ASSESMENT OF GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY FOR YIELD AND ITS ATTRIBUTING TRAITS IN PIGEON PEA (*Cajanus cajan* L. Millsp.)

THESIS

Submitted in partial fulfilment of the requirements
for the Degree of

MASTER OF SCIENCE

IN

AGRICULTURE

(GENETICS AND PLANT BREEDING)

By

BURHADE SANKET TULSIDAS
(ADPM/21/2811)

DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, DAPOLI

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NOVEMBER, 2023

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Under the Guidance of

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DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation of the thesis entitled **"Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea (*Cajanus cajan* L. Millsp.)"** or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged and that no part of the thesis has been submitted for any other degree or diploma.

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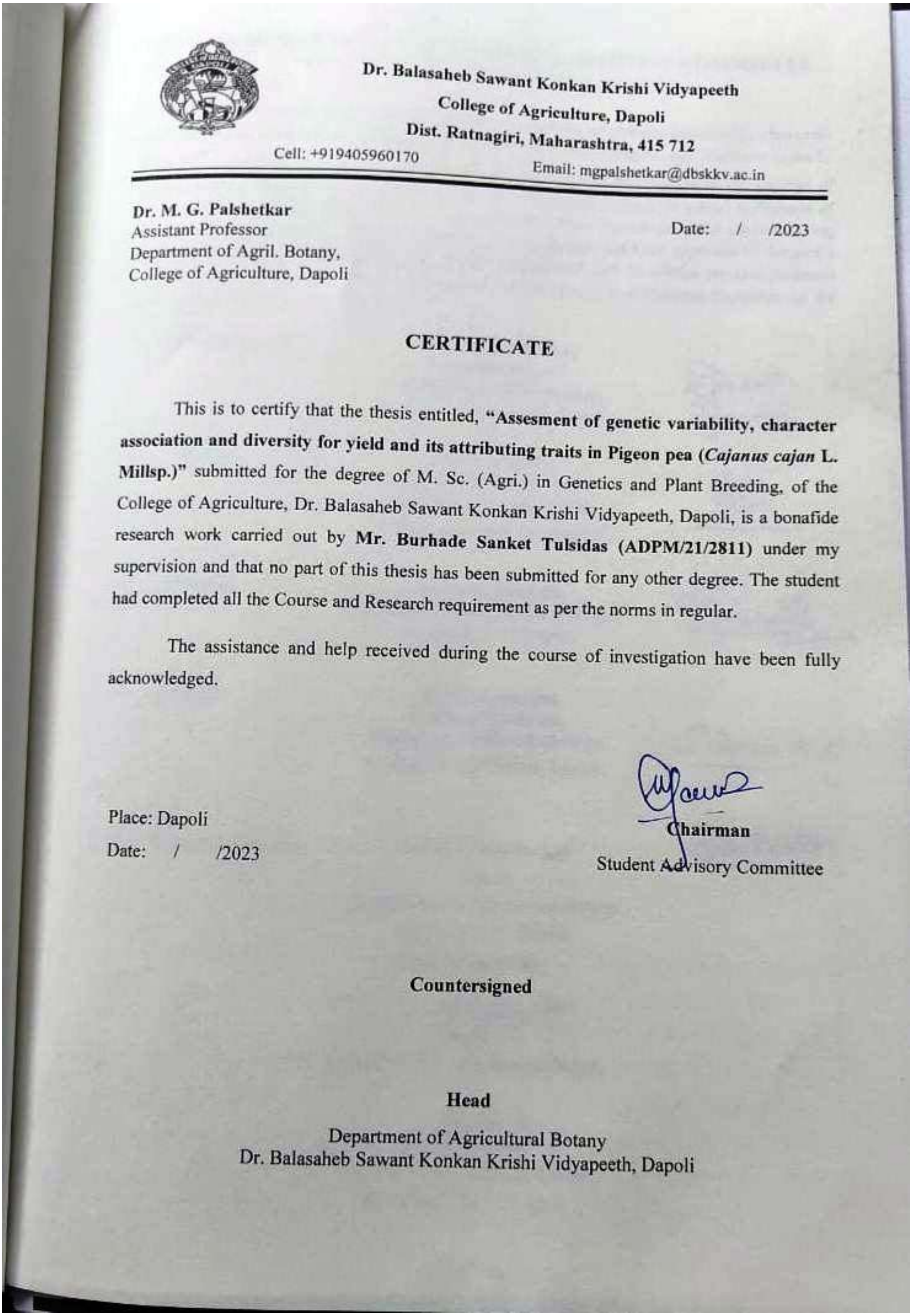

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The assistance and help received during the course of investigation have been fully acknowledged.

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This is to certify that the thesis entitled, **"Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea (*Cajanus cajan* L. Millsp.)"** submitted by **Mr. Burhade Sanket Tulsidas (ADPM/21/2811)** to the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, in partial fulfillment of the requirements for the degree of M.Sc. (Genetics and Plant Breeding) in the subject having Plant Physiology as Minor subject of Department Agril. Botany has been approved by Student's Advisory Committee, Board of Studies of the Department and Evaluated by One External Examiner after an open Viva Voice examination in the presence of External Examiner on the same held on dated २१ / ११ / 2023.

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Date: / / 2023 **(Burhade Sanket Tulsidas)**

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ABBREVIATIONS USED

% : Per cent
> : Greater than
< : Less than
* : Significant at 5% level of significance
** : Significant at 1% level of significance
ANCOVA : Analysis of covariance
ANOVA : Analysis of variance
@ : At the rate of
^{0}C : Degree Celsius
C.D. : Critical Difference
Cm : Centimetre
d.f. : Degree of freedom
EMS : Error mean sum of squares
Err. : Error
et al. : And others
m : Million
g : Grams
GCV : Genotypic coefficient of variance
PCV : Phenotypic coefficient of variance
ha : Hectare
h^2 : Heritability
i.e., : That is
K : Potassium
MSS : Mean sum of squares
N : Nitrogen
CV : Coefficient of Variation
S.E. : Standard error
SS : Sum of squares
viz., : Namely
GAM : Genetic advance as per percentage of mean
RBD : Randomized block design

Glossary

Genetic Variability: Genetic variability is either the presence of or the generation of genetic differences.

Heritability: Heritability is the amount of phenotypic (observable) variation in a population that is attributable to individual genetic differences.

Genotype: Genotype is the genetic makeup of an individual cell or organism that determines or contributes to its phenotype.

Genetic advance: Genetic advance is a measure of how much gain you may get from phenotypic selection for a trait.

Path analysis: Path analysis is a method to discern and assess the effects of a set of variables acting on a specified outcome via multiple causal pathways.

Genetic diversity: Genetic diversity is the biological variation that occurs within species.

Konkan: Konkan is the 700 km long rugged section of the western coast line of Arabian Sea which extends from Daman in the North to western side land of Maharashtra and Goa.

CHAPTER I

INTRODUCTION

Background Information:-

Pulse crop plays an important role in the Indian economy. They are often referred to as “poor man’s meat”, since they are a cheaper source of high-quality protein. Grain legumes or pulses occupy an important place in human’s food and nutritional requirements. They are important constituents in the diets of a very large number of people, especially in the developing countries and are a good source of protein which helps to supplement cereal diets, improving their nutritive values. The presence of different types of proteins and their smaller molecules, including alkaloids, isoflavones, polyphenols and a variety of oligosaccharides, make legume seeds unique in providing nutraceuticals. For centuries a combination of cereals and pulses has been a good source of improved nutrition for people all over the world. Besides, pulses are also important for increasing soil health through biological nitrogen fixation with sustainability of the cropping system, crop diversification and natural resource management.

It is cultivated worldwide on 5.40 m ha with an annual production of 4.48 m t and mean productivity of 827 kg ha-1 (FAOSTAT, 2021). In India, pigeon pea is cultivated on 3.88 m ha with a production of 2.84 m t and productivity of 733 kg ha^{-1} (FAOSTAT, 2021). In Maharashtra pigeon pea was cultivated on 20.98 Lha with total production of 12.66 LT during 2021. (Source-Kharif prospects, Bhopal)

The name pigeon pea was first reported for plants used in Barbados where seeds were considered most useful as feed for pigeons. In India, the Sanskrit name ‘Adhuka’ or ‘Adhaki’ became arhar, the ‘Dravidian Tuvarai’ or ‘Tuviri’, (used in Sanskrit since 300-400 AD) became Tur (Lal and Singh, 1998). Presently, Pigeon pea is known by several trade names such as Arhar, Redgram, Tur, Angola pea and Congo pea etc. Hooker (1879) classified the genus *Cajanus* into a single species, *Cajanus indicus,* whereas, Duthie and Fuller (1883) reported two species, *Cajanus flavors* and *Cajanus bicolor* under the genus Cajanus and were called as ‘tur’ and ‘arhar,’ respectively.

Pigeon pea is usually grown in tropical/subtropical in a wide range of soils (from sandy to heavy soils, pH of 5.0 to 8.0) and can not tolerate even light frost during any stage of its growth, however, it appears to be better adapted to marginal climatic conditions as compared to the other pulse crops.

The poor productivity of pigeon pea in Konkan region might be due to cultivation of traditional landraces by the farmer’s, which frequently suffer from several biotic and abiotic stresses resulting in poor yield. Due to high rainfall and water logging condition production of pigeon pea is affected. Improper agronomic practices, such as, low plant population, inadequate fertilizer application, insufficient weeding and inappropriate use of fungicides and herbicides are the other constraints limiting the productivity besides, environmental (low temperature, frequent drought, easily erodible soils with poor water holding capacity) and socio- economic (lack of roads, marketing infrastructure and exploitation by middlemen) factors. Outbreak of severe pest is one of the reason for poor productivity of pigeon pea in Konkan region. Soil type also plays an important role in production of pigeon pea.

Among various grain legumes grown, pigeon pea (*Cajanus cajan (L.))* is the second most important crop of India, belonging to family- fabaceae, subfamily-faboideae, tribe-Phaseoleae, subtribe-cajaninae, genus – *Cajanus* and species – *cajan* with chromosome number 2n = 22. According to Vander Maesen (1990) pigeon pea originated in India and spread to other countries quite early endowed with several unique characteristic. Based on the vast natural genetic variability in local germplasm and the presence of numerous wild relatives, the centre of origin is africa from where it travelled to East Africa and by means of the slave trade to the American continent. The genus, *Cajanus* comprises 32 species, of which 17 species are distributed in Asia, 14 in Australia, and one in West Africa. Of these, *Cajanus cajan* is the only domesticated species and *Cajanus cajanifolius* is supposed to be the most probable progenitor of pigeonpea through single gene mutation. Besides, eleven related genera including Rhynchosia, Eriosema, Dunbaria, Flemingia, and Paracalyx have been described in the subtribe, Cajaninae (van der Maesen, 1990).

It is an important grain legume mostly being cultivated in Africa, Asia and America. It is mostly consumed as dry split dal besides several other uses of various parts of pigeon pea plant. It is an excellent source of protein, supplementing energy rich cereal diets in a mainly vegetarian population.

Importance and need of the study:-

In Konkan region of Maharashtra, Pigeon pea is commonly cultivated on bunds of rice fields during *kharif* season. The aim of the experiment is to develop high yielding, early maturing varieties which acclimatize with climatic conditions of Konkan region. This study helps to find high yielding genotypes with low infestation of pod borer.

Pigeon pea is a hardy, widely adapted and drought tolerant crop. It has a range of maturity which helps in its adaptation in a wide range of environments and cropping systems. It is grown either as a sole crop or intercrop with urd bean, mung bean, castor, sorghum, soybean, cotton, maize and groundnut. Being drought tolerant and hardy crops, they can thrive well on marginal and less fertile soils under poor management and rainfed conditions. Moreover, they fix atmospheric nitrogen with the help of Rhizobium spp., releases soil-bound phosphorus, recycles the soil nutrients and adds organic matter and other nutrients and has potential to utilize limited moisture and nutrients available in soil. Thus, with all unique characters, Swaminathan (1981) has termed pulses as "Unique Jewels' ' in Indian crop husbandry.

The protein content of commonly grown pigeon pea cultivars ranges between 17.9-24.3 g 100-1 (Salunkhe *et al*., 1986) for whole grain samples and between 21.1-28.1 g 100-1 for split seed. Wild species of pigeon pea have been found to be a promising source of high protein content; genotypes have been developed with a protein content as high as 32.5% (Singh *et al*., 1990). The high dietary fibre in pigeon pea lowers risk of diabetes, heart ailments and gastrointestinal diseases. Pigeon pea also provides a substantial amount of micronutrients such as vitamin E, vitamin B6, folic acid, iron, potassium, magnesium, calcium, phosphorus, sulphur and zinc. Pigeon pea comes to the rescue of millions of people from clutches of chronic malnutrition as it is a cheap and easily accessible source of protein and micronutrients for the majority of the vegetarian population. Pigeon pea is also used as fodder, feed, fuel, functional utility (for making baskets, huts, fences, etc.), fertilizer (fixes atmospheric nitrogen and releases phosphorus), forest use (reforestation, lac production) and even for pharmaceutical purposes (Mula and Saxena, 2010).

Objectives of the study: -

Keeping in view, the above important aspects, the present investigation was carried out with following objectives:

1. To ascertain the extent of variability present in germplasm lines for yield and its attributing characters.
2. To estimate Correlation and Path coefficient for yield and its related traits.
3. To study the nature and extent of diversity among genotypes.

Hypothesis: -

This study helps to select prominent genotypes for future breeding programmes.

Scope and limitations of the study: -

Scope - This study helps in development of high yielding varieties with early maturing and tolerance to pod borer. Pigeon pea is grown on bunds of rice fields in Konkan region. Due to a lack of irrigation infrastructure during the Rabi season, farmers are reluctant to produce pigeon pea crop.

There is a scarcity of early duration varieties suitable for Konkan conditions during *Kharif* season. In *Kharif* season there is abundant rainfall and vegetative growth in Konkan region but yield and production is not in that proportion. This study helps to find out early maturing varieties with high yield and production.

Non-adoption of improved management practices and lack of proper scientific research have turned out to be the low productivity and production. Now a days, per capita per day consumption of pulses has declined to about 30 g as against 80 g recommended by WHO and FAO (FAOSTAT, 2021). Since the demand for pigeon pea is ever increasing and area available for expansion is limited, research now needs to focus on the genetic enhancement of yield through novel genetic approaches for achieving higher production and productivity of pigeon pea.

Limitation:

1) Pigeon pea is often a cross-pollinated crop, it is an entomophilous crop and it’s difficult to maintain the genetic purity.
2) Pod borer is a more severe pest of pigeon pea in the Konkan region of Maharashtra.
3) Affects survival of seedlings under water logging conditions.

CHAPTER II

REVIEW OF LITERATURE

Pigeon pea (*Cajanus cajan* (L.) Millsp) is a leguminous crop belonging to the family Fabaceae and is one of the important *kharif* pulse crops grown in India. India and Central Asia are the centres of origin of Pigeon pea. However, a thorough understanding of the genetic diversity between populations is very important for any crop improvement programme to be successful. The available literature on Pigeon pea have been reviewed under the following headings:

1. Genetic Variability

2. Correlation and Path coefficient

3. Genetic Diversity

1. To ascertain the extent of variability present in germplasm lines for yield and its attributing characters.

The success of any breeding programme depends upon the extent and magnitude of genetic variability existing in the germplasm. The assessment of variability present in the crop helps in successful utilization of plant characters for developing suitable variety for yield and stability. Variability studies enable the breeder in determining most suitable genotypes for selection using genetic parameters like genetic coefficient of variation, heritability and genetic advance. The reports available on variability of various characters in Pigeon pea are given below;

Singh *et al.* (2013) studied significant variability for all the traits under study. UPAS 120 yielded the highest seed yield per plant (39.21 g), followed by ICPL 88034 (35.66 g) and PA 134 (35.65 g). The high yield of UPAS 120 was attributed by high number of seeds per pod and pod length. Similarly, high yield of ICPL 88034 was contributed by primary branches per plant, pod length and 100-seed weight. The range of PCV was observed from 4.56 to18.59 % for the traits under study which provides a picture of the extent of phenotypic variability in the population. The PCV was notes moderate for the characters like seed yield per plant (18.59 %), followed by pods per plant (18.04%) and primary branches per plant (12.22%). Maximum GCV was observed for seed yield per plant (17.84%) followed by pods per plant (17.80) and primary branches per plant (10.94).

Kumar *et al.* (2014) studied 38 genotypes of Pigeon Pea for genetic variability. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2 b), genetic advance and correlation for yield and its attributes were computed. The minimum difference between PCV and GCV values for all characters indicated minimum environmental influence. Moderate to high PCV and GCV were recorded for days to fifty percent flowering (DFF) (27.41, 25.64), number of pods per plant (30.69, 2.06), number of seed (19.39, 18.23), grain yield (34.13, 29.42) and straw yield (26.24, 25.03). Respectively the characters *viz*. DFF, test weight, pod length and number of primary branches showed high heritability along with moderate or low genetic advance and could be improved by inter mating superior genotypes of population developed from combination breeding. Out of 38, eight genotypes *viz*., ICPL 87 (3.72 t/ha), Manak (3.59 t/ha), BSMR-736 (3.67 t/ha), BSMR-853 (3.36 t/ha), MAL-13 (3.15 t/ha), GC-11-39 (3.17 t/ha), NDA-1 (2.92 t/ha) and Virsa Bahar (2.81 t/ha) were found promising for yield and yield contributing traits.

Ali *et al.* (2015) evaluated hundred pigeon pea genotypes tested in a 10 × 10 simple lattice design. The objectives of the study were to estimate the genetic variability and heritability. The analysis of variance revealed a highly significant difference ($p \leq 0.01$) for most traits. High phenotypic (PCV) and genotypic coefficient of variation (GCV) was recorded for harvest index and biomass yield per plant. High heritability coupled with high expected genetic advance as percent of mean was recorded for 100-seed weight, seed yield per plot, plant height, biomass yield per plant and harvest index. Therefore, the present study indicated that there is sufficient genetic variability in pigeon pea germplasm that could be used as a base for improvement of the yield and other important attributes of this crop through direct selection and hybridization.

Ekka and Tigg (2019) carried out an investigation with 16 genotypes of pigeon pea for genetic variability studies. The analysis of variance revealed significant differences among the genotypes for all the characters studied except number of pods per cluster. Seed yield and number of seeds per pod had the high magnitude of genotypic coefficient of variation and phenotypic coefficient of variation which is an indicative of the genetic variability that exists in the Pigeon pea genotypes. The high magnitude of heritability was recorded for the seed yield and number of secondary branches per plant. Genetic advance as percentage of mean was recorded as high for the seed yield, number of seeds per pod and number of secondary branches per plant. High heritability coupled with high genetic advance was found for seed yield, number of seeds per pod and number of secondary branches per plant which indicated the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters.

Patro *et al.* (2019) carried out research including early duration variety to study the variability at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *Kharif*, 2018. High variability was recorded for grain yield indicating ample variation which can be further exploited. Grain yield also recorded high heritability coupled with high GAM indicating preponderance of additive gene action. Days to 50% flowering also recorded high heritability and high GAM and these two traits are highly and significantly associated in positive direction. High yielding varieties are more expected in late maturing varieties, however, LRG 274 which is an early duration variety can be utilized in future breeding to develop early maturing high yielding varieties.

Rao and Rao (2019) studied the genetic variability in 24 Pigeon pea [*Cajanus cajan* (L.) Mill sp.] Genotypes. Analysis of variance revealed the existence of significant differences among genotypes for all characters studied. The magnitude of PCV and GCV was moderate to high for the number of pods per plant, number of branches per plant. High heritability was recorded for test weight, days to maturity, days to 50% flowering, and number of pods per plant. High heritability combined with high genetic advance was recorded for test weight and number of pods per plant, indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purposes.

Patel and Patel (2020) studied variability in pigeon pea genotypes. Two genotypes i.e NP 09-41 and NP-09-46 recorded white colour and the same genotypes are identified as high yielder too. While other genotypes are light, reddish or dark brown in colour These traits can be used for identifying individual germplasm. Ten genotypes were grouped into two major groups. Five genotypes grouped under 1st group and the other five genotypes grouped under 2nd. NP-09-46, 43, 49, 47 and 50 falls under the first group while NP-09-41, 48, 44, 45 and 42 falls under another group. Based on per se performance genotype *viz*., NP-09-43, Np-09-41, NP-09-46 and NP-09-49 recorded highest yield per hectare and medium duration genotype recorded as NP-09-45 and 47. Hence, it can be considered that high yielding genotypes are grouped under 1st while in second group medium yielding genotypes are grouped representing high genetic variability among the germplasm.

Rao and Rao (2020) evaluated Forty-eight Pigeon pea genotypes for yield and yield component characters indicated the existence of considerable genetic variation in the present investigation. The components of variance revealed that the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. Heritability in broad sense was higher in most of the characters *viz*., test weight, days to maturity, days to 50 per cent flowering, seed yield per plant, number of pods per plant and number of branches per plant. High heritability coupled with high genetic advance as percent of mean was observed for seed yield per plant, number of pods per plant and test weight indicating the role of the additive gene in expressing these traits.

Sahu and Ekka (2020) evaluated sixty genotypes of Pigeon pea for genetic variability, heritability and genetic advance. Analysis of variance revealed that the mean sum of squares due to genotypes were highly significant for all the characters indicating existence of sufficient variability among the genotypes. Among the different yield attributing traits, the number of pods per cluster had the highest magnitude of GCV and PCV. The high magnitude of GCV and PCV was observed for number of pods per cluster followed by secondary branches per plant number of pod clusters per plant, number of pods per plant, seed yield per plant which is an indicative of the genetic variability exists in the pigeon pea germplasm accessions. High heritability coupled with high genetic advance as percentage of mean was found for number of pods per cluster, secondary branches per plant, number of pod clusters per plant, number of pods per plant, seed yield per plant, which indicated that the predominance of additive gene action in the expression of these characters

Fousiya *et al.* (2021) studied genetic variability among sixty-four vegetable pigeon pea genotypes for ten quantitative and quality traits. Highly significant differences existed among the genotypes for all the ten characters studied. Phenotypic coefficients of variation (PCV) were found higher than the genotypic coefficient of variation (GCV) for all the traits. PCV and GCV values were moderate for the traits *viz*., fresh pod length, fresh pod width, the number of beans per pod, bean length, bean width, protein content and fibre content. High heritability was observed for fresh pod length, fresh pod width, the number of beans per pod, hundred fresh bean weight and total soluble sugars. High heritability coupled with high genetic advance as per cent of mean was observed for fresh pod length, fresh pod width, hundred fresh bean weight and total soluble sugars indicating the additive gene effect. The genotypes *viz*., CVPP-20-002, CVPP-20-023, CVPP-20-017, CVPP-20-031, CVPP-20-032 and CVPP-20-061 showed a good performance for quantitative and nutritional traits and were superior over the check varieties. The promising genotypes identified for different vegetable traits could be used in the breeding programme to develop vegetable/dual purpose varieties in pigeon pea.

Hussain *et al.* (2021) studied 20 pigeon pea extra- early introgression lines along with the checks in RCBD for genetic variability and other genetic parameters for 10 agronomic traits. High heritability coupled with high genetic advance was observed for days to flowering, days to 50% flowering, days to maturity, plant height, the number of pods per plant, pod weight per plant, and grain yield per plant, signifying that these traits are governed by additive gene action. Simple selection may be useful for these traits. Further, using PCA analysis, it was found that these traits are ideal for pigeon pea improvement through the selection. Promising lines *viz*., ICPP 171540, ICPP 171541, ICPP 171542, ICPP 171546, ICPP 171556, ICPP 171559, ICPP 171561, ICPP 171564, ICPP 171566, ICPP 171578, ICPP 171579, and ICPP 171581, and ICPP 171578 were identified in extra-early determinate groups. These promising lines should be evaluated in multi-season/ location for further utilization.

Pashwan *et al.* (2021) examined the genotypic and phenotypic variation, genotypic and phenotypic coefficient of variation, heritability (h^2) and genetic advance. The genotypes of all traits studied showed significant variability, and the analysis of variance showed that there were highly significant differences among the 12 pigeon pea genotypes of the 14 quantitative traits studied. From the current investigation it is concluded that among the 12 pigeon pea genotypes based on average yield, 912, 901, 902, and 907 were found superior and showed the maximum seed yield. Among these 12 genotypes, they were found to provide the best results for 912. The maximum genotype and phenotypic variation of plant height and harvest index were recorded. Record the maximum GCV and PCV of each plant, the number of pods per plant, and the weight of each pod. The high heritability of seed yield, plant height, harvest index, number of pods per plant and seed yield per plant were recorded for each plot. High heritability and high genetic progress are recorded as a percentage of the average seed yield for each plot.

Bhagat *et al.* (2022) studied variability, in 16 genotypes of pigeon pea. The results indicated that the genotypes showed significant variability for all the traits studied. The components of variance revealed that the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. The highest GCV and PCV was recorded for seed yield followed by biological yield. Heritability in broad sense was higher in most of the characters *viz*., number of pods per plant followed by seed yield^{-1}, number of primary branches per plant, number of seeds per pod, pod length, days to 50% flowering, number of pods per cluster, days to maturity and days to flower initiation. Seed yield, biological yield, number of pods per cluster, pod length and number of primary branches per plant all had the highest genetic advance as a percentage of mean. It suggests that these characters are controlled by additive gene activity and that selection will aid in the growth of similar characters.

