“GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS IN SEED COWPEA [*Vigna unguiculata* (L.) Walp]”

by

Miss. Patil Ashwini Rajkumar

Reg. No. 019/036

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

in partial fulfilment of the requirements for the degree of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY

POST GRADUATE INSTITUTE,
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APPROVED BY

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2021

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
there of has not been submitted
by me or other person to any
other University or Institute
for Degree or
Diploma

Place : MPKV, Rahuri
Dated : / /2021

(Patil A.R.)

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CERTIFICATE

This is to certify that the thesis entitled **"GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS SEED COWPEA [*Vigna unguiculata* (L.) Walp]"** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist.- Ahmednagar, Maharashtra (India), in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING),** embodies results of piece of bonafide research work carried out by **Miss. PATIL ASHWINI RAJKUMAR** under my guidance and supervision and that no part of the thesis has been submitted to any other degree or diploma.

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Place : MPKV, Rahuri
Date : / /2021

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Place : M.P.K.V., Rahuri. (A.R. Patil)

Date : / /2021

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LIST OF ABBREVIATIONS

%	Percent
b.s.	Broad sense
C.D.	Critical difference
C.V.	Coefficient of variation
cm	Centimeter
Cov.	Co-variance
d.f.	Degrees of freedom
et al.	And others (et alia)
Fig.	Figure
g	Gram
GA	Genetic advance
GCV	Genotypic coefficients of variation
h^2	Heritability
ha	Hectare
i.e.	That is (idest)
kg	Kilogram
MSS	Mean sum of squares
No.	Number
PCV	Phenotypic coefficient of variation
r	Correlation coefficient
RBD	Randomized Block Design
RSLG	Rahuri Sorghum Local Germplasm
S.E.	Standard Error
S.S.	Sum of squares
via	By the way of, by means of
viz.	Videlicet (Namely)
Vs	Versus
Σ	Summation

ABSTRACT

“GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS IN SEED COWPEA (*Vigna unguiculata* L. Walp).”

by

Miss. PATIL ASHWINI RAJKUMAR

A candidate for the degree of
MASTER OF SCIENCE (AGRICULTURE)
in
AGRICULTURE BOTANY
2021

Research Guide	**: Dr. G. C. Shinde**
Department	**: Agricultural Botany**
Major discipline	**: Genetics and Plant Breeding**

The present study entitled “Genetic Diversity and Path Coefficient Analysis in Seed Cowpea [*Vigna unguiculata* (L.) Walp]” was conducted at Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri with the objectives to estimates the genetic diversity and the association and cause effects of yield contributing traits with seed yield.

The 33 genotypes of cowpea were sown in a randomized block design with two replications and observations were recorded on randomly selected five plants for fourteen characters *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), number of main branches, number of pods per plant, pod length cm), number of seeds per pod, test weight (g), seed yield per plant (g), seed yield per plant (kg/ha), protein content (%), tannin content, digestibility (%) and cocking time.

The analysis of variance revealed that the mean sum of squares due to genotypes for all the characters except digestibility were highly significant, which indicated presence of appreciable amount of variability among the genotypes for the all characters except digestibility.

Form the mean performance, it is observed genotypes CP-41, CP-01R, CP-13R, CP-01, PCP-1110, PCP-1404, PMCP-1016, PCP-1809, PCP-1814, Phule Pandhari and Phule Sonali were the best genotypes having desired *per se* performance for yield components.

The high magnitude of GCV and PCV were found for plant height, number of pods per plant and seed yield per plant. The estimation of genotypic and phenotypic coefficient of variation indicates the amount of genetic and non-genetic variation present for different desirable characters. Higher magnitude of GCV and PCV for these traits indicated presence of high degree of variability and better scope for selection.

High heritability estimates accompanied with high genetic advance percent of mean was noticed for plant height, number of pods per plant, seed yield per plant, number of branches, test weight and days to 50 % flowering while, high estimates of heritability coupled with moderate genetic advance percent of mean were observed for the characters days to maturity, number of seeds per pod and tannin content which is due to additive gene action and direct selection for such traits is rewarding in crop improvement.

The characters number of pods per plant, plant height, test weight, pod length leaf and crude protein showed positive and significant correlation with seed yield per plant at genotypic level. The characters days to 50% flowering, days to maturity, pod length, plant height and number of branches and other characters plant height, number of branches and number of pods were found significantly and positively inter correlated.

The maximum positive direct effect on seed yield per plant was recorded by number of pods per plant followed by pod length, number of seeds per pod and test weight. The characters days to maturity and number of main branches showed moderately positive direct effect on seed yield per plant. The number of branches, number of pods per plant and pod length contributed indirectly towards seed yield per plant.

The 33 genotypes were grouped into six clusters. Cluster I was the largest with 24 genotypes, followed by cluster III with 4 genotypes, followed by cluster IV with 2 genotypes. Cluster II, V and VI were monogenotypic. Clustering pattern indicated that genetic diversity and geographic diversity are not related.

The maximum inter cluster distance showed by cluster I and cluster VI (31.31) followed by cluster III and VI (29.49), cluster II and VI (27.39), cluster I and IV (27.26), cluster III and IV (21.10) and cluster IV and V (20.94).

The characters *viz.,* days to 50% flowering, plant height, number of pods per plant and test weight contributed maximum for divergence.

Based inter-cluster distance cluster mean and *per se* performance, the genotypes viz., CP-04, CP-10, CP-10R, PCP-1411, CP-37, CP-10R,CP-39 and Phule Sonali are suggested to utilize for future breeding programme.

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1. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous leguminous crop belongs to family Leguminoseae (Mackie and Smith, 1935) with a diploid chromosome number of 2n=2x=22 (Darlington and Wylie, 1955). Cowpea is in cultivation from very ancient times in the tropics of old world. Vavilov (1951) recognized India and Africa as a main centre of origin, while China is the secondary. Cowpea, self pollinated crop belongs to family Leguminosae, subfamily Fabaceae and genus *Vigna*. The genus *Vigna* is a pantropical genus of about 170 species, out of these 120 in Africa, twenty two (South-East Asia and India) and a few in America and Australia (Faris, 1965)

Cowpea is a tropical grain legume which plays nutritional role of the tropics and sub tropics, especially in Sub-Saharan Africa, Asia, Central and South America (Singh *et al*., 1997). Cowpea young leaves, pods and beans contain vitamins and minerals and therefore it is used for human consumption and animal feeding (Nielson *et al*., 1997) It is also one of oldest legume used as protein source for humans and livestock (Steele, 1972).

Dry seeds of cowpea are used to prepare several meal and snacks dishes. It contains high amount of quality protein (23.4 %), carbohydrate (60.3 %), fat (1.8 %) and sufficient amount of calcium (76 mg/100gm), iron (57 mg/100gm) and vitamins such as thiamine (0.92 mg/100g.), riboflavin (0.18 mg/100g.) and nicotinic acid (1.9mg/100g) (Chatterjee and Bhattaacharya, 1986).

Due to its nutritional value, it is gaining popularity in developing and under developed countries. Like other legumes, cowpea fixes atmospheric nitrogen, and thus contributes to the maintain soil nitrogen levels. One of the more remarkable things about cowpea is that it thrives in dry environments.

Polyphenols also plays an important role in reduction of protein digestibility (Elias *et al.,* 1979). More protein containing high digestibility in cowpea. Cooking is the common processing method of pulses which required to remove anti nutritional factors and to ensure acceptable sensory quality. In normal practice pulses are usually soaked in water so as it saves time and energy before cooking (Fernandes *et al*., 2010).

Among cultivated legumes, the largest usable protein is in cowpea and it’s most important plant protein source as a valuable and dependable commodity crop for farmer and grain traders (Nwosu *et al.,* 2013). Cowpea is grown worldwide on 12.61 million ha with production about 5.59 million tons. The productivity is of 20-25 kg/ha (dpd.gov.in > Cowpea, Directorate of Pulses Development Report, 2019). In India, cowpea is cultivated in about 1.3 million ha area and production is of 2.1 million tones having a productivity of 607 kg/ha (www.cazri.res.in).

Understanding of genetic variability is very valuable to plant breeding programme, because it is helpful choosing the best yield traits for hybridization or selection For fruitful selection, knowledge of heritable and non-heritable components of variability is of imperative need. This may be done by estimating genetic parameters like genotypic coefficient of variation, heritability and genetic advance for yield and its related traits.

The productivity of selection in any breeding programme is based on the knowledge of character association. Although genotypic correlation provides an estimate of inherent association between the genes governing any two traits, phenotypic correlation denotes the extent of the observation having a relationship between two characters. Path analysis, which is used to formulate selection indices for genetic improvement, can be applied to estimate the cause effect of the character. If the correlation is due to direct effect it reflects true relationship and for improving the yield such characters can be selected.

A basic and fundamental practice that has been carried out is the genetic diversity assessment and assigning different genotypes/ inbred lines into different clusters. Genetically diverse parents for efficient hybrid production can be choose through biometrical procedure which gives the quantification of genetic diversity of that parent. High heterotic effects are mainly produced by genetically diverged parents, so that genetic diversity between the genotypes is very important (Falconer, 1960). Mahalanobis D^2 analysis is very functional implement in studying the nature and cause of diversity influential in the available germplasm.

Therefore, the present investigation entitled “Genetic diversity and path coefficient analysis in seed cowpea (*Vigna unguiculata* L.) WALP)." was undertaken with thirty genotypes along with three checks for following objectives.

1. To estimate genetic diversity.
2. To estimate association and cause effect of yield contributing traits with seed yield.

2. REVIEW OF LITERATURE

Success of any breeding programme depends on wise selection. The efficient selection depends upon the knowledge of genetic architecture of quantitative traits. In present chapter by keeping in view the objectives of the present investigation an attempt has been made to present in brief an account of previous research work under following heads :-

2.1 Genetic Variability
2.2 Correlation Coefficient
2.3 Path Coefficient Analysis
2.4 Genetic Diversity

2.1 Genetic Variability

Exploration of genetic variability in the available germplasm is a pre-requisite for any successful breeding programme. Distinction between genotype and phenotype was noticed by Johannsen (1909). From this it is clear that, interaction between genotype and environment is responsible for variability (Fisher, 1930). The total variance was partitioned into genotypic and phenotypic variances by using estimates of environmental variance from non-segregating population (Charles and Smith, 1939).

The estimation of heritability helps the plant breeder in selection of elite genotypes. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. Allard (1960) expressed the genetic advance as the product of selection intensity, heritability and phenotypic standard deviation of a character.

Anbuselvem *et al.* (2000) reported high estimates of heritability and genetic advance in cowpea for plant height and days to 50 per cent flowering indicating the preponderance of additive gene action.

Kalaiyarasi and Palanisamy (2000) studied traits *viz.*, plant height, number of branches per plant, pod length, seed yield per plant in cowpea and observed both GCV and PCV were moderate for plant height, pod length and seed yield per plant.

Nehru and Manjunath (2001) evaluated 40 genotypes of cowpea and observed higher estimates of PCV for pods/plant followed by cluster/plant, primary branches/plant and yield/plant. High heritability and genetic advance expressed as per cent of mean were noticed for pods/plant and moderate for plant height, 100-seed weight and yield/plant.

Kumar *et al.* (2002) observed a wide range of genetic variability for most of the characters in their studies. High heritability was recorded for green fodder yield/plant, number of days to 50 % flowering, plant height and dry fodder yield/plant. Genetic advance was higher for green fodder yield, plant height and number of days to 50 % flowering.

Singh and Verma (2002) evaluated 600 lines of cowpea for genetic variation 8 quantitative traits of cowpea. High coefficient of variation was recorded for seed yield, plant height, 100-seed weight and number of pods/peduncle. Moderate variation was recorded for number of days to 50 % flowering and pod length. Minimum variability was observed for number of days to maturity and number of seeds/pod.

Pal *et al.* (2003) evaluated 40 diverse genotypes of vegetable type cowpea for assessing genetic variability for 13 traits. The phenotypic coefficient of variation was greater than genotypic coefficient of variation for most of traits. Relatively high phenotypic and genotypic coefficients of variation were recorded for plant height, number of primary branches/plant, number of peduncles/plant, number of pod/plant and green pod yield/plant.

Venkatesan *et al.* (2003) evaluated 20 genotypes of cowpea for 12 traits and recorded significant variation among the genotypes for all the traits studied and greatest variation was recorded for plant height. The magnitude of the PCV was higher than that of the GCV. Plant height, number of pods per plant, pod length, 100 seed weight, seed yield and dry matter production had high heritability. High heritability coupled with high genetic advance was observed for plant height, dry matter production and seed yield.

Prasanthi (2004) reported high coefficient of genotypic and phenotypic variations in 22 cowpea genotypes for plant height, pods per plant, 100 seed weight, seed yield and fodder yield while moderately high values for pod length and seeds per pod.

Resmi *et al.* (2004) reported high heritability coupled with high genetic advance for pod yield per plant, pods per kg, inflorescence per plant, pod weight and keeping quality of pods indicating scope of selection for improvement of these characters.

Malarvizhi *et al.* (2005) carried out genetic variability, heritability and genetic advance studies for 13 characters of 60 genotypes of fodder cowpea. The analysis of variance revealed that the genotypes varied significantly for all characters indicating existence of considerable variation for all the characters. High heritability and genetic advance was noticed for number of branches per plant and plant height.

Zarger *et al.* (2005) evaluated 32 genotypes of cowpea and estimated variability parameters for seven traits. Significant variation among the genotypes was evident for all the traits studied. The magnitude of the phenotypic coefficient of variation was higher than that of the genotypic coefficient of variation for all the traits studied. High GCV and PCV were recorded for plant height, number of pods/plant, seed yield/plot and 100-seed weight. High heritability coupled with high genetic gain was observed for plant height, number of pods/plant, seed yield/plot and 100-seed weight.

Girish *et al.* (2006) assessed genetic variability in 100 cowpea genotypes for eleven quantitative characters. Wide range of variability was observed for most quantitative characters. Plant height and seed yield showed highest phenotypic and genotypic variance, while primary and secondary branches showed lowest variances. The magnitude of phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance was high for seed yield/plant, number of pods/plant and plant height. Days to first flower opening, days to 50 % flowering and days to maturity had a low genetic advance.

Mary and Gopalan (2006) carried out analysis of variance for the thirteen characters and showed the presence of significant genotypic differences indicating the presence of sufficient variability in the materials. In F_3 and F_4 generations, estimates of GCV and PCV indicates that almost all the characters were less influenced by the environment and the variability exists in these characters are under the genetic influence. The genotypic coefficients of variation were highest for the characters plant height, number of branches and leaf weight in both the generations.

