | 1.55 | 93.72 |
| 6 | 1.48 | 95.20 |

vectors accounted for 82.52 per cent of the total variability produced by all the characters under study. The remaining four vectors absorbed only 12.68 per cent of the variability. So, they were not considered.

### 4.4.2 Canonical graph

The canonical variables were derived for 81 genotypes using the first two principal components and plotted on the graph (Fig. 7). The $Z_1$ axis refers to first vector and $Z_2$ to the second vector. Most of the genotypes accumulated almost equally and spatially arranged on both the sides of $Z_1$ axis, along the $Z_2$ axis, all the genotypes accumulated towards the right side of the $Z_2$ axis. The entries showed a wider distribution on the graph in general. In the second vector, the genotype 40 (T-21) was on the top and the genotype 61 (ICPL-85010) at the bottom. The remaining genotypes distributed within the extremes.

### 4.4.3 Clustering using canonical graph

Eighty one genotypes were arbitrarily grouped into 15 clusters as showed in Fig. 7 and the entries prevalent in them are given in Table 8.

Among these, cluster X was the biggest with 22 entries followed by the clusters V, VI, VII, XI with 11, 9, 8 and 6 entries, respectively. Clusters III, VIII and XIII had five

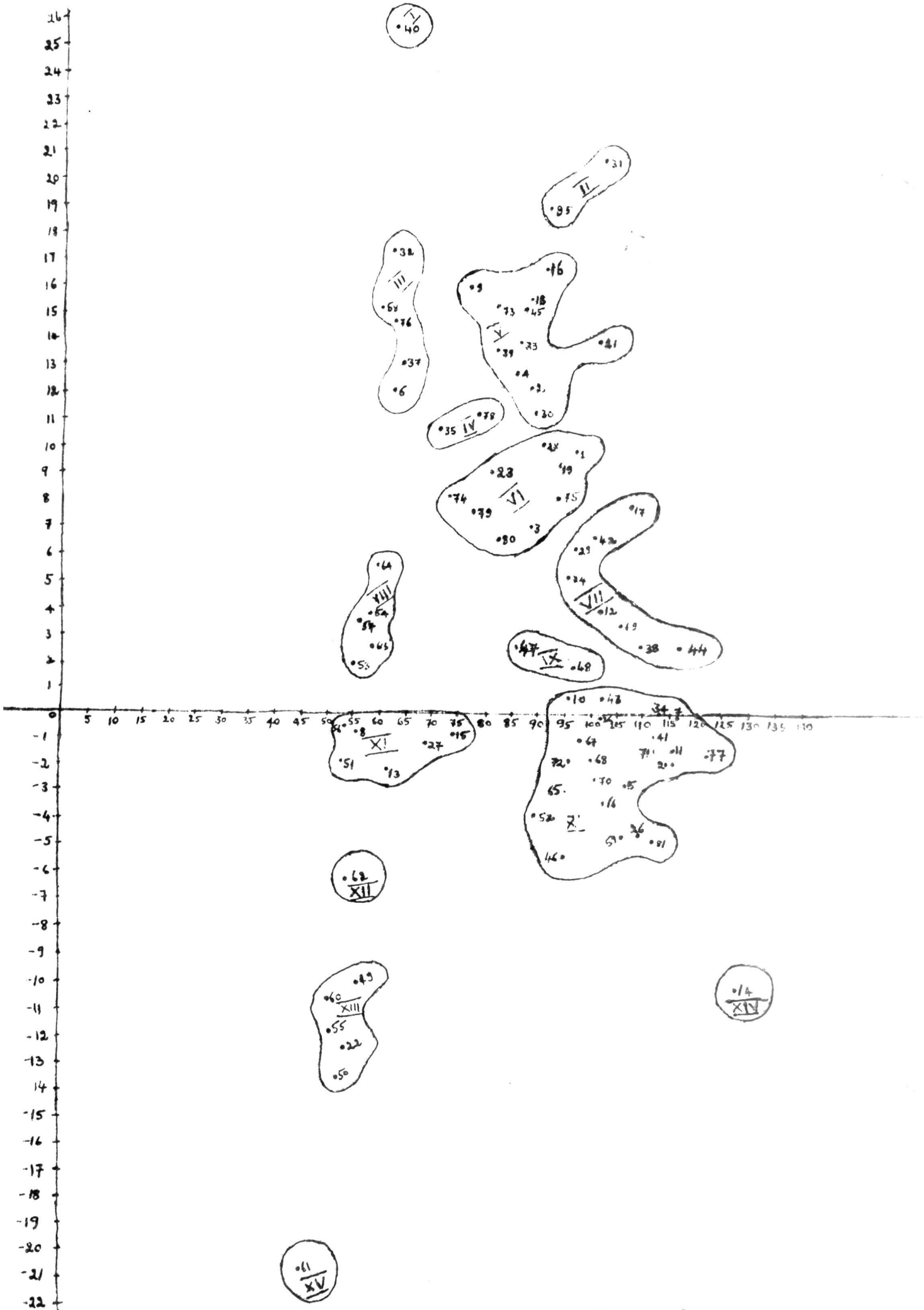


FIG.7: The canonical cluster formed on the graph.

Table 8. Clusters formed on canonical graph.

| Cluster No. | Number of accessions | Accession Numbers |
|---|---|---|
| I | 1 | 40 |
| II | 2 | 25, 31 |
| III | 5 | 32, 58, 76, 37, 6 |
| IV | 2 | 35, 78 |
| V | 11 | 9, 16, 18, 73, 45, 33, 39, 21, 4, 2, 30 |
| VI | 9 | 1, 19, 28, 23, 75, 3, 80, 79, 74 |
| VII | 8 | 17, 42, 29, 24, 12, 69, 38, 44 |
| VIII | 5 | 64, 54, 57, 63, 53 |
| IX | 2 | 47, 48 |
| X | 22 | 10, 43, 34, 7, 36, 41, 67, 72, 68, 71, 11, 77, 20, 70, 5, 65, 66, 52, 59, 26, 81, 46 |
| XI | 6 | 56, 8, 15, 27, 51, 13 |
| XII | 1 | 62 |
| XIII | 5 | 49, 60, 55, 22, 50 |
| XIV | 1 | 14 |
| XV | 1 | 61 |

entries each. Whereas, clusters II, IV and IX had two entries each and all other four clusters were solitary.

### 4.4.4 $D^2$ analysis

The square of the distance ($D^2$ values) between two entries, calculated as the sum of the squares of the differences between the mean values of all the 16 transformed variables, were used for final grouping of the entries. Since each entry produced 80 combinations, 3240 $D^2$ values were obtained for 81 genotypes.

### 4.4.5 Clustering of the entries

Tochers (Singh and Chaudhary, 1977) method was followed to group the entries into different clusters. Using this technique, 81 genotypes fell into 14 clusters. Cluster II was the biggest having 20 entries followed by the cluster I which had 14 entries. Cluster III and IV had 13 entries each, cluster VI and V with 7 and 4 entries, respectively, and cluster VII and VIII had 2 entries each. The remaining six clusters were solitary. The number of entries, name of the entries and the clusters to which they belong is mentioned in the Table 9. The clusters resulted were superimposed on canonical graph as represented in Fig. 8.

### 4.4.6 Inter-cluster and intra-cluster $D^2$ values

The intra-cluster and inter-cluster distances ($D^2$ values) are presented in Table 10. The intra-cluster $D^2$

Table 9. The $D^2$ clusters and the entries included in them.

| Cluster No. | No. of accessions | Accession No. | Name of the accession | Place of the origin |
|---|---|---|---|---|
| I | 14 | 5 | ICPL-87051 | ICRISAT |
| | | 7 | JJAL-16 | Madhya Pradesh |
| | | 11 | ICPL-87119 | ICRISAT |
| | | 17 | GAUT-88-24 | Gujarat |
| | | 20 | SPMA-11 | Madhya Pradesh |
| | | 24 | ICPL-92002 | ICRISAT |
| | | 26 | GS-1 | Karnataka |
| | | 29 | KM-10 | Madhya Pradesh |
| | | 38 | C-11 | Maharashtra |
| | | 41 | KM-61 | Madhya Pradesh |
| | | 42 | PBNA-47-1 | Maharashtra |
| | | 44 | PBNA-47-2 | Maharashtra |
| | | 71 | ICPL-8357 | ICRISAT |
| | | 81 | ICPL-227 | ICRISAT |
| II | 20 | 2 | BDN-2 | Maharashtra |
| | | 3 | JJAL-15 | Madhya Pradesh |
| | | 4 | MWT-2 | Maharashtra |
| | | 9 | AKT-8912 | Maharashtra |
| | | 16 | JJAL-11 | Madhya Pradesh |
| | | 18 | BDN-1 | Maharashtra |
| | | 23 | KM-79 | Madhya Pradesh |
| | | 25 | ICP-8863 | ICRISAT |
| | | 28 | KM-34 | Madhya Pradesh |
| | | 30 | BWR-23 | Maharashtra |
| | | 33 | ICC-47 | ICRISAT |
| | | 35 | AKT-9013 | Maharashtra |
| | | 39 | AKT-88-11 | Maharashtra |
| | | 45 | PBNA-672 | Maharashtra |
| | | 47 | BDN-699 | Maharashtra |
| | | 73 | ICP-8744 | ICRISAT |
| | | 74 | ICP-8755 | ICRISAT |
| | | 78 | ICP-8752 | ICRISAT |
| | | 79 | ICP-4865 | ICRISAT |
| | | 80 | MRG-66 | Madhira |

