VARIABILITY STUDIES IN COWPEA [*Vigna unguiculata* (L.) Walp.] GENOTYPES

by

Miss. Bankar Varsha Popat
(Reg. No. 021/308)

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

in partial fulfillment of the requirements for the degree

of

MASTER OF SCIENCE (HORTICULTURE)

in

VEGETABLE SCIENCE

DEPARTMENT OF HORTICULTURE

POST GRADUATE INSTITUTE
MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI – 413 722, DIST. - AHMEDNAGAR
MAHARASHTRA, INDIA.
2024

VARIABILITY STUDIES IN COWPEA [*Vigna unguiculata* (L.) Walp.] GENOTYPES

by

Miss. Bankar Varsha Popat
(Reg. No. 021/308)

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

in partial fulfillment of the requirements for the degree

of

MASTER OF SCIENCE (HORTICULTURE)

in

VEGETABLE SCIENCE

APPROVED BY

Dr. Sharmila Shinde
(Chairman and Research Guide)

Dr. D.B. Kshirsagar
(Committee Member)

Mrs. D.D. Patil
(Committee Member)

Dr. B.M. Bhalerao
(Committee Member)

DEPARTMENT OF HORTICULTURE
POST GRADUATE INSTITUTE
MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI – 413 722, DIST. – AHMEDNAGAR
MAHARASHTRA, INDIA.
2024

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 Institution

for a Degree or

Diploma

Place : MPKV., Rahuri

Date : / /2024

(Varsha P. Bankar)

Dr. Sharmila Shinde
Assistant Professor,
Department of Horticulture,
Mahatma Phule Krishi Vidyapeeth,
Rahuri-413 722, Dist. Ahmednagar,
Maharashtra, India.

CERTIFICATE

This is to certify that the thesis entitled, **"VARIABILITY STUDIES IN COWPEA [*Vigna unguiculata* (L.) Walp] GENOTYPES"** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri Dist. Ahmednagar (M. S.) in partial fulfillment of the requirement for the award of the degree of **MASTER OF SCIENCE (HORTICULTURE)** in **VEGETABLE SCIENCE,** embodies the results of a piece of *bona fide* research work carried out by **Miss. BANKAR VARSHA POPAT,** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

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

Place : MPKV., Rahuri (S. R. Shinde)

Date : / /2024 Research Guide

Dr. B.T. Patil
Head,
Department of Horticulture,
Mahatma Phule Krishi Vidyapeeth,
Rahuri – 413 722, Dist. Ahmednagar,
Maharashtra State, INDIA

CERTIFICATE

This is to certify that the thesis entitled, **"VARIABILITY STUDIES IN COWPEA [*Vigna unguiculata* (L.) Walp] GENOTYPES"** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri Dist. Ahmednagar (M. S.) in partial fulfillment of the requirement for the award of the degree of **MASTER OF SCIENCE (HORTICULTURE)** in **VEGETABLE SCIENCE,** embodies the results of a piece of *bona fide* research work carried out by **Miss. BANKAR VARSHA POPAT,,** under the guidance and supervision of **Dr. SHARMILA SHINDE,** Assistant Professor, Department of Horticulture, MPKV., Rahuri and that no part of this thesis has been submitted for any other degree or diploma.

Place : MPKV., Rahuri
Date : / /2024 (B.T. Patil)

Dr. V.S. Shirke
Associate Dean,
Post Graduate Institute,
Mahatma Phule Krishi Vidyapeeth,
Rahuri-413 722, Dist. Ahmednagar,
Maharashtra State, INDIA

CERTIFICATE

This is to certify that the thesis entitled, **“VARIABILITY STUDIES IN COWPEA [*Vigna unguiculata* (L.) Walp] GENOTYPES”** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri Dist. Ahmednagar (M. S.) in partial fulfillment of the requirement for the award of the degree of **MASTER OF SCIENCE (HORTICULTURE)** in **VEGETABLE SCIENCE,** embodies the results of a piece of *bona fide* research work carried out by **Miss. BANKAR VARSHA POPAT,** under the guidance and supervision of **Dr. SHARMILA SHINDE,** Assistant Professor, Department of Horticulture, MPKV., Rahuri and that no part of this thesis has been submitted for any other degree or diploma.