Naher *et al*. (2006) studied 68 cowpea accessions and revealed that, wide range of variations were present for days to 50 % flowering, duration of flowering, number of racemes per plant, days to pod maturity, pod length, pod width, number of pods per peduncle, number of pods per plant, dry matter content of edible pod, 100 seeds weight and yield per plant. Phenotypic coefficient of variation was little higher than the genotypic coefficient of variation for all the traits. The low differences between the phenotypic and genotypic coefficient of variations indicated low environmental influences on the expression of the characters.

Saini (2007) in variability studies in 60 genotypes of cowpea, high estimates of GCV and PCV were recorded for clusters/plant, seed yield/plant and plant height whereas, moderate estimate of PCV along with high estimate of GCV were recorded for branches/plant and pods/plant. Moderate estimates of GCV along with low estimates of PCV were recorded for pod length and seeds/pod. High estimates of heritability was observed for days to maturity, test weight and seed yield/plant whereas, moderate estimates of heritability were recorded for cluster/plant, days to 50 % flowering, plant height and pods/plant.

Suganthi and Murugan (2008) studied 30 genotypes of cowpea and reported a high genotypic coefficient of variation than phenotypic coefficient of variation for all the characters. Maximum phenotypic and genotypic coefficient of variation was recorded for seed yield/plant followed by pods/plant and clusters/plant. High heritability was recorded for seed yield/plant followed by seeds/pod, pod length and hundred seed weight. Genetic advance as per cent of mean was higher for seed yield/plant followed by pods/plant and clusters/plant. Seed yield had positive and significant association with pod length.

Tamgadge *et al.* (2008) evaluated 30 genotypes of cowpea and reported that the phenotypic coefficient of variation was greater than genotypic coefficient of variation, number of cluster/plant, diameter of pod and number of seeds/pod manifested high heritability coupled with low genotypic coefficient of variation and genetic advance.

Vishwanath *et al.* (2009) studied on 41 genotypes of cowpea and reported existence of relatively high degree of variability for plant height, peduncle length, number of peduncles and pods/plant, pod length, pod weight and pod yield/plant. Higher estimates of heritability coupled with the higher genetic advance for plant height, number of peduncles/plant, number of days to flower and pod yield/plant.

Bhadru and Navale (2012) studied the heritability parameters in F2 and F3 populations of two crosses of cowpea. Higher magnitude of heritability and genetic advance was reported in F3 as compared to F2 population in both crosses. Number of pods per plant, days to maturity, number of seeds per pod, pod length, 100 seed weight and seed yield per plant recorded higher heritability and genetic advances.

Manggoel *et al.* (2012) in a study on 10 cowpea accessions observed significant variability for days to 50 % flowering, number of peduncles/plant, flower/plant, pods/plant, seed/pod, pod length, 100-seed weight and grain yield. The phenotypic coefficient of variation and genotypic coefficient of variance were high for the traits studied, except pod length and seeds/pod.

Kumar *et al.* (2013) studied 40 genotypes of cowpea originated from different sources. Based on the analysis, they observed that seed yield and number of clusters had high PCV, GCV, heritability and genetic advance as per cent of mean, which suggested that direct selection for these traits would be fruitful in genetic improvement of cowpea.

Nwosu *et al.* (2013) in variability studies of 5 cowpea genotypes for sixteen characters reported high heritability and genetic advance as per cent of mean for clusters per plant, pods per plant, peduncle length, pod length, dry pod weight, hundred seed weight, seeds per pod, number of seeds per plant and seed yield per plant.

Thorat and Gadewar (2013) in genetic variability studies observed high heritability for almost all characters. High heritability coupled with high genetic advances observed for plant height, number of pods/plant and number of branches/plant and high GCV observed for leaf area index followed by days to 50 % flowering.

Vavilapalli *et al.* (2013) assessed the heritability and genetic advance for different characters in 22 diverse genotypes of bush cowpea. High heritability coupled with high genetic advance were observed for all characters studied, except days to first flowering and days to first harvest indicating these characters are governed by additive gene action.

Chattopadhyay *et al.* (2014) studied 60 genotypes of vegetable cowpea and found higher estimates of broad sense heritability coupled with higher genetic advance for number of pods/plant, pod yield/plant, pod weight, number of seeds/pod and pod length.

Diriba Shanko *et al.* (2014) in variability studies revealed significant differences among the forty nine accessions for all the characters studied. High phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance were found for the characters viz., yield per plant, number of pods per plant, and 100-seed weight.

Kharde *et al.* (2014) studied genetic variability in 20 genotypes of cowpea for yield and related characters. The results showed significant differences among the genotypes for all the characters. The phenotypic and genotypic coefficients of variation were higher for plant height, pod length, average pod weight, pod yield per plot, number of seeds per pod and number of pods per plant along with high heritability estimates and high expected genetic advance.

Nath and Tajane (2014) studied genetic variability in 44 cowpea genotypes. High estimates of GCV were observed for green forage yield per plant, dry matter yield per plant, branches per plant in forage cowpea. The magnitude of PCV was more than GCV for all characters.

Om Vir and Singh (2014) studied 33 indigenous and exotic accessions of cowpea for genetic variability during summer and kharif seasons. The high degree of genetic variability was estimated during both seasons for seed yield per plant (g), 100-seed weight (g.), pod length, number of seeds per pod, number of pods per plant, number of pods per cluster, number of branches per plant, number of cluster per plant, plant height (cm), number of days to 50 % flowering and number of days to maturity. The moderate to high heritabilities coupled with moderate to high expected genetic advance were observed for all studied traits.

Sapara *et al*. (2014) assessed genetic variability in 40 genotypes of cowpea. Significant differences among the genotypes for all the characters studied except pod width. The values of phenotypic coefficient of variation were higher than their genotypic coefficient of variation for all the characters indicating the influence of environmental factors. The estimates of genotypic and phenotypic coefficient of variation were high for number of pods per plant, 100 fresh seed weight, plant height, 10 pod weights and green pod yield per plant.

Khanpara *et al.* (2016) studied variability in 60 diverse genotypes of vegetable cowpea and observed high heritability estimates along with high genetic advance for green pod yield per plant, plant height, pod length, pod width, number of seeds per pod, number of pods per plant, 10 pod weight, number of pods per cluster and 100 seed weight.

Patel *et al.* (2016a) reported high heritability and genetic advance in cowpea for green pod yield per plant, very high heritability for plant height at final harvest.

Lal Hira *et al.* (2017) evaluated eighty nine genotypes for yield and yield-attributing traits for genetic variation. High values of genotypic and phenotypic coefficient of variations, broad sense heritability and genetic advance were observed for plant height, pod yield/plant, number of peduncles and pods/plant, pod weight and pod length.

Sarath and Reshma (2017) assessed 22 genotypes of cowpea for variability study. The high degree of variability was observed for all the characters. High magnitude of the PCV, GCV, heritability and genetic advance was observed for plant height, grain yield per plant and length of pods. Seeds per pod and protein content exhibited low PCV and GCV, but high heritability and low genetic gain. The difference between the phenotype coefficient of variation and genotype coefficient of variation were found maximum in pod weight, followed by number of pods per plant and test weight.

Sharma *et al.* (2017) estimated variability of ten parameters in 30 genotypes and revealed that least differences between the estimates of GCV and PCV for most of the characters. Higher estimates of GCV and PCV were observed for plant height, primary branches per plant, seed yield per plant and test weight. Maximum heritability and maximum genetic gain was found for test weight followed by plant height, primary branches per plant, seed yield per plant and harvest index.

Havaraddi and Deshpande (2018) revealed highly significant differences among 30 genotypes for 8 characters. High PCV and GCV values were recorded for the traits seed yield and number of pods per plant. Plant height showed moderate PCV and GCV values.

Manjudevi and Jayamani (2018) evaluated 180 genotypes of cowpea for 13 biometrical traits. High heritability coupled with high genetic advance was observed for plant height, number of racemes per plant, peduncle length, number of pods per plant, number of clusters per plant, pod length, 100 seed weight and single plant yield.

Rout *et al.* (2018) reported significant differences among the 13 genotypes for all the parameters studied indicating the presence of sufficient variability in the studied material. High magnitude of PCV and GCV were observed for pod yield per hectare, pod yield per plant, number of pods per plant and number of harvests.

Sabale *et al*. (2018) in an experiment with 23 F_2 generation genotypes revealed that phenotypic variances were higher than genotypic variances for all the characters. The high phenotypic and genotypic coefficient of variation was observed for seed yield per plant, number of pods per plant, number of clusters per plant and number of primary branches per plant, while lowest GCV and PCV was observed for days to first flowering and days to maturity.

Singh *et al.* (2018) evaluated a collection of 32 cowpea genotypes for eleven quantitative characters. All the characters under study showed considerable amount of variability. Phenotypic coefficient of variability was higher than genotypic coefficient of variability. A perusal of coefficient of variability indicates that PCV and GCV were quite high for number of pods per plant and seed yield per plant. Moderate PCV and GCV were recorded for seed yield per plant, leaf : stem ratio, plant height and pod length while lowest observed in leaf length, number of branches per plant, leaf width, days to maturity and days to flower initiation.

Gupta *et al.* (2019) found significant difference among 27 cowpea genotypes for quantitative characters which indicates the diverse genetic nature of base population. The coefficient of phenotypic variation was slightly greater than those of genotypic variation for almost all the characters.

Manohara *et al*. (2019) noticed significant differences among the 23 genotypes for the eleven characters. The estimate of Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation were high for seed yield, straw yield, pods per plant and 100 seed weight.

Olunloyo *et al.* (2019) reported high magnitude of broad sense heritability along with moderate to high genetic advance as percentage of mean for days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant.

Sharma *et al.* (2019) observed high heritability coupled with high genetic advance for the characters viz., seed yield per plant, plant height, days to 80% maturity, green pod weight, days to 50 % flowering and pods per plant.

Verma *et al.* (2019) studied the genetic variability for growth and yield traits in F2 generation of 24 hybrids of cowpea. Wide range of variability was observed for all the traits except number of branches per plant and pod width. The high genotypic coefficient of variation was recorded for number of pods per plant, number of pods per cluster, mean pod weight and 100-seed weight. Higher heritability estimates coupled with high genetic advance as per cent of mean were observed for plant height, number of branches per plant, flowers per cluster, pods per cluster, per cent pod set, days to last harvest, pod length, pod weight, number of seeds per pod, 100 seed weight and pod yield per plant.

Yadav and Duddukar (2019) showed highly significant differences among cowpea genotypes for 13 yield contributing characters studied. Maximum genotypic and phenotypic variance was recorded for plant height, days to maturity, pods per plant and biological yield. Maximum GCV and PCV were recorded for pods per plant, primary branches per plant and pod length. High heritability coupled with high genetic advance as per cent of mean was recorded for pods per plant, primary branches per plant and plant height.

Das *et al.* (2020) in genetic variability studies revealed substantial amount of genetic variability among the genotypes. In general, phenotypic coefficients of variation were higher in magnitude than genotypic coefficient of variation. The characters pod yield per plant and plant height at maturity showed comparatively higher estimates of genotypic and phenotypic coefficients of variation indicating high level of variability and ample scope for effective improvement.

Purohit *et al.* (2020) evaluated forty-two genotypes of grain cowpea to estimate variability parameters. High estimates phenotypic and genotypic variance was observed for yield per hectare. High estimate of PCV and GCV was observed for yield per plot. High heritability with high genetic advance was observed for plant height, yield per hectare and yield per plant. Moderate heritability and genetic advance were observed for days to 50 % flowering while low heritability with low genetic advance was observed for leaf length.

2.2 Correlation Coefficient

In plant breeding, correlation coefficient analysis is very useful as it provides measure of the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield through indirect selection. The literature available on this aspect has been reviewed as under:

Singh and Verma (2002) evaluated 600 lines of cowpea for 8 quantitative traits. Seed yield was positively correlated with 100-seed weight and pod length. Pod length and plant height were positively correlated with 100-seed weight. A negative correlation between 100- seed weight and number of pod/peduncle, number of days to 50 % flowering and days to maturity was observed.

Belhekar *et al.* (2003) revealed that the seed yield per plant exhibited positive and significant correlation with plant height, number of flowers per plant, first pod maturity, complete maturity, number of pods per plant and 100 seed weight both at the phenotypic and genotypic levels in F2 generation. However, it showed a negative and significant correlation with the number of pods per peduncle and seed index.

Venkatesan *et al.* (2003) carried out correlation analysis using 20 diversified genotypes of cowpea for 12 component characters including seed yield. Characters branches/plant, clusters/plant, pods/plant, pods/cluster and pod yield had positive correlation with seed yield both at genotypic and phenotypic level.

Kumawat and Raje (2005) evaluated 50 genotypes of cowpea reported that the seed yield/plant had significant positive correlations with branches/plant, clusters/plant, pods/plant, biological yield/plant and harvest index. These characters also had positive correlation among themselves, except correlation of harvest index with biological yield/plant. Seed yield/plant had significantly negative correlation with days to 50 % flowering and days to maturity.

Patil *et al.* (2005) revealed that seed yield per plant had positive and highly significant correlation with plant height at genotypic levels and number of pods per plant at both phenotypic and genotypic levels.

Saini (2007) evaluated 60 genotypes of cowpea and observed that seed yield/plant had positive significant correlation with seeds/pod. Whereas, it had negative significant correlation with days to maturity, In addition, days to maturity also had negative significant correlation with test weight. Days to maturity had positive significant correlation with days to 50 % flowering. Among other yield attributing traits, clusters/plant and seed/pods were positively and significantly correlated with pods/plant and pod length, respectively. Clusters/plant was negatively and significantly correlated with test weight.

Thorat and Gadewar (2013) observed that the days to maturity had highly significant positive correlation with days to 50 % flowering both genotypically and phenotypically. Protein content was significant but negatively associated with days to maturity. Number of clusters/plant showed strong positive significant correlation with protein content. Pod length exhibited significant positive correlation with protein content. Number of seeds/pod exhibited positive significant correlation with protein content and strongly correlated with pod length. Seed yield/plot exhibited strong positive significant correlation with clusters/plant, number of pods/plant. It also shows moderately positive significant correlation with protein content.