Table 9 contd..)

| Cluster No. | No. of accessions | Accession No. | Name of the accession | Place of the origin |
|---|---|---|---|---|
| III | 13 | 6 | Panth-A-8507 | Uttar Pradesh |
| | | 8 | AF-239 | Punjab |
| | | 32 | Pusa-33 | Bihar |
| | | 37 | Panth-A-104 | Uttar Pradesh |
| | | 51 | Pusa-952 | Bihar |
| | | 53 | H-88-25 | Haryana |
| | | 54 | AL-604 | Punjab |
| | | 56 | Pusa-951 | Bihar |
| | | 57 | PA-128 | Not known |
| | | 58 | UPAS-120 | Uttar Pradesh |
| | | 63 | H-90-10 | Haryana |
| | | 64 | H-90-11 | Haryana |
| | | 76 | ICP-4595 | ICRISAT |
| IV | 13 | 10 | KM-33 | Madhya Pradesh |
| | | 12 | Kanakapura Local | Karnataka |
| | | 34 | TTB-7 | Karnataka |
| | | 36 | ES-90 | Karnataka |
| | | 43 | AKT-9221 | Maharashtra |
| | | 48 | Hoskote Local | Karnataka |
| | | 65 | Sel-13 | Karnataka |
| | | 66 | Sel-20 | Karnataka |
| | | 67 | Sel-45 | Karnataka |
| | | 68 | Sel-5 | Karnataka |
| | | 69 | Sel-9 | Karnataka |
| | | 70 | HPL-40 | Haryana |
| | | 72 | ICPl-8357 | ICRISAT |
| V | 4 | 1 | BDN-627 | Maharashtra |
| | | 19 | KM-29 | Madhya Pradesh |
| | | 52 | PA-116 | Not known |
| | | 75 | ICP-9238 | ICRISAT |
| VI | 7 | 22 | ICP-870101 | ICRISAT |
| | | 49 | ICPL-87 | ICRISAT |
| | | 50 | Pusa-953 | Bihar |
| | | 55 | Pusa-955 | Bihar |
| | | 60 | Pusa-954 | Bihar |
| | | 61 | ICPL-85010 | ICRISAT |
| | | 62 | AL-607 | Punjab |

Table 9 contd..)

| Cluster No. | No. of accessions | Accession No. | Name of the accession | Place of the origin |
|---|---|---|---|---|
| VII | 2 | 21 | GAUT-86-20 | Gujarath |
| | | 31 | KM-84 | Madhya Pradesh |
| VIII | 2 | 13 | ICPL-890300 | ICRISAT |
| | | 27 | ICPL-88034 | ICRISAT |
| IX | 1 | 14 | Japan Super | Not known |
| X | 1 | 77 | ICP-5466 | ICRISAT |
| XI | 1 | 46 | Hyd-3C | Karnataka |
| XII | 1 | 59 | KE-71 | Madhya Pradesh |
| XIII | 1 | 15 | ICPl-87091 | ICRISAT |
| XIV | 1 | 40 | T-21 | Uttar Pradesh |

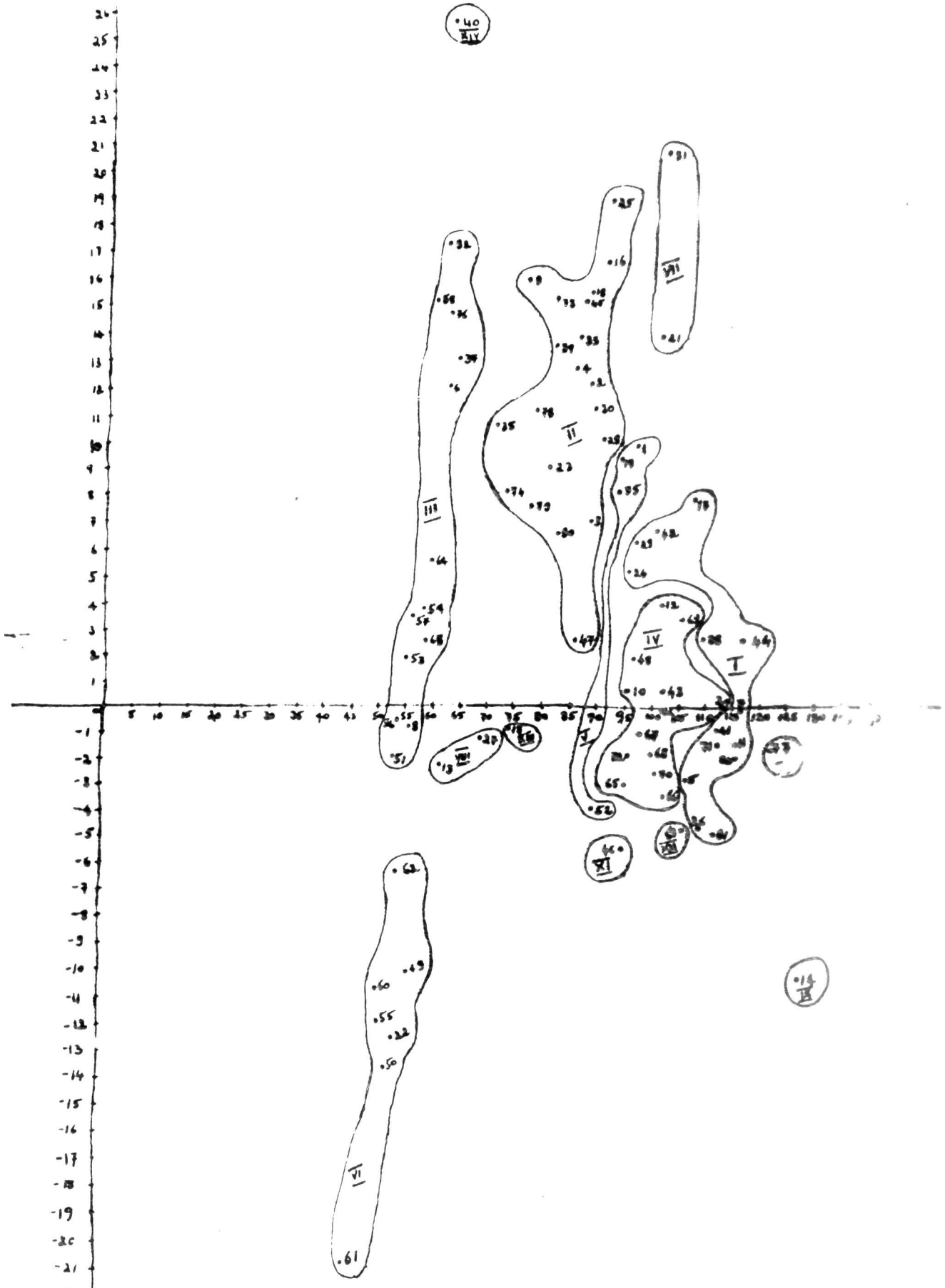


Fig.8:The $D^2$ clusters superimposed on Canonical graph.

Table 10. Inter-cluster (above diagonal) and intra-cluster (diagonal) $D^2$ values for 14 clusters in pigeonpea.

| Cluster No. | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII | XIII | XIV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 259.85 | 979.11 | 2781.39 | 448.92 | 531.76 | 3597.81 | 547.86 | 2183.59 | 947.56 | 480.7 | 936.53 | **389.91** | 2180.27 | 3087.38 |
| II | | 273.09 | 964.61 | 975.20 | 523.60 | 4180.92 | 535.61 | 880.12 | 2606.94 | 1884.98 | 1023.99 | 1057.13 | 1162.38 | 1077.17 |
| III | | | 235.62 | 2653.22 | 1629.81 | 667.69 | 2202.91 | 420.49 | 5438.31 | 4431.15 | 2418.78 | 2697.79 | 1260.85 | 639.54 |
| IV | | | | 335.44 | 678.03 | 3460.37 | 668.94 | 2095.21 | 965.53 | 904.06 | 558.49 | 418.08 | 1893.03 | 2800.00 |
| V | | | | | 271.93 | 2442.76 | 640.44 | 1337.26 | 1952.66 | 1052.15 | 918.42 | 524.07 | 1929.33 | 1845.69 |
| VI | | | | | | **370.74** | 3324.83 | 5567.17 | **6047.34** | 5378.64 | 2710.10 | 3231.26 | 1489.41 | 1764.78 |
| VII | | | | | | | **88.03** | 1967.47 | 1729.17 | 1178.88 | 1198.95 | 814.34 | 1783.98 | 1928.86 |
| VIII | | | | | | | | 150.96 | 2720.85 | 3628.89 | 1516.86 | 2181.44 | 692.98 | 1002.19 |
| IX | | | | | | | | | 0.00 | 651.26 | 1532.69 | 996.59 | 3294.36 | 5853.27 |
| X | | | | | | | | | | 0.00 | 1732.07 | 775.24 | 3735.61 | 4922.58 |
| XI | | | | | | | | | | | 0.00 | 825.78 | 1217.92 | 2273.64 |
| XII | | | | | | | | | | | | 0.00 | 2248.94 | 3054.47 |
| XIII | | | | | | | | | | | | | 0.00 | 1540.14 |
| XIV | | | | | | | | | | | | | | 0.00 |

values ranged from 0.0 (cluster number IX, X, XI, XII, XIII and XIV) to 370.74 (cluster number VI). The other intra-cluster distances lying between these values. There were six solitary clusters viz., IX, X, XI, XII, XIII and XIV possessing single entries in them and had no intra-cluster distances.