Place : MPKV., Rahuri

Date : / /2024 (V.S. Shirke)

ACKNOWLEDGEMENT

In my first place, I would like to thank Almighty God and my parents for showering their blessings upon me and fills me with courage and confidence to fulfill the desired task. Formal words cannot carry the fragrance of emotions; however, they are the only means of expressing emotions in such acknowledgment. I think it is the matter of great pleasure to glance back and recall the faces and spirits in the form of teachers, parents and parents who contributed to reach this destination.

I feel my immense priviledge to express my deep sense of heartful gratitude with highest veneration to my research guide **Dr. S.R. Shinde**, Assistant Professor, Department of Horticulture, MPKV Rahuri, Dist. Ahmednagar, Maharashtra for her immense insight, constructive criticism, unfailing enthusiasm, valuable advice with appreciation and to work purposively was always a great source of inspiration.

I owe my deep and sincere thanks to other members of the advisory committee, **Dr. D.B. Kshirsagar**, Associate professor, Department of Horticulture, MPKV., Rahuri. **Mrs. D.D. Patil**, Junior Vegetable Breeder, AICRP on Vegetable, Department of Horticulture, MPKV., Rahuri. **Dr. B.M. Bhalerao,** Assistant professor, Department of Biochemistry, MPKV, Rahuri for their valuable suggestions and encouragement throughout the course of research work.

I am sincerely thankful to **Dr. B.T. Patil**, Head, Department of Horticulture and all other scientists, teachers and staff of Department of Horticulture, for their valuable suggestions, help and co-operation.

I am thankful to **Dr. P.G. Patil**, Vice Chancellor, MPKV, Rahuri and **Dr. V.S. Shirke,** Associate Dean, PGI, MPKV, Rahuri for providing me an opportunity to study in such a reputed institute.

Special thanks goes to **Dr. M. N. Bhalekar**, Ex. Senior Vegetable Breeder, AICRP, Department of Horticulture MPKV, Rahuri for their constant support and extreme help at my high time during my research and **Dr. B.T. Patil,** Senior Vegetable Breeder, AICRP, Department of Horticulture MPKV, Rahuri, **Dr. J. K. Dhemre**, Associate Professor, Department of Horticulture, PGI, MPKV, Rahuri, **Tushar bhau, Shri. Sandeep Salve**, **Rambhau Magar**, Department of Horticulture, MPKV, Rahuri for their valuable support.

I am very thankful to all staff members of All India Coordinated Research Project on Vegetable Crops, for their constant support, valuable advice, prompt guidance and for providing me the necessary help during my research work.

I would like to thank to my Late Father ***Popat Gopinath Bankar*** *who taught me everything I know and loved me unconditionally. You will be deeply missed. Words are not enough to express my gratitude, love and affection to my mother* ***Smt. Kanchan Popat Bankar****, Brother* ***Mr. Devesh Popat Bankar*** *for their love, care, sacrifices and encouragement.*

I am cordially thankful to my seniors ***Vaishanavi didi, Hemlata didi, Rutuja didi, Shubhangi didi, Komal didi*** *and all other seniors for their help, suggestions, guidance and encouragement.*

I like to express special thanks to my classmates ***Shubhangi, Varshini, Akshata, Sunayana, Praful, Mayuresh, Ram, Ruturaj and Sumit*** *for their help and guidance.*

I express my deep appreciation and heartiest thanks to my best friends ***Rupali, Pratiksha, Pooja, Pranali, Sakshi, Madhura, Dhananjay, Ganesh*** *and* ***Vaibhav*** *for their superb understanding, their endless love and constant support and whose company kept me happy throughout the tenure of my work.*

I am also deeply obliged to all authors and scientists, past and present, whose contributions were of immense help to understand there research findings as their literature has been aptly cited to undertake the present investigation.

I express my profound thanks to one and all concerned that directly/indirectly helped me in this endeavour. While every effort has been made to acknowledge the helps rendered, any omission there in is inadvertent. I am also thankful to Mahatma Phule Krishi Vidyapeeth, Rahuri for providing me an opportunity to undertake my master studies.