Kharde *et al.* (2014) studied correlation study for seed yield its attributes and indicated that average pod weight, pod length, leaf area, number of seeds per pod, number of cluster per plant, number of pods per plant, number of pods per cluster, plant height and protein content had significant positive correlation with the pod yield per plot.

Om Vir and Singh (2014) in 33 indigenous and exotic accessions of cowpea revealed that number of seeds per pod, number of pods per plant, number of pods per cluster, number of cluster per plant, days to 50 % flowering and days to maturity had positive and significant correlations with seed yield per plant.

Lal Hira *et al.* (2017) in character association studies showed that pod yield/plant had strong positive correlation with pod weight, number of peduncles and pods/plant, pod length and number of seeds/pod, while negative correlation with days to 50 % flowering at genotypic and phenotypic levels.

Mohankumar *et al.* (2017) revealed that number of primary branches, number of secondary branches, number of cluster per plant and number of pods per plant had significantly higher correlation coefficient to seed yield per plant.

Yadav and Duddukar (2019) in correlation studies reported that days to 50 % flowering, days to 50 % pod setting, pods per plant, 100 seed weight, harvest index and biological yield showed highly significant positive association with seed yield at both phenotypic and genotypic levels. While plant height is significant negative correlation with the seed yield at both phenotypic and genotypic levels.

Das *et al.* (2020) in correlation studies revealed strong positive association of pod yield plant^{-1}, hundred grain weight with grain yield plant^{-1}.

2.3 Path Coefficient Analysis

The correlation studies are helpful in measuring the association between yield and yield components, they do not provide the exact picture of the direct and indirect causes of such association which can be had through path analysis (Wright, 1921). Thus, the path coefficient analysis is very helpful to pin-point the important yield components which can be utilized for construction of selection indices. The available literature on path coefficient analysis was reviewed and has been presented here:

Digee *et al.* (2001) studied path analysis in 9 cowpea lines and their 30 hybrids and reported that dry matter production had the highest positive direct effect on seed yield followed by harvest index. Other characters viz., plant height, branch number, cluster number and test weight exhibited negative direct effect on yield

Vidya and Ommen (2002) in path coefficient analysis emphasized the importance of the characters length of harvesting period, number of pods per plant, pod length, pod girth, pods per cluster and pod weight.

Henry *et al*. (2003) reported the greatest positive direct effects of number of clusters, pods and seeds per plant, and 100-seed weight on seed yield. Whereas, the number of days to maturity and flowering exhibited the greatest negative direct effects on seed yield per plant. Thus, selection for higher seed yield should involve early-maturing genotypes with high 100-seed weight, and number of clusters and pods per plant.

Narayanankutty *et al.* (2003) studied 37 divergent genotypes of vegetable cowpea for 12 traits and path analysis indicated that the number of pods/plant, followed by average weight of pods and number of pickings had the greatest positive direct effect on yield. The direct effects of pod length and number of days to first picking were low, mainly due to high indirect effects via average weight of pods and number of pods/plant.

Venkatesan *et al.* (2003) in path analysis studies of 20 cowpea genotypes for 10 characters showed the positive direct effect of number of pods/plant, pod length, number of clusters/plant, number of seeds/pod, and 100-seed weight on seed yield.

Peksen and Artk (2004) studied 6 genotypes of cowpea and path analysis revealed that pod length had the highest direct positive effect on seed yield/plant, followed by 100-seed weight and pods/plant. On the other hand, seed yield/plant was directly and negatively affected by first pod height and branches/plant.

Anbumalarmathi *et al.* (2005) carried out path analysis in 26 cowpea genotypes and reported that pods/plant, seeds/pod and 100-seed weight had high direct effect on single plant yield. Clusters/plant showed high indirect effect through pods/plant on grain yield.

Mittal and Singh (2005) studied 30 progenies of cowpea varietal cross Cowpea 99 x BS, for seed yield and its traits. Path analysis revealed that pods/plant, pod length, 100-seed weight and days to flowering had high positive direct effects on seed yield. Pods/cluster influenced seed yield positively via pods/plant.

Lal *et al.* (2007) observed maximum positive direct effect of number of pods per plant on pod yield followed by pod weight, number of peduncles per plant and pod length.

Vishwanath *et al.* (2009) evaluated 41 genotypes of cowpea and reported that pod weight exerted the maximum positive direct effect on pod yield followed by number of pods/plant and pod length.

Kumari *et al.* (2010) in path coefficient analysis found that days to fifty per cent flowering, plant height, pods/plant had positive direct effect on yield except days to maturity, branches/plant, seeds/pod and hundred seed weight which showed negative direct effects.

Singh *et al.* (2010) carried out path coefficient analysis with 25 genotypes of cowpea and found that the stem weight had maximum and positive direct effect on green fodder yield at phenotypic and genotypic level followed by leaves weight and dry matter yield. Biological yield and dry matter per cent had negative direct effect on green fodder yield.

Bhadru and Navle (2011) noticed that number of pods per plant had highest magnitude of direct effects on seed yield per plant followed by test weight, biomass at harvest and number of branches per plant.

Huque *et al.* (2012a) path analysis studies revealed that number of pods per plant, pod length (cm), number of clusters per plant and primary branches per plant were the major direct contributors to pod yield per plant.

Cokkizgin *et al.* (2013) from path analysis studies found that the number of plant had positive and highest direct effect on the seed yield while seed weight/plant had negative and highest direct effect on the seed yield.

Nwofia *et al.* (2013) observed that number of pods/plant had higher positive direct effect as well as correlation on pod yield than other yield traits, Number of pods/plant and seeds/plant showed negative direct effects on pod yield even though they had significant positive correlation to pod yield. The indirect effects of the two traits through number of pods/plant were positive and high and seemed to be the cause of the significant correlation between the traits and pod yield.

Kharde *et al.* (2014) reported that the characters pod length, plant height, primary branches per plant, number of pods per cluster and average pod weight had positive direct effect on the pod yield.

Kwaga (2014) from path coefficient analysis suggested that number of pods per plant, plant height and 100 seeds weight can be considered as selection criteria in cowpea.

Khandait *et al.* (2016) reported that per plant, number of branches, days to first flowering had the maximum negative direct effect on pod yield per plant followed by days to 50 % flowering, number of seeds per pod and pods per cluster.

Patel *et al.* (2016) reported the highest positive direct effect on green pod yield per plant by pod length followed by days to 50 % flowering, number of pod per plant and height at final harvest.

Patel *et al.* (2016) in path coefficient analysis indicated the highest positive direct effect on green pod yield per plant by pod length followed by days to 50 per cent flowering, shelling %, number of pods per plant, sugar content and plant height at final harvest.

Dinesh *et al.* (2017) revealed that seed yield was primarily influenced by number of pods per plant and 100 seed weight which had maximum direct effect on seed yield per plant. They also suggested that traits like number of pods per plant and 100 seeds weight could be used as selection criteria for grain yield improvement in segregating population.

Lal Hira *et al.* (2017) found the maximum direct positive effect on pod yield/plant by pod weight followed by number of pods/plant.

Jogdhande *et al.* (2017) carried out path coefficient analysis in 30 cowpea genotypes for different yield and yield contributing traits and reported that number of branches per plant, number of nodes per plant, number of cluster per plant, number green pods per plant, number of pods per plant, number of seeds per pod, pod weight (g), pod yield per plot and percentage of protein content exhibited positive direct effects on pod yield per plot.

Phogat *et al.* (2017) done path coefficient analysis in 30 cowpea genotypes and showed that the dry fodder yield per plant had the highest positive and direct contribution towards green fodder yield/plant followed by days to 50 % flowering, plant height, leaf: stem ratio indicating that selection for these characters would bring about improvement in green fodder yield of cowpea.

Das *et al.* (2018) determined path coefficient analysis clearly revealed that biological yield per plant, harvest index, pods per plant and plant height were the major direct contributors to seed yield.

Palve *et al.* (2018) from path coefficient analysis revealed that the characters number of pods per plant, 100 seed weight, primary branches per plant, plant height, pod length, number of seeds per pod had positive direct effect on pod yield 20 per plot. While traits like number of pods per cluster, number of clusters per plant, pod diameter, pod length, average pod weight, primary branches per plant, 100 seed weight, plant height and leaf area contributed indirect effect towards the yield.

Tsegaye *et al.* (2018) in path coefficient analysis of 30 cowpea genotypes observed positive direct effect of seeds per pod, number of pods per plant,100 seed weight, harvest index, number of nodes per plant on seed yield. So, those traits are the major direct contributors to grain yield.

Paghadar *et al.* (2019) carried path coefficient analysis in 60 vegetable cowpea genotypes and showed high positive direct influences on pod yield per plant through number of primary branches per plant and pod length.

Yadav and Duddukar (2019) in path coefficient analysis studies revealed that days to 50 % flowering, pods per plant, clusters per pod, harvest index, biological yield had direct positive effect on seed yield at both phenotypic and genotypic levels. Primary branches per plant showed direct and negative effect on seed yield at both phenotypic and genotypic levels. Pod length, 100 seed weight, showed direct and positive effect on seed yield at genotypic level.

Das *et al.* (2020) in path analysis studies indicated that the characters number of pods plant^{-1} and days to first pod maturity bearing direct positive effect on grain yield, could be the selection criteria for genetic improvement of grain yield plant^{-1} in cowpea population

2.1 Genetic Diversity

Genetic diversity arises due to geographical separation or genetic barrier to cross ability. Several methods have been developed for measuring divergence between population using multivariate such as multiple regression discriminate function (Fisher, 1936) and D^2 statistic (Mahalanobis, 1936). Out of these methods, D^2 statistic is a powerful tool in quantifying the degree of genetic divergence among the relative contribution of different components to the total divergence. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. The available literature is reviewed here:

Jayaprakash *et al.* (1974) based on the estimations of genetic divergence grouped 60 lines of cowpea from twelve countries into 21 clusters. They noticed wide diversity in material from the same geographical region.

Thiyagarajan *et al*. (1988) assessed the genetic divergence of 12 hybrids and their 7 parents of cowpea and grouped genotypes into 7 clusters. The parents fall into 5 clusters and hybrids also in another 5 clusters. The characters days to 50 per cent flowering, 100-seed weight and plant height contributed the most to genetic divergence.

Vishwanathan *et al.* (1998) grouped 72 cowpea genotypes into 5 clusters and 100 seed weight contributed maximum (33.5 %) to the divergence.

Ushakumari *et al.* (2000) studied fifty genotypes of cowpea and grouped into thirteen clusters by Mahalanobis statistics. Among the yield attributing characters, seeds per pod, number of branches, number of pods per cluster and pod length were the important traits contributed for the divergence.

Anbuselvan *et al.* (2001) evaluated 50 genotypes of cowpea for seed yield and its component on the basis of D^2 statistic analysis, the genotypes were grouped into 4 clusters. The days to 50 % flowering had maximum contribution (35.2 %) towards the genetic divergence followed by number of primary branches (14.5 %), pod length (14.0 %) and number of seeds/pod (9.1 %)

Borah and Khan (2002) evaluated sixty fodder cowpea cultivars and grouped them into 10 clusters. Dry matter yield, green fodder yield and plant height were recorded the highest contribution to total genetic divergence.

Narayanankutty *et al.* (2003) studied genetic variability and divergence in thirty seven genotypes of cowpea which revealed significant differences for all the characters under study. The thirty-seven genotypes were grouped into eleven clusters. They seem to be number of branches per plant, test weight, biomass (dry weight) at harvest and number of pods per plant contributed considerably towards divergence.

Nigude *et al.* (2004) evaluated 45 genotypes of cowpea for genetic diversity and grouped genotypes into 5 clusters. The number of branches/plant, test weight, biomass (dry weight) at harvesting and number of pods/plant had contributed considerably toward divergence.

Venkatesan *et al.* (2004) assessed genetic divergence in 20 genotypes of cowpea and indicated considerable diversity in the material. The genotypes were grouped into six clusters. Clustering pattern indicated the absence of parallelism between geographic origin and genetic diversity. The characters *viz.,* clusters per plant, pods per clusters, pods per plant and seed yield per plant contributed maximum towards the total divergence.

Kumawat and Raje (2005) in genetic diversity studies, grouped 50 genotypes of cowpea into six clusters. The seed yield/plant had maximum contribution the total genetic divergence followed by seeds/pod, days to 50 % flowering, plant height and reproductive period.

Anbumalarmathi and Nadarajan (2007) studied 26 genotypes of cowpea for nine characters for genetic diversity. The genotypes were grouped into seven clusters. Cluster I was the largest with 9 genotypes and cluster VII contained only one genotype. Single plant yield contributed maximum towards divergence followed by 100-seed weight.

Bhandari and Verma (2007) grouped 22 cowpea genotypes into seven clusters. Maximum intra cluster distance was observed in cluster III while maximum inter cluster distance was in between V and VII. Crude protein content, dry matter digestibility, dry matter yield and number of leaves per plant were found major contributor towards genetic divergence.

Saini (2007) performed a study on 60 genotypes of cowpea by using Mahalanobis D^2 statistics and grouped 60 genotypes into 9 clusters. Days to maturity and test weight appeared to be the most important traits contributing maximum towards genetic divergence.

Sulnathi *et al.* (2007) studied genetic divergence in 56 genotypes of cowpea using D^2 statistics for thirteen yield contributing characters. Fifty six genotypes were grouped into nine clusters. Cluster I had the maximum number of genotypes and characters viz., days to maturity, 100 seed weight and days to flowering were the highest contributors to D^2 values. The geographical diversity was not related to genetic diversity.

Valarmathi *et al.* (2007) evaluated 68 genotypes of cowpea for genetic diversity. All the accessions were grouped into twelve clusters. Days to maturity had the greatest contribution to genetic divergence, followed by 100-seed weight, while the number of branches/plant and the number of seeds/pod contributed least among the accessions.

Nagalakshmi *et al.* (2010) assessed genetic diversity in 66 genotypes of cowpea using Mahalanobi's D^2 statistics. The genotypes were grouped into 23 clusters. The characters grain yield/plant contributed maximum to the total divergence followed by 100-seed weight and days to 50 % flowering. Number of branches/plant had least contribution to the total divergence followed by petiole length. The existence of wide genetic diversity among the genotypes from the same geographical location was obviously seen.

Kiran and Krishna (2013) examined the existence of genetic divergence among the 22 cowpea genotypes by employing Mahalanobis's D^2 statistics. They observed that genotypes were grouped into four clusters showing the genetic diversity rather geographical diversity.