The inter-cluster $D^2$ values varied from 389.91 (I and XII) to 6047.34 (VI and IX). The other inter-cluster $D^2$ values were lying between these two values.

# DISCUSSION

# V. DISCUSSION

Improvement through breeding programme in any crop depends on the presence of genetic variability in the germplasm material available. The utility of such material in the germplasm could be judged based on the knowledge of the extent of variability and the genetic diversity available in the material. With a view to estimate the variability and the amount of diversity available in the pigeonpea crop, in the present study, 81 genotypes were evaluated for their genetic potential by studying grain yield and other quantitative characters. The results obtained through statistical analysis of the data are discussed under the following heads.

1. Genetic variability studies
2. Correlations between yield and its components
3. Path coefficient analysis, and
4. Genetic diversity studies

## 5.1 Genetic variability studies

The results of the analysis of variance for the 16 quantitative characters studied revealed highly significant differences among the genotypes both at five per cent and one per cent levels of significance.

Genetic variability is a basic need for breeders to improve the crops by adopting suitable selection criterion

based on type of variability existing in the material. The genotypes exhibited considerable amount of variability for all the 16 characters viz., days to 50 per cent flowering (51.0 to 102.5 days), days to maturity (109.5 to 170.0 days), straw weight (5.76 to 76.51 g), plant height (28.9 to 117.3 cm), branches per plant (5.2 to 13.5), pods per plant (43.0 to 122.1 g), pod weight (14.65 to 50.5 g), pod length (4.5 to 6.5 cm), pod width (0.62 to 0.91 cm), seeds per pod (3.4 to 4.35), yield per plant (6.54 to 38.4 g), shelling per cent (41.93 to 64.6%), length of pod bearing branches (4.6 to 38.36 cm), 100-seed weght (7.1 to 12.7 g), specific gravity (0.75 to 0.84 g/ml) and harvest index (18.76 to 32.76).

The wide range of variation indicates the scope for selection of suitable basic material in breeding for further improvement. The range in the mean values reflects the extent of phenotypic variability present in the material.

The genotypes like, Japan Super, C-11, KE-71, TTB-7, ICPL-87091, ES-90 and BDN-699 can be choosen for further selection, since they exhibited superiority for most of the characters (Table 11).

High phenotypic coefficient of variation was observed for days to 50 per cent flowering, straw weight, plant height, branches per plant, pods per plant, pod weight, yield per plant and length of pod bearing branches; moderate values

Table 11. Elite genotypes for 16 quantitative traits.

| Character | Genotypes |
|---|---|
| $X_1$ | Japan Super (102.50), C-11 (102.50), ICPL-227 (99.00), ICPL-8357 (98.50), KM-61 (98.00) |
| $X_2$ | Japan Super (170.00), ICPL-87119 (167.50), C-11 (167.50), PBNA-672 (166.00), IC-5466 (166.00) |
| $X_3$ | KE-71 (76.51), AKT-9221 (73.76), C-11 (67.14), GAUT-88-24 (65.74), Japan Super (62.28) |
| $X_4$ | KM-84 (177.30), GAUT-86-30 (154.85), KM-34 (146.60), Sel-13 (146.00), PBNA-47-2 (145.70) |
| $X_5$ | ES-90 (13.50), TTB-7 (13.30), Pusa-33 (13.10), PBNA 47-2 (11.60), UPAS-120 (11.50) |
| $X_6$ | ICP-4595 (12.21), ES-90 (120.50), TTB-7 (111.70), Hyd-3C (110.65), Panth-A 8507 (111.35) |
| $X_7$ | KE-71 (50.46), AKT-9221 (47.16), Sel-45 (46.71), TTB-7 (45.50), AKT-9013 (45.18) |
| $X_8$ | ICPL-87091 (6.55), KM-10 (6.16), BDN-699 (6.15), ICPL-890300 (6.13), ICPL-85010 (6.11) |
| $X_9$ | C-11 (0.91), ICPL-87091 (0.91), BDN 699 (0.91), Japan Super (0.86), Panth-A 8507 (0.83) |
| $X_{10}$ | BDN 699 (4.35), ICPL-87091 (4.30), Japan Super (4.25), C-11 (4.25), KM-10 (4.20) |
| $X_{11}$ | KE-71 (38.40), TTB-7 (29.59), AKT-9013 (28.20), ES-90 (28.04), MRG-66 (28.33) |
| $X_{12}$ | MRG-66 (64.63), KE-71 (64.58), Kanakapura Local (64.47), ICPL-84071 (64.26), GAUT 88-24 (63.57) |
| $X_{13}$ | T-21 (38.36), KM-84 (37.80), Pusa-33 (36.70), BDN-627 (33.01), AKT-8912 (32.51) |
| $X_{14}$ | ICPL-87091 (12.70), GAUT 86-30 (12.35), BDN-699 (12.35), ICPL 87119 (12.15) |
| $X_{15}$ | AL-604 (0.84), PBNA-672 (0.82), Sel-5 (0.82), TTB-7 (0.82), C-11 (0.82) |
| $X_{16}$ | Pusa-952 (32.76), AF-239 (32.34), BDN-627 (32.21), Pusa-951 (31.29), H 90-11 (30.96) |

$X_1$ = Days to 50 per cent flowering
$X_2$ = Days to maturity
$X_3$ = Straw weight (g)
$X_4$ = Plant height (cm)
$X_5$ = Branches per plant
$X_6$ = Pods per plant
$X_7$ = Pod weight (g)
$X_8$ = Pod length (cm)
$X_9$ = Pod width (cm)
$X_{10}$ = Seeds per pod
$X_{11}$ = Yield per plant (g)
$X_{12}$ = Shelling per cent
$X_{13}$ = Length of pod bearing branches (cm)
$X_{14}$ = 100-seed weight (g)
$X_{15}$ = Specific gravity (g/ml)
$X_{16}$ = Harvest index

of PCV were observed for days to maturity, pod length, pod width, seed weight and harvest index, whereas, seeds per pod, shelling per cent and specific gravity exhibited low phenotypic coefficient of variability. Breeders cannot depend on the knowledge of phenotypic variability alone to improve the crops. The most important information they have to obtain is the genotypic coefficient of variability, which is heritable and reliable for effective selection. High genotypic coefficient of variability values were observed for days to 50 per cent flowering, straw weight, pods per plant, yield per plant and length of pod bearing branches. Days to maturity, plant height, branches per plant, pod weight, pod width and 100-seed weight showed moderate genotypic coefficient of variability. Low GCV values were observed for pod length, seeds per pod, shelling per cent, specific gravity and harvest index. The results obtained in the present study are in confirmation with the findings of Malhotra and Sodhi (1977), Jagshoran (1983), Balyan and Sudhakar (1985a), Sindhu et al. (1985), Natarajan et al. (1990), Sunil Holkar et al. (1991).

The coefficient values indicated considerable amount of variability existing for all the characters studied except for pod length, seeds per pod, shelling per cent and specific gravity. Very low difference between PCV and GCV values were observed for days to 50 per cent flowering, days to maturity

and seeds per pod indicating little influence of environment on the expression of genotypes. Environmental factors had a moderate influence on all the other characters.

The coefficient of variation reveals the extent of variability present for different characters and it does not indicate the heritable portion. To obtain the magnitude of heritable portion of the variability, it is essential to know the heritability estimates of the different characters. The heritability estimate separates the variance due to environmental effects from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. As such the heritability in broad sense includes both additive and non-additive gene effects (Hanson et al., 1956) were estimated.

Very high heritability estimates were observed for days to 50 per cent flowering, days to maturity, straw weight, pods per plant, pod width, seeds per pod, yield per plant, length of pod bearing branches and 100-seed weight. These results are in confirmity with the findings of Jogshoran (1983), Balyan and Sudhakar (1985a), Natarajan et al. (1990), Sunil-Holkar et al. (1991), Khapre and Nerkar (1992) and Ghodke et al. (1994). The results of these characters revealed considerable genotypic component of variability which might be of much value in the selection programme.