Mourya *et al.* (2022) evaluated 34 pigeon pea genotypes for genetic variability study during the year 2021- 2022. The analysis of variance revealed that there was a significant amount of variation for all the characters. Days to maturity, plant height, number of secondary branches, days of 50% flowering, 100 seed weight, number of primary branches, biological yield, seed yield per plant, harvest index, number of pods per plant and number of seeds per pod showed high heritability value. High estimate of (phenotypic coefficient of variance and genotypic coefficient of variance) PCV and GCV were observed for the number of secondary branches, number of primary branches and days to maturity while moderate estimate of PCV and GCV were observed for plant height, 100 seed weight, days to 50% flowering, seed yield per plant, number of pods per plant and harvest index.

2. To estimate Correlation and Path coefficient for yield and its related traits.

Correlation studies are useful in developing an effective basis of phenotypic selection in plant populations; it may also be helpful for minimising the number of attributes for which simultaneous selection must be exercised. Correlation study measures the mutual relationship between various characters and helps in determining the component characters on which selection can be used for improvement in yield. The reports available on correlation of various characters in Pigeon pea are given below;

Jaggal *et al.* (2012) studied the correlation and path coefficient analysis for 14 characters in 135 pigeon pea (*Cajanus cajan* (L.) Millsp) genotypes. The positive and significant association was recorded by the characters *viz*., harvest index and straw yield among themselves and also with seed yield. However, negative and significant association was noticed by plant height, days to fifty per cent flowering and days to maturity against seed yield at both genotypic and phenotypic levels. Plant height, days to fifty per cent flowering and days to maturity exhibited positive and significant association among themselves at both genotypic and phenotypic levels. The characters *viz*., number of branches per plant, days to fifty per cent flowering, days from flowering to maturity and test weight exhibited the positive direct effects at genotypic and phenotypic path coefficient levels.

Nag and Sharma (2012) studied 45 pigeon pea germplasm lines for path coefficient. The path coefficient analysis revealed that, the number of pod clusters plant $^{-1}$ had the highest direct effect on seed yield. Whereas, the characters namely number of pods plant^{-1} and days to maturity had the highest indirect effect on seed yield *via* the character's number of pods plant^{-1} and days to 50% flowering.

Saroj *et al*. (2013) estimated the phenotypic and genotypic correlation and path coefficient, for grain yield and yield traits in 70 pigeon pea genotypes. Correlation and Path coefficient analysis (genotypic and phenotypic) revealed that pods per plant (0.858*), 100-seed weight (0.370), days to 50% flowering (0.458*), primary branches (0.357*) and secondary branches (0.302*) had maximum direct effect resulting in significant positive correlation with grain yield per plant. These traits can be used to improve the grain yield of pigeon pea.

Techale *et al.* (2013) estimated correlation coefficients and path coefficients on yield and its contributing traits. Seed yield had positive and significant phenotypic and genotypic association with plant height, biomass yield per plant, pods per plant, seeds per plant, days to maturity, days to flowering, seeds per pod, reproductive phase and seed yield per plant. Phenotypic path analysis showed that, days to maturity had the highest positive direct effect on seed yield followed by plant height and seeds per plant whereas; genotypic path analysis revealed that, maximum direct effect on seed yield was exerted by days to flowering and reproductive phase followed by seeds per plant and plant height. Thus, seeds per plant and plant height were the potent contributors to seed yield which could be used as indirect selection criteria. The results from correlation and path coefficient analyses showed that selection for yield improvement through days to flowering, plant height, seeds per plant, pod filling duration and biomass yield per plant appeared promising.

Pandey *et al.* (2016) evaluated 23 Pigeon pea genotypes in a randomized block design during *Kharif* 2012–13. The objective of this research was to assess inter-relationships, direct and indirect effects among yield and its components for genetic improvement of pigeon pea. The analysis of variance revealed highly significant differences for all characters under study among the genotypes. Considering the correlation analysis, biological yield per plant, pods per plant, 100-seed weight, harvest-index and secondary branches per plant had highly significant positive correlation with seed yield. Path analysis identified biological yield per plant followed by harvest-index, pods per plant, days to maturity, primary branches per plant 100-seed weight and seeds per pod as most important direct yield components while biological yield per plant and harvest-index as most important indirect components. Hence, these traits should be given much emphasis at the time of devising selection strategy to achieve a quantum jump in pigeon pea yield.

Narayanan *et al.* (2018) evaluated 21 genotypes of pigeon pea to investigate the nature and magnitude of association of seed yield with major agronomic characters *viz*., plant height (cm), days to 50 per cent flowering, days to maturity, number of branches, number of pods per plant and 100 seed weight (g). This research also focussed on finding the direct and indirect effect of the various yield contributing characters on seed yield by path coefficient analysis. Correlation studies revealed the positive and significant relationship of number of pods per plant, days to 50 per cent flowering, number of branches per plant with seed yield. The path coefficient analysis indicated that characters *viz*., plant height, number of pods per plant, days to 50 per cent flowering, and days to maturity should be considered as selection indices in seed yield improvement programmes as they recorded highest direct effects on seed yield per plant.

Pal *et al.* (2018) conducted experiment with 20 different genotypes of pigeon pea during *kharif* 2016 in three different environments. In each environment each genotype was sown in a six-row plot of four metre length in randomised block design with three replications. Observations were recorded on ten different characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plants, number of secondary branches per plants, number of pod per plants, number of seed per pods, main shoot length (cm), 100 seed weight (g) and seed yield per plot (g)on five randomly plants of each genotype in each replication. Over all the environments, seed yield per plot is significantly and positively correlated to the days to 50% flowering, days to maturity and number of pods per plant. Days to maturity, number of pods per plant and number of seed per pods not only had direct effect but also positively and significantly associated with seed yield per plot in all the three environments.

Pushpavalli *et al.* (2018) evaluated 49 Pigeon pea genotypes. Path coefficient analysis revealed that days to maturity exhibited maximum direct effect followed by the number of pods/plants.

Thanga *et al.* (2019) evaluated fifty-seven pigeon pea genotypes to study correlation and path coefficient in pigeon pea. Character association studies indicated that number of racemes, number of secondary branches, number of primary branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, and 100 seed weight were strongly associated with seed yield. Path coefficient analysis revealed that days to 50 per cent flowering and number of pods per plant had a high positive direct effect on seed yield. Pod size had a moderate direct effect on seed yield. Hence due emphasis should be given on the number of pods per plant for improvement of seed yield in pigeon pea.

Devi *et al*. (2020) conducted an experiment to study correlation coefficient and Path coefficient analysis in eleven pigeon Pea genotypes. The correlation studies showed that, seed yield per plant showed significant and positive correlation with secondary branches per plant both at phenotypic and genotypic level and at genotypic level with number primary branches per plant, number of secondary branches per plant, number of pods per plant and test weight.

In path coefficient analysis, the number of pods per plant exhibited a high and positive direct effect on the seed yield per plant followed by the number of secondary branches and days to maturity. The study on the correlation and path analysis concluded that out of the eleven genotypes, PA-291 can be used as a promising genotype since it exhibited high number of primary and secondary branches, high number of pods per plant, high test weight and high seed yield per plant.

Kandarkar *et al.* (2020) studied 27 genotypes of pigeon pea for correlation and path coefficient analysis for grain yield and its yield contributing characters so as to identify genotypes with desirable attributes for utilization in the crop improvement program. Association studies revealed that seed yield kg per ha showed the highest significant positive correlation with the number of pods per plant (0.8671) followed by plant spread (0.8046), number of branches per plant (0.7098) and number of seeds per pod (r= 0.5023). Direct selection for the number of pods per plant (0.392), number of branches per plant (0.358) and plant spread (0.35) may be advantageous for selecting the high yielding genotypes in pigeon pea. Indirect effects of the number of branches per plant on seed yield *via* the number of pods per plant (0.308) and plant spread (0.223). Hence, this character seems to be an important contributor to seed yield and must be considered in the selection for high seed yield.

Tharageshwari and Hemavathy (2020) studied Correlation between yield and yield attribute component traits in ninety-three genotypes of pigeon pea revealed that single plant yield had positive and highly significant association with pod weight per plant, number of pods per plant and shelling percentage. The selection criteria can be done based on these characters for seed yield will give successful results for yield improvement in pigeon pea. Path coefficient analysis of different traits on single plant yield recorded that trait *viz*., pod weight per plant, number of pods per plant and shelling percentage showed highest positive direct effect. Hence selection on these studied characters might be useful in pigeon pea yield improvement.

Chisa *et al.* (2021) conducted a study on the relationship between seed yield and agronomic traits to identify key traits for selection. Agronomic traits, including yield and its components genotype mean data was subjected to correlation, path coefficient. The results showed a strong positive and significant correlation between number of pods per plant and seed yield in both medium and short duration genotypes. The number of pods per plant had a high direct effect on seed yield in both medium and short duration with values of (0.43) and (0.63) respectively. Number of branches and pod length exhibited high direct effect (0.30-0.99) for medium duration. However, seed yield per plant was an important predictor of seed yield in short duration while seed yield per plant, 100 seed weight and number of seeds per pod were key predictors of seed yield in medium duration genotypes. Therefore, these traits should be targeted for seed yield improvement in pigeon pea.

Ramasamy *et al. (2021)* evaluated 15 genotypes of pigeon pea to study the correlation and path analysis for seed yield and its contributing characters. Racemes per plant show positive and highly significant correlation with grain yield per plant to emerge as most important associates of seed yield. Studies on path analysis identified the characters *viz*., racemes per plant, total number of pods and pod bearing length as the most important direct yield contributing traits which merit due consideration at the time of devising selection strategy aimed at developing high yielding varieties in pigeon pea. The information was fetched together after applying various statistical tools in order to make the outcomes of association studies for the various pigeon pea breeding programmes.

3. To study the nature and extent of diversity among genotypes.

Consideration of genetic diversity existing in a population is the basic requirement for effective improvement programmes. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right type parents for purposeful hybridization. Accumulation of different desirable traits spread over the diverse genotypes into one genotype is important for the rapid advancement in yield improvement of any crop. The reports available on diversity of various characters in pigeon pea are given below;

Hamid *et al.* (2010) evaluated one hundred germplasm lines of pigeon pea for variation in morphological and agronomic traits for selection of cultivar potentially suitable for growing under rice-based cropping system. A wide range of variation was found in twelve quantitative traits, according to cluster analysis the genotypes of pigeon pea were grouped into seven clusters, each cluster with greater similarities. Plant height, days to flowering and pods per plant were the discriminating variables mostly contributed in grouping the genotypes, pods per plant played the most dominant role in explaining the maximum variance. Genotypes grouped in 1, 4 and 7 clusters were early maturing and high yielder as compared to the other cluster members. Genotype 21 (ICP7143) representing group 1 showed promising for its short stature nature. However, genotype 32 (ICP7989) representing group 4 produced the highest yield with the shortest maturity duration.

Songok *et al.* (2010) revealed genetic relationships among 88 pigeon pea accessions from a presumed centre of origin and diversity, India and a presumed secondary centre of diversity in East Africa were evaluated using six microsatellite markers. Forty-seven (47) alleles were detected in the populations studied, with a mean of eight alleles per locus. Populations were defined by region (India and East Africa) and sub-populations by country in the case of East Africa and State in the case of India. Greatest genetic diversity in terms of number of alleles, number of rare alleles and Neis unbiased estimate of gene diversity (H) was found in India as opposed to East Africa. This supports the hypothesis that India is the centre of diversity and East Africa is a secondary centre of diversity.

Pandey et al. (2013) assessed nature and extent of genetic diversity were assessed among 23 parents of pigeon pea hybrids. Based on relative magnitude of D the genotypes were grouped into five different non-overlapping clusters. Cluster III, having 8 genotypes, emerged with highest number of entries; cluster I, II and V were constituted by four genotypes each while cluster IV, comprising three genotypes, had least number of entries. The highest contribution in manifestation of genetic divergence was exhibited by 100- seed weight followed by pods per plant, days to maturity, harvest index, biological yield per plant, days to 50% flowering and seed yield per plant. The maximum intra-cluster distance was observed for cluster III, followed by cluster IV, cluster I and cluster V. The highest inter-cluster distance was recorded between cluster II and IV followed by cluster I and IV and cluster V and II. The crossing between entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in pigeon pea.

Kumar *et al.* (2014) evaluated twenty-seven genotypes of pigeon pea and studied thirteen quantitative characters. Genetic divergence was estimated using Mahalanobis's statistics (D^2) and principal component analysis. Cluster analysis revealed 27 genotypes were grouped into 6 clusters. The lines chosen from the same ecogeographic region were found scattered in different clusters which indicated that genetic diversity and geographic distribution were not necessarily related. The inter cluster distances were higher than the intra-cluster distance reflecting wider genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between cluster I &IV whereas the highest intra-cluster distance was found in cluster II indicated that the highly divergent types existed in these clusters. Days to maturity was found to be the maximum contributors towards the total divergence. The genotypes from these clusters may be used as potential donors for future hybridization programmes to develop early pigeon pea variety with good grain yield.

Kumara *et al.* (2014) studied the genetic diversity on various morphological traits, yield and yield related components of pigeon pea. The experiment was laid out with randomized complete block design involving nineteen advanced breeding lines of pigeon pea with three replications. The range for days to 50 per cent flowering, days to 80 per cent pod maturity, plant height, number of pods per plant, 100 seed weight, seed yield per plant and seed yield per hectare was 109 to 119 days, 102 to 154 days, 116.8 to 188.2cm, 37.4 to 216.2 pods per plant, 8.17 to 11 g, 20.4 to 45.8 g, 314.78 to 1203.6 kg/ha respectively. Genotypes were grouped into three clusters, based on various morphological traits, yield and yield related components, which indicated the presence of appreciable amount of genetic diversity. The seed yield per ha was the largest contributor (41.03 per cent) followed by number of pods per plant (34.11 per cent) and pod bearing length (27.52 per cent) towards the divergence.

Satapathy and Panigrahi (2014) studied Mahalanobis D-square (D^2) technique for yield and yield contributing traits for 26 genotypes of pigeon pea. These genotypes were grouped into eight clusters. Cluster VI had maximum divergence with eight genotypes followed by cluster V having five genotypes. The inter cluster distance was greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accession. The maximum and minimum divergence was revealed between cluster V with VIII (58.028) and cluster II with III (13.150) respectively. Cluster VIII exhibited high mean values for number of primary branches per plants, pod weight, 100 seed weight, harvest index and yield/plant. Cluster IV recorded high mean values for plant height, root length and days to maturity. The genotypes of cluster VIII with IV, VIII with VII and VIII with VI are most divergent with high mean for many characters including yield per plant and can be successfully utilized in hybridization programmes to get desirable transgressive segregants.

Kumar *et al.* (2015) assessed genetic diversity among 73 genotypes comprising of cultivars and stable inter-specific derivatives from pigeon pea (*Cajanus cajan* x *C. scarabaeoides*) based on thirteen agro-morphological and quality traits and 42 genic microsatellite markers. Cluster analysis based on Tocher's methods of pooled field data of agro morphological traits from all three environments and two locations grouped pigeon pea genotypes into nine clusters. Genetic divergence was mainly contributed by days to 50% flowering (30.14%) followed by100 seed weight (20.78%) and protein content (12.56%). The range of polymorphic information content (PIC) for microsatellites was 0.055- 0.695. A total of 104 alleles were amplified with 42 SSR markers with an average of 2.48 alleles per locus. The first three principal coordinates explained 60.17% and 57.22% of the accumulated variation in case of agro morphological traits and microsatellite data respectively. The information accrued is potential for broadening the genetic base in pigeon pea.

Pandey *et al.* (2016) studied genetic diversity among 120 genotypes of pigeon pea along with three checks in augmented design during *Kharif*, 2011-12. The Non-hierarchical Euclidean cluster analysis grouped all the genotypes into twelve distinct non-overlapping clusters indicating the existence of a high degree of genetic diversity in the materials. The crossings between the members of diverse clusters separated by high inter-cluster distances are likely to throw desirable segregants. In this context, very high inter cluster distances were recorded between cluster VI and XII, cluster V and XII, cluster II and IX, cluster VI and XI, cluster II and VI and cluster V and IX. Considering the mean performance for different characters of genotypes belonging to diverse clusters, the promising genotypes for exploitation as parents in breeding programme were NDAGC 2011-4, NDAGC 2011-42 and NDAGC 2011-2 of cluster II; NDAGC 2011-34 and NDAGC 2011-27 of cluster V; NDAGC 2011-16, NDAGC 2011-41, NDAGC 2011-88, NDAGC 2011-104 and NDAGC 2011-103 of cluster VI; IC 525504 and Pusa 33 of cluster IX and IC 525456, IC 525408 and IC 525463 of cluster XII. It may be concluded that crosses between diverse genotypes belonging to clusters separated by high inter-cluster distances with desired means are likely to produce transgressive segregants may be advocated for developing high yielding pigeon pea varieties.

Choudhary *et al.* (2019) assessed fourteen land races with three checks were characterised for various characteristics *viz*., total grain yield, plant height, days to 50% flowering, days to harvest, total biological yield, number of seeds per pod, shelling percentage and 100 seed weight. Cluster analysis indicated significant genetic variability among tested genotypes which provides an opportunity for crop improvement through hybridization of selected genotypes present in distant clusters. The data was further subjected to PCA (principal component analysis) and genotype by trait biplot analysis. The first three principal components accounted for 77% of total variation indicating wide genetic variability among the genotypes. All the genotypes clustered into two major clusters with nine and eight genotypes each. Promising genotypes *viz*., IC-611232, IC-611230 and IC-611256 can be successfully incorporated in the pigeon pea breeding programme.

Reddy and Jayamani (2019) conducted an experiment to determine the genetic diversity among sixteen pigeon pea land races for eleven characters. Highly significant differences existed among the genotypes for all the eleven characters studied. High heritability was observed for days to 50% flowering, number of pods per plant, number of seeds per pod,100 seed weight, shelling percent, days to maturity, single plant yield and seed fibre content. High heritability coupled with high genetic advance as per cent of mean was observed for 100 seed weight and single plant yield indicating the additive gene effect, hence further improvement of these characters would be possible through direct selection. The genotypes with specific traits could be selected and used in the crossing programme to improve the yield and protein content in pigeon pea.

Sharma *et al.* (2019) evaluated a set of 68 Pigeon pea germplasm lines for the assessment of genetic diversity. Investigation elucidated a wide range of genetic divergence among germplasm lines for seven yield related characters. Mahalanobis D^2 analysis grouped 68 genotypes into nine clusters. Cluster I was the largest consisting of 18 genotypes, followed by cluster VI with 11, and cluster II and cluster III with 9 genotypes each. Cluster VIII was the smallest with only one genotype. The highest intra cluster distance was observed in cluster VII (39.4) followed by cluster XI (32.7) and I (31.2) indicating high variability within the cluster. Cluster VIII showed highest mean values for plant height (293.5), secondary branches per plant (28.0) and test weight (8.3), while cluster IX revealed highest mean values for number of pods per plant (341.2) and seed yield per plant (71.7). While cluster II showed lowest mean for most of the characters *viz*., secondary branches/plant (14.2), number of pods (72.8), number of seeds per pod (2.9) and seed yield per plant (14.9). So, the promising genotypes with good yield attributing traits *viz*., plant height, number of pods/plants, number of seeds per pod and 100-seed weight can be selected and could be further used in crossing programs for the selection of desirable transgressive segregants.

Qutadah *et al.* (2019) assessed genetic diversity among 57 pigeon pea accessions comprising release varieties, farmer varieties and reference varieties. All the accessions were grouped into eight different non-overlapping clusters. Among them cluster I, having 17 accessions, emerged with highest number of entries followed by cluster V with 9 accessions, cluster III with 7 accessions, cluster IV with 6 accessions, cluster VI, VII and VIII constituted by 5 accessions each while cluster II, comprised 3 accessions, had least number of entries. The highest contribution in manifestation of genetic divergence was exhibited by 100-seed weight followed by days to maturity, plant height and days to 50% flowering. In this context highest inter-cluster distance was recorded between cluster V and VII followed by cluster IV and VI, IV and VII, III and VII while cluster I and III had lowest inter-cluster distance. The promising accessions identified were Bumba Tumur, BDN-2, Chaita Arhar, BSMR-736, Karanja Tuar, Dehati Arhar Lal and Belianga of cluster III; UPAS- 120, Paras, Manak, Dehati Arhar-2, Pusa-992 and Vamban-1 of cluster IV, Ram Arhar, HJP-7, Agahani, Manika Arhar and HJP-9 of cluster VI and NTH-77, Lal Rahri, Desi Arhar-1, Arhar Manpur Pahadi and Rehhe Arhar of cluster VII for exploitation in hybridization programme for development of superior pigeon pea cultivars.

Yohane *et al.* (2020) assessed the genetic diversity among diverse pigeon pea accessions to select complementary and unique genotypes for breeding. Eighty-one pigeon pea accessions were evaluated in six environments in Malawi using a 9 × 9 alpha-lattice design with two replications. The cross-tabulation analysis revealed a significant genotype variation on plant growth, flower, and seed traits. The combined analysis of variance identified genotypes MWPLR 14, ICEAP 01170, ICEAP 871091, and ICEAP 01285 as early maturing varieties, while Kachangu, MWPLR 16, TZA 5582, No. 40, and MWPLR 14 were identified as high-yielding genotypes. The correlation analysis revealed a significant positive correlation between grain yield and a hundred seed weight (HSWT) ($r = 0.50$, $p < 0.01$), suggesting the usefulness of this trait for selection. The nonlinear principal component analysis identified grain yield (GDY), days to 50% flowering (DTF), days to 75% maturity (DTM), number of pods per plant (NPP), number of racemes per plant (NRP), 100 seed weight (HSWT), leaf hairiness (LH), and number of seeds per pod (NSP) as the most discriminated traits among the test genotypes. The cluster analysis using morphological traits delineated the accessions into three clusters. The selected high-yielding and early-maturing genotypes may be recommended as parental lines for breeding and grain yield improvement in similar agro-ecologies.

Jayamani *et al.* (2021) conducted a study on genetic analysis and diversity involving 68 early duration pigeon pea based on 12 quantitative traits. The 68 pigeon pea genotypes were grouped into seven clusters based on Mahalanobis D^2 statistic. The cluster II contains the maximum number of genotypes (44 genotypes) followed by cluster V with 10 genotypes. The maximum inter cluster distance (22.18) was observed for clusters VI and VII and the minimum distance (7.76) was between clusters III and IV. The cluster II recorded the maximum average cluster mean for traits *viz*., plant height (143.02 cm), pod bearing length (83.47 cm), the number of clusters per plant (91) and single plant yield (41.79 g). The highest per cent contribution to genetic diversity is rendered by days to fifty per cent flowering (21.12%) and the lowest contribution is observed for pod bearing length (0.83%). The genotypes CO2R (61 days) of cluster VI and ICPL19024 (64 days) of cluster I had reduced days to fifty per cent flowering and can be utilized in the breeding of early maturing pigeon pea genotypes. The genotypes *viz*., ICPL19002, ICPL19004, ICPL19007, ICPL19009, ICPL19010, ICPL19018 and ICPL19028 were found to be superior for yield and yield attributing traits. Genotypes identified in the present study, could be used to develop varieties with early maturity and increased yield in pigeon pea.

CHAPTER III

MATERIALS AND METHODS

The information regarding the trial details and analytical methodology used during this investigation, titled " Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea. (*Cajanas cajan* L. Millsp.*)*," has been provided below under the following headings.

3.1 Experimental site

3.2 Experimental materials

3.3 Methodology

3.4 Observation recorded

3.5 Statistical analysis

3.1 EXPERIMENTAL SITE:

The current study was conducted during the *Kharif* 2022 at Educational and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri in Maharashtra. Geographically, Dapoli is located in the tropical region at 17°45' North latitude and 73°12' East longitude. It is 250 metres above mean sea level with warm, humid weather all year round. The typical rainy season runs from June to September, with an average annual rainfall of 3500 to 4000 mm. The pH range of the lateritic soil at the experimental site was 5.6 to 8.0. During the experimentation period, meteorological observations were gathered from meteorological observatory, Department of Agronomy, College of Agriculture, Dapoli.

3.2 EXPERIMENTAL MATERIALS:

The 41 genotypes were collected from different sources selected as experimental material is given below in **Table 3.1.**

Table 3.1. List of experimental material

Sr. No	Germ-plasm Name	Source	Sr. No	Germ-plasm Name	Source
1	IPAWD 22-2	NBPGR-Kanpur	2	IPAWD 22-3	NBPGR-Kanpur
3	IPAWD 22-4	NBPGR-Kanpur	4	IPAWD 22-6	NBPGR-Kanpur
5	IPAWD 22-7	NBPGR-Kanpur	6	IPAWD 22-9	NBPGR-Kanpur
7	IPAWD 22-10	NBPGR-Kanpur	8	IPAWD 22-12	NBPGR-Kanpur
9	IPAWD 22-14	NBPGR-Kanpur	10	IPAWD 22-17	NBPGR-Kanpur
11	IPAWD 22-20	NBPGR-Kanpur	12	IPAWD 22-24	NBPGR-Kanpur
13	IPAWD 22-25	NBPGR-Kanpur	14	IPAWD 22-26	NBPGR-Kanpur
15	IPAWD 22-27	NBPGR-Kanpur	16	IPAWD 22-29	NBPGR-Kanpur
17	IPAWD 22-31	NBPGR-Kanpur	18	IPAWD 22-32	NBPGR-Kanpur
19	IPAWD 22-35	NBPGR-Kanpur	20	IPAWD 22-36	NBPGR-Kanpur
21	IPAWD 22-37	NBPGR-Kanpur	22	IPAWD 22-44	NBPGR-Kanpur
23	IPAWD 22-46	NBPGR-Kanpur	24	IPAWD-22-47	NBPGR-Kanpur
25	IPAWD 22-49	NBPGR-Kanpur	26	IPAWD-22-51	NBPGR-Kanpur
27	IPAWD 22-54	NBPGR-Kanpur	28	IPAWD-22-56	NBPGR-Kanpur
29	IPAWD 22-57	NBPGR-Kanpur	30	IPAWD-22-60	NBPGR-Kanpur
31	Loacl-1	Ratnagiri	32	Local-2	Amaravati
33	Local-3	Pune	34	Local-4	Satara
35	Local-5	Dharashiv	36	Local-6	Nagar
37	Local-7	Akola	38	Local-8	Kolhapur
39	Konkan Tur -1	Dapoli	40	BDN 711	VNKMV
41	BDN - 13- 41	VNKMV			

3.3 METHODOLOGY:

3.3.1 Experimental details

Randomized block design was used to conduct the experiment with two replications. The seed was dibbled at 60 cm distance between row to row and 60 cm distance between plant to plant. Each plot had about 10.80 m × 1.20 m area (excluding the space between each treatment), with 2 rows per genotype. Each row contains 18 plants thus there were 36 plant population per plot. Experiment details are explained in Table No. 3.2.