Tigga and Tandekar (2013) conducted a study of genetic diversity on 22 genotypes of cowpea. 22 genotypes were grouped into four clusters. Non-overlapping clusters showed genetic diversity rather than geographical diversity.

Chattopadhyay *et al.* (2014) evaluated 60 genotypes of cowpea using Mahalanobis D^2 statistics and reported that genotypes were grouped into 7 clusters. The characters number of seeds/pod, pod yield/plant and pod weight contributed most towards the genetic divergence.

Vavilapalli *et al.* (2014) evaluated 32 genotypes of cowpea for genetic diversity. The genotypes were grouped into 6 clusters. The pod yield/plant contributed maximum divergence, pod weight and plant height.

Chandrakar *et al.* (2016) studied genetic diversity among 21 genotypes of vegetable cowpea. The genotypes showed low quantum of divergence and grouped into five clusters. Maximum number of genotypes (9) was accommodated in cluster-II.

Lal Hira *et al.* (2017) in genetic diversity analysis grouped 89 genotypes into twelve clusters. Plant height contributed highest towards divergence (29.37 %) followed by number of peduncles/plant (26.30 %), number of pods/plant (18.39 %) and pod weight (16.42 %).

Patel *et al.* (2017) evaluated 32 cowpea genotypes to estimate the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into eight clusters.

Purohit *et al*. (2020) evaluated 42 genotypes of grain cowpea to estimate genetic divergence. Genotypes were grouped into 8 clusters. Maximum inter-cluster distance was observed between cluster VI and VII while maximum intracluster distance was observed in cluster V. Inter-cluster distance was higher than intra-cluster distance.

3. MATERIAL AND METHODS

The present investigation, entitled “Genetic Diversity and Path Coefficient Analysis in Seed Cowpea [*Vigna unguiculata* (L.) Walp]”was conducted at Post Graduate Institute, M.P.K.V Rahuri during kharif 2019-20.

The details of material used and methods applied to carry out the genetic variability studies, experimental design adopted and statistical procedures followed are as below.

3.1 Material

The material for the present study consisted of 30 indigenous genotypes and 3 released varieties of cowpea collected from Pulses and Oilseed Crops Research and Training Centre, Pandharpur, Dist. Solapur. The list of genotypes presented in Table 3.1.

3.2 Methods

3.2.1 Experimental design

The land selected for experiment was brought to fine tilt by ploughing followed by harrowing. The 33 (30 + 3 checks) genotypes were sown in RBD with 2 replications. Each genotype had a single row of 5.0 meter length and spacing between pant to pant and rows was 10 and 45 cm, respectively.

3.2.2 Sowing and cultural practices

Sowing was carried on 23 July, 2020 by following dibbling method. The recommended dose of 25:50:00 NPK (kg/ha) was applied at the time of sowing. Experimental plot was kept weed free. Rrecommended agronomic practices were followed to maintain the good crop condition..

3.3 Observations Recorded

Five competitive plants were randomly selected from each genotype and the observations were recorded for quantitative characters except days to maturity and 50 % flowering. The average was worked out from these five plants for the statistical computation and further used for the genetic diversity study. Mean days to 50 % flowering and days to maturity was recorded on plot basis. The observations recorded on each character are mentioned below.

3.3.1 Days to 50 % flowering (No.)

The number of days required from the date of sowing to the date on which 50 % of the plants in each genotype flowered were counted and expressed in whole number.

Table 3.1 Genotypes of cowpea

Sr. No.	Genotype	Pedigree	Source
1	PCP-1403	PCP-1123 × PCP-1606-10	ARS, Pandharpur
2	PCP-1124	RC-101 × Phule Vithai-7-15	ARS, Pandharpur
3	PCP-1404	PCP-112-13 × PCP-1606-10	ARS, Pandharpur
4	PCP-1409	PCP-1123 × PCP-1602-2	ARS, Pandharpur
5	PMCP-1018	Phule Phandhari (mutant)	ARS, Pandharpur
6	CP-07	C152 × V16	UAS, Bangalore
7	PCP-1408	PCP-1123 × PCP-1602-2	ARS, Pandharpur
8	CP-04	VCP-12-065	PRC Vamban
9	CP-10	GC-2 × GC-713	SDAU, Srinagar
10	CP-16	Selection from Bidoli local	SKRU, Bikaner
11	CP-17	Answara × Bhagyalaxmi	RARS, Pittambi
12	CP-38	DC-16	PRC Vamban
13	CP-41	Phule CP -05040	ARS, Pandharpur
14	CP-39	PGCP-28	GPAU & T Panthnagar
15	CP-01(Red)	RC -101	RARI Durgapur
16	CP-02(Red)	GC-3	SDAU,Srinagar
17	PCP-1110	RC-101 × Phule Vithai-2-3-1	ARS, Pandharpur
18	PCP-1402	PCP-1123 × PCP-1602-6	ARS, Pandharpur
19	PMCP-1016	Phule pandhari (mutant)	ARS, Pandharpur
20	PCP-1106	RC-101 × Phule Vithai-1-3-3	ARS, Pandharpur
21	PCP-1411	PCP-1123 × PCP-1602-13	ARS, Pandharpur
22	CP-05	RC 101 × Ajmer selection	RARI, Durgapura
23	CP-06	RC 101 × RC-19	RARI, Durgapura
24	CP-12	VCM8 × TC701	ARS, Pandharpur
25	CP-03 (Red)	VCP-13-001	PRC Vamban
26	CP-36	PTB-1	PARS Pittambi
27	CP-13	Vamban-1 × COCP-7	PRC, Vamban
28	CP-37	Pant Lobia-1	GPAU & T Pantnagar
29	CP-09 (Red)	GC-516 × GC-203	SDAU,Srinagar
30	CP-10(Red)	GC-2 × GC-0713	SDAU, Srinagar
31	Phule Pandhari	VCM-8 × V572	ARS, Pandharpur
32	Phule Sonali	RC-101 × Phule Vithai-7-1-4	ARS, Pandharpur
33	Phule Vithai	VCM8 × Komlean Safed	ARS, Pandharpur

Note : CP = Cowpea PCP = Pandharpur Cowpea PMCP = Pandharpur Mutated Cowpea

3.3.2 Days to maturity (No.)

Number of days required from the date of sowing to complete maturities were recorded an expressed in whole number.

3.3.3 Plant height (Cm)

Plant height of randomly selected five plants in each replication was measured in centimeters from ground level to the tip of main axis and averaged.

3.3.4 Number of main branches /plant (No.)

The number of branches of the randomly selected five plants in each replication were counted at maturity and averaged

3.3.5 Number of pods / plant (No.)

Total number of pods of the five randomly selected plants counted at maturity.

3.3.6 Pod length (Cm)

Pod length of five randomly selected plants was measured in centimetre at harvesting.

3.3.7 Number of seeds / Pod (No.)

Numbers of seeds of five well filled and undamaged pods randomly selected from the selected plants for observations were counted and averaged.

3.3.8 Test weight (100 seed weight) (g)

100 seeds of genotypes were counted from both the replications and weight (g) was recorded and averaged.

3.3.9 Seed yield / plant (g)

Seed yield /plant was measured in grams by taking seed weight of five plant and averaged.

3.3.10 Seed yield/ha (Kg)

Seed harvested from net plot form each replication of each genotypes was multiplied by hectare factor and calculated as kg per hectare.

Parameters

3.3.11 Protein content (%)

The seed protein content in percentage was estimated by using NIRS (Near Infrared spectroscopy) at Plant Physiology Laboratory, Department of Agricultural Botany, MPKV, Rahuri.

3.3.12 Tannin (mg/100 g)

The seed tannin content in mg per 100 gm was estimated by using NIRS (Near Infrared spectroscopy) at Plant Physiology Laboratory, Department of Agricultural Botany, MPKV, Rahuri.

3.3.13 Digestibility

Digestibility calculated by *in vitro* digestion method.

3.3.14 Cooking time

Cooking time calculated by simple cooking method.

3.4 Statistical Analysis

For statistical analysis, the mean values of each genotypes from both replications for fourteen characters were used.

3.4.1 Analysis of variance (ANOVA)

The analysis of variance was done as per procedure outlined by Panse and Sukhatme (1985).

Source of variation	Degree of freedom	MSS	Expected mean sum of squares
Replications	r – 1	MSSRep	σ^2 e + t. σ^2r
Genotypes	g – 1	MSS.Gen.	σ^2 e + r. σ^2r
Error	(r – 1) (g – 1)	MSSE	σ^2 e
Total	(rt – 1)		

Where,

r = Number of replications

t = Number of genotypes

3.4.2 Test of significance

If the variance ratio (MSSTrt/MSSE) was greater than the tabulated value of F, the differences were considered as significant and we could reject the null hypothesis. If it was lower than the table value, the differences were considered to be non-significant and we would accept the null hypothesis.

3.4.3 Variability parameters.

3.4.3.1 Mean

Mean is calculated by dividing the sum of all observations in a sample by their number. In present study mean was calculated by following formula.

$$\text{Mean} = \frac{\sum X}{N}$$

Where,

$\sum X$ = Summation of all the observations for character in each replication.

N = Corresponding number of observations.

3.4.3.2 Range

It is the difference between the lowest and the highest values present in the observations included in a sample. The lowest and highest value for each character was taken as range.

3.4.3.3 Variance

It is estimated as the sum of squares of deviations of all observations of a sample from its mean divided by the degrees of freedom.

3.4.3.3.1 Genotypic variance

Genotypic variance was calculated by following formula.

$$\sigma^2 g = \frac{\text{MSSTrt} - \text{MSSE}}{r}$$

Where,

MSSTrt = Treatment mean sum of squares

MSSE = Error Mean sum of squares

r = Number of replications

3.4.3.3.2 Phenotypic variance

Phenotypic variance was calculated by following formula.

$\sigma^2 p$ = Genotypic variance + Environmental variance

Where,

Environmental variance = Mean sum of squares due to error

3.4.3.4 Standard error of mean

Standard error of means was calculated by following formula:

$$\text{SED} = \sqrt{\frac{2\text{MSSE}}{r}}$$

3.4.3.5 Critical difference

Critical difference was calculated by following formula:

$$\text{CD} = \sqrt{\frac{2\text{MSSE}}{r}} \times t\alpha$$

Where,

$t\alpha$ = "t" table value at error degree of freedom at 5% level of significance

r = Number of replications.

MSSE = Mean sum of square due to error

3.4.3.6 Coefficients of variation

It is an important measure of variability and is the per cent ratio of standard deviation of a sample to its mean. PCV and GCV were estimated by formula given by Burton (1952).

$$\text{PCV} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100 = \frac{\sqrt{\sigma^2 p}}{X} \times 100$$

$$\text{GCV} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100 = \frac{\sqrt{\sigma^2 g}}{X} \times 100$$

3.4.3.7 Heritability (broad sense)

Heritability denotes the proportion of phenotypic variance that is due to genotype and hence heritable. Heritability (h^2) was worked out by using formula suggested by Lush (1949) and Burton and Devane (1953).

By Johnson *et al*. (1955), Heritability values are categorized as follows:

Low	: Less than 30%
Moderate	: 30-60%
High	: More than 60%

$$h^2 \ (broadsense) = \frac{\sigma^2 g}{\sigma^2 p} x \, 100$$

Where,

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

3.4.3.8 Genetic advance

The genetic advance that means expected genetic gain was worked out by using the formula suggested by Lush (1949) and Johnson *et al*. (1955).

$$\text{GA} = k \ \sigma_p h^2 (bs)$$

Where,

K = Selection differential in standard units which is 2.06 at 5% of selection intensity (in present study)

h^2(bs) = Heritability

σp = Phenotypic standard deviation

3.4.3.9 Genetic advance as % of mean (GAM)

$$\text{GAM (\%)} = \frac{\text{GA}}{\text{Grand mean}} \text{ x } 100$$

Genetic advance as % of mean values are categorized as follows:

High : More than 20 %

Moderate : 10-20 %

Low : Less than 10 %

3.4.4 Correlation

The genotypic and phenotypic correlation coefficients were worked out as suggested by Singh and Choudhary (1977).

3.4.4.1 Phenotypic correlation coefficients

$$\text{rp} = \frac{\text{Phenotypic covariance (X.Y.)}}{\sqrt{\text{Variance Xg . Variance Yg}}}$$

Where,

rp = Correlation coefficient (p) between character X and Y

p = Phenotypic

3.4.4.2 Genotypic correlation coefficient

$$rg = \frac{\text{Genotypic covariance (X.Y.)}}{\sqrt{\text{Variance Xg . Variance Yg}}}$$

Where,

rg = Correlation coefficient (genotypic)between character X and Y

g = Genotypic

‘t’ test given by Panse and Sukhatme, 1985 was used for testing the significance of correlation coefficients.

3.4.5. Genotypic path analysis

Genotypic path analysis was carried out as per procedure given by (Dewey and Lu (1959).

Genotypic path coefficients were obtained by solving a set of simultaneous equations in the form.

$r_{ny} = P_{ny} + r_{n2}P_2y + r_{n3}P_3y + \ldots\ldots$

Where,

r_{ny} = Genotypic correlation between one component and seed yield

P_n = Genotypic path coefficients between that character and seed yield

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

Matrix A Matrix B

$$\begin{bmatrix} r\,1\,y. \\ r\,2\,y. \\ r\,n\,y. \end{bmatrix} \quad \begin{bmatrix} r11 & r12 & r13 \ldots\ldots\ldots\ldots r1n \\ r21 & r22 & r23 \ldots\ldots\ldots\ldots r2n \\ rn1 & rn2 & rn3 \ldots\ldots\ldots\ldots 1 \end{bmatrix}$$

Where,

$r_{12} = r_{21}$ and so on.

r_1y = Genotypic correlation between one component character and yield

The matrix B was inverted (B) and path coefficients (Pij) were obtained as

(Pij) = A x (B)

The indirect effects of a particular character *via* other characters were calculated by multiplying direct paths and correlation coefficients particular between these characters separately.

Indirect effect = rij x Pij

Where,

$i = 1$ to 10

$j = 1$ to 10

$Pij = P_1y.\ P_2y....... P_{ny}$

The residual factor, i.e. unaccounted variation in yield for these associations, was calculated from the following formula.

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

Where,

$R^2 = P1yr1y + P_2yr_2y + P_3yr_3y + ... + P_nyr_ny$

Where,

$P_1y.\ P_2y\ ....\ Pny$ = Path values

$r_1y.r_2y\ ......r_ny$ = Correlation coefficients

The scales for path coefficients (Lenka and Mishra (1973)

Value for Direct or Indirect effect	Rate or Scale
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
More than 1.00	Very high

3.4.6 Genetic divergence

3.4.6.1 D^2 analysis

The D-square was carried out as per D^2 statistic given by Mahalanobis (1936) and as suggested by Rao (1952).