Moderate heritability values were obtained for plant height, branches per plant, pod weight, pod length, shelling per cent, specific gravity and harvest index. This suggests that these traits are prone for considerable influence by extraneous factors.

Heritability estimates in broadsense do not serve as true indicator of the genetic potentiality of the genotypes, since their scope is restricted by their interaction with the environment. It is advisable to consider the predicted genetic advance along with heritability estimates as a tool in the selection programme for better efficiency in selection.

High heritability estimates with high genetic advance were noticed for days to 50 per cent flowering, straw weight, pods per plant, pod width, yield per plant, length of pod bearing branches and 100-seed weight. The characters days to maturity and seeds per pod have shown high heritability with moderate genetic advance. These findings are in concordant with those of Jagshoran (1983), Balyan and Sudhakar (1985a), Sindhu et al. (1985), Natarajan et al. (1990) and Sunil-Holkar et al. (1991). High heritability and genetic advance might be due to additive gene action, while non-additive and additive gene interactions could be associated with characters possessing high heritability estimates coupled with moderate genetic advance. Moderate heritability

estimates coupled with high genetic advance were noticed for plant height, branches per plant and pod weight. The characters pod length and harvest index have shown moderate heritability estimates with moderate genetic advance, while shelling per cent and specific gravity showed moderate heritability with low genetic advance indicating lesser proportion of genotypic component in the total variability, suggesting, these traits might be conditioned by non-additive gene effects and thus selection based on these characters may not be effective.

In general, high estimates of genotypic and phenotypic coefficient of variability, heritability and genetic advance as per cent of mean were observed for days to 50 per cent flowering, straw weight, pods per plant, yield per plant and length of pod bearing branches.

## 5.2 Correlation between yield and its components

The phenotype of a plant is the result of interaction of a large number of factors. Therefore, the final yield is the sum total of all the effects of several component characters and thus it is a polygenically controlled character. These characters may be either related positively or negatively with each other and yield. Genetic correlation between various plant characters may arised because of linkage, pleiotrophy or developmentally induced functional

relationships (Harland, 1939). In the present investigation, both genotypic and phenotypic correlations were worked out for yield and its contributing characters.

Days to 50 per cent flowering, days to maturity, straw weight, plant height, branches per plant, pods per plant, pod weight, pod width, seeds per pod, shelling per cent and 100-seed weight exhibited significant positive association with grain yield at both genotypic and phenotypic levels. Earlier investigators also reported simiar results in pigeonpea (Balyan and Sudhakar, 1985; Patil et al., 1989; Henry and Krishna, 1990; Natarajan et al., 1990; Jahargirdar et al., 1991; Patel and Patel, 1992; Viramgama and Goyal, 1994; Byre Gowda et al., 1996). The magnitude of association between grain yield and pod weight was the highest at both the levels in positive directions.

Days to 50 per cent flowering showed positive significant correlation with grain yield and all the other characters. These results are in confirmity with the findings of Holkar et al. (1991) and Ganesh Murthy and Stephan Dorairaj (1990). Days to maturity also showed significant association with grain yield and its components. This is in accordance with the findings of Chaudhary et al. (1988), Ganesh Murthy and Stephan Dorairaj (1990), Khapre and Nerkar (1992) and Gamber et al. (1996).

Positive correlation was found between straw weight and grain yield and most of its component characters. It suggests that selection for higher straw weight is desirable. This corroborates with the findings of Merkar and Nerkar (1987a), Balakrishnan and Natarajarathnam (1989), Khapre and Nerkar (1992) and Paul et al. (1996).

Plant height showed positive significant association with grain yield and all the component characters except pod length, seeds per pod and harvest index. The results indicated that tall lines are likely to be effective in breeding for high yield. Earlier investigators also reported similar results in pigeonpea (Natarajan et al., 1990; Khapre and Nerkar, 1992; Patel and Patel, 1992; Viramgama and Goyal, 1994; Byre Gowda et al., 1996).

Branches per plant exhibited a positive and significant assocation with grain yield and other yield components except pod length, length of pod bearing branches, specific gravity and harvest index. So selection for higher branching genotypes is desirable. Similar reports were made by Ganesh Murthy and Stephan Dorairaj (1990), Henry and Krishna (1990), Viramgama and Goyal (1994) and Paul et al. (1996).

Pods per plant had a positive significant association with grain yield per plant. This was in confirmity with the findings of Holkar et al. (1991), Jahargirdar et al. (1991),

Khapre and Nerkar (1992), Patel et al. (1992), Viramgama and Goyal (1994), Byre Gowda et al. (1996) and Paul et al. (1996). Pod weight showed significant positive association with grain yield per plant and other component characters. This corroborates with the findings of Bhongale et al. (1987).

Pod width was positively and significantly correlated with grain yield and other yield components except with plant height, pods per plant, specific gravity and harvest index, where it was non-significant.

Seeds per pod showed significant positive association withu grain yield and all other yield components except, plant height, specific gravity and harvest index. This was in confirmity with the findings of Henry and Krishna (1990) and Byre Gowda et al. (1996). So, selection of genotypes which produces more number of seeds per pod is beneficial.

Hundred seed weight manifested a positive significant association with grain yield and other components except pods per plant, length of pod bearing branches and specific gravity. So, selection for higher test weight is likely to improve the grain yield per plant (Holkar et al., 1991; Jahargirdar et al., 1991; Viramgama and Goyal, 1994; Byre Gowda et al., 1996).

Pod length exhibited non-significant positive association with grain yield. This is in confirmity with the findings of Viramgama and Goyal (1994). This character also had positive significant association with pod weight, seeds per pod and 100-seed weight and interestingly had negative and significant association with length of pod bearing branches.

Harvest index showed significant and negative association days to 50 per cent flowering, days to maturity, straw weight and 100-seed weight. This is in confirmity with the findings of Merkar and Nerkar (1987a) and Ganesh Murthy and Stephan Dorairaj (1990).

While reviewing the studies on correlations, it has been observed that strength and direction of correlation in different character combinations depends on the nature of the experimental material and environmental condition in which they have been studied (Falconer, 1960). However, in pigeonpea, based on the present study, it can said that more emphasis should be given for pod weight, straw weight, pod per plant, branches per plant, shelling per cent, plant height, days to 50 per cent flowering, days to maturity, seeds per pod, pod width and 100 seed weight, as they showed very high degree of positive correlation with grain yield.

## 5.3 Path coefficient analysis

The estimation of correlation coefficients do not consider the dependence of one variable on another independent variable. Path coefficient analysis first suggested by Wright (1921) and later demonstrated its use in plant selection by Dewey and Lu (1959) being a statistical tool provides an effective measure of direct and indirect effect of contributing traits to the final product i.e., grain yield. In order to obtain cause and effect relationship between yield per se and eight yield contributing components were studied in pigeonpea through path coefficient analysis was carried out and the results are discussed below.

Pod weight showed the highest positive direct effect (0.881) on grain yield. This is in accordance with the findings of Merkar and Nerkar (1987a), Paul et al. (1996) and Paul and Upadhyaya (1991). The pod weight had low positive indirect influence on grain yield through days to 50 per cent flowring, plant height, branches per plant, pods per plant and seeds per pod.

The other components, days to 50 per cent flowering (0.0579), plant height (0.0629), pods per plant (0.0233) and seeds per pod (0.0045) had low positive direct effects on grain yield. Their indirect effects via pod weight alone was moderate to very high as evident from the Table 5.

Days to maturity (-0.0026) and 100-seed weight (-0.011) had very low negative direct effects on grain yield. These characters also showed very low indirect influence through other characters except pod weight.

So, improvement of pod weight would be mainly helpful in increasing the grain yield in these genotypes.

## 5.4 Genetic diversity studies

For an effective breeding programme, the precise information about the extent of genetic divergence is very crucial. To know the spectrum of diversity, the assemblage and assessment of divergence in the germplasm is essential.

The multivariate analysis is utilized for quantifying the degree of divergence between populations to understand the trend of evolutionary pattern and to assess the relative contribution of different components to the total divergence. The application of multivariate analysis to measure divergence between biological population has been successfully established by many workers (Nair and Mukherji, 1960; Murthy et al., 1965; Arunachalam and Ram, 1967; Ram and Panwar, 1970; Shawe et al., 1972; Narayan and Macefield, 1976).

Genetic diversity between populations is the result of difference in gene frequencies and any measure of genetic divergence must reflect these difference.

Phenotypic diversity is usually considered as an indication of underlying genetic differences. However, in recent years the success and usefulness of multivariate technique in quantification of genetic diversity has been demonstrated.