Table 3.2. Experimental details

1	Crop	:	Pigeon pea
2	Spacing	:	60x60 cm
3	Experimental design	:	Randomized Block Design
4	No. of Genotypes	:	38 + 3 checks
5	No of plants per line	:	18
6	Plot size	:	10.80 x 1.20 m
7	Recommended dose of fertilizer	:	25 kg N: 50 kg P_2O_5
8	Season	:	*Kharif* 2022
9	Date of sowing	:	2 August, 2022

3.3.2 Cultural practices

The experiment was carried out on lateritic soil with a normal fertility level. In order to bring the soil to fine tilth (soil health), the preliminary tillage operations were properly carried out. The total fertilizer dose applied per hectare was 25 kg N and 50 kg P_2O_5. Half of the nitrogen in the form of urea was applied at the time of sowing and the other half was applied one month later. The operation like gap filling was done 7 days after sowing so as to maintain one plant per hill and maintain the plant population. In order to maintain a good stand of crop, recommended package of practices was carried out as and when necessary.

3.4 OBSERVATIONS RECORDED:

Five plants were selected randomly from each genotype for recording observations in the field. The average values from these five plants were used for the statistical computation and further worked out for the genetic diversity analysis. The technique adopted to record each of the observation and details of the observations recorded have been given below.

1) Days to initiation of flowering

Number of days to initiation of flowering was counted from date of sowing to the appearance of first flower.

2) Days to 50 per cent flowering

The number of days were counted from the date of sowing to the date on which 50 per cent of the plants in a plot flowered.

3) Days to maturity

The numbers of days were counted from the date of sowing to the date on which 90 per cent of the plants showed drying up, confined by the hardiness of the seeds.

4) Plant height (cm)

Plant height was measured from ground level to the tip of main axis of the plant at the time of maturity and expressed in centimetres.

5) Number branches per plant

The total branches were counted and recorded at the time of maturity.

6) Number of pods per plant

The total number of pods counted on selected individual plants at the time of harvest.

7) Number of seeds per pod

Number of seeds per pod was counted from each of the selected pod from sampled five plants at maturity.

8) Pod length (cm)

It was measured in centimetres from the base to the tip of pod.

9) Test weight

The weight of randomly selected 100 seeds from each germplasm was recorded in grams.

10) Per cent pod borer damage

Per cent pod borer damage was calculated by using formula.

$$\text{Per cent pod borer damage} = \frac{\text{Number of damaged pods}}{\text{Total number of effective pods}} \times 100$$

11) Seed yield per plant (g)

All the pods of individual selected plants were harvested, threshed, dried and seed yield per plant was recorded in grams.

12) Seed yield per plot

Each plot had about 10.80 m × 1.20 m area (excluding the space between each treatment), with 2 rows per genotype. Each row contains 18 plants thus there were 36 plants population per plot. All the pods from the plot were harvested, threshed, dried and seed yield per plot was recorded in grams.

13) Harvest index (%)

Harvest index was calculated by dividing economic yield by biological yield in percentage of plants selected for observation.

14) Protein content (%)

The fat free oven dried 60 mesh flour sample of 0.5 g was digested with 15 ml concentrated H_2SO_4 (sp.gr.1.84) using 1 g catalyst mixture K_2SO_4:$CuSO_4$ in 10:1 proportion respectively. Samples were kept on hot plate for heating at 150 ºC for half an hour, 3ml of H_2O_2 was added in heated sample temperature was increased up to 200-250 ºC. Again, after half an hour 2-3 ml of H_2O_2 was added to avoid foaming while digestion of sample.

Samples were digested till the sample turns colourless from blackish brown. These digested samples were cooled at room temperature and 50 ml volume was prepared from digested sample, by using volumetric flask. Out of 50 ml sample prepared 5 ml sample was taken for distillation and transferred to distillation unit for estimation of nitrogen by micro Kjeldahl method (A.O.A.C.). Percent nitrogen was multiplied with 6.25 as conversion factor to obtain protein content in percent.

3.5 STATISTICAL ANALYSIS:

The available data on individual characters were subjected to the method of analysis of variance which is commonly used in the Randomized Block Design (Panse and Sukhatme, 1985). The analysis of variance was done as given below in **Table No 3.3**

3.5.1 Analysis of variance (ANOVA):

Table No. 3.3 : Analysis of Variance (ANOVA)

Source of Variation	D.F.	M.S.S.	Expected M.S.S.
Replication	(r-1)	RMS	$\sigma^2e + \sigma^2r$
Treatment	(g-1)	GMS	$\sigma^2e + \sigma^2g$
Error	(r-1) (g-1)	EMS	σ^2e

Where,

r = Number of replications

g = Number of genotypes

MSS = Mean sum of squares

σ^2e = Environmental variance

σ^2g = Genotypic variance

σ^2r = Replication variance

The genotype mean sum of square (GMS) was tested against error mean sum of square (EMS) by ‘F’ test for n_1 = (g-1) and n_2 = (r-1) (g-1) degrees of freedom.

3.5.2 Estimation of mean and range:

Mean value of each character was worked out by dividing the total by corresponding of observations.

$$\underline{X} = \frac{\Sigma X_i}{n}$$

Where,

$\underline{X}$ = Mean of character

$\sum X_i$ = Total of the character

n = Number of observations

Range: The lowest and highest values from the mean of each character were recorded as range.

Coefficient of variation (C.V) = $\frac{S.D}{g} \times 100$

Where,

Standard Deviation (S.D) = $\sqrt{\frac{1}{n}}(X-\underline{X})^2$

Classification of genotypes:

Genotypes were classified based on population mean and critical difference. The classification helps in identifying the superior as well as inferior genotypes. The classification was done as below;

Above average (>)	: Population mean + C.D.
Medium	: Population mean ± C.D.
Below average (<)	: Population mean – C.D.

3.5.3 Estimation of components of variation:

The environmental $(\sigma^2 e)$, phenotypic $(\sigma^2 p)$ and genotypic $(\sigma^2 g)$ variances were calculated as:

1. Environmental variance

$$(\sigma^2 e) = \text{EMS}$$

2. Genotypic variances

$$(\sigma^2 g) = \frac{GMS-EMS}{r}$$

3. Phenotypic variances

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

Where,

GMS=Genotypic mean sum of squares

EMS=Error mean square

r=Number of replications

3.5.4 Estimation of standard error of mean and standard error of difference:

a) Standard error of mean:

$$\text{SEm} \pm = \sqrt{\sigma^2 e/r}$$

b) Standard error of difference between two means was calculated as S.E. of difference of mean (SED)

$$\text{SED} = \text{SE}_{\text{m}} \times \sqrt{2}$$

3.5.5 Estimation of Coefficient of Variation:

The genotypic and phenotypic coefficient of variation was calculated as per the formula given by Burton and De Vane (1953).

1. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \sqrt{\frac{\sigma^2 e}{\underline{X}}} \times 100$$

2. Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \sqrt{\frac{\sigma^2 p}{\underline{X}}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

$\underline{X}$ = Mean of characters

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

i) Low : Less than 10 (%)
ii) Moderate: 10-20 (%)
iii) High : More than 20 (%)

3.5.6 Estimation of Heritability:

Heritability in broad sense estimated for various characters by using the formulae suggested by Lush (1949). It is estimated from the total genetic variances.

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

Where,

$\sigma^2 g$ = Genotypic variances

$\sigma^2 p$ = Phenotypic variances

As suggested by Johnson et al. (1955), heritability values are categorized as follows:

i) Low : Less than 30 (%)

ii) Moderate : 30-60 (%)

iii) High : More than 60 (%)

3.5.7 Estimation of genetic advance (GA)

Improvement in the mean genotypic value of selected plant over the parental population is known as genetic advance. The genetic variability is directly proportional to the genetic advance. The genetic advance is generally high with the characters having, high heritability and vice versa. It is calculated by the formula suggested by Johnson *et.al* (1955).

1. Genetic advance

$$\text{G.A.} = \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p \times k$$

2. GA as per cent of mean = $\frac{GA}{\underline{X}} \times 100$

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

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

k = Selection differential at 5% selection intensity

$\underline{X}$ = Mean of character

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

i) Low : Less than 10 (%)
ii) Moderate : 10-20 (%)
iii) High : More than 20 (%)

3.6 Correlation coefficient

Analysis of co-variance was carried out by taking two characters at a time and error was used as environmental co-variance.

ANOVA for phenotypic and genotypic co-variances

Source of variation	d. f.	Mean products
Replication	(r-1)	-
Genotypes	(g-1)	GMP
Error	(r-1)(g-1)	EMP
Total	(rg-1)	-

Where,

r = Number of replications

g = Number of treatments

GMP = Genotype mean sum of products

EMP = Error mean sum of products

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

Environmental co-variance = (CoVe1.2) =EMP

Genotypic co-variance = (CoVg 1.2) = $\frac{GMP-EMP}{r}$

Phenotypic co-variance = (CoVg 1.2) = (CoVe1.2) + (CoVg 1.2)

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

1. Phenotypic correlation coefficient (r_p)

Phenotypic correlation coefficient was derived as:

$$r_p1.2 = \frac{CoVp\ 1.2}{\sqrt{(\sigma^2 p1)\ (\sigma^2 p2)}}$$

Where,

r_p1.2 = Phenotypic correlation between character 1 and 2

CoVp 1.2 = Phenotypic co-variance between character 1 and 2

$\sigma^2 p1\ and\ \sigma^2 p2$ = Phenotypic variances of characters 1 and 2 respectively.

2. Genotypic correlation coefficient (r_g)

Genotypic correlation coefficient was obtained by the formula

$$r_g1.2=\frac{CoVg\ 1.2}{\sqrt{(\sigma^2 g1)\ (\sigma^2 g2)}}$$

Where,

$r_g1.2$ = Genotypic correlation between character 1 and 2

CoVg 1.2 = Genotypic co-variances between character 1 and 2

$\sigma^2 g1$ and $\sigma^2 g2$ = Genotypic variances of character 1 and 2 respectively.

The significance of genotypic and phenotypic correlation coefficient was tested by using 't' test.

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

Where,

r = Correlation coefficient

n= Total number of observations

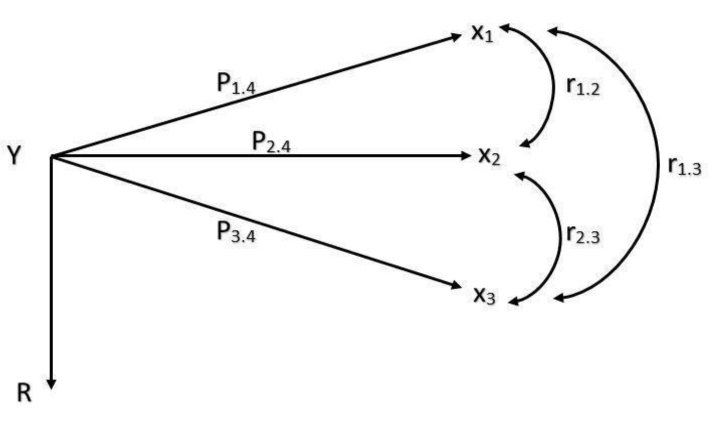
The calculated 't' value is tested with table 't' value for respective (n-2) degrees of freedom for significance.

3.7 Path Coefficient analysis:

To establish a cause and effect relationship, the genotypic and phenotypic correlation coefficients were partitioned in direct and indirect effect by path analysis as suggested by Dewey and Lu (1959). The first step in path analysis is to prepare a path diagram based on cause and effect relationship.

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effect.

The concept behind this is that yield is the function of various components like x_1, x_2, x_3 then these components show following type of association with one another.



From the above figure, it is clear that yield is the result of x_1, x_2 and x3 and some other undefined factors designated by 'R'. The double arrowed lines indicate mutual association as measured by correlation coefficients and the single arrowed line represented direct influence as measured by path coefficients Pij.

Path coefficients were obtained by solving a set of simultaneous equation of the form,

$$r_{ny} = p_{ny} + r_{n2} + 4n_2p_y + 4n_3 + \ldots\ldots$$

Where,

r_{ny} = represented correlation between one component and

yield

p_{ny} = represented path coefficient between one component and the yield

r_{n2} = represented correlation between that character and each of the other yield components in turn

Matrix A	Matrix B		
r_{1y}	1	$r_{1.2}$	$r_{1.3}$................ r_{1n}
$r_{2.1}$	1	$r_{2.3}$............... r_{2n}	
r_{ny}	r_{n1}	r_{n2}	r_{n3} 1

Where,

$r_{1.2} = r_{1.2}$ and so on.

r_{1y} = Correlation between one component character and yield

The ‘B’ matrix (P_{ij}) were obtained as -

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

The indirect effect of a particular character through other characters was obtained by multiplication of direct path and particular correlation coefficients between these characters separately.

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

Where,

i = 1 to n

j = 1 to n

$$P_{ij} = P_1Y_1, P_2Y_2, ---- \quad P_nY_n$$

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factor (s) were diagrammatically presented.

The residual factors i.e., variation in yield unaccounted for by these association was calculated from the following formula,

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

Where,

$$R^2 = (P1yr1y + P2yr2y + P3yr3y \ldots\ldots\ldots\ldots + Pnyrny)$$

Where,

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

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

The path coefficient is rated based on the scales given below: (Lenka and Mishra, 1973)

0.00 – 0.09 = Negligible

0.10 – 0.19 = Low

0.20 – 0.29 = Moderate

0.30 – 0.99 = High

>1.00 = Very high

3.8 GENETIC DIVERGENCE:

The genetic divergence between forty-one genotypes was estimated using Mahalanobis (1949) using D^2 statistic techniques D^2 value between ith and jth genotypes for ‘P’ characters was calculated as

$$D^2ij = \sum (\underline{Y}_{it} - \underline{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of ith genotype for ‘t’ character

Y_{jt} = Uncorrelated mean values of jth genotype for ‘t’ character

$D^2ij = D^2$ between ith and jth genotype

The various steps involved in estimation of D^2 values are given below:

3.8.1 Test of significance:

Variance was calculated for all fourteen characters investigated and test of significance was carried. Analysis of covariance (ANOVA) for the character pairs was estimated on the basis of mean values. From these estimates, a dispersion table was prepared. After testing the differences between the genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done by using V statistic which in turn utilize Wilk's criterion (Rao, 1952)

Wilk's criterion '^' $|E|/|E+V|$

= Determination of error matrix

= Determination of (genotypes + error) sum of squares and sum of product matrix.

Then the value of 'V' statistic was worked out using Wilk's lambda criterion V' (stat)-m log e'^'

$$Z = \frac{\sqrt{pq}}{n}$$

Where,

P= number of characters

q= number of genotypes

n= degree of freedom (for error+ genotypes)

e= 2.7183

'V' (stat) is distributed as x^2 with pq degrees of freedom.

3.8.2 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation values of the difference in mean values of various characters of the two genotypes i.e., d^2ij. Therefore, transformation of correlated variables to uncorrelated one was done before working out the D^2 values. Transformation was done by using pivotal consideration method.

3.8.3 Computation of D^2 values

For given a combination of 'i' and 'j' genotype, the mean deviation i.e.,$\underline{Y}_{it}$ -$\underline{Y}_{ji}$ for t= 1, 2………p variables were computed and D^2 values were calculated as sum of squares deviations

$$D^2ij = \sum (\underline{Y}_{it} - \underline{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for't' character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for't' character

D^2ij= D^2 between i^{th} and j^{th} genotype

3.8.4 Testing the significance of D^2 values

The D^2 value obtained for a pair of genotypes was taken as the calculated value of x^2 and tested against tabulated x^2 at p degree of freedom where,"P"is the number of characters considered.

3.8.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution toward divergence between two entries (di= yit- yjt).

Rank 1st was given to the highest mean difference and rank p to the lowest difference, where P is the total number of characters considered percentage contribution of each character towards genetic divergence was calculated using the formula:

Percentage contribution of character × = $\frac{N}{M}\times 100$

Where,

N= Number of genotype contributions where the character was ranked first

M= All possible combinations of genotypes considered

3.8.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done by using Tocher's method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should have a smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotype into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all the combinations for each genotype were arranged in the increasing order of their magnitude. To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average D^2 value from the first two genotypes was considered and so on. At certain stage when it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. The process was continued till all the genotypes were included in one or the other clusters.

3.8.7 Intra and inter cluster distance

Average intra cluster distance:

For the measurement of intra cluster distance, the formula used was

$$\sum Di^2/n.$$

Where,

$\sum Di^2$ = Sum of distance between all possible combinations (n) of the populations included in a cluster

n = Number of clusters

Average inter cluster distance:

Clusters were taken one by one and their distance from other clusters was calculated. The distance between the two clusters as the sum of D^2 value between the number one clusters to each of the member of each cluster divided by the product of number of genotypes in both the clusters under consideration. The square root of the average D^2 value gave the genetic distance ‘D’ between the clusters. Based on D^2 value (inter cluster distance), the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Averages inter cluster distance} = \frac{D2}{n1 \times n2}$$

When n1 and n2 are the number of genotypes in cluster 1 and cluster 2, respectively. Based on the ‘D’ values, the genotypes were categorized as indicated below.

CHAPTER IV

RESULTS AND DISCUSSION

Results of the present experiment entitled ‘Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea’. (*Cajanus cajan* L. Millsp.) Which was undertaken at the Educational and Experimental Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli during *kharif*, 2022-23 are presented in this chapter under the following four heads:

4.1 Genetic variability

4.2 Correlation analysis

4.3 Path coefficient analysis

4.4 Genetic Diversity

4.1 GENETIC VARIABILITY:

4.1.1 Analysis of Variance

The analysis of variance for different characters evaluated in the present study is given in Table 4.1. The analysis of variance showed highly significant differences between germplasms for all the traits indicating the presence of wide genetic variation for different characters among genotypes of pigeon pea. The genotypic and error mean sum of squares are also used for analysis of genotypic and phenotypic variances.

4.1.2 Mean performance and range of variability

The mean performance of genotypes, critical difference, standard error and range of variation for 41 pigeon pea genotypes for fourteen characters studied are presented in Table 4.2.

Table 4.1. Analysis of variance for 14 quantitative characters in pigeon pea.

Sr. No.	Characters	Mean Sum of Squares		
		Replication (1)	Treatment (40)	Error (40)
1	Days to initiation of flowering	16.695	95.240	12.060
2	Days to 50 per cent flowering	24.258	93.498	6.357
3	Days to maturity	95.947	101.850	10.613
4	Plant height at harvest (cm)	17.609	138.764	37.393
5	Number of branches per plant	0.158	1.626	0.236
6	Number of pods per plant	54.580	147.635	15.043
7	Number of seeds per pod	0.149	0.061	0.025
8	Pod length (cm)	0.531	0.064	0.085
9	Test weight (g)	0.144	2.913	0.191
10	Percent pod borer damage	70.068	524.561	76.266
11	Seed yield per plant (g)	29.519	68.749	7.823
12	Seed yield per plot (g)	780.597	1354.174	108.997
13	Harvest index (%)	0.844	24.398	0.916
14	Protein content (%)	16.677	1.189	1.040

Table 4.2. Mean performance of 41 Pigeon pea genotypes for different quantitative characters.

Characters	Days to flower initiation	Days to 50% flowering	Days to Maturity	Plant height (cm)	Number of Branches	Number seeds per pod	Number of pods per plant	Percent pod borer damage	Test weight (g)	Protein content (%)	Harvest Index (%)	Pod length (cm)	Seed yield per plant (g)	Seed yield per plot (g)
IPAWD-2	91.10	109.50	177.20	116.20	6.60	3.10	145.50	38.20	7.80	20.10	35.15	4.60	20.80	420.0
IPAWD-3	94.50	113.80	182.30	130.00	6.90	2.60	148.40	45.60	8.85	21.25	34.80	4.35	17.70	394.0
IPAWD-4	93.30	109.90	179.60	123.20	6.30	3.15	131.20	43.00	9.70	21.00	33.70	4.40	16.40	392.0
IPAWD-6	89.20	109.00	175.20	142.80	7.90	3.00	146.10	59.70	8.70	21.25	35.72	4.55	21.20	410.0
IPAWD-7	89.00	108.20	180.10	141.60	7.95	3.25	160.70	49.90	9.10	22.98	41.00	4.45	33.40	475.0
IPAWD-9	91.40	110.00	181.00	135.10	7.50	3.05	150.20	49.10	7.60	21.20	35.45	4.30	19.30	402.5
IPAWD-10	93.40	107.90	182.10	132.60	7.10	2.80	148.60	42.70	8.45	22.25	36.75	4.40	20.10	414.0
IPAWD-12	97.10	114.50	185.80	144.50	7.80	2.90	128.00	60.20	8.75	21.00	32.80	4.30	16.10	389.0
IPAWD-14	93.80	112.70	180.30	136.20	7.30	3.25	151.30	81.00	8.50	21.55	32.90	4.20	19.20	414.5
IPAWD-17	90.50	110.50	169.00	146.30	8.10	2.95	144.00	32.20	8.60	21.25	36.40	4.40	19.90	407.0
IPAWD-20	83.80	103.30	167.50	126.90	8.60	3.30	149.20	58.90	8.65	21.85	34.05	4.05	17.10	397.5
IPAWD-24	79.20	99.00	165.50	140.80	6.60	3.15	155.10	62.00	8.60	20.25	35.73	4.35	19.50	402.5
IPAWD-25	86.80	102.50	182.50	138.10	7.10	3.20	156.10	22.50	9.60	22.78	42.90	4.60	35.80	475.0
IPAWD-26	91.70	111.80	174.30	146.70	6.70	3.05	141.50	71.30	7.40	21.41	31.00	4.85	15.30	385.0
IPAWD-27	93.70	107.20	177.60	138.00	6.85	3.35	143.30	68.20	7.75	21.35	37.10	4.55	22.30	419.0
IPAWD-29	98.70	115.50	162.00	135.70	7.80	3.20	148.30	38.30	8.40	21.00	33.90	4.55	19.00	411.0
IPAWD-31	91.50	111.50	174.10	129.70	7.20	3.10	148.80	35.30	8.00	20.38	38.80	4.55	26.00	389.5
IPAWD-32	87.00	102.00	162.60	141.10	7.20	3.20	129.20	74.20	9.55	19.55	28.75	4.50	13.50	380.0
IPAWD-35	84.50	104.80	173.30	124.70	6.80	3.05	142.00	74.10	8.65	21.85	33.75	4.40	18.40	400.0
IPAWD-36	92.00	111.70	182.60	139.00	7.50	3.00	156.70	34.90	10.95	21.16	43.20	4.65	37.00	485.0
IPAWD-37	92.00	111.60	180.40	122.20	6.90	3.20	143.90	48.50	9.75	22.25	32.75	4.50	17.10	427.5
IPAWD-44	76.90	95.20	160.40	139.20	9.10	3.35	149.50	76.90	9.35	20.30	31.70	4.45	17.20	391.0
IPAWD-47	98.70	116.50	183.20	143.30	7.20	3.05	152.40	52.00	8.80	22.30	33.10	4.50	19.80	406.0

Characters	Days to flower initiation	Days to 50% flowering	Days to Maturity	Plant height (cm)	Number of Branches	Number seeds per pod	Number of pods per plant	Percent pod borer damage	Test weight (g)	Protein content (%)	Harvest Index (%)	Pod length (cm)	Seed yield per plant (g)	Seed yield per plot (g)
IPAWD-49	93.80	112.30	170.10	129.80	7.40	3.05	153.40	69.90	8.80	21.93	32.70	4.40	19.70	400.0
IPAWD-51	92.20	107.80	162.50	141.50	7.50	3.10	153.40	85.40	9.70	21.09	35.60	4.40	20.50	407.5
IPAWD-54	91.30	109.20	172.50	120.50	7.20	3.10	152.65	43.60	9.40	21.83	37.60	4.65	28.10	410.0
IPAWD-56	99.00	116.50	184.50	139.90	7.70	3.15	142.60	30.50	10.80	21.64	33.10	4.35	26.10	413.5
IPAWD-57	89.80	109.70	175.50	120.30	5.50	2.95	127.70	71.70	8.75	20.30	32.10	4.70	15.10	384.0
IPAWD-60	102.90	121.60	185.30	143.60	9.10	3.10	163.30	39.90	8.30	21.81	40.60	4.35	29.70	465.0
LOCAL 1	99.70	118.30	174.85	141.50	7.80	3.20	152.20	44.50	9.45	22.15	38.25	4.50	21.30	413.5
LOCAL 2	105.00	119.00	177.60	145.00	7.35	3.10	144.90	80.10	10.35	21.80	35.00	4.30	18.20	405.0
LOCAL 3	101.80	120.70	176.10	144.60	7.50	3.30	145.50	56.15	10.55	22.80	32.60	4.40	30.30	426.5
LOCAL 4	95.60	110.20	173.80	139.40	7.25	2.90	151.60	71.70	8.70	22.05	31.90	4.25	22.30	415.0
LOCAL 5	99.60	119.60	180.70	142.70	7.60	3.10	155.00	47.40	12.30	22.15	31.95	4.60	23.30	420.0
LOCAL 6	92.20	115.40	177.40	138.80	7.40	3.40	142.80	63.10	9.70	21.00	33.05	4.35	21.00	413.5
LOCAL 7	101.20	120.40	182.90	146.70	7.40	3.40	164.60	47.90	9.30	22.25	43.60	4.80	36.00	477.0
LOCAL 8	101.10	122.00	180.50	144.20	6.90	3.05	144.50	61.50	9.25	21.85	39.00	4.15	18.00	396.5
BDN 711	106.30	122.20	173.30	127.30	4.50	2.75	135.40	47.10	12.22	21.70	33.10	4.10	18.50	398.0
BDN 1341	105.80	124.90	180.50	126.40	4.70	2.75	138.90	26.00	11.75	20.70	33.40	4.10	21.20	412.5
K.TUR	106.30	124.60	187.20	136.40	6.70	3.05	148.80	43.00	11.80	21.90	31.10	4.30	23.40	422.0
Mean	93.97	112.29	176.07	136.02	7.23	3.09	147.18	53.82	9.32	21.49	35.19	4.43	21.84	412.5
C.V.	3.70	2.25	1.85	4.50	6.73	5.13	8.22	16.23	4.69	4.75	2.72	6.62	12.80	9.17
S.E.	2.46	1.78	2.30	4.32	0.34	0.11	2.74	6.18	0.31	0.72	0.68	0.21	1.98	7.38
C.D. 5%	7.02	5.10	6.58	12.36	0.98	0.32	7.84	17.65	0.88	NS	1.94	NS	5.65	21.10
Range Lowest	76.90	95.20	160.40	116.20	4.50	2.60	127.70	22.50	7.40	19.55	28.75	4.05	13.50	380.0
Range Highest	106.30	124.90	187.20	146.70	9.10	3.40	164.60	85.40	12.30	22.98	43.60	4.85	37.00	485.0

1. Days to initiation of flowering

Days to initiation of flowering is an important trait in any crop development programme. It ranged from 76.90 days (IPAWD-44) to 106.30 days (BDN-711) with the general mean of 93.97 days. Among all genotypes 25 genotypes showed early initiation of flowering than the general mean whereas 13 genotypes and 3 checks had taken more days for initiation of flowering. The early initiation of flowering was observed in IPAWD-44 (76.90 days), which was followed by IPAWD-24 (79.2 days) and IPAWD-20 (83.8 days). Late initiation of flowering was reported in BDN-711 and K.TUR (106.30 days) followed by BDN 1341 (105.8 days) and LOCAL-2 (105 days). Priyanka *et al.*, (2016) and Pashwan *et al.*, (2021) found similar variation for days to initiation of flowering and wide range of flowering between checks and genotypes in pigeon pea.