Place : MPKV., Rahuri. (Varsha P. Bankar)

Date : / / 2024

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF ABBREVIATIONS AND SYMBOLS

Abbreviations		Description
°C	:	Degree Celsius
%	:	Per cent
/	:	Per (or)
AICRP	:	All India Co-ordinated Research Project
ANOVA	:	Analysis of Variance
C.D.	:	Critical difference
C.V.	:	Coefficient of variance
Cm	:	Centimeter (s)
DAS	:	Days After Sowing
DSI	:	Disease Severity Index
et al.	:	et alli (Co-workers)
Fig.	:	Figure (s)
G	:	Gram (s)
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent mean
GCV	:	Genotypic coefficient of variation
H	:	High
h^2	:	Heritability
ha	:	Hectare (s)
HR	:	Highly resistant
HS	:	Highly susceptible
i. e.	:	that is
kg	:	Kilogram (s)
L	:	Low
M	:	Medium
MPKV	:	Mahatma Phule Krishi Vidyapeeth
MR	:	Medium Resistant
PCV	:	Phenotypic coefficient of variation
PDI	:	Percentage Disease Incidence
q	:	Quintal
R	:	Resistant
RBD	:	Randomized Block Design
RH	:	Relative Humidity
S	:	Susceptible
S.E.	:	Standard Error
viz.	:	Videlicet (Namely)

ABSTRACT

"VARIABILITY STUDIES IN COWPEA (*Vigna unguiculata* (L.) Walp) GENOTYPES"

By

Miss. Bankar Varsha Popat

A candidate for the degree of

MASTER OF SCIENCE (HORTICULTURE)

in

VEGETABLE SCIENCE

2024

Research Guide	:	**Dr. Sharmila Shinde**
Department	:	**Horticulture**

The present experiment entitled "Variability studies in cowpea (*Vigna unguiculata* (L.) Walp) genotypes" was completed during *Summer* 2022 at AICRP on Vegetables, MPKV, Rahuri. This experiment consists of twenty-three genotypes and one standard check, arranged in a randomised block design with three replications.

The genotypes were studied for the variability, heritability, genetic advance, association studies, path analysis along with divergence for various growth and yield contributing characters *viz.* days to 50 % flowering (Days), days to first pod harvest (Days), number of pods per plant (No.), number of seeds per pod, fresh pod length (cm), fresh pod width (cm), average pod weight (10 Pods), number of primary branches/plant, leaf area (cm square), vine length (m), yield per plant (g). The qualitative characters and incidence of disease and pests were also studied.

The analysis of variance revealed the significant difference among the genotypes for all the characters. Phenotypic coefficient of variation estimates was slightly higher than genotypic coefficient of variation. High estimates of heritability (b.s.) was observed for all the characters studied.

Appreciable amount of variability was observed for all the characters studied. The average pod weight (10 pods), number of pods per plant, fresh pod length, vine length, leaf area (cm^2) and yield per plot (kg) had high estimate of GCV and PCV, while moderate GCV and PCV values showed by yield per hectare (q/ha), fresh Pod Width (cm), number of primary branches per plant , number of seeds per pod.

Abstract contd…. **Miss. Varsha P. Bankar**

The estimates of high heritability (broad sense) per cent values were high for average pod weight (10 pods) (g), number of pods per plant, leaf area (cm^2), fresh pod length and vine length (m), yield per plot (kg) and yield per hectare (q/ha), fresh pod width (cm), number of seeds per pod, days to 50 % flowering (Days), days to first pod harvest (Days).

In correlation studies it was estimated that the yield per plant had significant positive association with number of seeds per pod, number of primary branches per plant, fresh pod width, vine length and for yield per plant had non-significant association with days to 50 % flowering, days to first pod harvest, number of pods per plant, fresh pod length, average pod weight and leaf area (cm^2).

In path analysis it was found that the character average pod weight showed very high positive direct effect on pod yield per plant followed by days to first pod harvest and number of pods per plant. High positive direct effect was shown by vine length and fresh pod length. The characters such as number of primary branches per plant and number of seeds per pod exhibit low positive direct effect whereas leaf area exhibit negligible direct effect on pod yield per plant whereas, days to 50 per cent flowering exhibit negative very high direct effect on yield per plant.

The genetic divergence revealed that there was prescence of genetic diversity among all the twenty three genotypes studied. These genotypes were further divided into four clusters, from which Cluster I was largest consisting of twenty genotypes while cluster II, III and IV were monogenotypic in nature. The maximum intra cluster distance were found in cluster I.