To assess the diversity in the population of diverse origin, usually two important methods viz., canonical variate analysis and Mahalanobis $D^2$ statistic are employed. The application of $D^2$ statistic in finding diverse parents for hybridization to be more efficient than choosing parents based on ecogeographic diversity (Ram and Panwar, 1970; Ziauddin Ahmed et al., 1980; Hazarika and Singh, 1986).

In the present study, 81 genotypes of pigeonpea were included for the assessment of nature of genetic diversity by multivariate analysis.

In the canonical variate analysis the number of variables were reduced to a linear functions called canonical vectors which accounts for most of the variations produced by these variables. The first two canonical vectors accounted 82.52 per cent of the total variability produced by all sixteen characters under study (Table 7). The first two canonical vectors were used to obtain graphical depiction of the genetic distances of the 81 genotypes. Days to 50 per cent flowering, plant height, pod width, length of pod

bearing branches and harvest index were the variables which contributed to the genetic diversity. Similar results were reported by Viramgama and Goyal (1994), Santos et al. (1994), Sarma and Roy (1994), Sandhu et al. (1993) and Singh and Govil (1988).

The 81 entries have been spatially distributed on the canonical graph indicating that a great deal of diversity in the germplasm. Accession-61 (ICPL-85010) and 40 (T-21) were found most divergent (Fig. 8). These entries showed wide differences in their mean performance across all the 16 characters (Appendix 1).

The arbitrary clustering of the entries on the canonical graph resulted in 15 clusters. It was observed that there was no perfect pattern of association between the origin of the entry and the cluster in which it was included. It is because of such of the entries which did not remain isolated as separate entries representing the diversified geographic regions of their origin were grouped in clusters possessing entries from heterogenous origin and is due to overlapping and gene flow in the material. Hence, there was no apparent parallelism between the genetic divergence and the geographic origin. This could be due to the free movement of the breeding material from place to place (Shwe et al., 1972; Mehindritta et al., 1971; Sarvaliya and Goyal, 1994; Viramgama and Goyal, 1994; Jaghshoran, 1989).

## $D^2$ analysis

In the Mahalanobis $D^2$ analysis, actual genetic distance between the entries were estimated.

Based on the $D^2$ values, 81 genotypes were grouped into 14 clusters (Table 9). It was observed that there is no perfect relation between genetic diversity and geographic diversity as evident from the grouping of varieties from heterogenous geographic origin in one cluster. It could be because of the free exchange of breeding material from one place to another. Similar results were obtained by Arunachalam and Ram (1967) in sorghum and by Viramgama and Goyal (1994) and Jagshoran (1989) in pigeonpea.

Out of 14 clusters, 6 were solitary and may be due to their geographic barriers preventing gene flow among those genotypes.

The $D^2$ clusters were superimposed on the canonical graph and a comparison of this with the canonical variate analysis was made. The absence of exact similarity between $D^2$ cluster and canonical variate anlaysis is due to the fact that the clustering through $D^2$ analysis is based on the criteria fixed subjectively whereas, in canonical variate analysis, it is based on the arbitrary scale. But the results of canonical variate analysis and $D^2$ analysis were almost similar indicating the perfect agreement of clusters

formed through them. Similar results of similarity between the clusters of the two types of analysis were reported by Arunachalam and Ram (1967), Shwe et al. (1972) and Singh (1991).

Out of the six solitary clusters formed, the three clusters viz., cluster IX (Japan Super), XI (Hyd-3C) and XII (KE-71) were found to be superior with respect to grain yield and other yield attributes as revealed from cluster means for 16 traits (Table 12).

Inter-cluster and intra-cluster $D^2$ values

The inter-cluster and intra-cluster $D^2$ values are given in Table 10. The intra-cluster $D^2$ value of any cluster is less than the intercluster $D^2$ value of any two closely related clusters. The intra-cluster $D^2$ values ranged from 88.03 (cluster VII) to 370.74 (cluster VI). The inter-cluster $D^2$ values ranged from 389.91 (between cluster I and XII) to 6047.34 (between cluster VI and IX). Six entries remained as solitary clusters.

It could be concluded that significant genetic diversity exists among the 81 genotypes selected for study for most of the important characters. This could be attributed to long term selection in different direction by both natural and human forces.

Table 12. Mean values of the 16 characters for the 14 clusters.

| | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 87.86 | 158.18 | 46.46 | 123.88 | 9.51 | 74.73 | 34.15 | 5.29 | 0.76 | 3.88 | 20.63 | 59.44 | 20.28 | 10.39 | 0.80 | 25.87 |
| II | 71.48 | 152.33 | 38.48 | 119.85 | 8.44 | 73.01 | 31.45 | 5.06 | 0.73 | 3.71 | 18.65 | 58.81 | 27.52 | 9.56 | 0.80 | 26.98 |
| III | 62.54 | 142.04 | 31.58 | 110.26 | 9.18 | 75.03 | 29.91 | 5.24 | 0.73 | 3.83 | 17.09 | 56.00 | 21.54 | 8.72 | 0.81 | 28.65 |
| IV | 82.27 | 152.27 | 51.96 | 131.91 | 10.14 | 86.47 | 39.57 | 5.19 | 0.75 | 3.88 | 22.88 | 59.99 | 22.89 | 9.74 | 0.80 | 26.49 |
| V | 76.25 | 148.13 | 30.76 | 102.96 | 7.35 | 82.65 | 29.87 | 4.86 | 0.64 | 3.68 | 16.32 | 57.64 | 24.53 | 8.26 | 0.79 | 27.15 |
| VI | 65.29 | 135.43 | 25.76 | 82.14 | 6.85 | 57.26 | 22.84 | 5.3 | 0.75 | 3.71 | 12.34 | 51.46 | 39.99 | 9.35 | 0.81 | 25.62 |
| VII | 83.75 | 162.00 | 57.37 | 166.08 | 7.25 | 66.05 | 32.42 | 5.23 | 0.76 | 3.58 | 19.68 | 60.62 | 34.38 | 11.08 | 0.80 | 21.80 |
| VIII | 71.00 | 153.00 | 30.23 | 97.28 | 8.02 | 69.10 | 29.27 | 5.63 | 0.70 | 4.03 | 16.60 | 56.46 | 21.17 | 8.83 | 0.81 | 27.96 |
| IX | 102.25 | 170.00 | 62.28 | 126.10 | 9.60 | 75.50 | 39.60 | 5.68 | 0.86 | 4.25 | 23.36 | 59.05 | 21.51 | 10.85 | 0.81 | 23.38 |
| X | 82.00 | 166.00 | 47.46 | 128.30 | 9.70 | 94.60 | 32.83 | 4.66 | 0.68 | 3.70 | 19.70 | 60.13 | 25.80 | 8.00 | 0.81 | 24.62 |
| XI | 68.00 | 150.50 | 43.89 | 112.40 | 7.50 | 110.65 | 43.40 | 5.58 | 0.82 | 3.95 | 24.79 | 59.62 | 24.54 | 10.50 | 0.80 | 29.23 |
| XII | 93.50 | 147.00 | 76.51 | 130.80 | 11.00 | 110.00 | 54.15 | 5.05 | 0.74 | 3.80 | 38.40 | 64.58 | 29.35 | 9.25 | 0.80 | 25.48 |
| XIII | 68.00 | 157.00 | 45.91 | 103.70 | 9.50 | 52.10 | 34.53 | 6.59 | 0.91 | 4.30 | 19.74 | 57.44 | 21.50 | 12.70 | 0.81 | 24.62 |
| XIV | 53.50 | 139.00 | 39.91 | 126.00 | 9.10 | 102.50 | 35.55 | 5.45 | 0.73 | 3.60 | 19.45 | 53.88 | 38.36 | 9.20 | 0.80 | 26.74 |

$X_1$ = Days to 50 per cent flowering
$X_2$ = Days to maturity
$X_3$ = Straw weight (g)
$X_4$ = Plant height (cm)
$X_5$ = Branches per plant
$X_6$ = Pods per plant
$X_7$ = Pod weight (g)
$X_8$ = Pod length (cm)
$X_9$ = Pod width (cm)
$X_{10}$ = Seeds per pod
$X_{11}$ = Yield per plant (g)
$X_{12}$ = Shelling per cent
$X_{13}$ = Length of pod bearing branches (cm)
$X_{14}$ = 100-seed weight (g)
$X_{15}$ = Specific gravity (g/ml)
$X_{16}$ = Harvest index

Genetic divergence studies aids in the choice of suitable parents for hybridization for realising heterosis. In the present study, it is observed that considerable amount of genetic diversity is present amongst the entries in respect of yield and yield attributes. The intercrossing of the genotypes should generate large variability and selection could be adopted for high yielding varieties.

Six solitary clusters were observed to be superior, such superior clusters are cluster IX (Japan Super), X (ICP-5466), XI (Hyd-3C), XII (KE-71), XIII (ICPL-87091) and XIV (T-21). The inter-crossing of these diverse genotypes would generate heterotic effect and broad spectrum of variability in the segregating generation and selection could be adopted for identification of superior segregants for the development of high yielding cultivars.