2. Days to 50 per cent flowering

Significant differences were observed among 41 genotypes of pigeon pea studied for days to 50 per cent flowering character. The general mean for days to 50 per cent flowering was 112.29 days and ranged from 95.20 days (IPAWD-44) to 124.90 days (BDN 1341). Among all genotypes 23 genotypes observed early while other 15 genotypes and 3 checks have taken more days to 50 per cent flowering than the general mean. The minimum days to 50 per cent flowering was observed in genotype IPAWD-44 (95.20 days) followed by IPAWD-24 (99 days) and IPAWD-25 (102.5days). The maximum days taken for 50 per cent flowering were recorded in genotype BDN 1341 (124.90 days) followed by K.TUR (124.60 days) and BDN 711 (122.20 days). Fousiya *et al.* (2021) and Gowsalya *et al.*, (2016) noted significant variation for fifty percent of flowering among check.

3. Days to maturity

All the 41 genotypes displayed significant differences for this trait. Days to maturity ranged from 160.40 days (IPAWD-44) to 187.20 days (K.TUR) with the general mean 176.07 days. Within 41 genotypes, 17 genotypes and 1 check (BDN 711) matured earlier than the general mean whereas 21 genotypes and 2 checks (BDN 1341 and K.TUR) took more days for maturity than the general mean. The minimum days to maturity was recorded by genotype IPAWD-44 (160.40 days) followed by IPAWD-29 (162 days) and IPAWD-51 (162.50 days). The maximum days to maturity was observed in genotypes K.TUR (187.20 days) followed by IPAWD-12 (185.80 days) and IPAWD-60 (185.30 days). Early maturity was noticed by Pashwan *et al.* (2021) and delay maturity in check was observed by Kumar *et al.* (2014).

4. Plant Height (cm)

The plant height varied from 116.20 cm (IPAWD-2) to 146.70 cm (IPAWD-26) with average of 136.02 cm. 14 genotypes and 2 checks (BDN 711 and BDN 1341) reported dwarf stature of the plant while 24 genotypes and 1 check (K.TUR) observed for tallness than the mean plant height. Among all the 41 genotypes, IPAWD-2 (116.20 cm) reported minimum plant height followed by IPAWD-57 (120.30 cm) and IPAWD-54 (120.50 cm). The maximum plant height was recorded in genotype IPAWD-26 (146.70 cm) followed by LOCAL-2 (145.00 cm), LOCAL-3 (144.60 cm). Similar type of findings was obtained by Rao and Rao (2020) and Singh *et al.* (2013) for plant height.

5. Number of branches per plant

Data concerning to the number of branches per plant ranged from 4.50 (BDN-711) to 9.10 (IPAWD-60) with overall average of 7.23 branches per plant. 16 genotypes and 3 checks recorded lesser number of branches per plant whereas 22 genotypes recorded more number of branches per plant than average number of branches per plant. The minimum number of branches per plant was observed in BDN-711 (4.50) followed by BDN.1341 (4.70) and IPAWD-57 (5.50). Whereas maximum number of primary branches per plant was observed in IPAWD-60 (9.10) followed by IPAWD-20 (8.60) and IPAWD-17 (8.10). Similar kind of results was noticed by Pashwan *et al.* (2021) and Priyanka *et al.* (2016) for number of branches per plant.

6. Number of seeds per pod

The number of seeds per pod varied from 2.60 (IPAWD-3) to 3.40 (LOCAL-7) with average 3.09. Among 41 genotypes, 15 genotypes and 3 checks had less and 23 genotypes had higher number of seeds per pod than average, respectively. Minimum number of seeds per pod was observed in IPAWD-3 (2.60) followed by BDN 711 and BDN 1341 (2.75) whereas LOCAL 7 (3.40) reported maximum number of seeds per pod followed by IPAWD-44 (3.35) and LOCAL-3 (3.30). Similar results were recorded by Priyanka *et al., (2016*), and Anu *et al.,* (2017).

7. Number of pods per plant

Differences among genotypes were significant for this number of pods per plant. The number of pods per plant ranges from 127.70 (IPAWD-57) to 164.60 (LOCAL-7) with the general mean of 147.18 pods per plant. Among all the genotypes under study, 17 genotypes and 2 checks (BDN 711 and BDN 1341) and 21 genotypes and 1 check (K.TUR) were found with less and a greater number of pods per plant than the average respectively. The minimum number of pods per plant was reported in IPAWD-57 (127.70) followed by IPAWD-12 (128.0) and IPAWD-32 (129.20) while genotypes LOCAL-7 (164.60) recorded maximum number of pods per plant followed by IPAWD-60 (163.30) and IPAWD-7 (160.70). Similar kind of results were obtained by Anu *et al.,* (2017), Punia *et al.,* (2014) for number of pods per plant.

8. Percent Pod borer damage

In case of percent pod borer damage, the general mean of pod borer damage was 53.82 with range 22.50 (IPAWD-25) to 85.40 (IPAWD-51). 19 genotypes and 3 checks (BDN 711, BDN 1341, K.TUR) and 19 genotypes were recorded for less and a greater percent pod borer damage than the overall mean respectively. The lesser number of pod borer damage was recorded IPAWD-25 (22.50) followed by BDN 1341 (26.0) and IPAWD-56 (30.50). The maximum number of pod borer damage was reported in IPAWD-51 (85.40) followed by IPAWD-14 (81.00) and LOCAL-2 (80.10). The results were in agreement with Pashwan *et al.* (2021).

9. Test weight (g)

Data regarding test weight varied between 7.40 g (IPAWD-26) to 12.30 g (LOCAL-5) with an overall mean of 9.32 g. Among the genotypes studied 23 genotypes and 15 genotypes and 3 checks (BDN 711, BDN 1341, K.TUR) were found for below and above test weight than general mean, respectively. The lowest weight was observed in IPAWD-26 (7.40 g) followed by IPAWD-9 (7.60 g) and IPAWD-27(7.75 g). The highest test weight was recorded in LOCAL-5 (12.30 g) followed by BDN-711 (12.22 g) and K.TUR (11.75 g). Similar type of results was recorded by Kumar *et al.* (2014) and Fousiya *et al.* (2021) for high test weight than mean value of checks for their bold appearance.

10. Protein content (%)

The protein content varied from 19.55 % (IPAWD-32) to 22.98 % (IPAWD-7) with general mean of 21.49%. Among all 41 genotypes, 18 genotypes and 1 check (BDN 1341) showed lower protein content and 20 genotypes and 2 checks (BDN 711 and K.TUR) showed more protein content than the general mean. The lower protein content was exhibited by genotype IPAWD-32 (19.55%) followed by IPAWD-2 (20.10%) whereas highest protein content was recorded in genotype IPAWD-7 (22.98%) followed by LOCAL-3 (22.80%). Similar results were noticed by Pashwan *et al.* (2021) for protein content.

11. Harvest index (%)

The harvest index was ranged from 28.75% (IPAWD-32) to 43.60 % (LOCAL-7) with the general mean of 35.19 %. 21 genotypes and 3 checks (BDN 711, BDN 1341, K.TUR) had lower harvest index while 17 genotypes recorded for higher harvest index than the general mean. The genotype IPAWD-32 (28.75%) showed lowest harvest index followed by IPAWD-25 (31.0%) and K.TUR (31.10%) while genotype LOCAL-7 (43.60%) exhibited highest harvest index followed by IPAWD-36 (43.20 %) and IPAWD-25 (42.90 %). Similar type of results was recorded by Kumar *et al.* (2014), Fousiya *et al.* (2021) and Pashwan *et al.* (2021) for low harvest index.

12. Pod length (cm)

The average variation in pod length varied from 4.05 (IPAWD-20) to 4.85 (IPAWD-26) with the mean value of 4.43. Among all, 20 genotypes and 3 checks (BDN 711, BDN 1341, K.TUR) were with a less pod length than the general mean, while 18 genotypes had a greater number of pod length than the general mean. The lowest number of pod length was reported in IPAWD-20 (4.05) followed by BDN 711 (4.10) and LOCAL-8 (4.15). The genotype IPAWD-26 (4.85) showed maximum pod length followed by LOCAL-7 (4.80), IPAWD-57(4.70). Similar type of findings was obtained by Rao and Rao (2020) and Anu *et al.,* (2017) for pod length.

13. Seed yield per plant (g)

The wide range of variation was observed for this trait. The range of variation was 13.50 g (IPAWD-32) to 37.0 g (IPAWD-36) with general mean of 21.84 g. Among all the 41 genotypes, 26 genotypes and 2 checks (BDN 711 and BDN 1341) and 12 genotypes and 1 check (K.TUR) were reported for low and high seed yield per plant than the general mean, respectively. The genotypes IPAWD-32 (13.50 g), IPAWD-57 (15.10 g) and IPAWD-26 (15.30 g) were recorded with low seed yield per plant. The maximum seed yield per plant was reported in genotype IPAWD-36 (37.0 g) followed by LOCAL-7 (36.0 g) and IPAWD-25 (35.80 g). Such kind of results was reported by Mourya *et al.* (2022) for seed yield per plant.

14. Seed yield per plot (g)

The Seed yield per plot varied from 380.0 g (IPAWD-32) to 485.0 g (IPAWD-36) with mean value 412.5 g. Among all, 25 genotypes and 2 checks (BDN 711 and BDN 1341) and 13 genotypes and 1 check (K.TUR) were reported low and higher for seed yield per plot than mean performance, respectively. The genotype IPAWD-32 (380.0 g) recorded low seed yield per plot followed by IPAWD-60 (384.0 g) and IPAWD-26 (385.0 g). The highest seed yield per plot was observed in genotype IPAWD-36 (485.0 g) followed by LOCAL-7 (477.0 g) and IPAWD-25 (475.0 g). The results are in agreement with Singh *et al.* (2013) for low seed yield per plot by one of the checks than mean.

4.1.3 Components of variation

The total variation between the genotypes were subdivided into genotypic, phenotypic and environmental variance. The estimates of variance due to these three components for fourteen characters among 41 genotypes of pigeon pea are given in Table 4.3.

The magnitude of phenotypic variance was higher than genotypic variance for all the characters under study. The phenotypic variance for various characters varied from 0.08 (pod length) to 731.59 (seed yield per plot). The phenotypic variance was highest for seed yield per plot (731.59) followed by percent pod borer damage (300.41) and plant height (88.08), number of pods per plant (81.34), days to maturity (56.23), days to flower initiation (53.65), days to 50 % flowering (49.93), seed yield per plant (38.29). It was moderate for harvest index (12.66), whereas it was lowest for pod length (0.08) followed by number of seeds per pod (0.04), number of branches per plant (0.93), protein content (1.12), test weight (1.55). Similar results were in confirmed by Patro *et al.* (2019) and Ekka and Sahu (2019) for plant height and pod length. Pashwan *et al.* (2021) for plant height, pod length, number of branches per plant.

Table 4.3. Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances for 14 quantitative characters of pigeon pea.

Sr. No.	Characters	σ^2_p	σ^2_g	σ^2_e
1	Days to initiation of flowering	53.65	41.59	12.06
2	Days to 50 per cent flowering	49.93	43.57	6.36
3	Days to maturity	56.23	45.62	10.61
4	Plant height at harvest (cm)	88.08	50.69	37.39
5	Number of branches per plant	0.93	0.70	0.24
6	Number of pods per plant	81.34	66.30	15.04
7	Number of seeds per pod	0.04	0.02	0.03
8	Pod length (cm)	0.08	0.01	0.09
9	Test weight (g)	1.55	1.36	0.19
10	Percent pod borer damage	300.41	224.15	76.27
11	Seed yield per plant (g)	38.29	30.46	7.82
12	Seed yield per plot (g)	731.59	622.59	109
13	Harvest index (%)	12.66	11.74	0.92
14	Protein content (%)	1.12	0.07	1.04

The genotypic variance was higher in magnitude over environmental variance in all characters except number of seeds per pod, pod length and protein content. The highest genotypic variance was noticed in seed yield per plot (622.59) followed by pod borer damage (224.15), number of pods per plant (66.30), plant height (50.69), days to maturity (45.62), days to 50% flowering (43.57), days to flower initiation (41.59) and seed yield per plant (30.46). The moderate genotypic variance was noted for harvest index (11.74). The lowest magnitude of genotypic variances was observed in pod length (0.01), number of seeds per pod (0.02), protein content (0.07) followed by number of branches per plant (0.70). Similar type of findings was obtained by Pashwan *et al.* (2021) for highest genotypic variance for plant height and moderate for pod length, number of branches per plant.

The magnitude for environmental variance was higher for seed yield per plot (109.0) followed by percent pod borer damage (76.27) and plant height (37.39). It was moderate for number of pods per plant (15.05), days to flower initiation (12.06) and days to maturity (10.61), whereas it was lowest for number of seeds per pod (0.03), number of pod length (0.09), test weight (0.19), number of branches per plant (0.24), harvest index (0.92), protein content (1.04), days to 50 % flowering (6.36), seed yield per plant (7.82). Similar type of results was recorded by Kumar *et al.* (2014) and Fousiya *et al.* (2021) for lowest environmental variance for test weight, harvest index and protein content.

This classification (GCV and PCV) was done based on the standard scale given by the Sivasubramanian and Menon (1973).

4.1.4 Coefficient of variation

Genotypic and phenotypic coefficient of variation for 14 characters of pigeon pea was estimated and are presented in Table 4.4.

Table 4.4. Estimates of genetic parameters for 14 quantitative characters in pigeon pea.

Sr. No.	Characters	PCV (%)	GCV (%)	ECV (%)	h^2b (%)	GA	GAM (%)
1	Days to initiation of flowering	7.79	6.86	3.70	77.50	11.70	12.45
2	Days to 50 per cent flowering	6.29	5.88	2.25	87.30	12.70	11.31
3	Days to maturity	4.26	3.84	1.85	81.10	12.53	7.12
4	Plant height at harvest (cm)	6.90	5.23	4.50	57.50	11.13	8.18
5	Number of branches per plant	13.35	11.53	6.73	74.60	1.48	20.52
6	Number of pods per plant	19.12	17.26	8.22	81.50	15.14	32.10
7	Number of seeds per pod	6.74	4.38	5.13	42.10	0.18	5.85
8	Pod length (cm)	6.19	2.35	6.62	14.40	0.08	1.84
9	Test weight (g)	13.36	12.51	4.69	87.70	2.25	24.14
10	Percent pod borer damage (%)	32.20	27.82	16.23	74.60	26.64	49.50
11	Seed yield per plant (g)	28.33	25.27	12.80	79.60	10.14	46.43
12	Seed yield per plot (g)	23.77	21.93	9.18	85.10	47.42	41.67
13	Harvest index (%)	10.11	9.74	2.72	92.80	6.80	19.32
14	Protein content (%)	4.92	1.27	4.75	6.70	0.15	0.68

The results showed that, phenotypic coefficient of variation (PCV) was greater in magnitude than the respective genotypic coefficient of variation (GCV). The characters *viz.*, percent pod borer damage (32.20%), seed yield per plant (28.33), seed yield per plot (23.77), showed highest phenotypic coefficient of variation. Mourya *et al.* (2022), Pashwan *et al.* (2021) and Singh *et al.* (2013) reported phenotypic coefficient of variation (PCV) was greater in magnitude than genotypic coefficient of variation (GCV).

Moderate phenotypic coefficient of variation was observed for number of pods per plant (19.12), test weight (13.36%), number of branches per plant (13.35%), harvest index (10.11%). The lowest magnitude of phenotypic coefficient of variation was reported in days to maturity (4.26%) followed by protein content (4.92%), pod length (6.19 %), days to 50% flowering (6.29), plant height (6.90%), number of seeds per pod (6.74%) and days to initiation of flowering (7.79%). Kumar *et al.* (2014) and Fousiya *et al.* (2021) observed highest phenotypic coefficient of variation for seed yield per plant (28.33), seed yield per plot, Pashwan *et al.* (2021) and Singh *et al.* (2013) found similar results for lowest magnitude of phenotypic coefficient of for plant height and test weight.

The amount of genetic variation present in the 41 genotypes was worked out in terms of genotypic coefficient of variation (GCV). The highest genotypic coefficient of variation was recorded in percent pod borer damage (27.82 %), followed by seed yield per plant (25.27%) and seed yield per plot (21.93 %). The moderate GCV was observed in traits, *viz.*, number of pods per plant (17.26%), test weight (12.51%), number of branches per plant (11.53%), whereas lowest GCV was seen in harvest index (9.74), days to initiation of flowering (6.86), days to 50 % flowering (5.88), plant height (5.23%), number of seeds per pod (4.38%), days to maturity (3.84%), pod length (2.35 %), protein content (1.27 %). Pashwan *et al.* (2021) and Singh *et al.* (2013) observed moderate GCV for test weight and lowest GCV for plant height, number of seeds per pod, days to maturity characters in Pigeon pea.

This classification (GCV and PCV) was done based on the standard scale given by the Sivasubramanian and Menon (1973).

4.1.5 Heritability and genetic advance

The estimate of heritability and genetic advance for 14 different characters are presented in Table 4.

Heritability in broad sense varied from 6.70% (protein content) to 92.80% (Harvest index). High heritability was observed for harvest index (92.80%) followed by test weight (87.70%), days to 50% flowering (87.30%), seed yield per plot (85.10%), number of pods per plant (81.50%), days to maturity (81.10 %), seed yield per plant (79.60%), days to flower initiation (77.50%), percent pod borer damage (74.60%), number of branches per plant (74.60%), plant height (57.50%), number of seeds per pod (42.10%). Lowest heritability was found in pod length (14.40%) and protein content (6.70%). Such kind of results also exhibited by Rao and Rao (2020) and Patel and Patel (2020) for high heritability in harvest index and test weight. Pashwan *et al.* (2021) and Singh *et al.* (2013) observed low heritability in pod length and protein content.

The genetic advance ranged from 0.08 (pod length) to 47.42 (seed yield per plot). Seed yield per plot (47.42) reported moderate magnitude of genetic advance. Lowest magnitude of genetic advance was reported in percent pod borer damage (26.64), number of pods per plant (15.14), days to 50% flowering (12.70), days to maturity (12.53), days to flower initiation (11.70), plant height (11.13), seed yield per plant (10.14), harvest index (6.80), test weight (2.25), number of branches per plant (1.48), number of seeds per pods (0.18), protein content (0.15) and pod length (0.08). Mourya *et al.* (2022), Pashwan *et al.* (2021) and Singh *et al.* (2013) recorded similar findings for low magnitude of genetic advance for seed yield per plant, harvest index and test weight.

The genetic advance as per cent of mean (GAM) was varied from 0.68% (protein content) to 49.50% (percent pod borer damage). The highest GAM was reported in percent pod borer damage (49.50 %) followed by seed yield per plant (46.43 %), seed yield per plot (41.67 %), number of pods per plant (32.10 %), test weight (24.14 %) and number of branches per plant (20.52%). The moderate estimate of GAM was observed in harvest index (19.32%), days to flower initiation (12.45%) and days to 50% flowering (11.31%). The minimum magnitude of GAM was recorded for plant height (8.18), days to maturity (7.12), number of seeds per pod (5.85%), pod length (1.84%) and protein content (0.68 %). Highest GAM was reported by Pashwan *et al.* (2021) and Singh *et al.* (2013) for characters like test weight and number of branches per plant. Sahu *et al.* (2020) found moderate estimate of GAM in harvest index.

This classification of (Heritability, Genetic advance and Genetic advance as per cent of mean) was done based on the standard scale given by the Johnson *et al.* (1955).

4.2 CORRELATION ANALYSIS

The relationship between the seed yield and its component characters is crucial since the seed yield is a complicated character that depends on numerous independent features. Correlation analysis is crucial for determining the mutual association between yield and yield contributing characters. Therefore, correlation coefficients were calculated for all combinations of the characters under study at the phenotypic and genotypic levels.

4.2.1 Phenotypic correlation coefficient

Seed yield per plant showed highly significant positive correlation with days to maturity (0.360), number of pods per plant (0.595), harvest index (0.702), seed yield per plot (0.876). It has reported significant positive correlation with number of branches per plant (0.219) and protein content (0.315). It showed non-significant positive correlation with days to flower initiation (0.1165), days to 50% flowering (0.1479), plant height (0.1677), number of seeds per pod (0.2066), test weight (0.2054), pod length (0.1486). Seed yield per plant showed highly significant negative correlation with percent pod borer damage (-0.430). The similar results obtained by Tharageshwari and Hemavathy (2020) for highly significant positive correlation of seed yield per plant on seed yield per plot.

Days to flower initiation recorded highly significant positive correlation with days to 50 per cent flowering (0.920), days to maturity (0.496) and test weight (0.448). Significant positive correlation was reported with protein content (0.272) while non-significant positive correlation with plant height (0.1252), harvest index (0.0066), seed yield per plot (0.1422), seed yield per plant (0.1165). It reported non-significant negative correlation with number of seeds per pod (-0.1909), number of pods per plant (-0.0251), pod length (-0.1264) and significant negative correlation with number of branches per plant (-0.297), percent pod borer damage (-0.266). Non-significant positive correlation of days to flower initiation with plant height and harvest index were recorded by Ramasamy *et al.* (2021) and Kandarkar *et al.* (2020).

Days to 50 per cent flowering had highly significant positive correlation with days to maturity (0.514) and test weight (0.455) while significant positive correlation with protein content (0.252). It had non-significant positive correlation with plant height (0.1430), number of pods per plant (0.0077), harvest index (0.0331), seed yield per plot (0.1519), and seed yield per plant (0.1479). It had non-significant negative correlation with number of seeds per pod (-0.1740) and pod length (-0.1050). It had significant negative correlation with number of branches per plant (-0.237) and percent pod borer damage (-0.296). Similar results were recorded by Kandarkar *et al.* (2020) for non-significant positive correlation of days to 50% flowering on harvest index and seed yield per plant.

Days to maturity had highly significant positive correlation with protein content (0.376), seed yield per plant (0.360) and seed yield per plot (0.418). It reported significant positive correlation with harvest index (0.261) and non-significant positive correlation with plant height (0.0725), number of pods per plant (0.0905), test weight (0.1618), pod length (0.0084) while it showed non-significant negative correlation with number of branches per plant (-0.1422), number of seeds per pod (0.1136) and had highly significant negative correlation with percent pod borer damage (-0.378). Devi *et al*. (2020) and Saroj *et al*. (2013) reported similar results of days to maturity had non-significant positive correlation with plant height and test weight

Plant height had highly significant positive correlation with number of branches per plant (0.440). Significant positive correlation was reported with number of pods per plant (0.288) and protein content (0.283) while it showed non-significant positive correlation with number of seeds per pod (0.1967), percent pod borer damage (0.1538), test weight (0.0220), harvest index (0.1444), pod length (0.0668), seed yield per plot (0.1853), seed yield per plant (0.1677). Saroj *et al*. (2013) recorded similar findings for number of pods per plant was positively correlated with plant height.