Considering the above results it is concluded that the genotypes, *viz.*, RHRCP-04, RHRCP-05, RHRCP-03, RHRCP-18, RHRCP-09, RHRCP-08 and RHRCP-06 are potential parents for the future breeding programmes.

Pages 1 to 82

1. INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is an annual, self-pollinated legume belonging to the family Leguminaceae with a diploid chromosome number of 2n=2x=22. It is native to India but tropical and Central Africa is considered a secondary centre of origin. In India cowpea is cultivated for food, vegetables and fodder purpose (Arya *et al*., 2019). This crop has tremendous adaptability to various conditions and therefore it is cultivated from north Jammu Kashmir to south Tamil Nadu. Cowpea has been referred to as "Poor man's meat" because of their high protein content (20-25 %) (Sabale *et al*., 2018). It is considered one of the oldest legumes used as a protein source for humans and livestock. It is being used as a pulse in form of dry seed, immature pod and green leaf and growing twigs can be utilized as a vegetable. It is an important source of green as well as dry fodder. Cowpea is cultivated for both grain and fodder in all tropical and sub-tropical regions among fodder legumes (Nguyen *et al*., 2017).

Cowpea is one of the most important vegetable crops grown during rainy and summer seasons and it is well suited and well adapted to a wide range of climates and soils as it is relatively tolerant of sandy soil and low rainfall. The vegetable cowpea has been subdivided into five subspecies; three cultivated, *V. unguiculata*, *V. sesquipedalis* and *V. cylindrica* and two wild species *V. dekindtiana*, *V. mensenensis*.

In India, During 2017-18, the area under vegetable crops was 10.26 MHa with a production of 184.40 MT. Total vegetable production was highest in Uttar Pradesh (283.16 MT) followed by West Bengal (276.95 MT). In Maharashtra, the area under vegetable crops in 2017-18 was 726.20 (000 Ha) with a production of 12306.72 (000 MT) (NHB, 2017-18). The total area under beans in India is 145 (000 Ha) with a production of 390 (000 MT). As India is the second largest producer of vegetables with 2.8 per cent of the total cropped area under vegetables. An increase of 2.5 per cent per year in vegetable production is necessary to meet the recommended requirement of 300 g. (Annon, 2021). In India, cowpea is grown in an area of 3.9 MHa with a production of 2.21 MT.

Cowpea is a warm season, annual herbaceous legume crop and growth habit is pole type as well as bush type. It has a strong tap root system, the stem may be green or pigmented and the leaves are alternate and trifoliate with one symmetrical terminal leaflet and two asymmetrical leaflets. It has an auxiliary raceme inflorescence which bears several flowers at the top. Calyx is longitudinal robbed and tubular with 2-15 cm long sub-equal lobes. The corolla of the cowpea is perpendicular with an erect standard petal, spreading at the time of flower opening. Its wings are boat-shaped and enclose an androecium and gynoecium. Stamens are Diadelphous i.e. (9+1). Anthers present in cowpea flower are yellow and its ovary is monocarpellary which has many ovules in it and pods are pedant and linear. It is commonly known as crowder pea, black-eyed pea, lobia, barbatti, chawali, southern pea, long yard bean, asparagus bean, snake bean and china bean. It is one of the most important legume vegetable crops commonly grown throughout India for its long, tender green pods as vegetables and seeds as a pulse. It is also grown for silage, hay, pasture, all type of struck and as a source of protein, especially lysine (Joghdhande *et al*., 2016).

It is a fast-growing, highly palatable and nutritious grain, fodder and vegetable crop. Hence, it is considered to be the most important leguminous crop. The crop is gaining popularity in developing and underdeveloped countries, especially in arid regions of the world due to its nutritional value. Like other legumes, cowpea fixes atmospheric nitrogen and thus contributes to the available N levels in the soil. One of the more remarkable things about cowpea is that it thrives in dry environments. Cultivars are available that produce a good crop with as little as 300 mm of rainfall. It is being cultivated in the drier parts of the world where other food legumes cannot withstand. Also, it is shade tolerant and compatible as an intercrop. This makes it the crop of choice for an arid zone (Nagalakshmi *et al*., 2010).