# SUMMARY

## VI. SUMMARY

Eighty one genotypes of pigeonpea (*Cajanus cajan*) were evaluated in a simple lattice design with two replications based on 16 characters to ascertain the variability, correlation, path coefficient analysis of yield and yield contributing components and the magnitude of genetic diversity.

Wide range of variations were observed for the characters studied. The analysis of variance revealed significant differences among the genotypes for all the characters studied. Phenotypic coefficient of variability was found to be higher magnitude than the genotypic coefficient of variability. The PCV values were high for the characters days to 50 per cent flowering, straw weight, plant height, branches per plant, pods per plant, pod weight, yield per plant and length of pod bearing branches. Moderate values of PCV were obtained for days to maturity, pod length, pod width, 100-seed weight and harvest index. PCV values were low for seeds per pod, shelling per cent and specific gravity. High genotypic coefficient of variation was observed for the characters days to 50 per cent flowering, straw weight, pods per plant, yield per plant and length of pod bearing branches and the characters such as days to maturity, plant height, branches per plant, pod weight, pod width and 100-seed weight exhibited moderate values of GCV.

Heritability estimates in broadsense were very high for days to 50 per cent flowering, days to maturity, straw weight, pods per plant, pod width, seeds per pod, yield per plant, length of pod bearing branches and 100-seed weight. The characters plant height, branches per plant, pod weight, pod length, shelling per cent, specific gravity and harvest index have shown moderate heritability values.

The expected genetic advance was high for days to 50 per cent flowering, straw weight, plant height, branches per plant, pod weight, pod width, yield per plant, length of pod bearing branches and 100-seed weight. The characters days to maturity, pod length, seeds per pod and harvest index have shown moderate genetic advance values. The remaining characters have shown low genetic advance.

Grain yield had a significant positive correlation with days to flowering, days to maturity, straw weight, plant height, branches per plant, pods per plant, pod weight, pod width, seed per pod, shelling per cent and 100-seed weight. The characters pod length and harvest index exhibited positive but non-significant association with grain yield. Specific gravity had non-significant negative association with grain yield per plant.

The path coefficient analysis was carried out for the characters which exhibited highly significant associations

with grain yield. The study revealed maximum positive direct effect of pod weight on grain yield. Low positive direct effects were observed for the characters days to 50 per cent flowering, plant height, branches per plant, seeds per pod. The direct effects of days to maturity and 100-seed weight were low but negative. Days to 50 per cent flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod registered high positive indirect influences through pod weight. The indirect influence of 100-seed weight via pod weight was moderate.

It is evident from the canonical variate analysis and $D^2$ analysis that, 81 genotypes were found to account for greater magnitude of genetic diversity. In the canonical variate analysis, the first two canonical vectors accounted for 82.52 per cent of the total variability produced by all the 16 characters. Days to 50 per cent flowering, plant height, pod width, length of pod bearing branches and harvest index were found to be the most important characters contributing towards genetic diversity in the population. Hence, these potent variables could be used as parameters in selecting genetically diverse parents for hybridization programme. In $D^2$ analysis 14 clusters were resulted, out of which second cluster was the biggest having 20 genotypes followed by cluster number one consisting of 14 entries, cluster number three and four with 13 entries each and all

the other clusters were either small or solitary clusters. There were almost similar resutls obtained by both canonical variate and $D^2$ analysis with respect to clustering of the entries. The intra-cluster generalised distance (370.74) was maximum for cluster VI. The highest inter-cluster generalised distance (6047.34) was recorded between clusters VI and IX, while the clsuters I and XII were the least divergent (389.91). The lines included in these clusters were identified as promising for hybridization on the basis of divergence.

The findings of the present study are significant in the improvement of pigeonpea as it throws spectrum of diversity in the crop. The inter-crossing of the genotypes showing diversity should result in generating sufficient variability to operate selection in segregating populations. The study resulted in the identification of six solitary clusters representing widely diverse types with respect to the yield and yield component characters studied. The inter-crossing of these genotypes should result in generating sufficient variability to operate selection in segregating populations. The genotypes like Japan Super, C-11, K-71, ICPL-87091 and BDN-699 can be choosen for further selection. It is expected that from this study pigeonpea varieties can be synthesized to increase the production substantially.

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## VII. REFERENCES


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* = Original not seen.

# APPENDICES

APPENDIX-I

The mean values of 16 characters for the 81 pigeonpea genotypes

| Sl. No | Name of the genotype | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. | BDN-627 | 84.50 | 157.00 | 28.19 | 140.30 | 8.90 | 98.00 | 32.85 | 4.75 | 0.71 | 3.65 | 20.53 | 62.52 | 33.01 | 9.95 | 0.75 | 32.21 |
| 2. | BDN-2 | 81.00 | 160.50 | 54.08 | 129.00 | 7.70 | 92.75 | 36.15 | 5.16 | 0.73 | 3.60 | 21.89 | 60.36 | 32.45 | 9.45 | 0.78 | 24.22 |
| 3. | JJAL-15 | 78.00 | 151.00 | 42.32 | 126.90 | 7.30 | 92.00 | 32.15 | 4.51 | 0.62 | 3.60 | 20.13 | 62.57 | 27.20 | 8.30 | 0.81 | 27.01 |
| 4. | MWT-2 | 73.00 | 161.50 | 42.10 | 141.60 | 8.30 | 75.93 | 35.11 | 5.20 | 0.81 | 3.85 | 20.43 | 58.23 | 28.70 | 9.90 | 0.79 | 26.52 |
| 5. | ICPL-87051 | 73.50 | 157.00 | 37.87 | 112.20 | 8.80 | 57.30 | 28.05 | 5.60 | 0.74 | 3.90 | 16.71 | 59.14 | 22.55 | 10.15 | 0.81 | 25.27 |
| 6. | Panth-A 8507 | 68.50 | 150.50 | 44.74 | 119.20 | 10.60 | 111.35 | 44.70 | 5.41 | 0.83 | 3.90 | 26.52 | 59.30 | 25.79 | 10.28 | 0.82 | 28.84 |
| 7. | JJAL-16 | 74.00 | 143.50 | 31.98 | 99.60 | 8.70 | 54.50 | 23.90 | 5.08 | 0.71 | 3.70 | 13.57 | 54.65 | 14.10 | 9.48 | 0.81 | 25.45 |
| 8. | AP-239 | 54.00 | 130.00 | 13.31 | 94.80 | 8.50 | 51.00 | 19.98 | 5.50 | 0.72 | 3.90 | 10.72 | 53.78 | 21.15 | 8.30 | 0.79 | 32.34 |
| 9. | AKT-8912 | 67.50 | 151.00 | 39.91 | 134.95 | 8.60 | 72.33 | 31.84 | 4.99 | 0.69 | 3.65 | 18.35 | 57.04 | 32.51 | 9.00 | 0.81 | 25.56 |
| 10. | KM-33 | 79.00 | 162.00 | 60.36 | 127.70 | 8.00 | 89.45 | 34.46 | 5.10 | 0.70 | 3.85 | 20.45 | 59.56 | 30.00 | 9.55 | 0.79 | 22.50 |
| 11. | ICPL-87119 | 98.00 | 167.50 | 46.59 | 134.10 | 10.30 | 49.20 | 24.20 | 4.60 | 0.75 | 3.45 | 14.29 | 59.09 | 19.95 | 12.85 | 0.77 | 20.51 |
| 12. | Kanakapura Local | 91.00 | 162.00 | 54.51 | 142.60 | 11.30 | 99.60 | 33.36 | 4.81 | 0.74 | 3.75 | 25.38 | 64.47 | 21.05 | 9.45 | 0.80 | 26.91 |
| 13. | ICPL-890300 | 67.50 | 155.50 | 31.31 | 107.05 | 8.13 | 59.00 | 28.81 | 6.13 | 0.75 | 4.20 | 15.92 | 54.26 | 18.29 | 9.90 | 0.81 | 26.42 |
| 14. | Japan Super | 102.50 | 170.00 | 62.28 | 126.10 | 9.60 | 75.50 | 39.36 | 5.68 | 0.86 | 4.25 | 23.36 | 59.05 | 21.51 | 10.85 | 0.81 | 23.38 |
| 15. | ICPL-87091 | 68.00 | 157.00 | 45.91 | 103.70 | 9.50 | 52.10 | 34.53 | 6.55 | 0.91 | 4.30 | 19.74 | 57.44 | 21.50 | 12.70 | 0.81 | 24.62 |
| 16. | JJAL-11 | 62.00 | 146.50 | 35.08 | 118.85 | 7.70 | 84.50 | 32.40 | 5.08 | 0.72 | 3.70 | 17.62 | 51.72 | 24.65 | 8.02 | 0.80 | 27.85 |
| 17. | GAUT 88-24 | 93.50 | 157.00 | 65.74 | 142.30 | 11.30 | 80.10 | 42.36 | 5.50 | 0.81 | 4.05 | 26.93 | 63.57 | 22.20 | 10.35 | 0.80 | 24.93 |
| 18. | BDN-1 | 69.50 | 154.00 | 38.74 | 125.10 | 7.60 | 64.20 | 29.29 | 4.64 | 0.74 | 3.40 | 16.57 | 56.33 | 31.03 | 9.30 | 0.81 | 24.89 |
| 19. | KM-29 | 78.00 | 151.00 | 41.34 | 125.70 | 8.30 | 91.30 | 32.30 | 4.72 | 0.62 | 3.50 | 19.94 | 62.03 | 26.22 | 7.95 | 0.80 | 27.12 |
| 20. | SPMA-11 | 91.00 | 159.50 | 57.84 | 135.60 | 11.40 | 97.00 | 36.92 | 4.76 | 0.74 | 3.70 | 22.60 | 61.35 | 19.72 | 8.70 | 0.80 | 23.79 |
| 21 | GAUT 86-30 | 83.00 | 162.00 | 59.72 | 154.85 | 6.80 | 49.10 | 26.99 | 5.15 | 0.77 | 3.65 | 16.28 | 60.29 | 30.95 | 12.35 | 0.79 | 18.76 |
| 22 | ICPL-87010 | 65.00 | 140.00 | 24.64 | 103.30 | 6.30 | 47.10 | 24.55 | 5.67 | 0.80 | 3.80 | 13.69 | 54.15 | 19.15 | 10.75 | 0.80 | 27.92 |
| 23. | KM-79 | 76.50 | 154.00 | 35.29 | 69.20 | 8.20 | 77.10 | 32.55 | 4.99 | 0.73 | 3.60 | 19.98 | 60.26 | 30.95 | 9.90 | 0.79 | 28.22 |
| 24. | ICPL-92002 | 82.00 | 156.00 | 51.84 | 137.20 | 9.30 | 81.50 | 40.56 | 5.44 | 0.77 | 3.70 | 24.15 | 59.45 | 22.12 | 11.00 | 0.80 | 25.99 |
| 25. | ICP-8863 | 63.50 | 140.00 | 35.58 | 116.30 | 7.90 | 66.14 | 24.00 | 5.06 | 0.70 | 3.95 | 14.47 | 59.11 | 30.15 | 8.70 | 0.79 | 25.92 |