Number of branches per plant exhibited highly significant positive correlation with number of seeds per plant (0.390) and number of pods per plant (0.414), while significant positive correlation with seed yield per plot (0.227) and seed yield per plant (0.219). It showed non-significant positive correlation with percent pod borer damage (0.1144), protein content (0.1567), harvest index (0.2057), pod length (0.0263). It had significant negative correlation with test weight (-0.259). Positive correlation of number of branches per plant with pod length was observed by Pal *et al.* (2018) and Thanga *et al.* (2019).

Number of seeds per pod showed significant positive correlation with number of pods per plant (0.236) and seed yield per plot (0.223). It showed non-significant positive correlation with percent pod borer damage (0.1440), protein content (0.0910), harvest index (0.1127) pod length (0.1722) and seed yield per plant (0.2066). It reported non-significant negative correlation with test weight (-0.1227). Pal *et al.* (2018) ended with similar results for non-significant positive correlation of number of seeds per pod with harvest index.

Number of pods per plant recorded highly significant positive correlation with harvest index (0.55), seed yield per plot (0.595) and seed yield per plant (0.595) while significant positive correlation with protein content (0.347). It showed non-significant positive correlation with pod length (0.0970) while non-significant negative correlation with percent pod borer damage (-0.1870) and test weight (-0.0750). Techale *et al.* (2013) revealed significant positive correlation of number of pods per plant with protein content.

Table no 4.5 Estimates of phenotypic correlation coefficient between different characters in pigeon pea.

Characters	DFI	DFF	DTM	PH	NBPP	NSPP	NPPP	PPBD	TW	PC	HI	PL	SYPP	SYP.PL
DFI	1.0000	0.920**	0.496**	0.1252	-0.297*	-0.1909	-0.0251	-0.266*	0.448**	0.272*	0.0066	-0.1264	0.1422	0.1165
DFF		1.0000	0.514**	0.1430	-0.237*	-0.1740	0.0077	-0.296*	0.455**	0.252*	0.0331	-0.1050	0.1519	0.1479
DTM			1.0000	0.0725	-0.1422	-0.1136	0.0905	-0.378**	0.1618	0.376**	0.261*	0.0084	0.418**	0.360**
PH				1.0000	0.440**	0.1967	0.288*	0.1538	0.0220	0.283*	0.1444	0.0668	0.1853	0.1677
NBPP					1.0000	0.390**	0.414**	0.1144	-0.259*	0.1567	0.2057	0.0263	0.227*	0.219*
NSPP						1.0000	0.236*	0.1440	-0.1227	0.0910	0.1127	0.1722	0.223*	0.2066
NPPP							1.0000	-0.1870	-0.0750	0.357*	0.557**	0.0970	0.595**	0.595**
PPBD								1.0000	-0.2095	-0.1061	-0.386**	-0.0855	-0.380**	-0.430**
TW									1.0000	0.1329	-0.1298	-0.1603	0.1846	0.2054
PC										1.0000	0.252*	-0.0055	0.337*	0.315*
HI											1.0000	0.1642	0.688**	0.702**
PL												1.0000	0.1646	0.1486
SYPP													1.0000	0.876**
SYP.PL														1.0000

*Significant at 5 % level **Significant at 1 % level

Note: DFI- Days to flower initiation, DFF- Days to 50% flowering, DTM- Days to maturity, NBPP- Number of branches per plant, NSPP- Number of seeds per plant, NPPP- Number of pods per plant, PPBD- Percent pod borer damage, TW- Test weight, PL- Pod length, PH- Plant height, SYPP- Seed yield per plot, SYP.PL- Seed yield per plant, HI- Harvest index, PC- Protein content

Percent pod borer damage showed non-significant negative correlation with test weight (-0.2095), protein content (-0.1061) and pod length (-0.0855). It had highly significant negative correlation with harvest index (-0.386), seed yield per plot (-0.380) and seed yield per plant (-0.430). Ramasamy *et al.* (2021) and Techale *et al.* (2013) reported similar kind of results of percent pod borer damage had highly significant negative correlation with seed yield per plant.

Test weight showed non-significant positive correlation with protein content (0.1329), seed yield per plot (0.1846) and seed yield per plant (0.2054), Whereas significant negative correlation with harvest index (-0.1298) and pod length (-0.1603). Test weight showed non-significant positive correlation with seed yield per plant this was also observed by Jaggal *et al.* (2012) and Chisa *et al.* (2021).

Protein content recorded significant positive correlation with harvest index (0.252), seed yield per plot (0.337) and seed yield per plant (0.315), while non-significant negative correlation with pod length (-0.0055). Protein content showed non-significant positive correlation with harvest index, was also observed by Chisa *et al.* (2021) and Ramasamy *et al.* (2021).

Harvest index exhibited highly significant positive correlation with seed yield per plot (0.688) and seed yield per plant (0.702) and while non-significant positive correlation with pod length (0.1642). Pandey *et al.* (2016) and Devi *et al.* (2020) observed harvest index had highly significant positive correlation with seed yield per plant.

Pod length recorded non-significant positive correlation with seed yield per plot (0.1646) and seed yield per plant (0.1486). Similar results were noticed by Techale *et al.* (2013) for seed yield per plant.

Seed yield per plot had highly significant positive correlation with seed yield per plant (0.876). Similar results were noticed by Chisa *et al.* (2021) and Tharangeshwari (2020).

4.2.2 Genotypic correlation coefficient

Estimates of genotypic correlation coefficient between yield and yield contributing characters in 41 pigeon pea genotypes presented in Table 4.6

Seed yield per plant exhibited highly significant positive correlation with days to maturity (0.381), number of pods per plant (0.753), protein content (0.888), harvest index (0.804), seed yield per plot (0.902) while it was significant positively correlated with plant height (0.329) and number of seeds per pod (0.347). It exhibited non-significant positive correlation with days to flower initiation (0.2021), days to 50 per cent flowering (0.1967), number of branches per plant

(0.2063) and test weight (0.2170). It showed highly significant negative correlation with percent pod borer damage (-0.559) and pod length (-0.692). Ramasamy *et al.* (2021) and Kandarkar *et al.* (2020) found significant positive correlation of seed yield per plant with plant height and number of seeds per pod.

Days to flower initiation recorded highly significant positive correlation with days to 50 per cent flowering (0.992), days to maturity (0.565), test weight (0.523), protein content (0.897) and pod length (0.407). It reported significant positive correlation with plant height (0.264). It showed non-significant positive correlation with seed yield per plot (0.1864) and seed yield per plant (0.2021). It showed non-significant negative correlation with number of pods per plant (-0.0010) and harvest index (-0.0100). It had significant negative correlation with number of branches per plant (-0.294) and percent pod borer damage (-0.288), while highly significant negative correlation with number of seeds per pod (-0.409). Rao and Rao (2020) reported significant positive correlation for test weight and significant negative correlation for number of branches per plant.

Days to 50 per cent flowering showed highly significant positive correlation with days to maturity (0.575), test weight (0.511), protein content (0.917) and pod length (0.405) whereas non-significant positive correlation with plant height (0.2072), number of pods per plant (0.0350), harvest index (0.0098), seed yield per plot (0.1804) and seed yield per plant (0.1967). It showed significant negative correlation with number of branches per plant (-0.296) and per cent pod borer damage (-0.325). It had highly significant negative correlation with number of seeds per pod (-0.363). Ramasamy *et al.* (2021) and Techale *et al.* (2013) reported similar results for significant positive correlation with seed yield per plot and seed yield per plant.

Days to maturity recorded highly significant positive correlation with protein content (0.868), seed yield per plot (0.465) and seed yield per plant (0.381), while significant positive correlation with harvest index (0.262). It showed non-significant positive correlation with plant height (0.0390), number of pods per plant (0.1080), test weight (0.2044) and pod length (0.0446) while non-significant negative correlation was reported with number of branches per plant (-0.1982) whereas significant negative with number of seeds per pod (-0.353) and highly significant negative correlation with percent pod borer damage (-0.474). Pandey *et al.* (2016) observed highly significant positive correlation of days to maturity with seed yield per plant.

Plant height showed highly significant positive correlation with number of branches per plant (0.527). It showed significant positive correlation with number of seeds per pod (0.292), number of pods per plant (0.319), seed yield per plot (0.306) and seed yield per plant (0.329). It reported non-significant positive correlation with percent pod borer damage (0.2007), test weight (0.0206), protein content (0.0981) and harvest index (0.1985). It had non-significant negative correlation with pod length (-0.0385). Vaniarajan *et al.* (2021) and Rekha *et al.* (2013) reported positive highly significant for seed yield per plant and non-significant positive for test weight.

Number of branches per plant exhibited highly significant positive correlation with number of seeds per pod (0.604), number of pods per plant (0.564) and protein content (0.382) whereas had significant positive correlation with harvest index (0.237). It showed non-significant positive correlation with percent pod borer damage (0.0865), seed yield per plot (0.2101) and seed yield per plant (0.2063). It showed significant negative correlation with pod length (-0.251) and highly significant negative correlation with test weight (-0.378). Jaggal *et al.* (2012) and Chisa *et al.* (2021) observed number of branches per plant exhibited highly significant positive correlation with number of pods per plant.

Number of seeds per pod showed highly significant positive correlation with seed yield per plot (0.360). It had significant positive correlation with number of pods per plant (0.340), percent pod borer damage (0.337) and seed yield per plant (0.347). It showed non-significant positive correlation with protein content (0.1383), harvest index (0.1710). While it reported non-significant negative correlation with test weight (-0.1638) and highly significant negative with pod length (-0.471). The similar results obtained by Tharageshwari and Hemavathy (2020) for non-significant positive correlation of number of seeds per pod with harvest index.

Number of pods per plant recorded highly significant positive correlation with protein content (0.824), harvest index (0.673), seed yield per plot (0.769) and seed yield per plant (0.753). It showed non-significant negative correlation with percent pod borer damage (-0.1780), test weight (-0.0733). It had significant negative correlation with pod length (-0.310). Kumar (2021), Patel (2022) and Rekha *et al.* (2013) reported positive highly significant for harvest index and seed yield per plant.

Percent pod borer damage showed non-significant positive correlation with pod length (0.0545). Significant negative correlation was reported with test weight (-0.275) whereas had highly significant negative correlation with protein content (-0.513), harvest index (-0.481), seed yield per plot (-0.486) and seed yield per plant (-0.559). Significant negative correlation of percent pod borer damage with seed yield per plot and seed yield per plant was reported by Techale *et al.* (2013).

Table No 4.6 Estimates of genotypic correlation coefficient between different characters in pigeon pea.

Characters	DFI	DFF	DTM	PH	NBPP	NSPP	NPPP	PPBD	TW	PC	HI	PL	SYPP	SYPPL
DFI	1.0000	0.992**	0.565**	0.264*	-0.294*	-0.409**	-0.0010	-0.288*	0.523**	0.897**	-0.0100	0.407**	0.1864	0.2021
DFF		1.0000	0.575**	0.2072	-0.296*	-0.363**	0.0350	-0.325*	0.511**	0.917**	0.0098	0.405**	0.1804	0.1967
DTM			1.0000	0.0390	-0.1982	-0.353*	0.1080	-0.474**	0.2044	0.868**	0.262*	0.0446	0.465**	0.381**
PH				1.0000	0.527**	0.292*	0.319*	0.2007	0.0206	0.0981	0.1985	-0.0385	0.306*	0.329*
NBPP					1.0000	0.604**	0.564**	0.0865	-0.378**	0.382**	0.237*	-0.251*	0.2101	0.2063
NSPP						1.0000	0.340*	0.337*	-0.1638	0.1383	0.1710	-0.471**	0.360**	0.347*
NPPP							1.0000	-0.1780	-0.0733	0.824**	0.673**	-0.310*	0.769**	0.753**
PPBD								1.0000	-0.275*	-0.513**	-0.481**	0.0545	-0.486**	-0.559**
TW									1.0000	0.623**	-0.1317	0.424**	0.1695	0.2170
PC										1.0000	0.825**	0.465**	0.785**	0.888**
HI											1.0000	-0.411**	0.759**	0.804**
PL												1.0000	-0.463**	-0.692**
SYPP													1.0000	0.902**
SYP.PL														1.0000

*Significant at 5 % level **Significant at 1 % level

Note: DFI- Days to flower initiation, DFF- Days to 50% flowering, DTM- Days to maturity, NBPP- Number of branches per plant, NSPP- Number of seeds per plant, NPPP- Number of pods per plant, PPBD- Percent pod borer damage, TW- Test weight, PL- Pod length, PH- Plant height, SYPP- Seed yield per plot, SYP.PL-Seed yield per plant, HI-Harvest index, PC-Protein content.

Test weight exhibited highly significant positive correlation with protein content (0.623) and pod length (0.424). It had non-significant positive correlation with seed yield per plot (0.1695) and seed yield per plant (0.2170) whereas significant negative correlation with harvest index (-0.1317). Highly significant positive correlation for pod length was also observed by Kumar (2021) and Patel (2022).

Protein content exhibited highly significant positive correlation with harvest index (0.825), pod length (0.465), seed yield per plot (0.785) and seed yield per plant (0.888). Techale *et al.* (2013) reported highly significant positive correlation of protein content with pod length.

Harvest index showed highly significant positive correlation with seed yield per plot (0.759) and seed yield per plant (0.804), While it showed highly significant negative correlation with pod length (-0.411). Similar results were noticed Rekha *et al.* (2013) and Chisa *et al.* (2021) for seed yield per plot and seed yield per plant.

Pod length recorded highly significant negative correlation with seed yield per plot (-0.463) and seed yield per plant (-0.692). Significant negative correlation for seed yield per plant was reported by Patel (2022).

Seed yield per plot recorded highly significant positive correlation with seed yield per plant (0.902). Similar results were noticed by Chisa *et al.* (2021).

4.3 PATH COEFFICIENT ANALYSIS

The correlation coefficients were further partitioned in order to assess the direct and indirect effects of various characters on seed yield per plant. The direct and indirect effect for each character towards seed yield per plant recorded by path analysis are presented below.

4.3.1. Phenotypic path coefficient analysis

The phenotypic correlation was partitioned into direct and indirect effects are presented in the Table 4.7.

Days to flower initiation had negligible negative direct effect (-0.0924) on seed yield per plant. It reported positive indirect effect through number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage and pod length. It showed negative indirect effect through 50 % percent flowering, days to maturity, plant height, test weight, protein content, harvest index and seed yield per plot. The similar results were obtained by Tharageshwari and Hemavathy (2020) for negative direct effect on seed yield per plant.

Days to 50 per cent flowering had negligible positive direct effect (0.0496) on seed yield per plant. It had positive indirect effect through days to flower initiation, days to maturity, plant height, number of pods per plant, test weight, protein content, harvest index and seed yield per plot. It showed negative indirect effect through number of branches per plant, number of seeds per pod, percent pod borer damage and pod length. Techale *et al.* (2013) reported similar kind of results, reported positive direct effect of days to 50 per cent flowering on seed yield per plant.

Days to maturity had negligible positive direct effect (0.0193) on seed yield per plant. It reported indirect positive effect through, days to initiation of flowering, days to 50 per cent flowering, plant height, number of pods per plant, test weight, protein content, harvest index, pod length, seed yield per plot. It recorded indirect negative effect through number of branches per plant, number of seeds per pod, percent pod borer damage. Devi *et al*. (2020) found positive direct effect of days to maturity on seed yield per plant.

Plant height had negligible negative direct effect (-0.0042) on seed yield per plant. It showed negative indirect effect through days to initiation of flowering, days to 50 percent flowering, days to maturity, number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage, test weight, protein content, harvest index, pod length and seed yield per plot. Kandarkar *et al.* (2020) confirmed the similar kind of results for negative indirect effect on pod length and protein content.

Number of branches per plant had negligible positive direct effect (0.0176) on seed yield per plant. It reported positive indirect effect through plant height, number of seeds per pods, number of pods per plant, percent pod borer damage, protein content, harvest index, pod length and seed yield per plot. It showed negative indirect effect through days to flower initiation, days to 50 per cent of flowering, days to maturity and test weight. Tharageshwari and Hemavathy (2020) reported positive direct effect of branches per plant on seed yield per plant.

Number of seeds per pod had negligible positive direct effect (0.0402) on seed yield per plant. It showed positive indirect effect through plant height, number of branches per plant, number of pods per plant, percent pod borer damage, protein content, harvest index, pod length and seed yield per plot. Reported negative indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity and test weight. Similar results were reported by Thanga *et al.* (2019) for positive indirect effect on protein content, harvest index, pod length.

Table No 4.7 Path analysis for different characters at the phenotypic level in Pigeon pea.

Characters	DFI	DFF	DTM	PH	NBPP	NSPP	NPPP	PPBD	TW	PC	HI	PL	SYPP	SYP.PL
DFI	-0.0924	-0.0850	-0.0458	-0.0116	0.0274	0.0176	0.0023	0.0246	-0.0414	-0.0251	-0.0006	0.0117	-0.0131	0.1165
DFF	0.0457	0.0496	0.0255	0.0071	-0.0118	-0.0086	0.0004	-0.0147	0.0226	0.0125	0.0016	-0.0052	0.0075	0.1479
DTM	0.0096	0.0099	0.0193	0.0014	-0.0028	-0.0022	0.0018	-0.0073	0.0031	0.0073	0.0051	0.0002	0.0081	0.360**
PH	-0.0005	-0.0006	-0.0003	-0.0042	-0.0018	-0.0008	-0.0012	-0.0006	-0.0001	-0.0012	-0.0006	-0.0003	-0.0008	0.1677
NBPP	-0.0052	-0.0042	-0.0025	0.0078	0.0176	0.0069	0.0073	0.0020	-0.0046	0.0028	0.0036	0.0005	0.0040	0.219*
NSPP	-0.0077	-0.0070	-0.0046	0.0079	0.0157	0.0402	0.0095	0.0058	-0.0049	0.0037	0.0045	0.0069	0.0090	0.2066
NPPP	-0.0024	0.0007	0.0086	0.0275	0.0395	0.0225	0.0954	-0.0178	-0.0072	0.0340	0.0531	0.0093	0.0568	0.595**
PPBD	0.0224	0.0249	0.0318	-0.0129	-0.0096	-0.0121	0.0157	-0.0841	0.0176	0.0089	0.0324	0.0072	0.0320	-0.430**
TW	0.0605	0.0614	0.0218	0.0030	-0.0350	-0.0166	-0.0101	-0.0283	0.1349	0.0179	-0.0175	-0.0216	0.0249	0.2054
PC	-0.0006	-0.0006	-0.0009	-0.0006	-0.0004	-0.0002	-0.0008	0.0002	-0.0003	-0.0023	-0.0006	0.0000	-0.0008	0.315*
HI	0.0013	0.0066	0.0521	0.0288	0.0410	0.0225	0.1110	-0.0769	-0.0259	0.0503	0.1995	0.0328	0.1372	0.702**
PL	-0.0009	-0.0007	0.0001	0.0005	0.0002	0.0012	0.0007	-0.0006	-0.0011	0.0000	0.0011	0.0069	0.0011	0.1486
SYPP	0.0868	0.0927	0.2550	0.1131	0.1388	0.1362	0.3633	-0.2319	0.1127	0.2057	0.4199	0.1004	0.6103	0.876**
SYP.PL	0.1165	0.1479	0.360**	0.1677	0.219*	0.2066	0.595**	-0.430**	0.2054	0.315*	0.702**	0.1486	0.876**	1.0000

* Significant at 5% level **Significant at 1% level

Note: Bold figures indicate direct effects.

Note: DFI-Days to flower initiation, DFF- Days to 50% flowering, DTM- Days to maturity, NBPP- Number of branches per plant, NSPP- Number of seeds per plant, NPPP- Number of pods per plant, PPBD- Percent pod borer damage, TW- Test weight, PL- Pod length, PH- Plant height, SYPP- Seed yield per plot, SYP.PL- Seed yield per plant, HI- Harvest index, PC- Protein content.

Number of pods per plant had negligible positive direct effect (0.0954) on seed yield per plant. It had positive indirect effect through days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, protein content, harvest index, and pod length and seed yield per plot. It showed negative indirect effect through days to flower initiation, percent pod borer damage and test weight. The similar results were observed by Pushpavalli *et al.* (2018) for positive indirect on harvest index.

Percent pod borer damage had negligible negative direct effect (-0.0841) on seed yield per plant. It had positive indirect effect through days to flower initiation, days to 50 percent flowering, days to maturity, number of pods per plant, test weight, protein content, harvest index, pod length and seed yield per plot. It reported negative indirect effect through plant height, number of branches per plant and number of seeds per pod. The result was in accordance with the reports of Narayanan *et al.* (2018) for negative direct of percent pod borer damage on seed yield per plant.

Test weight had low positive direct effect on (0.1349) seed yield per plant. It showed positive indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, protein content and seed yield per plot. It had negative indirect effect through number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage, harvest index and pod length. Positive indirect effect on plant height was observed by Pushpavalli *et al.* (2018).

Protein content had negligible negative direct effect (-0.0023) on seed yield per plant. It had positive indirect effect through percent pod borer damage and pod length. It had negative indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of seeds pod, number of pods per plant, test weight and harvest index and seed yield per plot. Similar kind of results reported by Tharageshwari and Hemavathy (2020) for negative indirect effect on number of branches per plant.

Harvest index had low positive direct effect (0.1995) on seed yield per plant. It had positive indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, number of pods per plant, protein content, pod length and seed yield per plot. It had negative indirect effect through percent pod borer damage and test weight. Narayanan *et al.* (2018) noticed similar kind of results for positive direct effect on seed yield per plant.

Pod length had negligible positive direct effect (0.0069) on seed yield per plant. It showed positive indirect effect through days to maturity, plant height, number of branches per plant, number of seeds per pod, number of pods per plant, protein content, harvest index and seed yield per plot. It reported negative indirect effect through days to flower initiation, days to 50 per cent flowering, percent pod borer damage and test weight. The result was in confirmation with Pushpavalli *et al.* (2018), it had indirect effect through number of pods per plant.

Seed yield per plot had high positive direct effect (0.6103) on seed yield per plant. It had positive indirect effect through days to flower initiation, days to 50 percent flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, number of pods per plant, test weight, protein content harvest index and pod length. It had negative indirect effect through percent pod borer damage. Chisa *et al.* (2021) reported direct effect of seed yield per plot on seed yield per plant.

The residual effect of path analysis at phenotypic level was found be about **0.435**.

4.3.2 Genotypic path coefficient analysis

The genotypic correlation coefficients are partitioned into direct and indirect effect and are presented in the Table 4.8.

Days to flower initiation had low direct negative effect (-0.1785) on seed yield per plant. It showed positive indirect effect through number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage, harvest index. It reported negative indirect effect through days to 50 percent flowering, days to maturity, plant height, test weight, protein content, pod length and seed yield per plot. Saroj *et al.* (2013) recorded similar findings for positive indirect effect on number of seeds per pod and harvest index.

Days to 50 per cent flowering had high positive direct effect (0.5321) on seed yield per plant. It recorded positive indirect effect through days to flower initiation, days to maturity, plant height, number of pods per plant, test weight, protein content, harvest index, pod length and seed yield per plot. It showed negative indirect effect through number of branches per plant, number of seeds per pod and percent pod borer damage. Pal *et al.* (2018), ended with similar results for positive direct effect on seed yield per plant.

Days to maturity had negligible negative direct effect (-0.0619) on seed yield. It had positive indirect effect through number of branches per plant, number of seeds per pod, percent pod borer damage. It had negative indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, number of pods per plant, test weight, protein content, harvest index, pod length and seed yield per plot. Pandey *et al.* (2016) observed similar kind of results for positive indirect effect on number of branches per plant.

Plant height had low negative direct effect (-0.1872) on seed yield per plant. It showed positive indirect effect through pod length. Negative indirect effect was reported through days to flower initiation, days to 50 per cent flowering, days to maturity, number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage, test weight, protein content, harvest index, pod length and seed yield per plot. Saroj *et al.* (2013) recorded similar findings for negative indirect effect on number of pods per plant.

Number of branches per plant had high positive direct effect (0.3953) on seed yield per plant. It had positive indirect effect through plant height, number of seeds per pod, number of pods per plant, percent pod borer damage, protein content, harvest index and seed yield per plot. It had negative indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, test weight and pod length. Pal *et al.* (2018) recorded positive indirect effect of number of branches per plant on protein content and harvest index.

Number of seeds per pod had moderate direct effect (-0.2660) on seed yield per plant. It recorded a positive indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, test weight and pod length. It showed negative indirect effect through plant height, number of branches per plant, number of pods per plant, percent pod borer damage, protein content, harvest index and seed yield per plot. Techale *et al.* (2013) revealed positive effect on pod length and test weight.

Number of pods per plant had negligible positive direct effect (0.0787) on seed yield per plant. It reported positive indirect effect through days to 50 % flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, protein content, harvest index, pod length and seed yield per plot. It showed negative indirect effect through days to flower initiation, percent pod borer damage, test weight and pod length. Kandarkar *et al.* (2020) reported similar results for number of pods per plant on seed yield per plant.

Percent pod borer damage had low direct effect (0.1811) on seed yield per plant. It showed positive indirect effect through plant height, number of branches per plant, number of seeds per pod and pod length. It recorded negative indirect effect through days to flower initiation, days to 50 percent flowering, days to maturity, number of pods per plant, test weight, protein content, harvest index and seed yield per plot. Techale *et al.* (2013) reported similar kind of results for positive direct effect on seed yield per plant.