Cowpea stands well in dry environments, it is a noticeable characteristic of cowpea. It helps to improve soil fertility as it can fix nitrogen from the atmosphere. It has maximum forage as it has maximum vegetative growth and covers maximum ground area resulting in less soil erosion. Cowpea cultivation requires a pH of about 6-7 with a loamy type of soil with 250-300 mm rainfall and 27^0C temperature for pod formation and seed yield. It is cultivated in the dry zone of the world, where other leguminous crops cannot withstand hence it is known as "The Crop of Choice" (Wadghane *et al*., 2022).

Cowpea grain is a nutritious component in the human diet and livestock feed as well. The protein in cowpea grain is rich in amino acids, lysine and tryptophan in comparison with cereal grain. It is a good source of Protein (22–24 %), Carbohydrate (55–66 %), Iron (0.005 %) Calcium (0.08–0.11 %), Fat (1.9 %), CHO (63.6 %), Vitamin A (0.00074 mg), Thiamine (0.00014 mg), Riboflavin (0.00042 mg) and Niacin (0.00281 mg) (Krishnan *et al*., 2019). Tender pods as well as green- shelled seeds are used as a vegetable and as a pulse when dried. It is also suitable for green manuring, fodder cover and catch crop.

The present-day cultivars exhibit lower productivity, non-synchronous flowering and fruiting, less response to high doses of inputs like fertilizers, irrigation, tillage etc., non-suitability of the various cropping systems, lodging and shattering susceptible, long duration, complete or partial absence of genetic resistance to major insect pest and diseases like a mosaic virus, rust, powdery mildew and bacterial blight that cause considerable damage and poor harvest indices. The development of cultivars with early maturity, acceptable grain quality and resistance to some important diseases and pests has significantly increased the yield and cultivated area.

Cowpea includes various species which are mainly wild perennials, wild annuals and in cultivated forms. For a successful breeding programme, Genetic variability is the most important constituent. Collecting and evaluating any genotype of a crop creates greater scope for exploiting genetic diversity. A good amount of variability is present in cowpea for the characters like leaf length, leaf width, flowering, maturity, pods per plant, pod length, pod width, pods per plant, pod yield per plot, flower bud colour, pod shape, leaf shape etc. utilization of these characters in breeding programmes has not been fully used hence, it is necessary to study the genetic variability in various genotypes of cowpea.

Cowpea which is a high protein vegetable, suffers from alarmingly low yield, especially in south-east Asia. One of the major reasons was recognized as the non-availability of improved genotypes suitable for different cropping systems with greater suitability and general adaptability. Although, a large amount of variability is available for almost all the traits, even then very poor productivity for green pod yield had been recorded. The yield level of cowpea is low, which is mainly due to the non-availability of desirable high-yielding disease and insect- resistant varieties and poor management practices hence the high yield potential and quality are the main target for an effective breeding programme in this crop. For any crop improvement breeding programme, it is essential that study of genetic variability of that crop. The study of Genetic variability in cowpea is used for improvement in the selection of superior genotypes which helps in selection-based improvement in cowpea.

Correlation coefficient analysis gives an idea about the nature and intensity of association between two or more quantitative characters. It measures the relationship between yield and yield contributing characters. It simply gives a clear picture of the association between a pair of traits and indicates whether the improvement of the traits may be possible or not. Thus, selection of superior genotype from diverse genetic populations is possible through correlation (Palve *et al*., 2018).

The path analysis given by Dewey and Lu (1959) enables a critical analysis of a given correlation and the determination of the relative relevance of each element, as well as an efficient way to identify direct and indirect sources of association. This understanding makes it possible to simultaneously increase a number of characteristics and it also improves the efficiency of determining complex inherited traits. The genetic divergence among genotypes was estimated by using D^2 statistics (Mahalanobis, 1936).The average intra and inter cluster distances were calculated by the formulae given by Singh and Chaudhary (1977).

Considering the scope in increasing the production of cowpea the variability studies on twenty- three cowpea genotypes with the standard check will be undertaken at the farm of AICRP on Vegetables, Department of Horticulture, MPKV, Rahuri during the year 2022 with the following objectives.

1. To study the nature and extent of variability present in the different cowpea genotypes.
2. To study the correlation of yield and yield contributing characters.
3. To identify the most suitable and best-performing elite genotype.
4. To identify the elite genotypes for disease resistance.