3.4.6.2 Wilk's criteria

A simultaneous test of significance of difference in the values of a number of correlated variables with regard to the Pooled effect of the ten characters considered together was carried using Wilk's criteria (Wilk, 1932)

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

Where,

$|E|$ = Determinant of the error sum of squares and sum of products matrix

$|E+V|$ = Determinant of error sum of squares and sum of products plus population sum of squares and product matrix.

Significance of A was estimated by X as

$$X^2pq = V = -m \log, A$$

Where,

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

n = N, +............. + Nk-1, = Total number of observations - 1
p = Number of characters
q = K - 1
K = Number of genotypes

3.4.6.3 Mahalanobis's generalized distance (D^2)

The generalized distance between two genotypes is given by Mahalanobis (1936) as:

$$\underline{D^2 = i.\ J.\ di.dj}$$

Where,

λ ij= Reciprocal matrix to the common dispersion matrix

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

dj= Difference between the mean values of two population of j" character

3.4.6.4 Determination of gene constellation

In the present study, a method suggested by K.D. Tocher (Rao, 1952) for grouping the different lines into clusters was used. Two genotypes having smallest (D^2 values) distance from each other were considered. A third population having smallest average D^2 values from the first two genotypes was added. Then considered the nearest fourth population and so it was done for the remaining ones. At certain stage when it was felt that after adding only of the remaining entries, there was abrupt increase in the average D^2, that genotype was not added in that cluster and another cluster was formed. In this way clusters were formed till all the genotypes were included into one or the other cluster.

3.4.6.5 Average intra and inter-cluster D values

3.4.6.5.1 Average intra-cluster D²

$$D^2 = \frac{\sum Di^2}{n}$$

Where,

Di = Sum of distances between all possible combinations (n) of the population included in a cluster.

3.4.6.5.2 Average inter-cluster

$$D^2 = \frac{\sum \text{Distance between the population of cluster i and j}}{ni.nj}$$

Where,

ni = Number of populations in the cluster i

nj = Number of populations in the cluster j

3.4.6.6 Cluster means

The cluster mean was calculated by summing all the mean values of each genotypes belonging to a particular for each traits cluster, which was then divided by number of genotypes and thus cluster mean was obtained for each character.

3.4.6.7 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed as suggested Singh and Chaudhary (1977). From all combinations, each character was ranked on the basis of di = yi j – yi k values. Where, di = mean deviation yi j = mean of the jth genotype for the ith character and yi k = mean value of the kth genotype for the character. Rank ‘I’ is given to the highest mean difference and rank ‘P’ is given to the lowest mean difference Where, P is the total characters. For estimation of per cent contribution of characters towards divergence, the number of times that each character appeared in the first rank is computed.

4. RESULTS AND DISCUSSION

The present investigation entitled "Genetic Diversity and Path Coefficient Analysis in Seed Cowpea [*Vigna unguiculata* (L.) Walp]" was carried out at Post Graduate Institute (Department of Agril. Botany), Mahatma Phule Krishi Vidyapeeth, Rahuri during Kharif-2020-21 with a view to study genetic variability, correlation, path analysis and genetic diversity of thirty-three genotypes of cowpea. The obtained results were discussed under different subheadings.

4.1 Analysis of Variance
4.2 Mean Performance of Genotypes
4.3 Genetic Variability
4.4 Correlation Coefficient Analysis
4.5 Path Coefficient Analysis
4.6 Genetic Divergence

4.1 Analysis of Variance

The genotypes mean sum of squares were highly significant for all the characters except digestibility, which indicated presence of appreciable variability among the genotypes for the all characters studied except digestibility.

Table 4.1. Analysis of variance for fourteen characters of cowpea

Sr. No	Character	Replications	Genotypes	Error
	DF	**1**	**32**	**32**
1	Days to 50 % flowering	5.470*	123.577**	1.251
2	Days to maturity	1.227	96.315**	2.259
3	Plant height (cm)	5.470	608.241**	3.733
4	Number of main branches (No.)	0.349	8.711**	0.840
5	Number of pods / plant (No.)	0.049	23.841**	0.863
6	Pod length (cm)	0.011	5.869*	2.973
7	Number of seed / pod (No.)	0.022	2.539**	0.396
8	Test weight (g)	0.230	6.948**	0.340
9	Crude protein content (%)	0.445	1.502*	0.604
10	Tannin(mg/100 g)	0.0003	0.0050**	0.0007
11	Digestibility (%)	10.801	6.119	3.723
12	Cooking time (Minute)	0.530	3.130**	0.610
13	See yield per plant (g)	0.839	28.374**	1.750
14	See yield per plant (kg/ha))	7236.236	247154.249**	15247.380

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

Earlier workers *viz.,* Venkatesan *et al.* (2003), Vineeta *et al.* (2003), Malarvizhi *et al.* (2005), Zarger *et al.* (2005), Mary and Gopalan (2006), Manggoel *et al.* (2012), Diriba Shanko *et al.* (2014) Kharde *et al.* (2014) Sapara *et al.* (2014), Havaraddi and Deshpande (2018), Rout *et al.* (2018), Singh *et al.* (2018), Gupta *et al.* (2019) Manohara *et al.* (2019), Das *et al.* (2020) also found significant differences among genotypes for these traits of cow pea

4.2 Mean Performance of the Genotypes

The mean performances of 33 genotypes of cowpea for fourteen characters are given in Table 4.2.

4.2.1 Days to 50 % flowering (No.)

The range of variation in days to 50 per cent flowering was from 44.50 to 69.50 days with .general mean 55.59 days. Among all the genotypes, PCP-1409 (44.50 days) was early in flowering followed by CP-07 (46.50 days). Eleven genotypes were significantly earlier than general mean (55.59). The genotype CP-13R (69.50 days) was late in flowering followed by PCP-1411(68.50 days).

4.2.2 Days to maturity (No.)

The general mean of days required to maturity was 80.77 days. The variation in days to maturity ranged from 68.00 (CP-07) to 95 days (CP-17). The genotypes CP-07 (68.00) and CP-01 R (71.00) were significantly earlier for maturity than check Phule Sonali (74.50. Twelve genotypes were significantly earlier for maturity than general mean.

4.2.3 Plant height (Cm)

Plant height varies from 31.70 (PC-1124) to 96.50 cm (CP-39). Average mean of plant height was 45.83 cm. Four and six genotypes had significantly higher plant height over Check Phule Sonali (58.00 cm) and general mean (45.83 cm), respectively.

4.2.4 Number of main branches (No.)

The general mean of main branches/plant was 9.46. The variation in number of main branches per plant ranged from 6.90 (Phule Sonali) to 16.40 (CP-39). The genotype CP-39 (16.40), CP-09R (14.00) and CP-41(10.10) recorded significantly more number of main branches per plant than Phule Pandhari (6.90). Six genotypes produced significantly more number of main branches over the general mean.

4.2.5 Number of pods /plant (No.)

The general mean for pods/ plant was 14.03. The variation in pods/ plant ranged from 8.50 (PMCP-1016) to 20.70 CP-41). Two genotypes viz., CP-41 (20.70) and CP-13R (20.65) produced significantly higher pods/ plant over check Phule Sonali (17.05), while eight genotypes had significantly more number of pods than general mean (14.03).

4.2.6 Pod length (Cm)

The general mean for pod length was observed as 12.92 cm. The variation for pod length ranged from 9.49 to 16.49 cm. The PCP-1110 (16.49) recorded significantly more plant length than check Phule Vittai (12.88) and general mean (12.92). However, sixteen genotypes showed long pod length as compared to general mean.

4.2.7 Number of seeds/pod (No.)

The seeds per pod ranged from 8.10 (CP-41) to 12.30 (PMCP-1016) with general mean 10.55. None of genotype had recorded significantly more seeds/ pod than best check Phule Sonali (11.25) however, three genotypes *viz.,* PCP-1016 (12.30), CP-37 (12.10), PCP-1106 (12.10) had recorded significantly more seeds/ pod over general mean (10.55).

4.2.8 Test weight (g)

The general mean for 100 seed weight was 11.70 g and ranged from 7.15 (CP-03R) to 14.75 g (PCP-1124). Sixteen and ten genotypes had significantly more 100 seed weight than check Phule Sonali (10.90 g) and general mean.

4.2.9 Protein (%)

The protein content in per cent was varied from 17.20 to 21.11 per cent. The general mean for protein content was recorded as 19.76 per cent. Twenty genotypes showed numerically high protein content per cent as compared to general mean. The genotype Phule Vithai (21.11 %) had highest protein content followed by CP-01R (20.75 %), while the genotype CP-37 (17.20 %) had lowest protein content. None of the genotype was found significant over the check Phule Vithai (21.11 %).

4.2.10 Tannin (mg/100 g)

The tannin content was varied from 0.44 to 0.72 mg/100 g. The general mean for tannin content was recorded as 0.62 mg/100 g. Four genotypes had significantly low tannin content as compared to general mean. The genotypes *viz.,* CP-09R (0.44), PCP-1404 and PMCP-1018 (0.57) recorded significant low tannin content than Phule Pandhari (0.61)

4.2.11 Digestibility (%)

The variation for digestibility ranged from 63.40-70.50 per cent. General mean for digestibility was 66.45. Fifteen genotypes had higher digestibility and eighteen genotypes had lower digestibility. The genotype PCP-1106 (70.50) followed by CP-16 (70.25) and PCP-1124(68.85) had highest digestibility. The genotype PCP-1402 (63.40) followed by Phule Vithai and CP-39 (64.30).

4.2.12 Cooking time (minutes)

The variation for cooking time ranged from 21.75- 27.50. General mean for cooking time was 24.52. The genotypes CP-12 (27.50), PCP-1110 (26.50) and CP-16 (26.30) had more cooking time while the genotypes CP-05 (21.75) PCP-1404 and CP-39 (22.50) took less time for cooking.

4.2.13 Seed yield/ Plant (g)

The seed yield / plant ranged between 6.34 (CP-03R) to 22.42 g (CP-10R), having general mean 16.94 g. Ten genotypes recorded significantly higher seed yield/plant than general mean. The higher seed yield was recorded by CP-10R (22.42 g), CP-39 (21.88 g), Phule Sonali (20.91 g) and PCP-1411 (20.12g).

4.2.14 Seed yield /hectare (kg)

Seed yield/ha ranged from 591 kg (CP-03R) to 2092 kg (CP-10R). Ten genotypes produced significantly higher seed yield per ha than general mean. The genotypes CP-10R, Phule Sonali and PCP-1411 recorded the highest seed yield in kg/ha.

Form the mean performance, it is observed genotypes CP-41, CP-01R, CP-13R, CP-01, PCP-1110, PCP-1404, PMCP-1016, PCP-1809, PCP-1814, Phule Pandhari, Phule Vithai and Phule Rukmini were the best genotypes having desired *per se* performance for yield components.

Table 4.2. Mean performance of thirty three cowpea genotypes for seed yield and yield traits

Sr. No.	Genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of main branches	Number of Pods/ Plant	Pod length (cm)	Number of seed/ Pod	Test weight (g)	Crude protein content (%)	Tannin (mg/ 100 g)	Digestibi lity (%)	Cooking time (Minute)	Seed yield / plant (g)	Seed yield/ plot (kg/ha)
1	PCP1403	48.00	74.00	44.10	9.10	14.50	12.43	9.05	13.65	20.15	0.63	65.25	24.50	17.96	1676
2	PC-1124	52.50	81.00	31.70	10.20	11.60	13.93	11.30	14.75	19.53	0.62	68.85	23.50	19.30	1801
3	PP-1404	68.00	88.00	34.40	8.50	9.00	14.20	11.20	13.70	19.32	0.57	66.00	22.50	13.74	1282
4	CP-1409	44.50	73.00	35.10	7.90	10.00	11.14	11.40	10.80	19.90	0.59	66.25	23.50	12.27	1145
5	PMCP1018	54.00	84.50	39.40	7.80	11.00	12.10	11.10	12.10	19.91	0.57	65.85	23.25	14.73	1374
6	CP-07	46.50	68.00	40.45	9.00	11.10	13.87	8.60	13.00	20.11	0.61	66.90	24.50	12.32	1150
7	PCP-1408	54.00	79.50	40.20	11.50	13.00	13.59	11.60	12.50	20.25	0.70	66.50	23.80	18.83	1758
8	CP-04	63.00	87.50	68.85	11.50	12.30	13.69	11.40	14.30	19.38	0.61	64.75	24.00	19.95	1861
9	CP-10	67.00	87.50	52.45	8.20	14.90	14.99	9.60	13.85	19.99	0.59	68.75	23.50	19.80	1848
10	CP- 16	50.00	74.00	33.65	7.60	17.80	13.48	9.40	11.80	20.05	0.65	70.25	26.30	19.73	1841
11	CP- 17	66.00	95.00	60.40	8.40	15.85	14.30	10.60	10.15	19.93	0.59	65.50	24.60	17.03	1590
12	CP- 38	56.00	81.00	36.50	7.30	15.10	12.42	10.40	11.10	20.61	0.62	65.70	24.25	17.45	1629
13	CP-01 R	48.50	71.00	32.70	7.70	15.50	10.03	9.80	13.30	20.75	0.66	65.75	23.50	20.21	1886
14	CP-02 R	51.00	72.00	32.60	7.20	11.90	11.72	9.50	11.70	20.15	0.62	67.90	24.25	13.21	1233
15	PCP-1110	58.50	83.00	33.70	8.00	8.50	16.49	11.10	11.50	19.10	0.63	64.50	26.50	10.85	1012
16	PCP-1402	60.50	84.00	41.70	8.40	9.90	15.16	11.15	12.20	19.29	0.59	63.40	25.75	13.50	1259
17	PMCP-1016	47.00	74.00	36.50	7.30	8.50	11.90	12.30	12.90	20.02	0.64	66.50	26.00	13.45	1255
18	PCP-1106	66.50	91.50	48.10	8.90	12.65	14.15	12.10	12.90	19.79	0.66	70.50	25.20	19.76	1844
19	PCP-1411	68.50	85.50	37.30	9.80	13.75	15.03	11.60	12.65	20.02	0.64	64.80	25.35	20.12	1878
20	CP-05	48.00	73.50	35.50	7.10	18.60	10.00	9.10	11.60	20.09	0.69	64.50	21.75	19.54	1824
21	CP-06	57.50	4.50	34.70	10.10	15.40	10.62	10.40	9.85	19.96	0.66	65.20	25.50	15.82	1476
22	CP-12	52.00	76.50	47.70	11.00	18.30	12.16	11.60	8.75	19.93	0.66	67.50	27.50	18.56	1732

Table 4.2 contd….