Test weight had high positive direct effect (0.5058) on seed yield per plant. It had positive indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, protein content, pod length and seed yield per plot. It had negative indirect effect through number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage and harvest index. Kandarkar *et al.* (2020) and Ramasamy *et al.* (2021) reported similar results of test weight on seed yield per plant.

Protein content reported low negative direct effect (-0.1479) on seed yield per plant. It showed positive indirect effect through percent pod borer damage. Negative indirect effect was recorded through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of seeds pod, number of pods per plant, test weight, harvest index, pod length and seed yield per plot. Negative indirect effect of protein content on harvest index and pod length were expressed by Pal *et al.* (2018) and Thanga *et al.* (2019)

Harvest index had high positive direct effect (0.3473) on seed yield per plant. It showed positive indirect effect through days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, number of pods per plant, protein content and seed yield per plot. It reported negative indirect effect through days to flower initiation, percent pod borer damage test weight and pod length. Pandey *et al.* (2016) and Pal *et al.* (2018) observed similar kind of results for negative indirect effect of harvest index on test weight.

Pod length had high negative direct effect (-0.5871) on seed yield per plant. Positive indirect effect was reported through plant height, number of branches per plant, number of seeds per pod, number of pods per plant, harvest index and seed yield per plot. It showed negative indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, percent pod borer damage, test weight, protein content and pod length. Similar results noticed by Techale *et al.* (2013) for negative direct effect of pod length on seed yield per plant.

Table No 4.8 Path analysis for different characters at genotypic level in Pigeon pea.

Characters	DFI	DFF	DTM	PH	NBPP	NSPP	NPPP	PPBD	TW	PC	HI	PL	SYPP	SYP.PL
DFI	-0.1785	-0.1771	-0.1009	-0.0471	0.0524	0.0730	0.0002	0.0514	-0.0933	-0.1600	0.0018	-0.0726	-0.0333	0.2021
DFF	0.5279	0.5321	0.3059	0.1103	-0.1573	-0.1930	0.0186	-0.1727	0.2719	0.4878	0.0052	0.2152	0.0960	0.1967
DTM	-0.0350	-0.0356	-0.0619	-0.0024	0.0123	0.0219	-0.0067	0.0293	-0.0126	-0.0537	-0.0162	-0.0028	-0.0287	0.381**
PH	-0.0494	-0.0388	-0.0073	-0.1872	-0.0987	-0.0547	-0.0598	-0.0376	-0.0039	-0.0184	-0.0372	0.0072	-0.0572	0.329*
NBPP	-0.1161	-0.1169	-0.0783	0.2084	0.3953	0.2386	0.2230	0.0342	-0.1495	0.1510	0.0938	-0.0993	0.0830	0.2063
NSPP	0.1088	0.0965	0.0939	-0.0778	-0.1605	-0.2660	-0.0905	-0.0895	0.0436	-0.0368	-0.0455	0.1252	-0.0956	0.347*
NPPP	-0.0001	0.0028	0.0085	0.0251	0.0444	0.0268	0.0787	-0.0140	-0.0058	0.1056	0.0530	-0.0244	0.0605	0.753**
PPBD	-0.0521	-0.0588	-0.0859	0.0363	0.0157	0.0609	-0.0322	0.1811	-0.0497	-0.0929	-0.0870	0.0099	-0.0880	-0.559**
TW	0.2644	0.2585	0.1034	0.0104	-0.1914	-0.0828	-0.0371	-0.1389	0.5058	0.3149	-0.0666	0.2145	0.0857	0.2170
PC	-0.1326	-0.1356	-0.1285	-0.0145	-0.0565	-0.0205	-0.1985	0.0759	-0.0921	-0.1479	-0.1221	-0.0688	-0.2313	0.888**
HI	-0.0035	0.0034	0.0911	0.0689	0.0824	0.0594	0.2338	-0.1669	-0.0457	0.2866	0.3473	-0.1427	0.2636	0.804**
PL	-0.2389	-0.2375	-0.0262	0.0226	0.1475	0.2764	0.1818	-0.0320	-0.2490	-0.2731	0.2413	-0.5871	0.2720	-0.692**
SYPP	0.1071	0.1037	0.2670	0.1756	0.1207	0.2066	0.4418	-0.2794	0.0974	0.8987	0.4363	-0.2663	0.5748	0.902**
SYP.PL	0.2021	0.1967	0.381**	0.329*	0.2063	0.347*	0.753**	-0.559**	0.2170	0.888**	0.804**	-0.692**	0.902**	1.0000

Significant at 5% level **Significant at 1% level

Note: Bold figures indicate direct effects.

Note: DFI-Days to flower initiation, DFF- Days to 50% flowering, DTM- Days to maturity, NBPP- Number of branches per plant, NSPP- Number of seeds per plant, NPPP- Number of pods per plant, PPBD- Percent pod borer damage, TW- Test weight, PL- Pod length, PH- Plant height, SYPP- Seed yield per plot, SYP.PL- Seed yield per plant, HI- Harvest index, PC- Protein content.

Seed yield per plot had high positive direct effect (0.5748) on seed yield per plant. It showed positive indirect effect through days to flower initiation, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of seeds per pod, number of pods per plant, test weight, protein content and harvest index. It reported negative indirect effect through percent pod borer damage and pod length. Similar results noticed by Chisa *et al.* (2021) for negative indirect effect on pod length.

The residual effect of path analysis at genotypic level was found to be about **0.285.**

4.4 GENETIC DIVERGENCE

Genetic diversity prevailed among available material has immense scope in crop improvement for character of interest; the prime factor is estimation of the genetic distance. The genetic divergence can be estimated by using an effective statistical tool, Mahalanobis D^2 statistics, which gives clear idea about the diverse nature of the genotypes. The formation of clusters was done by following Tocher method suggested by Rao (1952). The results of the study are presented below.

4.2.1 Grouping of genotypes into various clusters

Based on magnitude of D^2 values 41 genotypes were grouped into Six clusters. The distribution of genotypes into different clusters are presented in Table 4.9.

Table no 4.9. **Grouping of Pigeon pea genotypes into different clusters by tocher method**

Cluster Group	No. of Genotypes	List of Genotypes and Source.
1 Cluster	27	IPAWD-49, LOCAL 4 (Satara), IPAWD-47, IPAWD-14, LOCAL 6(Ahmednagar), IPAWD-6, IPAWD-9, IPAWD-35, IPAWD-3, IPAWD-2, IPAWD-10, IPAWD-27, IPAWD-20, LOCAL 1(Ratnagiri), IPAWD-17, IPAWD-46, IPAWD-29, LOCAL 2(Amravati), LOCAL 8(Kolhapur), IPAWD-51, IPAWD-24, IPAWD-54, IPAWD-26, IPAWD-56, IPAWD-4, IPAWD-31 & LOCAL 3 (Pune)
2 Cluster	6	LOCAL 5 (Dharashiv), K.TUR (BSKKV, Dapoli), BDN 1341(VNKMV), BDN 711(VNKMV), IPAWD-37 & IPAWD-57
3 Cluster	5	IPAWD-25, IPAWD-36, IPAWD-7, LOCAL 7(Akola) & IPAWD-60
4 Cluster	1	IPAWD-44
5 Cluster	1	IPAWD-12
6 Cluster	1	IPAWD-32

Out of six clusters, cluster I was largest comprising 27 genotypes followed by cluster II with 6 genotypes, cluster III with 5 genotypes, cluster IV, cluster V and VI are solitary.

In **cluster I**, 21 genotypes originating from NBPGR- Kanpur and 6 from local collection. In **cluster II**, 2 genotypes originating from VNKMV- Parbhani, 2 genotypes from local collection and 2 from NBPGR Kanpur. In **Cluster III**, 4 genotypes originating from NBPGR- Kanpur and 1 from local collection. **Cluster IV, Cluster V, Cluster VI** consists of single genotype and it was originating from NBPGR- Kanpur. Kumar *et al.* (2014) grouped 27 genotypes of pigeon pea into six clusters, Jayamani *et al.* (2021) grouped 68 pigeon pea genotypes into seven clusters and Satapathy and Panigrahi (2014) grouped 26 pigeon pea genotypes into Eight clusters.

Tabl 4.10. Average intra and inter cluster D^2 values in 6 clusters in 41 genotypes of pigeon pea.

Cluster Distances						
	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Cluster 1	**41.59**	82.63	112.50	64.88	67.03	82.48
Cluster 2		**56.03**	183.85	141.99	85.12	106.73
Cluster 3			**42.79**	171.10	215.63	263.17
Cluster 4				**0.00**	102.13	48.45
Cluster 5					**0.00**	53.83
Cluster 6						**0.00**

Note: Diagonal values (**Bold**) are intra- cluster distances. Off-diagonal values are inter cluster distances.

Table 4.11. Average intra and inter cluster $\sqrt{D^2}$ values (D Values) in 6 clusters in 41 genotypes of pigeon pea.

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**
I	**6.44**	9.09	10.60	8.05	8.18	9.08
II		**7.48**	13.55	11.91	9.22	10.33
III			**6.54**	13.08	14.68	16.22
IV				**00**	10.10	6.96
V					**00**	7.33
VI						**00**

Note: Diagonal values (**Bold**) are intra- cluster distances. Off-diagonal values are inter cluster distances.

4.2.2 Average inter and intra cluster distance

The average intra and inter cluster D^2 and D values are presented in Table 4.10 and Table 4.11 respectively. The inter cluster distance, maximum divergence was noticed between cluster III and VI (16.22) followed by cluster III and V (14.68), cluster II and cluster III (13.55), cluster III and IV (13.08), cluster II and cluster IV (11.91), cluster I and cluster III (10.60), cluster II and cluster VI (10.33), cluster IV and cluster V (10.10), cluster I1 and cluster V (9.22), cluster I and cluster II (9.09), cluster I and V (8.18), cluster I and IV (8.05), cluster V and VI (7.33), cluster IV and VI (6.96) indicating that the genotypes included in these cluster may have different genetic architecture. The highest intra cluster distance was observed in cluster II (7.48) followed by cluster III (6.54) and by cluster I (6.44) and least distance for clusters IV, V, VI (00,00,00). Cluster VI was the most diverse as many other clusters displayed maximum inter cluster distance with it. Similar results were found by Yohane *et al.* (2020) and Choudhary *et al.* (2019).

4.2.3 Cluster mean for different characters:

The cluster mean performance for days to flower initiation varied from 76.90 days (Cluster IV) to 99.97 days (Cluster II) with mean population of 91.11 days. The genotypes from cluster IV exhibited early initiation of flowering whereas genotypes from cluster II were reported for late initiation of flowering. Similar results were recorded by Pandey *et al.* (2016).

The cluster mean performance for days to 50 per cent flowering ranged from 95.20 days (Cluster IV) to 118.77 days (Cluster II) with population mean of 109.17. The genotypes from cluster IV reported for early 50 per cent flowering whereas genotypes from cluster II were recorded for late 50 per cent flowering. Similar results were observed by Patil *et al.* (2019) and Choudhary *et al.* (2019).

The cluster mean performance for days to maturity varied from 160.40 days (Cluster IV) to 185.80 days (Cluster V) with population mean of 174.31. The genotypes from cluster IV recorded early maturity whereas genotypes from cluster V were reported for late maturity. Similar results were recorded by Kumara *et al.* (2014).

The cluster mean performance for plant height was ranged from 129.22 cm (Cluster II) to 144.50 cm (Cluster V) with the mean population of 138.61. The genotypes from cluster II were dwarf plant stature whereas genotypes from cluster V were reported for tallness among all. Results were in agreement with Choudhary *et al.* (2019).

The cluster mean performance for number of branches per plant was ranged from 5.98 (Cluster II) to 9.10 (Cluster IV) with population mean of 7.53. The genotypes from cluster II reported lesser number of branches per plant whereas genotypes from cluster IV recorded a greater number of branches per plant. Jayamani *et al.* (2021) noted similar results.

The cluster mean performance for number of seeds per pod varied from 2.90 (Cluster V) to 3.35 (Cluster IV) with population mean of 3.11. The genotypes from cluster V were observed for lesser number of seeds per pod whereas genotypes from cluster IV were recorded for a greater number of seeds per pod. Kumar *et al.* (2014) observed similar kind of results.

The cluster mean performance for number of pods per plant was varied from 28.00 (Cluster V) to 60.28 (Cluster III) with population mean of 42.64. The genotypes from cluster V were recorded for a smaller number of pods per plant whereas genotypes from cluster III were reported for a greater number of pods per plant. Sharma *et al.* (2019) reported similar kind of results.

The cluster mean performance for percent pod borer damage varied from 39.02 (Cluster III) to 76.90 (Cluster IV) with population mean of 58.96. The genotypes from cluster IIII were observed for less pod borer damage whereas genotypes from cluster IV were recorded for more pod borer damage. Similar results were observed by Jayamani *et al.* (2021)

The cluster mean performance for test weight varied from 8.75 g (Cluster V) to 11.10 g (Cluster II) with population mean of 9.52. The genotypes from cluster V were recorded for lower test weight whereas genotypes from cluster II were bold and were reported for higher test weight. Hamid *et al.* (2010) reported similar kind of results.

The cluster mean performance for protein content was varied from 19.55% (Cluster VI) to 22.19% (Cluster III) with mean population of 21.00. The genotypes from cluster VI were recorded for less protein content whereas genotypes from cluster III were reported for more protein content. Satapathy and Panigrahi (2014) noted similar kinds of results.

The cluster mean performance for harvest index varied from 28.75% (Cluster VI) to 42.26% (Cluster III) with mean population of 33.81. The genotypes from cluster VI were reported for low harvest index whereas genotypes from cluster III were observed for high harvest index. Sangok *et al.* (2010) reported similar kind of results.

The cluster mean performance for pod length was ranged from 4.30 cm (Cluster V) to 4.57 cm (Cluster III) with population mean of 4.43. The genotypes from cluster V were recorded for less pod length whereas genotypes from cluster III were reported for more pod length. Nag and Sharma (2012) ended with similar kind of results.

The cluster mean performance for seed yield per plot varied from 80.00 (Cluster VI) to 175.40 (Cluster III) with mean population of 108.69. The genotypes from cluster VI were observed for less seed yield per plot whereas genotypes from cluster III were recorded for more seed yield per plot.

The cluster mean performance for seed yield per plant was ranged from 13.50 g (Cluster VI) to 34.38 g (Cluster III) with mean population of 20.27. The genotypes from cluster VI were reported for lower seed yield per plant whereas genotypes from cluster III were observed for higher seed yield per plant. Kumar *et al.* (2014) reported similar kind of results.

4.2.4 Character contribution towards divergence

The contribution of different characters towards total divergence were illustrated in Table 4.12. The highest contribution towards divergence with its respective times ranked first were recorded for seed yield per plant (16.54%, 138) followed by seed yield per plot (13.65%, 114), test weight (9.63%, 80), harvest index (8.95%, 75), pod length (7.88%, 66), number of pods per plant (7.56%, 63), percent pod borer damage (5.85%, 49), protein content (5.65%, 47), days to maturity (5.61%, 4), number of seeds per pod (5.33%, 44), days 50 per cent flowering (4.17%, 35), days to flower initiation (3.78%, 32), plant height (2.084%,24), number of branches per plant (2.56 %, 21). Nag and Sharma (2012) and Kumar *et al.* (2014) ended with similar kind of results for seed yield per plant and plant height.

Table No. 4.12. Mean performance of clusters with their contribution towards total divergence.

Sr. No.	Characters	Clusters						Mean population	Contribution towards divergence (%)	Times ranked first
		I	II	III	IV	V	VI			
1	Days to flower initiation	93.34	99.97	94.38	76.90	97.10	87.00	91.11	3.78	32
2	Days to 50 % flowering	111.67	118.77	112.88	95.20	114.50	102.00	109.17	4.17	35
3	Days to maturity	174.78	179.60	182.68	160.40	185.80	162.60	174.31	5.61	47
4	Plant height (cm)	135.85	129.22	141.80	139.20	144.50	141.10	138.61	2.84	24
5	Number of branches per plant	7.31	5.98	7.81	9.10	7.80	7.20	7.53	2.56	21
6	Number of seeds per pod	3.09	2.97	3.19	3.35	2.90	3.20	3.11	5.33	44
7	Number of pods per plant	47.28	41.62	60.28	49.50	28.00	29.20	42.64	7.56	63
8	Percent pod borer damage	56.17	47.28	39.02	76.90	60.20	74.20	58.96	5.85	49
9	Test weight (g)	8.92	11.10	9.45	9.35	8.75	9.55	9.52	9.63	80
10	Protein content (%)	21.49	21.50	22.19	20.30	21.00	19.55	21.00	5.65	47
11	Harvest index (%)	34.96	32.40	42.26	31.70	32.80	28.75	33.81	8.95	75
12	Pod length (cm)	4.41	4.38	4.57	4.45	4.30	4.50	4.43	7.88	66
13	Seed yield per plot	106.09	110.67	175.40	91.00	89.00	80.00	108.69	13.65	114
14	Seed yield per plant	20.68	19.77	34.38	17.20	16.10	13.50	20.27	16.54	138

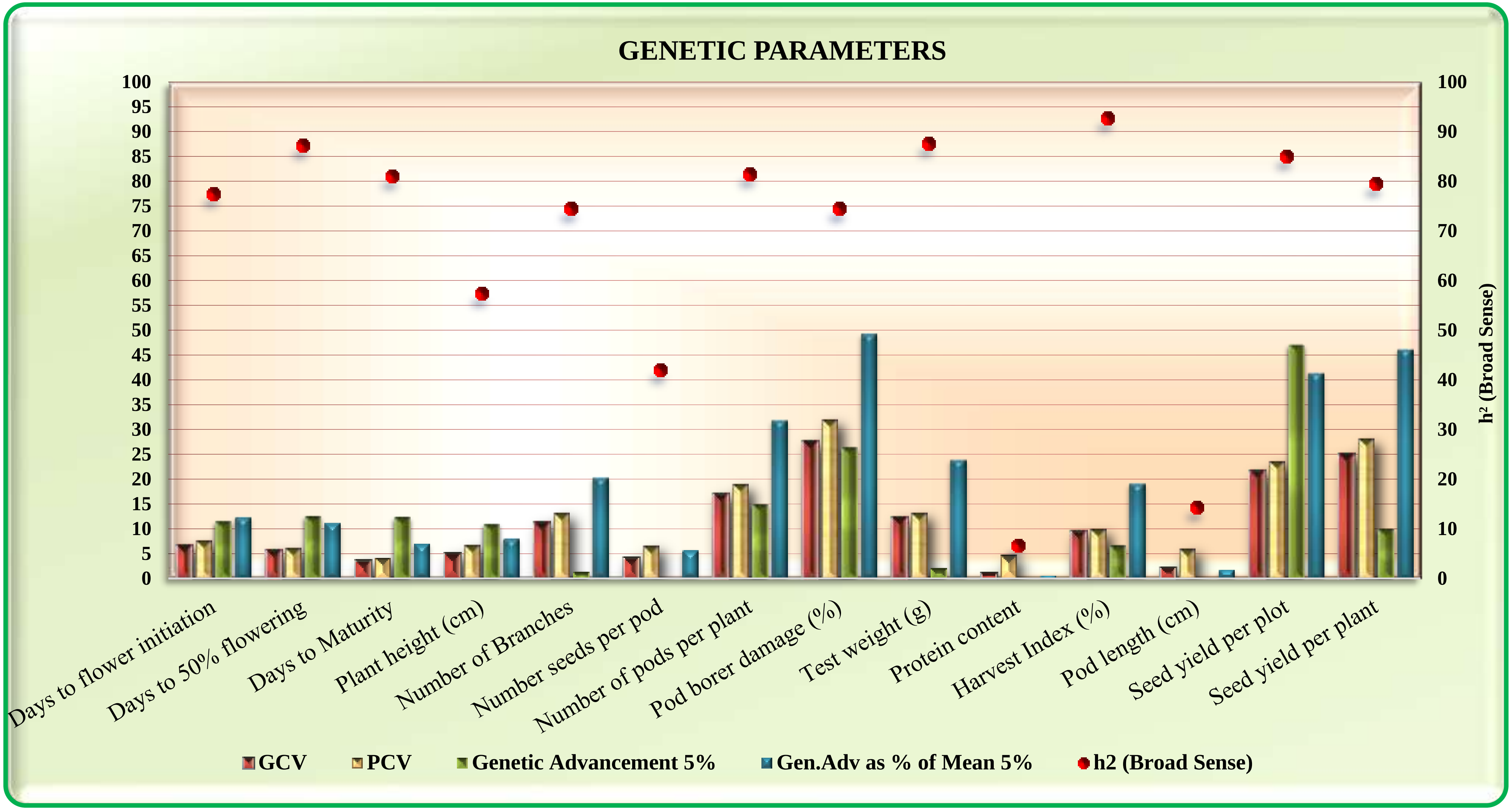


Fig.4.1 : Graphical comparison of GCV, PCV, GA, h^2 (Board sense) and GAM as per cent of mean for 14 characters in pigeon pea