2. REVIEW OF LITERATURE

Any breeding programme depends on the availability of variation selection practices. The knowledge of quantitative traits is required for the selection of elite genotypes. The statistical parameters viz., genetic variability, correlation and path analysis, heritability, genetic advance and genetic diversity. The Literature collected has been reviewed under the following sub-headings :

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation and path analysis

2.4 Genetic diversity

2.1 Genetic variability

Manggoel *et al*. (2012) showed significant ($P<0.05$) variability for days to 50 % flowering, number of peduncles plant^{-1}, flowers plant^{-1}, pods plant^{-1}, seeds pod^{-1}, pod length, 100-seed weight and grain yield. The magnitudes of the genotypic variance of these traits were higher than the environmental variance, indicating that the genotypic component was the major contributor to the total variance. The phenotypic coefficient of variation and genotypic coefficient of variation was high for the traits studied, except pod length and seeds pod^{-1}. These Field experiments were conducted to estimate genetic variability, heritability, correlations and path analysis of some reproductive characters on the grain yield of 10 cowpea accessions.

Sapara *et al*. (2014) carried out variability with forty genotypes of cowpea. Significant differences among the genotypes for all the characters studied except pod width indicate the existence of ample variability in the experimental material for all the characters. A high to moderate range of variation was observed for important yield components. The estimates of the genotypic and phenotypic coefficient of variation were high for several pods per plant, 100 fresh seed weights, plant height, 10 pod weights and green pod yield per plant. The values of the phenotypic coefficient of variation were higher than their genotypic coefficient of variation for all the characters indicating the influence of environmental factors.

Niar and Mehta (2014) treated Cowpea var. Pusa Komal with physical mutagen gamma rays (100, 200, 300, 400, 500 Gy) and chemical mutagen EMS (0.25, 0.30, 0.35, 0.40 and 0.45 %) to assess the genetic variability in M2 and M3 generation. Analysis of variance in M2 and M3 populations showed significant differences among the treatments for all the twelve yields and their attributing characters under study except protein per cent. For all the characters under study in both generations, the phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation. High GCV, as well as PCV, was obtained in M2 and M3 generation for traits of some primary branches per plant, protein per cent, yield per plant and hundred seed weight. High heritability estimates were recorded in protein per cent in M2 as well as M3 populations.

Meena *et al*. (2015) conducted a field experiment during the *kharif* season in 2013 to evaluate 72 genotypes of cowpea. The genotypic and phenotypic variance was recorded highest for plant height (358.69, 378.69) followed by pod wall proportion (38.30, 41.27) and lowest for primary branches per plant (0.30, 0.50). High GCV and PCV were recorded for plant height (38.65, 39.70) followed by 100- seed weight (25.68, 26.21) and pod wall proportion (20.49, 21.24). Whereas, a moderate estimate of GCV and PCV were recorded for seed yield per plant (15.93, 18.76) followed by pods per plant (14.86, 19.69), pod length (14.93, 16.28), primary branches per plant (12.77, 16.77) and seeds per pod (12.98, 14.76). High estimates of heritability along with high genetic advance as per cent of mean were recorded for the 100-seed weight (95.95, 51.81) and plant height (94.78, 77.52) which indicated the major role of additive gene action in the expression of these characters while high heritability along with moderate genetic advance as per cent of mean was recorded for pod wall proportion, seed yield per plant and pod length which indicated these characters was mainly governed by non-additive gene action.

Sharma *et al*. (2017) carried out a present investigation on 30 genotypes to study genetic parameters for ten characters at the Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Udaipur, Rajasthan, India. The estimates of genotypic parameters revealed that differences between the estimates of GCV and PCV were found least 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 were found for test weight followed by plant height, primary branches per plant, seed yield per plant and harvest index. These characteristics are governed by additive gene action and one should go for direct selection for these traits to improve in future.

Havaraddi and Deshpande (2018) evaluated 30 genotypes along with two checks for genetic variability and other related parameters in respect of eight quantitative characters during *Kharif* 2016. Analysis of variance revealed highly significant differences among genotypes for all the characters. A considerably high range of variation was observed for characters viz. Seed yield, days to fifty per cent flowering, plant height and the number of pods per plant. 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 whereas, the remaining traits exhibited low to moderate PCV and GCV values.

Magashi *et al*. (2018) conducted a field experiment on five Cowpea cultivars which were sown in a randomized block design (RBD) with three replications. The results showed high significant variability for all the tested traits except days to flowering and days to branching. All the PCV values were higher than the GCV values for each character and showed a similar pattern of changing over the characters. The highest heritability was recorded in favour of hundred seeds weight. Based on the results obtained it is concluded that genotypic variation can be used for effective selection based on phenotypic expression and the heritability value of a trait.