Sr. No.	Genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of main branches	Number of Pods/ Plant	Pod length (cm)	Number of seed/ Pod	Test weight (g)	Crude protein content (%)	Tannin (mg/ 100 g)	Digestibility (%)	Cooking time (Minute)	Seed yield / plant (g)	Seed yield/ plot (kg/ha)
23	CP-03R	54.00	81.00	31.90	10.40	9.70	9.49	8.80	7.45	19.97	0.62	69.25	25.75	6.34	591
24	CP- 36	49.00	79.50	39.10	9.40	9.80	14.00	11.20	13.70	18.89	0.63	67.90	25.50	15.06	1406
25	CP- 37	48.50	73.50	93.40	11.40	17.80	14.51	12.10	9.45	17.20	0.62	67.95	23.70	20.36	1900
26	CP- 09R	56.50	84.00	38.30	14.00	14.20	9.94	11.00	7.15	17.64	0.44	65.80	25.05	11.18	1043
27	CP-10R	45.50	74.50	37.20	9.20	15.90	13.53	11.30	12.50	19.93	0.64	66.90	24.50	22.42	2092
28	CP- 13R	69.50	92.50	89.20	10.00	20.65	13.66	8.90	10.85	20.02	0.72	66.75	25.50	19.92	1859
29	CP- 39	66.50	90.00	96.50	16.40	16.10	14.50	10.25	13.25	19.42	0.61	64.30	22.50	21.88	2042
30	CP- 41	49.00	79.00	43.15	12.20	20.70	12.24	8.10	11.40	19.50	0.63	67.40	24.50	19.15	1787
31	Phule Pandhari(c)	60.00	87.00	42.35	10.10	16.75	12.45	11.00	9.60	19.73	0.61	65.50	23.50	17.68	1650
32	Phule Sonali (C)	47.00	74.50	58.00	6.90	17.05	11.88	11.25	10.90	20.47	0.72	65.70	25.00	20.91	1951
33	Phule Vithai (C)	61.50	81.50	45.50	9.70	15.10	12.88	10.10	10.65	21.11	0.64	64.30	24.25	16.24	1516
	G. mean	55.59	80.77	45.83	9.46	14.03	12.92	10.55	11.70	19.76	0.62	66.45	24.52	16.94	1581
	S.E. ±	0.79	1.06	1.37	0.65	0.66	1.22	0.44	0.41	0.55	0.02	1.36	1.60	0.94	87
	CD at 5%	2.28	3.06	3.94	1.87	1.89	3.51	1.28	1.19	1.58	0.06	NS	2.15	2.69	252
	CV %	2.01	1.86	4.22	9.69	6.62	13.34	5.96	4.99	3.93	4.37	2.90	3.20	7.81	8.00

4.3 Parameters of Genetic Variability

Variability can be studied through biometric parameters like genotypic coefficient of variation, heritability (broad sense), and genetic advance. This would be of great help to breeder in evolving a selection programme for crop improvement.

The estimates of variability parameters for the 13 traits (Table 4.3), explained here as follows.

4.3.1 Variance

Estimation of phenotypic variance (σ^2p) and genotypic variance (σ^2g) were obtained for different traits (Table 4.3). The highest variances (V_p and V_g) were noticed in case of plant height (305.99 and 302.25), days to maturity (49.29 and 47.03) and seed yield/plant (15.06 and 13.31).

4.3.2 Coefficient of variation

The phenotypic coefficient of variations (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters. Less difference in the values of these variances suggested that the variability present among the genotypes was mainly due to genetic reason with minimum influence of environment and hence heritable. The genotypic estimates of variances (Vg), being the important help in the measurement of the contribution of the genotype to the expression of a particular trait.

Mary and Gopalan (2006) and Naher *et al*. (2006) also found less difference between GCV and PCV almost all the characters which indicated less environmental influence. Pal *et al.* (2003), Venkatesan *et al.* (2003), Zarger *et al.* (2005), Naher *et al*. (2006), Suganthi and Murugan (2008) Tamgadge *et al.* (2008), Manggoel *et al.* (2012) Sapara *et al*. (2014), Sabale *et al*. (2018), Singh *et al.* (2018), Gupta *et al.* (2019), Das *et al.* (2020) also reported higher values of PCV than GCV for characters studied indicating the influence of environmental factors.

The higher magnitudes of genotypic and phenotypic coefficient of variations were recorded for plant height (37.94 and 38.14), pods/ plant (24.16 and 25.05), seed yield per plant (21.53 and 22.90) and number of branches (20.97 and 23.10). Where- as, moderate values were observed for test weight (15.54 and 16.32) and days for 50 per cent flowering (14.07 and 14.21). However, days to maturity, length of pod, seeds/pod, crude protein content, tannin content, digestibility and cooking time showed low GCV and PCV except seeds/ pod and pod length which recorded moderate PCV.

The high magnitude of GCV and PCV were noticed for pods/ per plant, plant height, and seed yield /plant. It indicates that the amount of genetic and non-genetic variation were present for these characters. Higher GCV estimates for the traits indicated presence of high degree of variability and better scope for selection.

Earlier workers *viz.,* Nehru and Manjunath (2001) who also obtained high values of GCV and PCV in case of plant height, pods/plant, primary branches/plant and yield/plant; Singh and Verma (2002) for pods /plant, seed yield, plant height; Prasanthi (2004) for pods/plant, plant height, and green pod yield/plant; Zarger *et al.* (2005) in case of plant height, pods/plant, seed yield/plot; Girish *et al.* (2006) for seed yield/plant, number of pods/plant and plant height; Saini (2007) for seed yield/plant and plant height; Suganthi and Murugan (2008) in case of seed yield, pods/plant; Sarath and Reshma (2017) for plant height, grain yield per plant; Sharma *et al.* (2017) for plant height, branches/plant and seed yield/plant; Havaraddi and Deshpande (2018) for seed yield/plant and pods/ plant and Das *et al.(*2020) in case of plant height and seed yield/plant.

Sarath and Reshma (2017) reported low GCV and PCV in case of seeds/ pod and protein content which confirms the present findings.

4.3.3 Heritability (b.s.)

According to Lush (1949) heritability in broad sense is the ratio of total genotypic variance to phenotypic variance, expressed in percentage.

The heritability (b.s.) estimates ranged between 24.34 to 98.78 per cent. The highest heritability (98.78 %) was found for plant height, which was followed by days to flowering (98.00), days to maturity (95.42), pods/plant (93.02), test weight (90.66), seed yield /plant (88.38), tannin content (75.44) and seeds/ pod (73.04). Crude protein content (42.64), cooking time (36.46) and pod length (32.75 %) recorded moderate estimate, while digestibility had low estimate of heritability.

High heritability for plant height, pods/ plant, length of pod, test weight, seed yield was also reported by Venkatesan *et al.* (2003). Similarly, Girish *et al.* (2006) found higher estimates of broad sense heritability seed yield/plant, number of pods/plant and plant height; Suganthi and Murugan (2008) for seeds/pod, pod length and test weight; Bhadru and Navale (2012) for pods /plant, days to maturity, seeds/ pod, length of pod, test weight and seed yield /plant; Nwosu *et al.* (2013) for pods/ plant, , hundred seed weight, seeds/pod and seed yield/ plant; Diriba Shanko *et al* (2014) for yield/ per plant, pods/ plant, and 100-seed weight and Lal Hira *et al.* (2017) for plant height and pods/plant which confirms the present findings.

Moderate heritability for pod length was estimated for pod length which was in contradictory report of Nwosu *et al.* (2013) and Lal Hira *et al.* (2017)

4.3.4 Genetic advance

Without genetic advance, the estimates of heritability will not be of practical values and emphasized the concurrent use of genetic advance along with heritability Johnson *et al*. (1955). High heritability alone is not enough to make sufficient improvement though selection in genetic advance generation.

The higher values of genetic advance was found for plant height (35.59), days to 50 % flowering (15.95), maturity (13.80) and seed yield/ plant (7.07). All the remaining characters recorded low values for genetic advance.

4.3.5 Genetic advance as per cent of mean

Genetic advances as per cent of mean for 13 quantitative characters was ranged from 1.67 per cent (digestibility) to 77.67 (plant height). High estimate of genetic advance as per cent of mean (GAM) was recorded for plant height (77.67). It was followed by pods/plant (48.01), seed yield/ plant (41.70), number of branches (39.21), test weight (30.48) and days to 50 per cent flowering (28.69), whereas, moderate GAM was noticed for seeds/ pod (17.27), days to maturity (17.08), tannin content (13.29), length of pod (10.98). Low GMA was observed for crude protein content (4.56), cooking time (3.00) and digestibility (1.67)

The characters *viz.,* plant height, pods/ plant, seed yield /plant, main branches, test weight and days to 50 per cent flowering had high heritability estimates accompanied with high genetic advance as per cent of mean which indicates presence of additive gene action and direct selection for such traits is rewarding in crop improvement.

Similar findings were obtained by Zarger *et al.* (2005), Bhadru and Navale (2012), Thorat and Gadewar (2013), Diriba Shanko *et al.* (2014), Om Vir and Singh (2014), Sharma *et al.* (2017), Manjudevi and Jayamani (2018), Olunloyo *et al.* (2019), Sharma *et al.* (2019),Yadav and Duddukar (2019) for these traits.

High estimates of broad sense heritability and moderate genetic advance per cent of mean were found for days to maturity, seeds/ pod and tannin content. It also indicated that these characters are governed by an additive gene action.

Table 4.3. Variability parameters for seed yield and yield traits of thirty three seed cow pea genotypes

Sr. No.	Character	Mean	Range	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	ECV (%)	Heritability h² (bs)	Genetic Advance	Genetic Advance as % of Mean
1.	Days to 50 % flowering	55.59	44.50-69.50	61.16	62.41	14.07	14.21	2.01	98.00	15.95	28.69
2.	Days to maturity	80.77	68.00-95.00	47.03	49.29	8.49	8.69	1.86	95.42	13.80	17.08
3.	Plant height (cm)	45.83	31.70-96.50	302.25	305.99	37.94	38.17	4.22	98.78	35.59	77.67
4.	Number of main branches	9.46	6.90-16.40	3.94	4.78	20.97	23.10	9.69	82.40	3.71	39.21
5.	Number of Pods / Plant (No.)	14.03	8.50-20.70	11.49	12.35	24.16	25.05	6.62	93.02	6.73	48.01
6.	Pod Length (cm)	12.92	9.49-16.49	1.45	4.42	9.31	16.27	13.34	32.75	1.42	10.98
7.	Number of seed /pod (No.)	10.55	8.10-12.30	1.07	1.47	9.81	11.48	5.96	73.04	1.82	17.27
8.	Test Weight (g)	11.70	7.15-14.75	3.30	3.64	15.54	16.32	4.99	90.66	3.57	30.48
9.	Crude protein content (%)	19.76	17.20-21.11	0.45	1.05	3.39	5.19	3.93	42.64	0.90	4.56
10.	Tannin(mg/100 g)	0.62	0.44-0.72	0.00	0.00	7.43	8.55	4.24	75.44	0.08	13.29
11.	Digestibility (%)	66.45	63.40-70.50	1.20	4.92	1.65	3.34	2.90	24.34	1.11	1.67
12.	Cooking time (Minutes)	24.37	22.11-26.50	0.35	0.96	2.41	4.00	3.19	36.46	0.74	3.00
13.	Seed yield / plant (g)	16.94	6.34-22.42	13.31	15.06	21.53	22.90	7.81	88.38	7.07	41.70

4.4 Correlation Coefficient Analysis

Correlation coefficient is a statistical measure, for finding out the degree (strength) and direction of relationship between two or more variable. The correlation between characters may due to linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all**.**

Correlation studies would provide reliable information in nature extent and the direction of the selection especially when the breeder needs to combine high yield potential with desirable traits. The genotypic and phenotypic correlation coefficient of different traits with seed yield/ plant and their interrelations are given in Table 4.4 and are discussed here under following points.

4.4.1 Association of grain yield with other characters

The seed yield/plant had positive significant association at genotypic and phenotypic level with pods /plant (r_g= 0.692 and r_p= 0.669) followed by plant height (r_g= 0.470 and r_p= 0.448), test weight (r_g= 0.381 and r_p= 368), pod length (r_g= 295 and r_p= 0.239) and crude protein content (r_g 0.256 at genotypic level). It indicates dependence of these characters on each other.

Earlier workers viz., Singh and Verma (2002) also found significant positive correlation of characters 100-seed weight and pod length; Belhekar *et al.* (2003) plant height, pods/plant and 100 seed test weight; Patil *et al.* (2005) of plant height and pods / plant; Thorat and Gadewar (2013) pods/plant and protein content; Kharde *et al.* (2014) plant height, pods and protein content; Mohankumar *et al.* (2017) pods / plant ; Yadav and Duddukar (2019) pods /plant, test weight with seed yield which confirms the present findings.

The non significant association of seed yield at both the levels with days to 50 per cent flowering ($r_{g=}$ 0.111 and r_p= 0.109), days to maturity (r_g= -0.240.083 and r_p= 0.085), seeds / pod ($r_{g=}$ 0.046 and r_p= 0.123) was observed.

The magnitude of genotypic correlation coefficient were was higher than the phenotypic correlation coefficient for almost all the characters indicating strong association between these characters and they are useful in yield improvement.

4.4.2 Association among seed yield component traits

4.4.2.1 Days to 50 % flowering

It had significant positive correlation with days to maturity (r_g= 0.913 and r_p= 0.902), pod length (r_p= 0.643 and r_p= 0.397), plant height (r_p= 0.360 and r_p= 0.355) and number of branches (r_p= 0.278 and r_p= 0.241) at both the level. It showed non-significant positive association with pods/plant, seeds /pod, test weight and negative with crude protein content both at both the levels.

4.4.2.2 Days to maturity

Days to maturity displayed positive significant correlation with pod length (r_p= 0.493 and r_p= 0.344), plant height (r_p= 0.362 and r_p= 0.360), and number of branches (r_p= 0.346 and r_p= 0.299). It had positive non- significant association with pods/plant and seeds / pod and negative non- significant with test weight and crude protein.