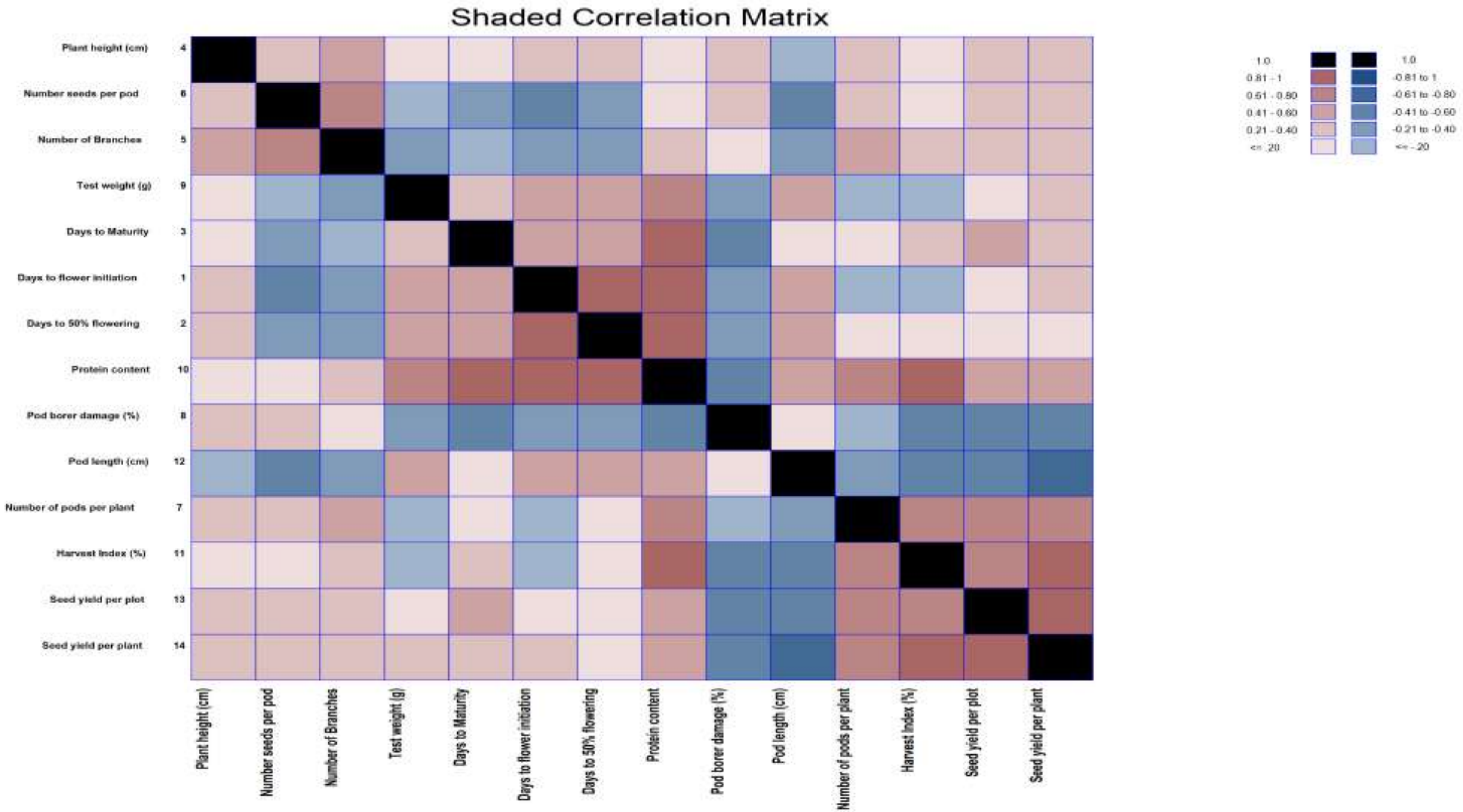


Fig. 4.2: Shaded correlation matrix of phenotypic correlation

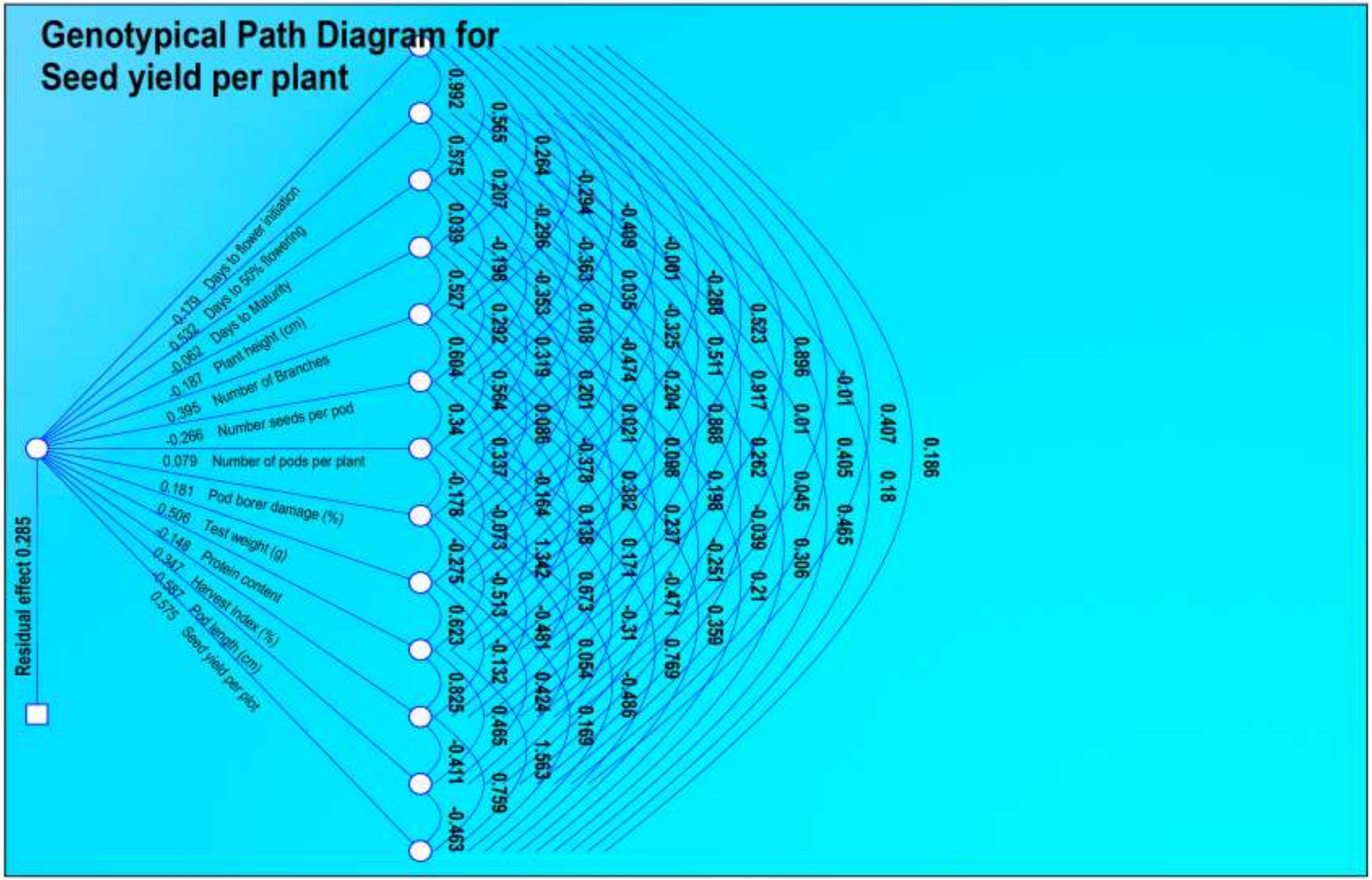


Fig. 4.5: Genotypical path diagram for seed yield per plant

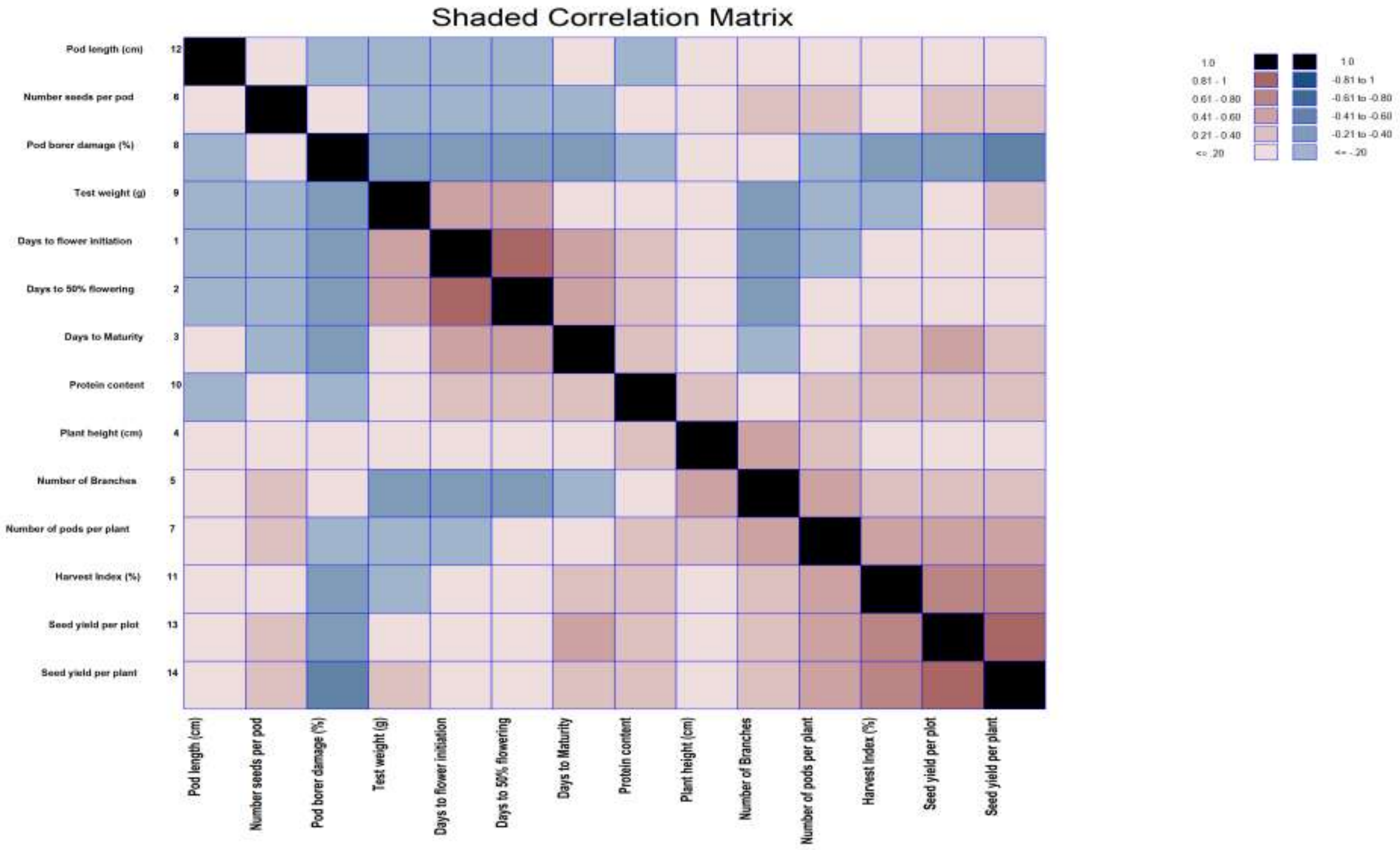


Fig. 4.3 : Shaded Correlation Matrix of Genotypic Correlation

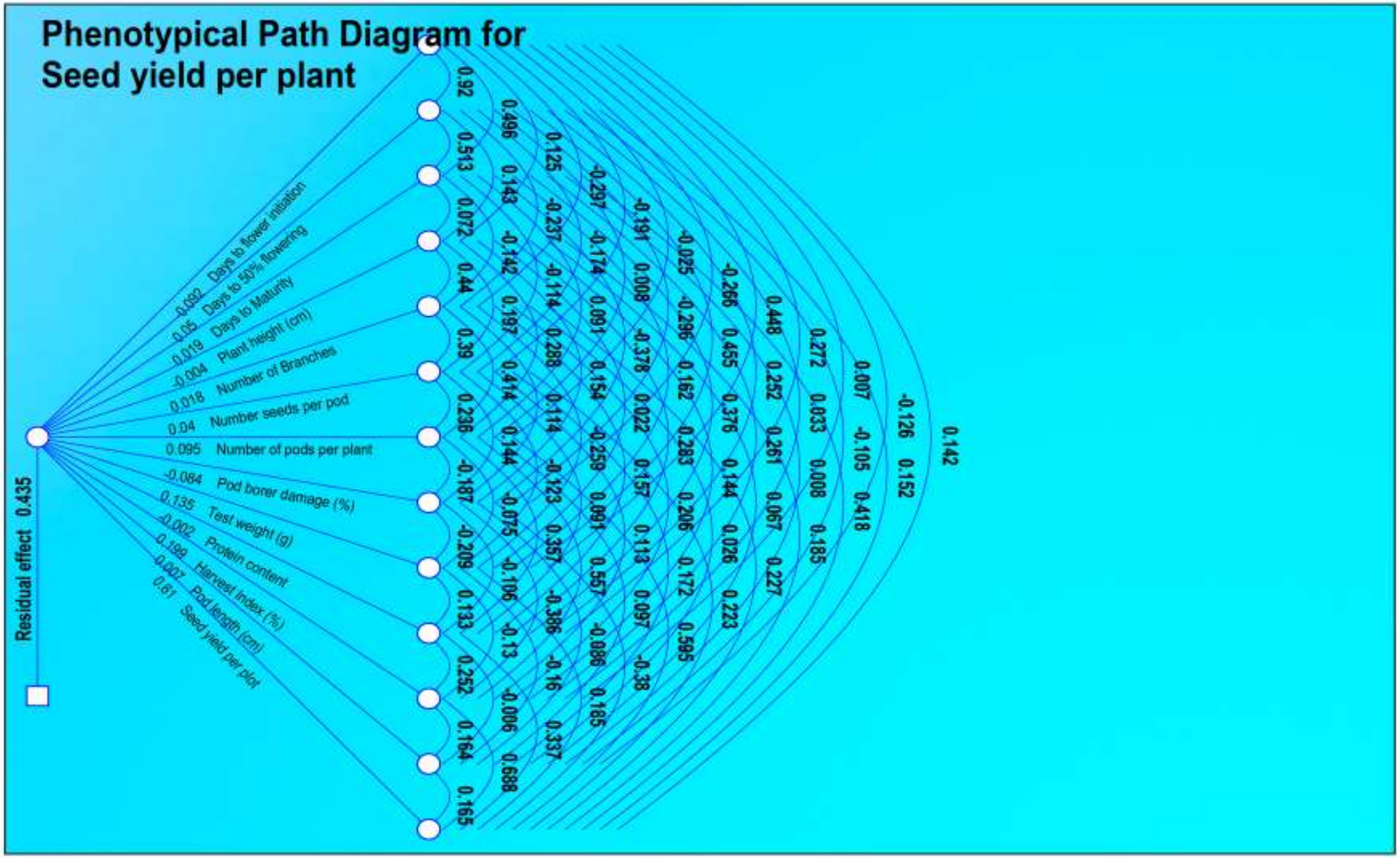


Fig. 4.4: Phenotypical path diagram for seed yield per plant

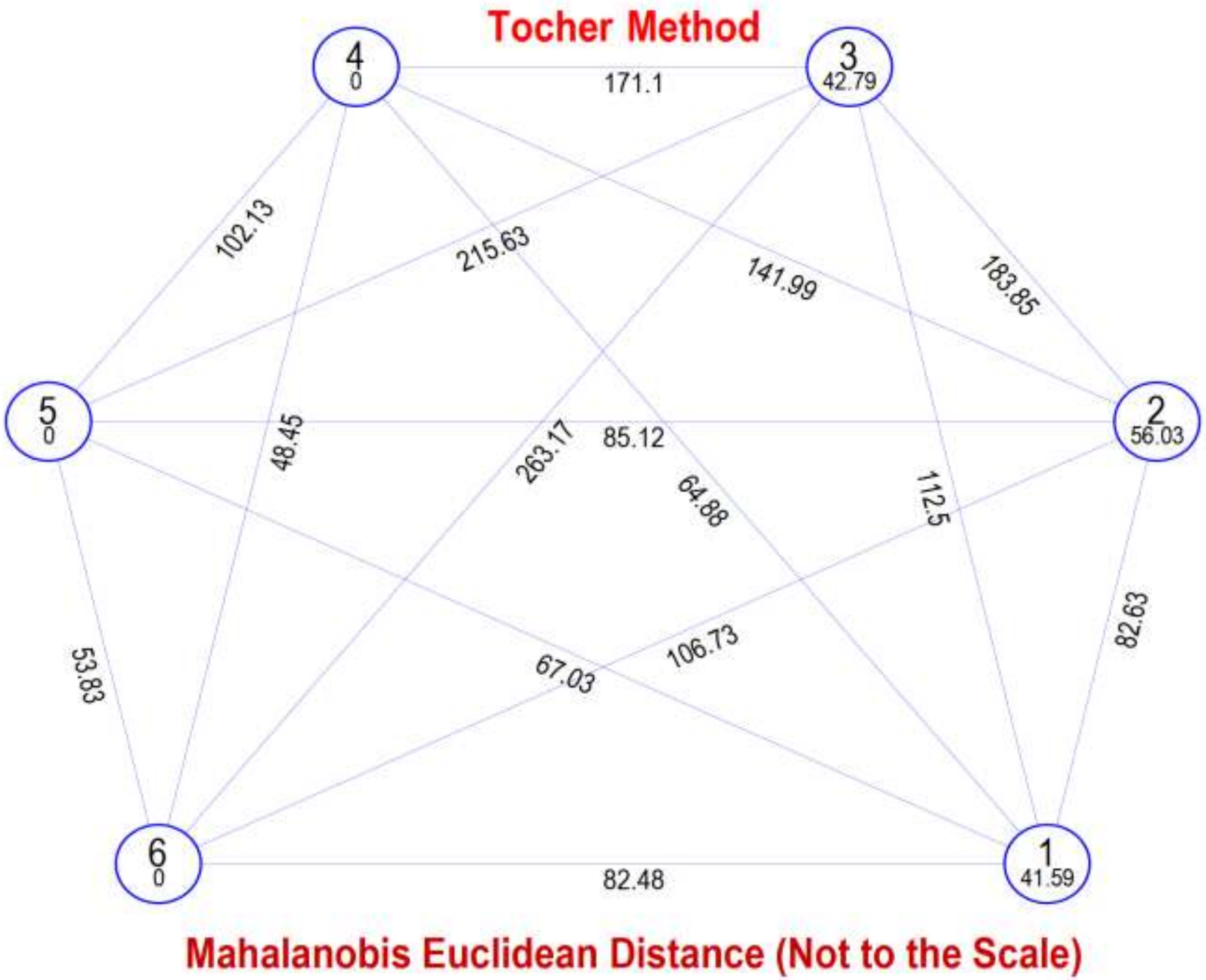


Fig. 4.7: Cluster Diagram (Tocher Method)

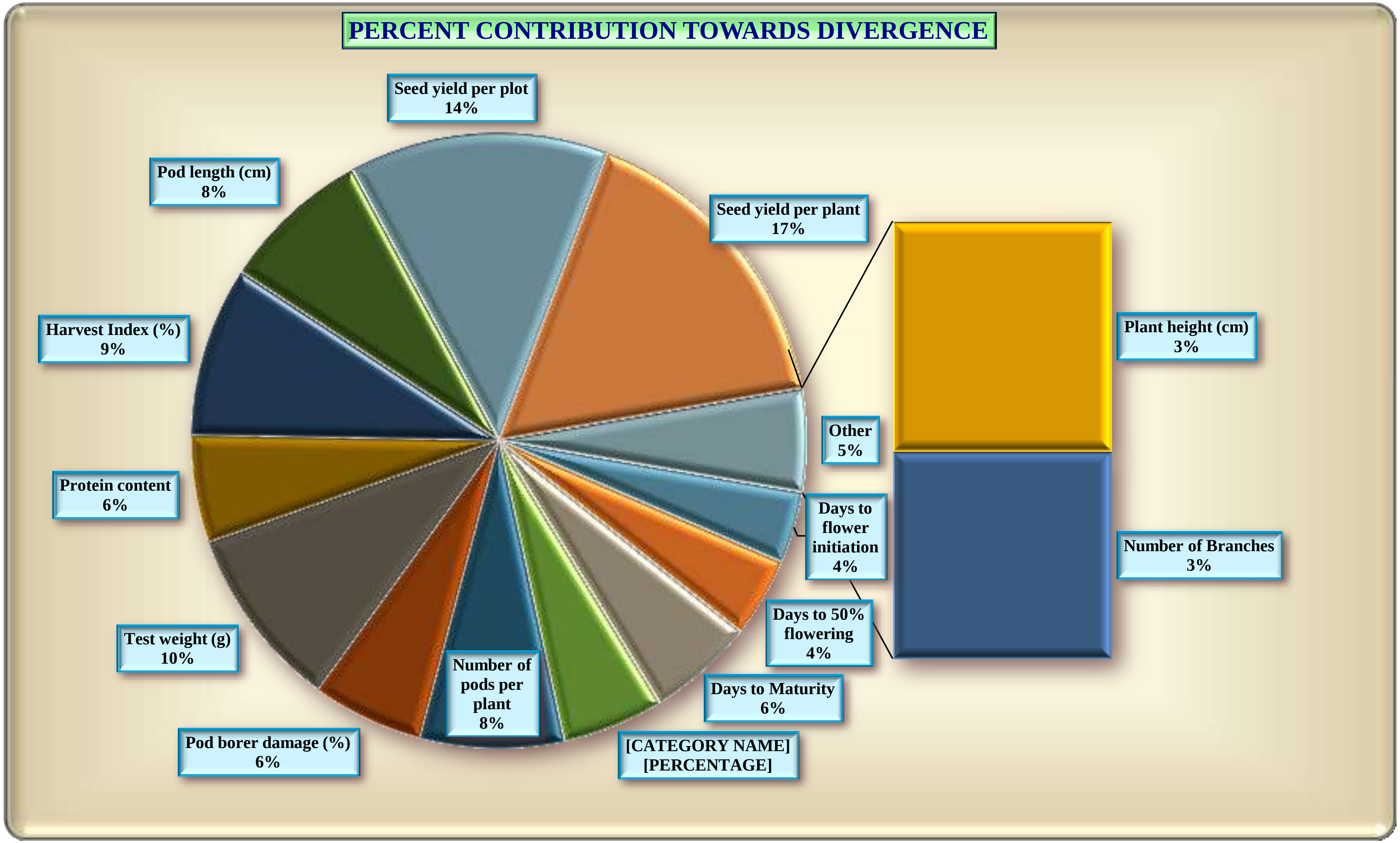


Fig. 4.8: Per cent contribution of various 14 characters towards divergence

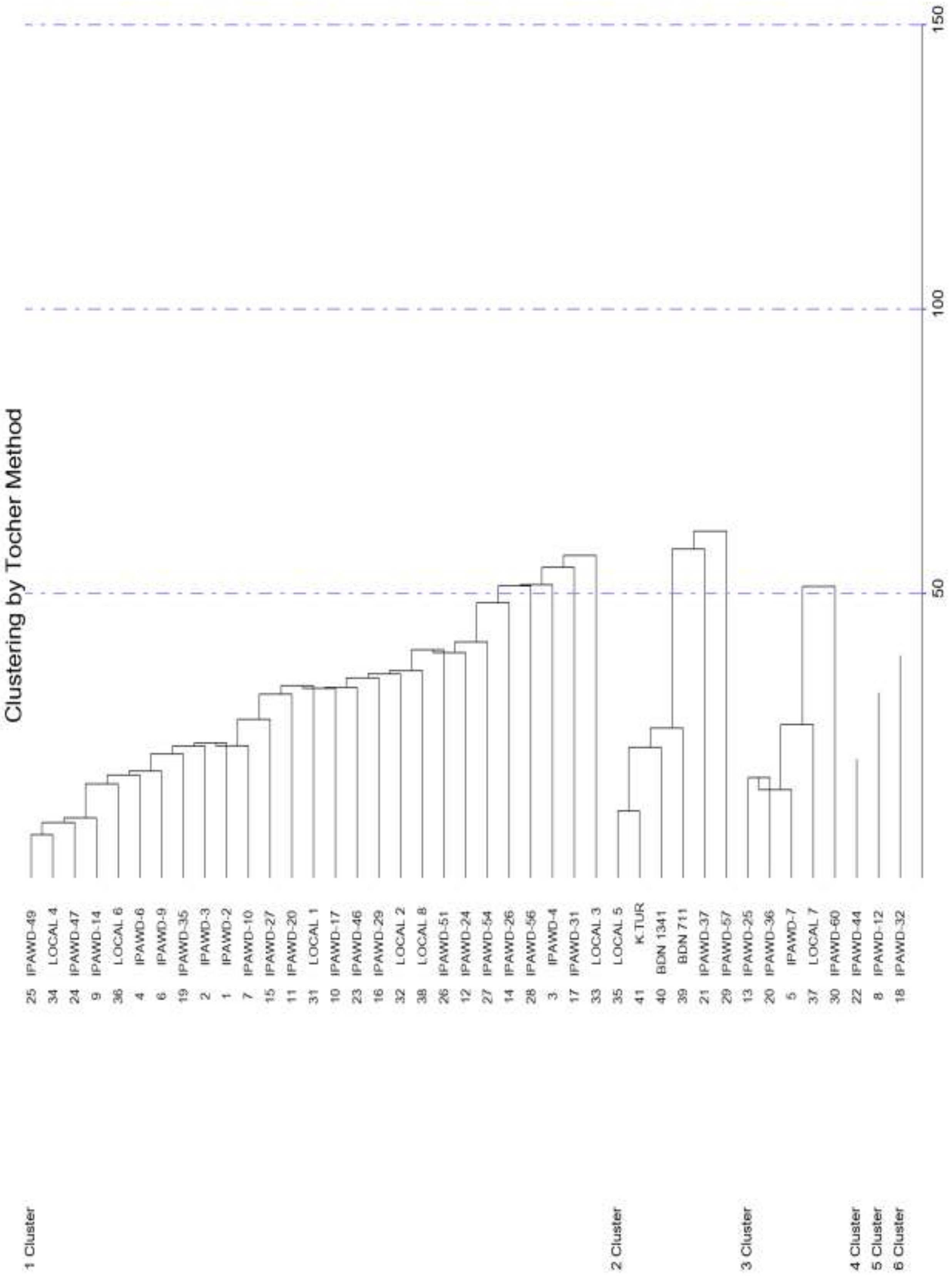


Fig. 4.6: Clustering by Tocher method (Dendrogram)

Plate No.1: General view of experimental plot

Dwarf Plant **Medium Plant** **Tall Plant**

Plate No. 2: Variation in growth habit

Plate No.4 : Variation in pod borer infestation

Plate No. 3:Variation in number of branches of pigeon pea genotypes

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation entitled "Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea. (*Cajanus cajan* L. Millsp.)", which was carried out at the Educational and Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *kharif*, 2022-23 with following objectives:

1. To ascertain the extent of variability present in germplasm lines for yield and its attributing characters.
2. To estimate Correlation and Path coefficient for yield and its related traits.
3. To study the nature and extent of diversity among genotypes.

Forty-one genotypes of Pigeon pea including three check (38+3) were grown in randomized block design with two replications during *kharif*, 2022-2023. Observations were recorded on fourteen different characters *viz*., days to flower initiation, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of seeds per pod, number of pods per plant, percent pod borer damage, test weight (g), protein content (%), harvest index (%), pod length (cm), seed yield per plot (g) and seed yield per plant (g).

The analysis of variance showed significant variation among the genotypes for all the 14 characters studied. The magnitude of mean sum of squares showed comparatively wide range of variation for the characters *viz.*, seed yield per plot, percent pod borer damage, number of pods per plant, plant height, days to flower initiation, days to maturity, days to 50 % flowering, seed yield per plant and harvest index whereas lowest variation noticed for protein content, pod length, number of branches per plant, test weight (g) and number of seeds per pod.

Among the genotypes IPAWD-44, IPAWD-24 and IPAWD-25 were earliest in days to flower initiation. IPAWD-44, IPAWD-24 and IPAWD-25 were early for days to 50 per cent flowering whereas IPAWD-44, IPAWD-29 and IPAWD-51 were taken least days to maturity. The maximum number of branches per plant were reported by IPAWD-60, IPAWD-20, IPAWD-17 genotypes and maximum plant height was found in IPAWD-26.

Maximum number of pods per plant observed in IPAWD-60, IPAWD-7 and LOCAL-7. Whereas maximum number of seeds per pod was found in LOCAL-7, IPAWD-44 and IPAWD-3. The genotypes IPAWD-51 and IPAWD-14 showed maximum percent pod borer damage. Days to maturity was highest in Konkan Tur and IPAWD-12. Maximum pod length shown by IPAWD-26. Maximum test weight recorded in LOCAL-5, BDN-711 and BDN 1341. Maximum seed yield per plant exhibited by IPAWD-36, IPAWD-25 and LOCAL-7. Highest harvest index recorded by LOCAL-7 while highest protein content found in IPWAD-7. Maximum highest seed yield per plot was observed in IPAWD-36.

The magnitude of phenotypic, genotypic variance stated that phenotypic variance was high in magnitude than genotypic variance for all the characters. The magnitude of phenotypic and genotypic variance was closer to each other for majority of the traits hence indicating less significant role of environment in the appearance of these characters. In general, phenotypic coefficient of variation (PCV) was higher in magnitude over genotypic coefficient of variation (GCV) for all the 14 characters. High phenotypic coefficient of variation was observed for the characters seed yield per plot, percent pod borer damage and plant height (cm) whereas it was low for the characters like number of seeds per pod, pod length (cm) and number of branches per plant. High genotypic coefficient of variation was observed in seed yield per plot, percent pod borer damage and number of pods per plant, while it was low for the characters like protein content, pod length (cm) and number of seeds per pod.