Devi and Jayamani (2018) evaluated one hundred and eighty genotypes of cowpea during *kharif* 2017. The high estimates of GCV was found in traits viz., number of pods per plant, number of clusters per plant, hundred seed weight and single plant yield. High heritability for plant height, days to 50 per cent of flowering, number of racemes per plant, peduncle length, number of pods per plant, number of clusters per plant, days to maturity, pod length, hundred seed weight and single plant yield. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of racemes per plant, peduncle length, number of pods per plant, number of clusters per plant, pod length, hundred seed weight and single plant yield. A high degree of variability was observed among the genotypes for different yield- contributing traits. This could be utilized in the breeding programme for the improvement of cowpea.

Gupta *et al*. (2019) conducted the trial on twenty-seven genotypes of cowpea which were sown in RBD with three replications and observations regarding eighteen characters were recorded at the Vegetable farm, RPCAU, Pusa, Samastipur during zaid-2017. Analysis of variance shows that there was a significant difference among all the eighteen quantitative characters which indicates the diverse genetic nature of the population. The coefficient of phenotypic variation was slightly greater than those of genotypic variation for almost all the characters showing that the existing variation is mainly governed by the genotypic factor and there is little influence of environment in the expression of the character.

Krishnan *et al*. (2019) Kerala Agricultural University, Kayam Kulam conducted experiment on Genetic Variability and Heritability studies in Cowpeas with fifteen genotypes of cowpea at ORARS Kayam Kulam. A high genotypic coefficient of variation, heritability in the broad sense and genetic advance were estimated for some of the characters. The genotype Kashi Kanchan recorded the maximum mean value for pod length, the number of seeds per pod and the seed index. The estimates of the phenotypic coefficient of variation for all yield parameters were higher than that of the genotypic Coefficient of variation. A high heritability value coupled with high genetic advance. The information on genetic variability among the existing cowpea genotypes will increase the efficiency of the cowpea improvement in terms of quality and quality.

Koraddi and Basavaraja (2019) accessed the variability, heritability and genetic advance of 13 genotypes of soybean. Observations on 11 characters were recorded. Analysis of variance revealed highly significant differences among the genotypes for all the characters. The range was maximum for plant height (39.27- 77.73) followed by several pods per plant (35.87- 61.40). The genotypic coefficient of variation and phenotypic coefficient of variation was high for pod weight per plant (g) followed by seed yield per plant (g) indicating the presence of wider adaptability for these traits in the genotypes studied, suggesting the less influence of environment in the expression of characters. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 % flowering, plant height (cm), number of pods per plant, number of seeds per pod, pod weight per plant, 100 seed weight, biomass and seed yield per plant indicating additive gene action and the ample scope for improvement in these traits through simple selection.

Pandiyan *et al*. (2020) evaluated twenty-eight cowpea entries at Agricultural Research Station, Virinjipuram for yield and its components during two seasons *Kharif* 2014 and *Rabi* 2015. Phenotypic and genotypic variability was observed for seed yield and component characters pods per plant and clusters per plant. The result indicated that the selected cowpea genotypes have shown a mean value for 50 % flowering was 45.00 days with a total of days 74.50 for full maturity. The plant height was 73.27 cm with 16.77 no. of pods per plant. High heritability and low genetic advance as a percentage of the mean were recorded for days to 50 % flowering, days to maturity and plant height suggesting that selection based on these Characters could be effective.

Panchta *et al*. (2020) evaluated fourteen genotypes of cowpea (*Vigna unguiculata (*L.) Walp) for character association during *kharif* 2017. The phenotypic coefficient of variation (PCV) estimates were invariably higher than their corresponding genotypic coefficient of variation (GCV) values. This suggests the environmental influence. High GCV and PCV were observed for seed yield per plot, days to 50 % flowering, days to maturity and plant height. The number of seeds per pod had a positive and significant correlation at the genotypic level with seed yield per plot. Two genotypes viz. GC 3 and PTBCP 4 were found resistant to Cowpea Yellow Mosaic Virus (CYMV) disease.