4.4.2.3 Plant height

Plant height had positive significant association with branches (r_g= 0.516 and r_p= 0.480), pod length (r_g= 0.471 and r_p= 0.281) and pods /per plant (r_g= 0.452 and r_p= 0.434) at both levels, respectively. Seeds/ per pod showed positive but positive non-significant correlation (r_g= 0.041 and r_p= 0.049) and negative non- significant correlation with test weight and crude protein at genotypic and phenotypic levels.

4.4.2.4 Number of main branches /per plant

Number of main branches per plant recorded positive significant correlation with pods /per plant (r_g= 0.274) at genotypic level and non-significant association (r_p= 0.214) at phenotypic level. It showed negative significant correlation (r_g= -0.577 and r_p= -0.440) at genotypic and phenotypic level respectively with crude protein content and negative non significant correlation with test weight. It had non significant positive correlation with seeds /per pod and pod length at both levels.

4.4.2.5 Number of pods/plant

Number of pods showed significant negative correlation with seeds / pod (r_g= -0.377 and r_p= -0.345) and test weight (r_g= -0.285 and r_p= -0.286) and negative non significant with pod length (r_g= -0.235 and r_p= -0.119) at both levels, respectively. It also showed positive but non-significant correlation (r_g= 0.118 and r_p= 0.063) with crude protein content.

Table 4.4. Genotypic (above diagonal) and phenotype correlations (below diagonal) among seed yield and yield contributing characters in thirty three cowpea genotypes

Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of main branches	Number of pods per plant	Pod length (cm)	Number of seed per pod	Test weight (g)	Crude protein content (%)	Seed yield per plant (g)
Days to 50 % flowering	**1.000**	0.913**	0.360**	0.278*	0.014	0.643**	0.095	0.071	-0.022	0.111
Days to maturity	0.902**	**1.000**	0.362**	0.346*	0.026	0.493**	0.162	-0.017	-0.157	0.083
Plant height (cm)	0.355**	0.360**	**1.000**	0.516**	0.452**	0.471**	0.041	-0.034	-0.461**	0.470**
Number of main branches	0.241*	0.299*	0.480**	**1.000**	0.274*	0.003	0.001	-0.200	-0.577**	0.179
Number of Pods Per Plant	0.013	0.017	0.434**	0.214	**1.000**	-0.235	-0.377**	-0.285*	0.118	0.692**
Pod Length (cm)	0.397**	0.344**	0.281*	0.093	-0.119	**1.000**	0.238*	0.718**	0.129	0.295*
Number of seed per pod	0.088	0.168	0.049	0.032	-0.345**	0.316**	**1.000**	0.080	-0.418**	0.046
Test Weight (g)	0.070	-0.020	-0.029	-0.189	-0.286*	0.361**	0.049	**1.000**	0.360**	0.381**
Crude protein content (%)	-0.024	-0.123	-0.260*	-0.440**	0.063	-0.320**	-0.291*	0.166	**1.000**	0.256*
Seed yield per plant (g)	0.109	0.085	0.448**	0.118	0.669**	0.239*	0.123	0.368**	0.088	**1.000**

* significant at P= 5 and ** significant P = 1 level of significance.

4.4.2.6 Pod length (cm)

Pod length exhibited positive and significant correlation with test weight (r_g= 0.718 and r_p= 0.361) and seeds/ pod (r_g= 0.238 and r_p= 0.316. However, it recorded negative but significant correlation with crude protein content at phenotypic level (-0.320) and non significant positive correlation (0.129) at genotypic level.

4.4.2.7 Number of seeds /pod (No.)

It had positive but non significant correlation with test weight (r_g= 0.080 and r_p= 0.049). It recorded negative significant association with crude protein content at genotypic level (r_g= -0.418 and r_p= -0.291) at both genotypic and phenotyic levels, respectively.

4.4.2.8 Test weight (g)

Test weight was significantly and positive correlation with crude protein content (r_g= 0.360) at genotypic level only.

4.5 Path Coefficient Analysis

Path coefficient analysis is an efficient statistical technique specially designed to partition the correlation coefficients into direct and indirect effect, provides the information on actual contribution of a character on the yield. This approach is more important to comprehend genetic makeup of a dependent character when the determining component characters are correlated. The results by the path coefficient analysis presented in Table 4.5.

Direct effect of any component trait on seed yield gives an idea about reliability of indirect selection to be made through that trait to bring about improvement in seed yield. If both correlation coefficient and the direct effect are positive and high and then correlation explains its true relationship and a selection for that character will be effective. If the correlation coefficient is positive, but the direct effect is negative, in such relations the indirect causal factors are to be considered simultaneously for selection, when correlation coefficient is negative but the direct effect is positive and high in such cases direct selection for such traits should be practiced to reduce the undesirable indirect effect.

The residual effect determines how best the causal factor accounts for variability of the dependent factor, seed yield. In this case if the value of residual effect is moderate or high, it indicates that besides the characters studied there is some other attributes which contributes for yield.

Genotypic Path

4.5.1 Direct effect

In present study, the characters *viz.,* pods / plant (1.120) showed highest positive direct effect on seed yield / plant which was followed by pod length (0.674), seeds/pod (0.369), test weight (0.215) and main branches/plant (0.213). However, days to maturity (0.146) and crude protein content (0.109) had positive but low effect on seed yield/ plant.

Higher values in desirable direction of path coefficients indicates the direct selection of those characters. Path correlation coefficient of pods/ per plant, pod length, seeds/plant, test weight and main branches/ plant indicated the direct selection of these characters. Number of days to 50 % flowering (-0.469) and plant height (-0.305) showed moderate negative direct effect on seed yield /plant.

4.5.2 Indirect effect

4.5.2.1 Days to 50 % flowering

Days to 50 % flowering exhibited high negative direct effect of magnitude (-0.469) on seed yield/ plant. The genotypic correlation of this trait with seed yield/ plant (0.111) was positive and non significant. It was due to high positive indirect effect *via* pod length (0.433), low positive indirect effect *via* days to maturity (0.134) and negligible positive indirect effect *via* main branches/plant (0.059), seeds/ pod (0.035), pods / plant (0.015) and test weight (0.015). Low negative indirect effect *via* days to maturity (-0.110) and negligible negative indirect effect via crude protein content (-0.002) was noticed.

4.5.2.2 Days to maturity

Days to maturity had low but positive direct effect of magnitude (0.146) on seed yield /per plant. It's genotypic association was positive and significant with seed yield/ plant (0.083). It was due to high positive indirect effect *via* pod length (0.332), negligible positive indirect effect *via* branches/plant (0.074), seeds/ pod (0.060) and number of pods per plant (0.030) and test weight (0.015). Days to maturity recorded high negative indirect effect *via* days to flowering (-0.428) and low to negligible negative indirect effect *via* plant height (-0.110), test weight (-004) and crude protein content (-0.001).

Table 4.5. **Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on seed yield in thirty three cow pea genotypes**

Sr. No.	Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of main branches	Number of Pods /Plant	Pod Length (cm)	Number of seed / pod	Test Weight (g)	Crude protein content (%)	Genotypic correlation Seed yield per plant (g)
1	Days to 50 % flowering	**-0.469**	0.134	-0.110	0.059	0.015	0.433	0.035	0.015	-0.002	0.111
2	Days to maturity	-0.428	**0.146**	-0.110	0.074	0.030	0.332	0.060	-0.004	-0.017	0.083
3	Plant height (cm)	-0.169	0.053	**-0.305**	0.110	0.506	0.317	0.015	-0.007	-0.050	0.470**
4	Number of main branches	-0.131	0.051	-0.157	**0.213**	0.307	0.002	0.001	-0.043	-0.063	0.179
5	Number of Pods / Plant	-0.006	0.004	-0.138	0.058	**1.120**	-0.158	-0.139	-0.061	0.013	0.692**
6	Pod Length (cm)	-0.302	0.072	-0.144	0.001	-0.263	**0.674**	0.088	0.154	0.014	0.295*
7	Number of seed / pod	-0.045	0.024	-0.012	0.000	-0.422	0.160	**0.369**	0.017	-0.046	0.046
8	Test Weight(g)	-0.033	-0.003	0.010	-0.043	-0.319	0.484	0.030	**0.215**	0.039	0.381**
9	Crude protein content (%)	0.010	-0.023	0.141	-0.123	0.132	0.087	-0.154	0.077	**0.109**	0.256*

Residual effect= 0.212

4.5.2.3 Plant height (cm)

Plant height exhibited high but negative direct effect of magnitude (-0.305) on seed yield / plant. However, it's correlation with seed yield/ plant (0.470**) was positive and significant. It was due to high positive indirect effect *via* pods/ plant (0.506), pod length (0.17), low positive indirect effect *via* branches/ plant (0.110), negligible positive indirect effect *via* bays to maturity (0.053) and seed/ pod (0.015). Plant height had also low negative indirect effect *via* days to 50 % flowering (-0.169) and negative negligible indirect effect through crude protein content (-0.050) and test weight (-0.007).

4.5.2.4 Number of main branches / plant (No.)

It showed moderate positive direct effect of magnitude (-0.213) on seed yield / plant. Positive non-significant correlation (0.179). The high positive indirect effect was noticed *via* pods / plant (0.307), negligible positive *via* days to maturity (0.051), pod length (0.002) and seeds per pod (0.001). It had also low negative indirect effect *via* plant height (-0.157), days to 50 % flowering (-0.131) and negligible *via* crude protein content (-0.063) and test weight (-043).

4.5.2.5 Number of pods/ plant (No.)

It exhibited very strong positive direct effect (1.120) on seed yield /plant. Its indirect effect were high low / negative *via* pod length (-0.158), seeds / pod (-0.139), plant height (-0.138), test weight (-0.061) and days to 50 % flowering (-0.006). It had also negligible positive indirect effect *via* number of branches (0.058) crude protein content (0.013) and days to maturity (0.04).

4.5.2.6 Pod length (cm)

Pod length showed positive and high direct effect of magnitude (0.674) on seed yield /plant. It’s correlation with seed yield/ plant (0.295*) was found to be positive and significant. It was due to low positive indirect effect *via* test weight (0.154), negligible and positive indirect effect *via* seeds /pod (0.088), days to maturity (0.072), crude protein content (0.004). It had also high negative indirect effect *via* days to 50 % flowering (-0.302), moderate/low negative indirect effect *via* pods/ plant (-0.263) and plant height (-0.144) .

4.5.2.7 Number of seeds / pod (No.)

Seeds / pod had high positive direct effect of magnitude (369) on seed yield per plant. However, its genotypic correlation with seed yield/ per plant (0.046) was positive but non- significant. The high negative indirect effect was observed *via* pods/ plant (-0.422) and negligible negative indirect effect *via* crude protein content (-0.046), days to 50 % flowering (-0.045) and plant height (-0.012).

4.5.2.8 Test weight (g)

Test weight exhibited moderate positive direct effect of magnitude (0.215) on seed yield per plant. However, it's correlation with seed yield /plant (0.381**) was positive and significant. The maximum positive indirect effect was noticed *via* pod length (0.484), and negligible positive *via* crude protein content (0.039), seeds / pod (0.030) and plant height (0.010). It also recorded negative indirect effect *via* pods/ plant (-0.349) and negligible negative *via* main branches (-0.043), days to 50 % flowering (-0.033) and days to maturity (-0.003).

4.5.2.9 Crude protein content (%)

Crude protein content exhibited positive but low direct effect of magnitude (0.109) on seed yield / plant. However, it's correlation with seed yield/plant (0.256*) was positive and significant. It was due to low positive indirect effect *via* plant height (0.141), pods per plant (0.132), pod length (0.087), test weight (0.077) and number of days to 50 % flowering (0.010). It had also low negative indirect effect *via* seeds/ pod (-0.154), main branches (-0.123) and days to maturity (-0.023).

In the present study, characters *viz.,* pods / plant, pod length and test weight recorded high to moderate magnitude of positive direct effect accompanied by highly significant correlation with seed yield/ plant, indicating through a perfect relationship between them. Thus, suggesting that selection these characters will be highly rewarding for improving the seed yield / plant.

The traits, main branches/plant, seeds/ pod also recorded of direct effect towards the seed yield/ plant, hence direct selection of these traits will be effective to improve seed yield/ plant.

The earlier workers *viz.,* Henry *et al*. (2003) and Tsegaye *et **al.*** (2018) also reported positive direct effect of pods /plant, seeds/ pod, test weight on seed yield of cowpea; Venkatesan *et al.* (2003) observed positive direct effect of pods/plant, length of pod, seeds/pod and 100-seed weight; Peksen and Artk (2004), Anbumalarmathi *et al.* (2005), Mittal and Singh (2005) and Yadav and Duddukar (2019) of pods/plant, pod length, and 100-seed weight and Bhadru and Navle (2011) of pods/plant , test weight and main branches on seed yield.

Days to 50 per cent flowering (-0.469) and plant height (-0.305) showed negative moderate direct effect on seed yield / plant.

Similar observations were also noticed by Digee *et al.* (2001) and Henry *et al*. (2003). However, Kumari *et al.* (2010) and Kwaga (2014) observed positive direct effect of plant height whereas, Kumari *et al.* (2010) found negative direct effect of days to maturity on seed yield /plant which is contradictory of present findings.

The residual effect (R= 0.212) is found low which suggested that the characters included in the study were sufficient to explain the variability in the dependent variables.

4.6 Genetic Divergence

4.6.1 Genetic divergence using mahalanobis's D^2 statistic

Multivariate analysis is useful in for quantifying the degree of divergence in germplasm collection of crop plants. In present study, genetic divergence among Thirty three genotypes of cowpea was quantitatively assessed by adopting Mahalanobis D^2 statistics based on grain yield and yield attributes.

4.6.2 Test with wilk's criterion and analysis of variance for dispersion of genotypes

Significant differences between genotypes based on the pooled effects of all the traits were tested by Wilk's 'λ' (Statistics) criterion. The significance of 'λ' (Statistics) values was tested by 'χ^2' at 320 degrees of freedom. The 'λ' (Statistics) value was 916.71**, suggesting that the genotypes differed significantly when all characters were considered simultaneously. The ANOVA of dispersion of thirty three genotypes is presented in Table 4.6.