Appreciable heritability estimates were observed for all the characters under evaluation. Highest heritability was observed for harvest index, test weight and days to 50 % flowering. Genetic advance found to be highest for seed yield per plot followed by percent pod borer damage. The character’s percent pod borer damage, seed yield per plot (g) and seed yield per plant (g) showed comparatively higher estimates of genetic advance as per cent of mean.

In present investigation, the phenotypic correlation coefficient was higher in magnitude than their genotypic counter parts for most of characters. Number of pods per plant, Harvest index and days to maturity exhibited highly significant positive correlation with seed yield per plant at both phenotypic and genotypic levels. The character’s test weight and days to 50 % flowering had non-significant positive correlation with seed yield per plant while percent pod borer damage had significant negative correlation with seed yield per plant at both phenotypic and genotypic level.

The seed yield is complex character and each character had its own effect for establishing correlation with yield. The path coefficient reported that the character’s test weight, days to 50 % flowering, number of branches per plant, number of seeds per pod, number of pods per plant, seed yield per plot, harvest index had positive direct effect on seed yield at both phenotypic and genotypic levels, while days to flower initiation, plant height and protein content had negative direct effect on seed yield per plant at genotypic and phenotypic levels. Simultaneously, at phenotypic level and genotypic level the traits like days to maturity, percent pod borer damage and pod length had positive and negative direct effect on seed yield per plant.

Forty-one genotypes were grouped into 6 different clusters on the basis of magnitude of D^2 values evaluated by Mahanlanobis D^2 analysis. Among forty-one genotypes, 27 genotypes were clustered into first (I) cluster, followed by cluster (II) with 6 genotypes, 5 genotypes were clustered in cluster (III), cluster (IV), cluster (V) and cluster (VI) had 1 genotype each. Inter cluster distance i.e. Divergence was highest between clusters III and VI (16.22), while intra cluster distance was maximum for cluster II (7.48).

Conclusion:

It is to be confessed that, broad range of variability was present between the genotypes studied for the different quantitative characters. High heritability coupled with high genetic advance per cent mean was observed for percent pod borer damage, seed yield per plot (g), seed yield per plant (g). The higher estimates of heritability coupled with high genetic advance as percent of mean shows additive gene action and make in suitable for direct selection. On the basis of correlation and path analysis, seed yield per plant could be improved through simultaneously selection of percent pod borer damage, number of seeds per pod, harvest index, number of branches per plant, plant height, pod length, number of pods per plant, test weight, protein content, and days to maturity. It is desirable to give more magnitude of weightage to these characters during selection programme.

The genotypes LOCAL-7 followed by IPAWD-36 and IPAWD-25 were observed as best performers in the genotypes studied. These had the highest seed yield per plant and also maximum yield attributing characters. The genotype LOCAL-5 had maximum test weight, LOCAL-7 had maximum number of pods per plant, protein content, harvest index and pod length. The genotype IPAWD-36 had highest seed yield per plot and IPAWD-26 had maximum pod length and IPAWD-27 had minimum percent pod borer damage. All the genotypes mentioned above have the potential to be used as promising genetic material in future breeding programmes.

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APPENDIX I

Meteorological observation during the period of experiment *kharif*, 2022-2023 at Dapoli

Period	**MW**	**Tmax**	**Tmin**	**RH-I**	**RH-II**	**Wind speed**	**Rain**	**RD**	**BSS**	**Epan**
		(oC)	**(oC)**	**(%)**	**(%)**	**(Kmph)**	**(mm)**	**day**	**(hrs.)**	**(mm)**
28.05 - 03.06	**22**	32.9	23.0	87	66	5.7	2.2	0	8.2	5.1
04.06 - 10.06	**23**	33.2	23.4	84	60	5.6	6.2	1	7.5	5.1
11.06 - 17.06	**24**	31.8	23.3	90	71	5.9	83.8	6	6.1	3.8
18.06 - 24.06	**25**	29.8	22.5	94	79	5.0	148.4	5	2.7	3.0
25.06 - 01.07	**26**	27.9	22.8	97	95	5.2	489.2	7	0.5	1.2
02.07 - 08.07	**27**	28.3	22.9	97	93	8.6	625.2	7	0.8	1.7
09.07 - 15.07	**28**	27.3	22.7	98	95	11.0	265.4	7	0.0	1.7
16.07 - 22.07	**29**	28.0	23.2	93	89	8.8	121.4	7	1.1	2.5
23.07 - 29.07	**30**	28.9	23.2	94	83	6.3	120.8	5	2.5	2.6
30.07 - 05.08	**31**	30.1	23.5	93	83	4.4	81.6	4	4.7	3.1
06.08 - 12.08	**32**	26.9	22.5	97	96	12.0	655.6	7	0.0	0.6
13.08 - 19.08	**33**	27.9	22.5	95	92	8.6	202.0	7	0.7	2.2
20.08 - 26.08	**34**	27.9	22.2	96	90	7.0	154.3	7	1.2	2.3
27.08 - 02.09	**35**	29.7	22.1	93	85	3.8	2.6	0	4.6	3.4
03.09 - 09.09	**36**	30.2	23.1	93	86	3.7	31.8	4	4.6	2.9
10.09 - 16.09	**37**	28.8	23.1	94	89	7.0	239.2	6	1.9	2.2
17.09 - 23.09	**38**	27.8	21.4	92	85	3.4	89.9	4	2.4	2.3
24.09 - 30.09	**39**	28.9	21.4	93	82	3.2	79.8	2	4.1	3.3
01.10 - 07.10	**40**	29.8	21.0	91	82	4.2	34.8	3	5.5	3.4
08.10 - 14.10	**41**	29.1	21.6	94	81	2.6	22.6	2	2.6	2.8
15.10 - 21.10	**42**	31.2	22.1	92	82	2.8	53.1	3	6.5	3.1
22.10 - 28.10	**43**	32.3	17.2	92	70	2.2	28.6	1	8.9	3.3
29.10 –04.11	**44**	31.9	15.2	88	62	5.5	0.0	0	10.2	3.6
05.11 –11.11	**45**	33.0	15.4	86	55	2.2	0.0	0	10.0	3.6
12.11 –18.11	**46**	32.8	15.0	91	50	2.2	0.0	0	9.9	3.9
19.11 –25.11	**47**	32.0	13.9	92	56	2.4	0.0	0	9.6	3.8
26.11 –02.12	**48**	32.9	16.6	93	52	2.4	0.0	0	8.5	4.0
03.12 –09.12	**49**	33.2	16.6	93	50	2.3	0.0	0	6.8	4.1
10.12 –16.12	**50**	32.1	17.7	92	53	2.5	0.0	0	5.5	3.8
17.12 –23.12	**51**	34.1	16.8	94	51	2.7	0.0	0	8.6	4.2
24.12 –31.12	**52**	32.2	14.4	92	55	2.7	0.0	0	8.4	4.0
							3559.5	**98**		

RD: Rainy days

BSS*: Bright Sun Shine hours

RH I: Morning Relative Humidity

RH II: Evening Relative Humidity

T max: Temperature Maximum

T min: Temperature Minimum

APPENDIX II

- **Determination of protein content**

The protein content of dry pods was determined by estimating the nitrogen content as per the modified Kjeldhal method and multiplying the nitrogen content with a factor 6.25 and expressed on per cent basis for each genotype.

Methodology for the Determination of Protein by Kjeldhal Method

Principle:

The protein content is determined from the organic Nitrogen content by Kjeldahl method. The various nitrogenous compounds are converted into ammonium sulphate by boiling with concentrated sulphuric acid. The ammonium sulphate formed is decomposed with an alkali (NaOH) and the ammonia liberated is absorbed in excess of standard solution of acid and then back titrated with standard alkali.

Apparatus

a. Kjeldahl digestion flask - 500 or 800 ml

b. Kjeldahl distillation apparatus, - same digestion flask fitted with rubber stopper through which passes lower end of efficient rubber bulb or trap to prevent mechanical carryover of NaOH during distillation or apparatus as shown below:

c. Conical flask, 250 ml

d. Burette 50 ml.

Reagents

a. Concentrated Sulphuric acid – sp. gr. 1.84

b. Sodium Hydroxide solution - 45%. Dissolve 450 gm of Sodium Hydroxide In 1000 ml water

c. Standard Sulphuric acid solution – 0.1 N

d. Standard Sodium Hydroxide solution – 0.1 N

e. Methyl Red Indicator solution - Dissolve 0.5 gm methyl red in 100 ml of Alcohol

Procedure

Weigh quickly about 0.5 g of the sample and transfer to a 500 or 800 ml Kjeldahl flask taking care to see that no portion of the sample clings to the neck of the flask. Add 0.7 gm of Mercuric oxide, 15 gm of Potassium Sulphate and 40 ml of concentrated sulphuric acid. Add two to three glass beads. Place the flask in an inclined position on the stand in the digestion chamber and digest. Heat the flask gently at low flame until the initial frothing ceases and the mixture boils steadily at a moderate rate.

During heating rotate the flask several times. Continue heating for about an hour or more until the colour of the digest is pale blue. Cool the digest and add slowly 200 ml of water. Cool, add a piece of granulated Zinc or anti bump granules and carefully pour down from the side of the flask sufficient Sodium Hydroxide solution (450gm/ litre) to make the contents strongly alkaline (about 110 ml) before mixing the acid and alkaline layer. Connect the flask to a distillation apparatus incorporating an efficient flash head and condenser. To the condenser fit a delivery tube which dips just below the surface of the pipette volume of standard acid contained in a conical flask receiver. Mix the contents of the digestion flask and boil until 150 ml have distilled into the receiver. Add 5 drops of methyl red indicator and titrate with 0.1 N Sodium hydroxide solutions. A blank was also run through all steps as above. Percent crude protein content of the sample was calculated by using the following formula:

% Crude Protein = 6.25* x %N (*. Correction factor)

$$\%N = \frac{(S - B) \times N \times 0.014 \times D \times 100}{\text{Wt. of the sample} \times V}$$

Where

S = Sample titration reading

B = Blank titration reading

N = Normality of HCl

D = Dilution of sample after digestion

V = Volume taken for distillation

0.014 = Milli equivalent weight of Nitrogen

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Investigation of genetic variability in pigeon pea for yield and its attributing traits. (*Cajanus cajan* L. Millsp.)

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Abstract

The study titled “Investigation of genetic variability in pigeon pea for yield and its attributing traits (*Cajanus cajan* L. Millsp.)" took place at the Research and Education farm, Botany Department, College of Agriculture, Dapoli, during the Kharif season of 2022. Across all 14 traits examined, the PCV(phenotypic coefficient of variation) surpassed the GCV (genotypic coefficient of variation) in magnitude. Notably, per plot seed yield, % pod borer damage, plant height exhibited high PCV. Conversely, per plot seed yield, % pod borer damage, pods / plant displayed high GCV.

Appreciable heritability estimates were noted across all evaluated traits, with the highest heritability observed for harvest index, test weight, and days to fifty% flowering. Genetic advance was most pronounced in per plot seed yield, followed by % pod borer damage. Moreover, % pod borer damage, per plot seed yield (g), seed yield / plant (g) showcased comparatively higher estimates of genetic advance as a percentage of mean.

In terms of performance, the genotypes LOCAL-7, IPAWD-36, and IPAWD-25 emerged as top performers, demonstrating the highest seed yield / plant and maximum yield-related characteristics. These genotypes hold promise as valuable genetic resources for future breeding programs.

Keywords: Genotype, variability, heritability, genetic advance etc.

Introduction

Pulse crops have a significant impact on Indian economy, often dubbed as the "Poor man’s meat" due to their affordability and high-quality protein content. Grain legumes or pulses hold a crucial position in meeting human dietary and nutritional needs. They serve as key components in the diets of many, particularly in developing nations, augmenting cereal-based diets and enhancing their nutritional value by providing valuable protein source. Throughout history, combination of cereals and pulses has consistently offered enhanced nutrition to people worldwide. Furthermore, pulses play vital role in bolstering soil health through biological N_2 fixation, fostering sustainable cropping systems, diversifying crops, and managing natural resources.

The pigeon pea, a crucial legume crop in rainfed agriculture within semiarid tropics, demonstrates high drought resistance and thrives in areas with less than 650 mm annual rainfall. It exists in both perennial and annual varieties, with the former lasting 3 to 5 years and the latter more suitable for seed production. Typically cultivated in tropical or subtropical regions across various soils (ranging from sandy to heavy, with pH levels from 5.0 to 8.0), pigeon peas cannot withstand even light frost during growth stages. However, compared to other pulse crops, they display superior adaptability to marginal climates. Genetic diversity epicenters for pigeon pea are found in Africa and India, with India regarded as the primary origin and West Africa as a secondary center. Pigeon pea are rich in protein and contains essentially amino acids such as methionine, lysine, and tryptophan.

Globally, pigeon pea cultivation spans 5.40 million hectares, yielding an annual production of 4.48 million metric tons, averaging a productivity of 827 kilograms per hectare (FAOSTAT, 2021). Specifically in India, pigeon pea is grown across 3.88 million hectares, resulting in a production of 2.84 million metric tons and a productivity of 733 kilograms per hectare (FAOSTAT, 2021). Notably, in Maharashtra alone, pigeon pea is cultivated over an average area of 20.98 lakh hectares in 2021, yielding total production of 12.66 lakh tons (Source - Kharif prospects, Bhopal).

Pigeon pea, a robust and adaptable crop, exhibits notable drought tolerance. Its varied maturity range facilitates adaptation to various environments and cropping systems. Farmers cultivate it both as a sole crop and in intercropping systems with urd bean, mung bean, castor, sorghum, soybean, cotton, maize, and groundnut. Its resilience to drought and hardy nature enables thriving in marginal, less fertile soils, even under poor management and rainfed conditions.

Materials and Methods

During the *kharif* season of 2022, the study was carried out at Educational and Research Farm within the Botany Department, College of Agriculture, located in Dapoli, Dist. Ratnagiri, Maharashtra. Throughout the experimentation phase, meteorological data was collected from meteorological observatory situated at the Department of Agronomy, College of Agriculture, Dapoli. The experiment employed a randomized block design with two replications, where each plot covered an area of approximately 10.80 meters × 1.20 meters, containing 2 rows per genotype. Within each row, there was 18 plants, summing up to total of 36 plants/plot. For field observations, five plants were chosen randomly from each genotype. A comprehensive record of 14 characteristics was collected, encompassing observations such as Days to flower initiation, Days to fifty% flowering, Days to maturity, No. of branches /plant, No. of seeds / plant, Pods / plant, % pod borer damage, Test weight, Pod length, Plant height, Seed yield / plant, Per plot seed yield, Harvest index, Protein content.

The data for individual characteristics underwent analysis of variance using the commonly applied method in the RBD, as outlined in (Panse and Sukhatme 1985) [6].

Results and Discussion

Components of Variation

The total variance among the genotypes was divided into genotypic, phenotypic, and environmental components. Across all studied characteristics, the magnitude of phenotypic variance exceeded that of genotypic variance. Phenotypic variance ranged from 0.08 (pod length) to 731.59 (per plot seed yield) for different traits. The highest phenotypic variance was observed for per plot seed yield, followed by % pod borer damage, plant height, pods / plant, days to maturity, days to flower initiation, days to fifty % flowering, seed yield / plant. The variance was moderate for harvest index, while it was lowest for pod length, followed by No. of seeds / pod, No. of branches / plant, protein content, test weight.

In all traits, except for No. of seeds / pod, pod length, and protein content, genotypic variance exhibited greater magnitude than environmental variance. The most substantial genotypic variance was observed in per plot seed yield, followed by pod borer damage, pods / plant, plant height, days to maturity, days to fifty % flowering, days to flower initiation, and seed yield / plant. Moderate genotypic variance was noted for harvest index. Pod length, No. of seeds / pod, protein content, followed by No. of branches / plant, displayed the lowest magnitude of genotypic variances. Pashwan et al. (2021) [7] similarly reported findings with the highest genotypic variance for plant height and moderate variance for pod length,No. of branches / plant.

Environmental variance showed greater magnitude for per plot seed yield, followed by % pod borer damage and plant height. It was moderate for No. of pods / plant, days to flower initiation, and days to maturity, while being lowest for No. of seeds / pod, pod length, test weight, No. of branches / plant, harvest index, protein content, days to fifty % flowering, seed yield / plant. Patro et al. (2019) [9] and Ekka and Sahu (2019) [12] similarly confirmed these results, particularly concerning plant height and pod length.

Table 1: Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances for 14 quantitative characters of pigeon pea.

Sr. No.	Characters	σ^2_p	σ^2_g	σ^2_e
1	Days to initiation of flowering	53.65	41.59	12.06
2	Days to fifty% flowering	49.93	43.57	6.36
3	Days to maturity	56.23	45.62	10.61
4	Plant height at harvest (cm)	88.08	50.69	37.39
5	No. of branches / plant	0.93	0.70	0.24
6	Pods / plant	81.34	66.30	15.04
7	No. of seeds / pod	0.04	0.02	0.03
8	Pod length (cm)	0.08	0.01	0.09
9	Test weight (g)	1.55	1.36	0.19
10	% pod borer damage	300.41	224.15	76.27
11	Seed yield / plant	38.29	30.46	7.82
12	Per plot seed yield	731.59	622.59	109
13	Harvest index (%)	12.66	11.74	0.92
14	Protein content (%)	1.12	0.07	1.04

Coefficient of variation

The findings indicated that the PCV surpassed the respective GCV in magnitude. % pod borer damage, seed yield / plant, and per plot seed yield exhibited the highest PCV. Moderate PCV was observed for the pods / plant, test weight, No. of branches / plant, harvest index. Kumar et al. (2014) [5] and Fousiya et al. (2021) [3] observed similar patterns, noting the highest PCV for seed yield / plant and per plot seed yield.

The lowest magnitude of PCV was recorded for days to maturity, followed by protein content, pod length, days to fifty% flowering, plant height, No. of seeds / pod, and days to initiation of flowering. Priyanka et al. (2016) [10] reported comparable results.

The genetic variation among the 41 genotypes was assessed in terms of GCV. The highest GCV was found in % pod borer damage, followed by seed yield / plant and per plot seed yield. Moderate GCV was observed in traits such as pods / plant, test weight,No. of branches / plant. The lowest GCV was seen in harvest index, days to initiation of flowering, days to fifty% flowering, plant height, No. of seeds / pod, days to maturity, pod length, and protein content. This categorization based on GCV and PCV utilized the standard scale provided by Sivasubramanian and Menon (1973) [14].

Heritability and genetic advance

The broad-sense heritability ranged from 6.70% (protein content) to 92.80% (Harvest index). It was recorded high for harvest index, followed by test weight, days to fifty% flowering, per plot seed yield, pods / plant, days to maturity, seed yield / plant, days to flower initiation, % pod borer damage, No. of branches / plant, plant height, No. of seeds / pod. Pod length and protein content exhibited the lowest heritability. Similar results indicating high heritability in harvest index and test weight were also reported by Rao and Rao (2020) [11] and Patel and Patel (2020) [8].

The genetic advance spanned from 0.08 (pod length) to 47.42 (per plot seed yield). Per plot seed yield exhibited a moderate level of genetic advance. Conversely, the lowest magnitude of genetic advance was observed in % pod borer damage, pods / plant, days to fifty% flowering, days to maturity, days to flower initiation, plant height, seed yield / plant, harvest index, test weight, No. of branches / plant, No. of seeds / pod, and protein content. Singh et al. (2013) [13] documented similar findings, particularly noting low magnitude of genetic advance for seed yield / plant, harvest index, test weight.

The genetic advance as a percentage of mean (GAM) ranged from 0.68% (protein content) to 49.50% (% pod borer damage). The highest GAM was seen in % pod borer damage, followed by seed yield / plant, per plot seed yield, pods / plant, test weight, and No. of branches / plant. Harvest index, days to flower initiation, days to fifty % flowering displayed a moderate estimate of GAM. The lowest magnitude of GAM was recorded for plant height, days to maturity, No. of seeds / pod, and pod length.

This categorization of Heritability, Genetic advance, and Genetic advance as a percentage of mean was determined following the standard scale outlined by Johnson et al. (1955) [4].

Table 2: Estimates of genetic parameters for 14 quantitative characters in pigeon pea

Sr. No.	Characters	PCV (%)	GCV (%)	ECV (%)	h^2b (%)	GA	GAM (%)
1	Days to initiation of flowering	7.79	6.86	3.70	77.50	11.70	12.45
2	Days to fifty% flowering	6.29	5.88	2.25	87.30	12.70	11.31
3	Days to maturity	4.26	3.84	1.85	81.10	12.53	7.12
4	Plant height at harvest	6.90	5.23	4.50	57.50	11.13	8.18
5	No. of branches / plant	13.35	11.53	6.73	74.60	1.48	20.52
6	Pods / plant	19.12	17.26	8.22	81.50	15.14	32.10
7	No. of seeds / pod	6.74	4.38	5.13	42.10	0.18	5.85
8	Pod length (cm)	6.19	2.35	6.62	14.40	0.08	1.84
9	Test weight (g)	13.36	12.51	4.69	87.70	2.25	24.14
10	% pod borer damage	32.20	27.82	16.23	74.60	26.64	49.50
11	Seed yield / plant	28.33	25.27	12.80	79.60	10.14	46.43
12	Per plot seed yield	23.77	21.93	9.18	85.10	47.42	41.67
13	Harvest index (%)	10.11	9.74	2.72	92.80	6.80	19.32
14	Protein content (%)	4.92	1.27	4.75	6.70	0.15	0.68

Conclusion

The study concluded that a broad range of variability existed among the genotypes across various quantitative traits. Traits like % pod borer damage, per plot seed yield (g), and seed yield / plant (g) exhibited high heritability coupled with a high genetic advance as a percentage of mean. This combination suggests an additive gene action and signifies their suitability for direct selection, indicating the need to prioritize this traits in selection programs.

Among genotypes studied, LOCAL-7, followed by IPAWD-36 and IPAWD-25, emerged as top performers, displaying the highest seed yield / plant and attributing maximum yield-related characteristics. LOCAL-5 exhibited the highest test weight, while LOCAL-7 excelled in the pods / plant, protein content, pod length, harvest index. IPAWD-36 displayed the highest per plot seed yield, IPAWD-26 had the maximum pod length, and IPAWD-27 showed the least % pod borer damage.

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THESIS ABSTRACT

a)	Title of the thesis	:**‘Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea’. (*Cajanus cajan* L. Millsp.)’**
b)	Full name of the student	: Mr. Burhade Sanket Tulsidas
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d)	Degree to be awarded	: M.Sc. (Agri.)
e)	Year of award of degree	: 2023
f)	Major subject	: Genetics and Plant Breeding
g)	Total number of pages in the thesis	: 75
h)	Number of words in the abstract	: 474
i)	Signature of student	: ________________
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The present investigation, entitled “Assesment of genetic variability, character association and diversity for yield and its attributing traits in Pigeon pea’. (*Cajanus cajan* L. Millsp.)” was conducted at Research and Education farm, Department of Agriculture Botany, College of Agriculture, Dapoli during *Kharif* 2022.

In general, phenotypic coefficient of variation (PCV) was higher in magnitude over genotypic coefficient of variation (GCV) for all the 14 characters. High phenotypic coefficient of variation was observed for the characters seed yield per plot, percent pod borer damage and plant height (cm). High genotypic coefficient of variation was observed in seed yield per plot, percent pod borer damage and number of pods per plant.

Appreciable heritability estimates were observed for all the characters under evaluation. Highest heritability was observed for harvest index, test weight and days to 50 % flowering.

Genetic advance found to be highest for seed yield per plot followed by percent pod borer damage. The character's percent pod borer damage, seed yield per plot (g) and seed yield per plant (g) showed comparatively higher estimates of genetic advance as per cent of mean.

The phenotypic correlation coefficient was higher in magnitude than their genotypic counter parts for most of characters. Number of pods per plant, Harvest index and days to maturity exhibited highly significant positive correlation with seed yield per plant at b phenotypic and genotypic levels. The character's test weight and days to 50 % flowering had non-significant positive correlation with seed yield per plant while percent pod borer damage had significant negative correlation with seed yield per plant at both phenotypic and genotypic level.

The path coefficient reported that the character's test weight, days to 50 % flowering, number of branches per plant, number of seeds per pod, number of pods per plant, seed yield per plot, harvest index had positive direct effect on seed yield at both phenotypic and genotypic levels, while days to flower initiation, plant height and protein content had negative direct effect on seed yield per plant at genotypic and phenotypic levels.

Forty-one genotypes were grouped into 6 different clusters on the basis of magnitude of D^2 values evaluated by Mahanlanobis D^2 analysis. Among forty-one genotypes, 27 genotypes were clustered into first (I) cluster, followed by cluster (II) with 6 genotypes, 5 genotypes were clustered in cluster (III), cluster (IV), cluster (V) and cluster (VI) had 1 genotype each. Inter cluster distance i.e., Divergence was highest between clusters III and VI (16.22), while intra cluster distance was maximum for cluster II (7.48).

The genotypes LOCAL-7 followed by IPAWD-36 and IPAWD-25 were observed as best performers in the genotypes studied. These had the highest seed yield per plant and also maximum yield attributing characters. All the genotypes mentioned above have the potential to be used as promising genetic material in future breeding programmes.

Key words: Genotype, Variability, heritability, Genetic advance *etc.*

VITAE

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9. Research Papers published

Title of paper

Burhade S T, Palshetkar M G, Pethe U B, Mahadik S G, Rathod R R, Misal S S, Shinde P S (2023). Investigation of genetic variability in pigeon pea for yield and its attributing traits. (*Cajanus cajan* L. Millsp). *The Pharma Innovation Journal*, **12**(11): 2384-2386.

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