Appendix-I contd..)

| Sl. No | Name of the gedotype | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 26. | GS-1 | 93.50 | 154.00 | 40.05 | 125.10 | 10.40 | 62.65 | 36.26 | 5.66 | 0.82 | 4.05 | 21.83 | 59.94 | 20.51 | 10.35 | 0.80 | 28.31 |
| 27. | ICPL-88034 | 74.50 | 150.50 | 29.14 | 92.50 | 7.90 | 79.20 | 29.72 | 5.12 | 0.64 | 3.85 | 17.39 | 58.65 | 24.05 | 7.75 | 0.81 | 29.50 |
| 28. | KM-34 | 73.00 | 162.00 | 40.67 | 146.60 | 6.80 | 77.55 | 37.25 | 5.26 | 0.79 | 3.90 | 22.34 | 60.04 | 29.20 | 11.10 | 0.78 | 28.67 |
| 29. | KM-10 | 67.00 | 157.00 | 33.15 | 107.09 | 8.00 | 57.70 | 28.16 | 6.16 | 0.74 | 4.20 | 16.41 | 57.82 | 17.41 | 10.50 | 0.80 | 26.79 |
| 30. | BWR-23 | 63.50 | 145.50 | 22.93 | 101.30 | 7.30 | 43.00 | 24.20 | 5.64 | 0.80 | 3.85 | 13.65 | 55.64 | 20.65 | 10.45 | 0.79 | 29.59 |
| 31. | KM-84 | 84.50 | 162.00 | 55.01 | 177.30 | 7.70 | 83.00 | 37.85 | 5.30 | 0.75 | 3.50 | 23.07 | 60.94 | 37.80 | 9.80 | 0.81 | 24.84 |
| 32. | Pusa-33 | 53.50 | 138.00 | 36.01 | 125.10 | 13.10 | 100.80 | 36.16 | 5.43 | 0.72 | 3.65 | 19.70 | 54.43 | 36.70 | 8.75 | 0.81 | 27.22 |
| 33. | ICC-47 | 63.50 | 142.50 | 31.69 | 99.70 | 9.00 | 45.00 | 22.54 | 5.35 | 0.81 | 3.50 | 13.52 | 60.02 | 21.80 | 10.40 | 0.83 | 25.74 |
| 34. | TTB-7 | 72.50 | 152.00 | 56.42 | 136.00 | 13.30 | 111.70 | 45.50 | 5.62 | 0.75 | 3.95 | 29.59 | 60.58 | 24.95 | 9.30 | 0.82 | 28.60 |
| 35. | AKT-9013 | 79.00 | 151.00 | 46.98 | 138.10 | 10.90 | 84.50 | 45.18 | 5.10 | 0.71 | 4.00 | 28.20 | 60.54 | 23.09 | 10.15 | 0.80 | 29.99 |
| 36. | ES-90 | 68.50 | 140.50 | 50.07 | 134.80 | 13.50 | 120.50 | 43.58 | 4.66 | 0.75 | 3.80 | 28.04 | 63.20 | 24.33 | 8.15 | 0.80 | 29.90 |
| 37. | Panth-A-104 | 72.50 | 157.00 | 39.05 | 114.40 | 9.30 | 59.30 | 28.07 | 5.37 | 0.73 | 3.90 | 17.05 | 60.63 | 24.40 | 9.95 | 0.81 | 26.01 |
| 38. | C-11 | 102.50 | 167.50 | 67.14 | 124.00 | 9.00 | 78.45 | 39.26 | 5.77 | 0.82 | 4.25 | 23.98 | 61.02 | 27.82 | 10.75 | 0.82 | 22.85 |
| 39. | ATK-88-11 | 76.50 | 154.50 | 39.39 | 140.50 | 9.00 | 78.90 | 36.32 | 4.95 | 0.72 | 3.70 | 23.07 | 63.21 | 30.15 | 10.00 | 0.78 | 30.78 |
| 40. | T-21 | 53.50 | 139.00 | 39.91 | 126.00 | 9.10 | 102.50 | 35.55 | 5.45 | 0.73 | 3.60 | 19.45 | 53.88 | 38.36 | 9.20 | 0.80 | 26.74 |
| 41. | KM-61 | 98.00 | 161.50 | 46.33 | 142.00 | 8.00 | 89.00 | 40.16 | 4.73 | 0.75 | 3.60 | 24.74 | 61.60 | 23.35 | 10.15 | 0.80 | 28.61 |
| 42. | PBNA-47-1 | 67.50 | 146.50 | 31.74 | 87.100 | 8.90 | 66.70 | 24.65 | 5.56 | 0.74 | 3.75 | 13.06 | 49.97 | 15.25 | 10.25 | 0.81 | 22.46 |
| 43. | AKT-9221 | 94.00 | 148.50 | 73.76 | 133.60 | 9.00 | 86.80 | 47.16 | 5.18 | 0.75 | 3.85 | 23.20 | 59.53 | 27.65 | 9.50 | 0.81 | 23.14 |
| 44. | PBNA-47-2 | 92.00 | 162.00 | 46.80 | 145.70 | 11.60 | 92.15 | 42.30 | 4.91 | 0.76 | 4.05 | 26.70 | 62.74 | 19.93 | 10.40 | 0.81 | 29.77 |
| 45. | PBNA-672 | 89.50 | 166.00 | 45.45 | 135.00 | 9.48 | 97.50 | 33.22 | 4.55 | 0.66 | 3.60 | 20.46 | 61.69 | 27.45 | 8.25 | 0.82 | 26.38 |
| 46. | Hyd-3C | 68.00 | 150.50 | 43.89 | 112.40 | 7.50 | 110.65 | 43.40 | 5.58 | 0.82 | 3.95 | 24.79 | 59.62 | 24.54 | 10.50 | 0.80 | 29.23 |
| 47. | BDN-699 | 69.00 | 158.00 | 45.10 | 106.70 | 9.10 | 50.00 | 33.61 | 6.15 | 0.91 | 4.35 | 21.09 | 58.00 | 21.00 | 12.35 | 0.81 | 24.86 |
| 48. | Hoskote Local | 81.50 | 152.50 | 51.36 | 134.90 | 10.20 | 80.80 | 40.28 | 5.49 | 0.75 | 3.70 | 23.10 | 57.60 | 22.25 | 11.65 | 0.79 | 25.22 |
| 49. | ICPL-87 | 63.50 | 143.50 | 27.19 | 98.80 | 8.40 | 43.90 | 19.20 | 5.09 | 0.79 | 3.50 | 11.51 | 60.61 | 23.25 | 9.86 | 0.82 | 25.54 |
| 50. | Pusa-953 | 66.50 | 146.00 | 34.38 | 83.40 | 7.05 | 69.70 | 25.55 | 5.30 | 0.72 | 3.70 | 14.59 | 54.13 | 15.55 | 9.95 | 0.81 | 23.53 |