Table 4.6. Analysis of variance for dispersion in thirty three cow pea genotypes

Source of variation	Degree of freedom (df)	Mean sum of squares
Genotype	32	1.9013E+09**
Error	63	5.0062E-01
Total	63	9.6576E+08

** Significant at 1% level V statistics at 320 df = 916.73

4.6.3 Mahalanobis's D^2 values

The mean values of thirty three genotypes [(X_1) – (X_2)] were transformed into standardized uncorrelated mean values [(Y_1) – (Y_2)]. The D^2 values were computed for all possible combination that is 33 (33-1)/2 =528 pairs of genotypes.

4.6.4 Cluster formation

As per Tocher's method (Rao,1952), thirty three genotypes were grouped into 6 clusters (Table 4.7) Cluster I was the largest with 24 genotypes, cluster III with 4 genotypes, followed by cluster IV with 2 genotypes. Cluster II, V and VI were solitory. These genotypes grouped in solitory clusters maintained separate identity and exhibited high genetic diversity with most of the other clusters.

Earlier workers *viz,* Nigude *et al.* (2004) were grouped 45 cowpea genotypes into 5 clusters; Venkatesan *et al.* (2004) grouped 20 genotypes into 6 clusters; Kumawat and Raje (2005) grouped 50 genotypes into 6 clusters; Naher *et al.* (2005) grouped 68 genotypes into 6 clusters; Anbumalarmathi and Nadarajan (2007) grouped 26 genotypes into 7 clusters; Saini (2007) grouped 60 genotypes into 9 clusters; Sulnathi *et al.* (2007) grouped 56 genotypes into 9 clusters; Tigga and Tandekar (2013) grouped 22 genotypes into 4 clusters; Chattopadhyay *et al.* (2014) grouped 60 genotypes into 7 clusters; Vavilapalli *et al.* (2014) grouped 32 genotypes into 6 clusters; Chandrakar *et al.* (2016) grouped 21 genotypes into five clusters; Lal Hira *et al.* (2017) 89 genotypes into 11 clusters; Patel *et al.* (2017) grouped 32 genotypes into 8 clusters and Purohit *et al*. (2020) grouped 42 genotypes into 8 clusters.

Clustering pattern of genotypes was random but it has clearly shown relationship with the characters for which they were bred. It indicates that genetic diversity and geographic diversity are not related.

Similar results were reported by earlier workers *viz.,* Rewale *et al.* (1995), Narayanankutty *et al.* (2003), Venkatesan *et al.* (2004), Naher *et al*. (2005), Sulnathi *et al.* (2007), Nagalakshmi *et al.* (2010) and Tigga and Tandekar (2013) in seed cowpea.

Table 4.7 Distribution of 33 cowpea genotypes into different clusters

Clusters	No. of genotypes included	Name of genotype
I	24	PCP-1124, PCP-1409, PMCP-1018, CP-07, PCP-1403, PCP-1408, CP- 16CP- 38, CP-01R, CP-02R, PCP-1110, PCP-1402, PMCP-1016, PCP-1106, CP-05, CP-06, CP-12, CP 03R, CP- 36, CP-41, CP-09R CP-10R, Phule Pandhari and Phule Vittai
II	1	CP-10
III	4	PCP-1411, CP-17, CP-04, PCP-1404
IV	2	CP-13R, CP-39
V	1	Phule Sonali
VI	1	CP-37

4.6.5 Intra and inter-cluster distance

The mean D values (Table 4.8) were used as measures of intra and inter cluster distance.

The highest intra cluster distance was found in cluster III (11.88) followed by cluster I (10.30), IV (8.32), and rest of cluster had zero intra cluster distance as they have only one genotype (monogenic).

The maximum inter cluster distance was noticed between cluster I and cluster VI (31.31) followed by cluster VI and III (29.49), cluster II and VI (27.39), cluster I and IV (27.26), cluster III and IV (21.10) and cluster V and IV (20.94). This indicated maximum divergence between genotypes grouped in these clusters. Minimum D values observed between cluster II and III (8.22).

Table 4.8 Average intra (bold) and inter cluster distance (D) and D^2 (in bracket) values for six clusters in thirty three cowpea genotypes

Cluster	I	II	III	IV	V	VI
I	**10.30 (106.09)**	13.69 (187.41)	14.35 (205.92)	27.26 (773.10)	14.00 (196)	31.31 (980.31)
II		**0.00**	8.22 (67.56)	18.11 (327.97)	14.83 (219.92)	27.39 (750.21)
III			**11.88 (141.13)**	21.10 (445.21)	16.75 (280.56)	29.49 (869.66)
IV				**8.32 (69.22)**	20.94 (438.48)	18.00 (324)
V					**0.00**	19.78 (391.24)
VI						**0.00**

4.6.6 Cluster means

The mean values of ten characters of different clusters is presented in the (Table 4.9).

4.6.6.1 Days to 50 % flowering

For days to 50 per cent flowering the genotypes in cluster V were early (47.00 days) followed by cluster VI (48.50 days), whereas, genotypes grouped in cluster IV (68.00 days) and cluster II (67.00 days) were late.

4.6.6.2 Days to maturity

On the basis of cluster means, cluster VI (73.50 days) matured earliest followed by cluster V (74.50 days). Cluster IV (91.25 days) was late in maturity followed by cluster III (89.00 days).

4.6.6.3 Plant height (cm)

Cluster means for plant height was maximum for cluster VI (93.40 cm) followed by cluster IV (92.85cm). The cluster I (38.41 cm) and cluster III (50.24 cm) recorded comparatively dwarf.

4.6.6.4 Number of main branches/plant

Cluster IV (13.20) recorded more main branches followed by cluster VI (11.40). Cluster V (6.90) had least number of branches.

4.6.6.5 Number of pods/ plant (No.)

It was found that cluster IV (18.38) had highest pods/plant which was followed by cluster VI (17.80), whereas, Cluster III (12.73) had least pods / plant.

4.6.6.6 Pod length (cm)

Cluster II (14.99 cm) had highest pod length whereas, low pod length was observed for cluster V (11.88 cm).

4.6.6.7 Number of seeds/pod (No.)

Cluster VI (12.10), cluster V (11.25) and cluster III (11.20) had more number of seeds per pod, whereas, cluster IV (9.58) and cluster II (9.60) had less number of seeds/pod

4.6.6 Test weight (g)

Cluster mean for test weight was maximum for cluster II (13.85) followed by cluster III (12.70) whereas, minimum test weight was in cluster VI (9.45) followed by cluster V (10.90).

Table 4.9. **Mean values of the six clusters for ten characters in thirty three cowpea genotypes**

Cluster No.	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of main branches	No. of Pods Per Plant	Pod Length (cm)	No. of seed per pod	Test Weight (g)	Crude protein content (%)	Seed yield per plant (g)
CL-I	52.94	78.81	38.41	9.21	13.56	12.49	10.48	11.54	19.85	16.06
CL-II	67.00	87.50	52.45	8.20	14.90	14.99	9.60	13.85	19.99	19.80
CL-III	66.38	89.00	50.24	9.55	12.73	14.31	11.20	12.70	19.66	17.71
CL-IV	68.00	91.25	92.85	13.20	18.38	14.08	9.58	12.05	19.72	20.90
CL-V	47.00	74.50	58.00	6.90	17.05	11.88	11.25	10.90	20.47	20.91
CL-VI	48.50	73.50	93.40	11.40	17.80	14.51	12.10	9.45	17.20	20.36

4.6.6.9 Crude protein content (%)

Cluster mean for crude protein content was maximum for cluster V (20.47 %) followed by cluster II (19.99 g) whereas, minimum crude protein content was found in cluster VI (17.20 %).

4.6.6.10 Seed yield/ plant (g)

Cluster mean for seed yield was maximum incase of cluster V (20.91) which was followed by cluster IV (20.90) and VI (20.36 g), whereas, minimum seed yield/ plant was found in cluster I (16.06 g).

4.7 Per cent Contribution of 10 Characters for Divergence

The utility of D^2 analysis, which is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The per cent contribution of ten characters towards genetic divergence is presented in Table 4.10.

The contribution of days to 50 % flowering was maximum (34.09 %) for genetic divergence followed by plant height (32.58 %), pods/ plant(10.98 %), test weight (8.71 %), days to maturity (3.60 %), pod length (3.22 %), main branches/plant (1.89 %) seed yield/ plant (1.89 %), crude protein (1.70 %) and seeds/ pod (1.33).

Thiyagarajan *et al.* (1988), Kumawat and Raje (2005), Sulnathi *et al.* (2007) and Nagalakshmi *et al.* (2010) also reported maximum contribution towards genetic divergence of characters *viz.,* days to 50 per cent flowering, test weight, plant height and pods/plant.

The pattern of group constellation proved the existence of significant amount of variability. Greater is the distance between to clusters, wider is the genetic diversity in the genotype. For hybridization programme the parents are selected by considering the genetic diversity, their *per se* performance and cluster mean for characters.

Based inter-cluster distance cluster mean and *per se* performance, the genotypes *viz.*, CP-04, CP-10, CP-10R, PCP-1411, CP-37, CP-10R,CP-39 and Phule Sonali are suggested to utilize for future breeding programme.

Table 4.10. Per cent contribution of 10 characters for divergence

Sr. No.	**Source**	**Number of times ranked first**	**Contribution (%)**
1	Days to 50 % flowering	180	34.09
2	Days to maturity	19	3.60
3	Plant height (cm)	172	32.58
4	Number of main branches	10	1.89
5	Number of Pods / Plant	58	10.98
6	Pod Length (cm)	17	3.22
7	Number of seed /pod	7	1.33
8	Test Weight (g)	46	8.71
9	Crude protein content (%)	9	1.70
10	Seed yield / plant (g)	10	1.89
		Total	**100**

5. SUMMARY AND CONCLUSIONS

The present investigation entitled "Genetic Diversity and Path Correlation in Seed Cowpea [*Vigna unguiculata* (L.) Walp]" was conducted at PGI (farm), M.P.K.V Rahuri with the following objectives:

1. To estimates the genetic diversity
2. To estimates the association and cause effects of yield contributing traits with seed yield between.

The thirty three cowpea genotypes were sown in a RBD with two replications and observations were recorded on randomly selected five plants for fourteen characters *viz.,* days to 50 % flowering, maturity, plant height, number of main branches, number of pods/ plant, pod length, number of seeds per/pod, test weight, protein content, tannin content, cooking time, digestibility, seed yield / plant and seed yield / ha.

5.1 Variability, Heritability and Genetic Advance

There were significant difference among the genotypes for all the characters except digestibility, which indicated presence of variability among the genotypes for these characters.

Form the mean performance, it is observed genotypes CP-41, CP-01R, CP-13R, CP-01, PCP-1110, PCP-1404, PMCP-1016, PCP-1809, PCP-1814, Phule Pandhari and Phule Sonali were the best genotypes having desired *per se* performance for yield components

Phenotypic variance was higher than genotypic one for seed yield and yield contributing traits, indicating the control of environmental factors on these traits. Less difference in the estimates of genotypic and phenotypic variance suggested that the variability present among the genotypes was mainly due to genetic reason with minimum influence of environment and hence heritable.

The high magnitude of GCV and PCV were found plant height, pods/plant and seed yield / plant. The estimates of GCV and PCV indicates the amount of genetic and non-genetic variation present for different desirable characters. Higher estimates of GCV and PCV for the traits indicated presence of high degree of variability and better scope for selection.

The characters, plant height, pods/plant, seed yield/plant, / main branches/plant, test weight and days to 50 per cent flowering showed high heritability estimates and genetic advance per cent of mean and high heritability estimates coupled with moderate genetic advance per cent of mean were noticed for days to maturity, seeds/ pod and tannin content which indicates presence of additive gene action and direct selection for such traits is rewarding in crop improvement.

5.2 Correlation and Path Analysis

The characters pods/plant, plant height, test weight, pod length and crude protein exhibited positive and significant genotypic correlation with seed yield / plant. The traits days to 50 % flowering, days to maturity, pod length, plant height and main branches/plant had significant correlation with each other, while the characters plant height, branches and pods/plant were found significantly and positively inter correlated.

Pods/ plant recorded maximum positive direct effect on seed yield/ plant followed by pod length, seeds/pod and test weight. The characters days to maturity and main branches/plant showed positive moderate direct effect on seed yield/plant. By considering the overall indirect effects the characters main branches, pods / plant and pod length contributed indirectly towards seed yield per plant.

5.3 Genetic Divergence

The 33 cowpea genotypes were grouped into 6 clusters. Cluster I had maximum 24 genotypes, followed by cluster III with 4 genotypes and cluster IV with 2 genotypes. Cluster II, V and VI were monogenotypic. Clustering pattern indicated that genetic diversity and geographic diversity are not related.

The highest inter cluster distance was observed between cluster I and cluster VI (31.31) followed by cluster VI and III (29.49), cluster II and VI (27.39), cluster I and IV (27.26), cluster III and IV (21.10) , cluster IV and V (20.94).

The present study the characters *viz.,* days to 50 % flowering, plant height, number of pods per plant and test weight contributed maximum for divergence.

Based inter-cluster distance cluster mean and *per se* performance, the genotypes viz., CP-04, CP-10, CP-10R, PCP-1411, CP-37, CP-10R,CP-39 and Phule Sonali are suggested to utilize for future breeding programme.

Conclusion:

From the above discussion it may be concluded that,

1. There were highly significant differences among the genotypes for all the characters except digestibility indicating that these traits are applicable to exploitation.
2. In the present investigation, plant height, pods/ plant and seed yield/ plant showed high/GCV and PCV which shows good scope for their improvement through selection.
3. High heritability (b.s.) and genetic advance as per cent mean was observed for plant height, pods/plant, seed yield/plant/main branches, test weight and days to 50 % flowering indicates that these characters were predominantly governed by additive gene effect and selection would be more effective for genetic improvement.
4. Seed yield/ plant exhibited positive significant relationship at genotypic and phenotypic level with pods/ plant, plant height, test weight, pod length and with protein content at genotypic level only.
5. In path analysis, pods /plant, pod length, seeds/plant, test weight and main branches / plant exhibited the positive direct effect on seed yield / plant.
6. All 33 genotypes under study were grouped into six clusters. The maximum intra cluster distance was found for cluster III and inter cluster distance between cluster I and VI.
7. Days to 50 % flowering showed maximum contribution towards divergence. It was followed by plant height, pods/ plant and test weight.
8. Based on inter-cluster distance, intra-cluster distance and *per se* performance the genotypes viz., CP-04, CP-10, CP-10R, PCP-1411, CP-37, CP-10R, CP-39 and Phule Sonali are suggested to utilize for future breeding programme.

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7. VITAE

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