Appendix-I contd..)

| Sl. No | Name of the genotype | $X_1$ | $X_2$ | $X_3$ | $X_4$ | $X_5$ | $X_6$ | $X_7$ | $X_8$ | $X_9$ | $X_{10}$ | $X_{11}$ | $X_{12}$ | $X_{13}$ | $X_{14}$ | $X_{15}$ | $X_{16}$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 51. | Pusa-952 | 53.00 | 130.00 | 11.00 | 71.00 | 6.00 | 58.70 | 20.99 | 5.42 | 0.72 | 3.70 | 10.49 | 49.96 | 20.80 | 7.75 | 0.83 | 32.76 |
| 52. | PA-116 | 66.00 | 125.00 | 27.84 | 53.20 | 6.00 | 63.50 | 26.14 | 4.89 | 0.62 | 3.60 | 10.48 | 49.14 | 15.65 | 7.10 | 0.80 | 21.16 |
| 53. | H-88-25 | 69.50 | 140.50 | 42.20 | 121.90 | 9.40 | 71.20 | 32.95 | 5.35 | 0.77 | 3.85 | 19.75 | 56.62 | 19.75 | 9.20 | 0.80 | 26.84 |
| 54. | AL-604 | 59.00 | 143.00 | 19.42 | 99.30 | 8.30 | 47.80 | 16.80 | 4.88 | 0.66 | 3.50 | 9.02 | 52.33 | 23.98 | 8.30 | 0.84 | 25.53 |
| 55. | Pusa-955 | 74.50 | 145.50 | 33.56 | 97.00 | 7.40 | 54.80 | 25.30 | 5.04 | 0.73 | 3.80 | 14.55 | 56.51 | 14.00 | 9.55 | 0.81 | 26.00 |
| 56. | Pusa-951 | 62.50 | 150.50 | 31.96 | 119.05 | 7.60 | 82.70 | 32.26 | 5.03 | 0.70 | 3.70 | 18.97 | 56.69 | 24.30 | 8.05 | 0.79 | 31.29 |
| 57. | PA-128 | 65.50 | 142.00 | 32.66 | 116.05 | 9.20 | 63.70 | 26.55 | 5.15 | 0.69 | 3.80 | 15.63 | 56.61 | 28.75 | 8.80 | 0.81 | 27.10 |
| 58. | Upas-120 | 72.50 | 148.00 | 54.16 | 127.30 | 11.50 | 80.40 | 42.73 | 5.57 | 0.75 | 4.15 | 23.61 | 55.64 | 24.10 | 8.90 | 0.80 | 26.14 |
| 59. | KE-71 | 93.50 | 147.00 | 76.51 | 130.80 | 11.00 | 110.00 | 50.46 | 5.05 | 0.74 | 3.80 | 38.40 | 64.58 | 29.35 | 9.25 | 0.80 | 25.48 |
| 60. | Pusa-954 | 66.00 | 123.00 | 27.82 | 52.80 | 5.40 | 62.80 | 20.86 | 5.01 | 0.62 | 3.80 | 9.47 | 45.15 | 13.90 | 7.26 | 0.80 | 19.34 |
| 61. | ICPL-85010 | 51.00 | 109.50 | 5.76 | 28.90 | 5.20 | 47.90 | 15.61 | 6.11 | 0.78 | 3.80 | 6.54 | 41.93 | 4.60 | 8.40 | 0.82 | 30.65 |
| 62. | AL-607 | 70.50 | 140.50 | 26.99 | 110.80 | 8.20 | 74.60 | 28.79 | 4.95 | 0.78 | 3.60 | 16.04 | 48.77 | 17.55 | 9.70 | 0.80 | 26.36 |
| 63. | H-90-10 | 59.50 | 142.50 | 26.92 | 106.30 | 8.50 | 76.80 | 29.12 | 5.01 | 0.71 | 3.65 | 15.74 | 52.60 | 21.80 | 8.61 | 0.81 | 28.22 |
| 64. | H-90-11 | 54.50 | 134.00 | 11.36 | 89.10 | 7.20 | 49.50 | 16.87 | 5.39 | 0.74 | 3.85 | 8.63 | 51.14 | 22.20 | 8.60 | 0.79 | 30.96 |
| 65. | Sel-13 | 93.50 | 157.00 | 60.42 | 146.60 | 10.90 | 75.80 | 39.84 | 5.39 | 0.80 | 4.15 | 24.12 | 60.54 | 20.70 | 9.80 | 0.82 | 24.09 |
| 66. | Sel-20 | 93.50 | 154.50 | 43.87 | 124.90 | 8.20 | 59.65 | 32.77 | 5.52 | 0.81 | 4.00 | 19.08 | 57.39 | 21.07 | 11.05 | 0.80 | 24.55 |
| 67. | Sel-45 | 80.50 | 156.00 | 48.28 | 133.00 | 9.18 | 84.50 | 46.71 | 5.34 | 0.72 | 4.15 | 27.41 | 57.37 | 23.30 | 9.75 | 0.80 | 29.12 |
| 68. | Sel-5 | 91.00 | 158.50 | 50.51 | 142.50 | 10.10 | 81.85 | 40.38 | 4.75 | 0.69 | 3.95 | 25.41 | 62.47 | 18.80 | 10.30 | 0.82 | 27.81 |
| 69. | Sel-9 | 69.50 | 138.50 | 41.36 | 128.35 | 9.20 | 68.70 | 32.15 | 5.41 | 0.75 | 3.85 | 19.67 | 59.42 | 21.55 | 9.00 | 0.80 | 27.99 |
| 70. | HPL-40 | 71.50 | 139.50 | 31.89 | 115.35 | 8.90 | 67.40 | 32.00 | 5.02 | 0.77 | 3.65 | 18.07 | 51.55 | 17.50 | 9.40 | 0.81 | 26.89 |
| 71. | ICPL-8357 | 98.50 | 162.00 | 40.24 | 130.70 | 7.50 | 72.60 | 32.36 | 5.10 | 0.75 | 3.80 | 20.41 | 63.06 | 23.93 | 9.51 | 0.80 | 28.11 |
| 72. | ICPL-84071 | 83.50 | 158.00 | 52.64 | 115.18 | 10.07 | 97.40 | 40.26 | 5.11 | 0.72 | 3.85 | 25.85 | 64.26 | 24.39 | 9.70 | 0.79 | 27.61 |
| 73. | ICP-8744 | 67.50 | 152.00 | 34.87 | 128.20 | 9.85 | 73.63 | 30.26 | 4.90 | 0.71 | 3.65 | 16.32 | 53.97 | 32.81 | 9.70 | 0.81 | 25.08 |
| 74. | ICP-8755 | 69.00 | 153.50 | 35.21 | 120.50 | 8.20 | 62.20 | 25.90 | 4.61 | 0.74 | 3.40 | 15.51 | 58.34 | 31.25 | 9.70 | 0.80 | 24.62 |
| 75. | ICP-9238 | 76.50 | 147.50 | 25.66 | 92.70 | 6.20 | 77.80 | 28.19 | 5.06 | 0.62 | 3.95 | 14.33 | 56.85 | 23.25 | 8.05 | 0.80 | 28.12 |
| 76. | ICP-4595 | 68.50 | 140.50 | 47.77 | 129.90 | 10.10 | 122.10 | 41.63 | 4.63 | 0.73 | 3.70 | 26.38 | 62.29 | 25.28 | 7.85 | 0.80 | 29.23 |
| 77. | ICP-5466 | 88.00 | 166.00 | 47.46 | 128.30 | 9.70 | 94.60 | 32.83 | 4.66 | 0.68 | 3.70 | 19.70 | 60.13 | 25.80 | 8.00 | 0.81 | 24.62 |
| 78. | ICP-8752 | 61.50 | 143.00 | 21.01 | 97.10 | 7.70 | 44.70 | 14.65 | 4.80 | 0.63 | 3.50 | 8.34 | 56.88 | 23.88 | 8.10 | 0.82 | 25.33 |
| 79. | ICP-4865 | 59.00 | 144.00 | 28.87 | 103.80 | 7.70 | 77.80 | 28.60 | 5.25 | 0.63 | 3.65 | 17.91 | 57.53 | 19.10 | 8.55 | 0.80 | 29.90 |
| 80. | MRG-66 | 82.50 | 156.00 | 57.32 | 118.30 | 10.40 | 100.40 | 43.76 | 5.03 | 0.71 | 3.80 | 28.33 | 64.63 | 22.40 | 9.74 | 0.80 | 28.22 |
| 81. | ICPL-227 | 99.00 | 163.50 | 39.32 | 130.10 | 9.90 | 107.30 | 47.21 | 5.15 | 0.75 | 3.65 | 23.25 | 58.49 | 20.08 | 10.95 | 0.81 | 29.34 |