Ugale *et al*. (2020) conducted a field experiment on Thirty-One genotypes of cowpea which were sown in a randomized block design with two replications, during *Kharif* 2018 at the Research farm, Department of Agricultural Botany, VNMKV, Parbhani. The results indicated high heritability was coupled with high genetic advance as per cent of mean was observed for all growth, flower attributes, earliness attributes and pod attributes except days to 50 % flowering and pod width indicating that these characters were less influenced by environmental effects and these characters were governed by additive genes and selection will be rewarding for improvement of such traits.

Vinay *et al*. (2022) evaluated thirty-two cowpea genotypes in randomized block design to assess the nature and magnitude of variability, heritability and genetic advance for ten quantitative traits at Regional Agriculture Research Station, Warangal, Professor Jayashankar Telangana State Agricultural University, Hyderabad. Analysis of variance unveiled that differences among the genotypes were significant for all the characters considered indicating the presence of a substantial amount of genetic variation among the germplasm studied. High estimates of GCV and PCV were recorded for clusters per plant, seed yield per plant, pods per plant, plant height and seeds per pod, while high estimates of heritability were recorded for all the characters under study. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, seed yield per plant, clusters per plant, pods per plant, test weight, seeds per pod, pod length and branches per plant suggesting predominance of additive gene effects and these characters could be improved through selection.

Wadghane *et al*. (2022) conducted a field experiment which is comprised of 30 cowpea genotypes that were evaluated for genetic variability for important quantitative and quality traits during the summer 2019 season. High heritability and high genetic advance were observed for days to 50 % flowering, leaf width, the number of nodes on the main stem, the number of main branches, the number of pods per plant, length of the pod, the number of seeds per pod, test weight, seed yield per plant, fat content, lignin content and host preference mechanism of pulse beetle on the grain of cowpea indicating that the characters are governed by additive gene action and the characters which can be improved by simple selection. On Mahalanobis D_2 statistics, the genotypes were grouped into four clusters. A maximum number of genotypes was observed in cluster I with 16 genotypes followed by clusters II and III with 8 genotypes each and cluster IV with solitary genotype.

2.2 Heritability and genetic advance

Vavilapalli *et al*. (2013) experimented to assess the genetic variability, heritability and genetic advance for different characters in 22 diverse genotypes of bush cowpea at the Department of Olericulture, College of Agriculture, Vellayani, Kerala, India. The high phenotypic coefficient of variation and genotypic coefficient of variation was observed for pod weight, plant height and pod length. High heritability coupled with high genetic advance was observed for all characters studied, except days to first flowering and days to the first harvest indicating these characters are governed by additive gene action.

Shanko *et al*. (2014) tested Forty-nine cowpea genotypes in a 7 x 7 triple lattice design at Haramaya University, Dire Dawa Tony farm with three replications in 2010/11. High phenotypic and genotypic coefficient of variation, heritability in a broad sense and genetic advance estimated for the characters viz., yield per plant, some pods per plant and 100-seed weight indicated the scope of improvement of these characters through selection.

Santos *et al*. (2014) estimated the genotypic and phenotypic correlations and analyze the direct and indirect effects of yield components on grain yield in 20 cowpeas (*Vigna unguiculata*) genotypes. The experimental design was in randomized blocks with 20 treatments and 4 replications. The character showed a low to moderate possibility of gain from indirect selection, with a greater possibility for success when joining multiple characters and a genotype of better performance.

Khanpara *et al*. (2015) evaluated sixty genotypes of vegetable cowpea for genetic variability, heritability and genetic advance. Analysis of variance revealed significant differences among the genotypes for all the12 characters studied. High heritability was observed for green pod yield per plant, plant height, pod length, pod width, number of seeds per pod, number of pods per plant, ten pod weight, number of pods per cluster and hundred fresh seed weight. These indicated that these traits were governed by additive gene action and responsive to further improvement of these traits.

Rambabu *et al*. (2016) experimented to study Genetic variability, heritability and genetic advance for some traits in Yard long bean for 41 genotypes. The maximum phenotypic and genotypic coefficient (PCV and GCV) was observed for the characters viz., number of pods per plant, pod length (cm) pod ascorbic acid content (mg/100g) and pod yield per plant (g). The High estimates of heritability (broad sense) was observed for pod length (99 %), pod girth (94 %), plant height (79 %), pod yield per plant (75 %), terminal leaf breadth (69 %), seed protein content (67 %), number of clusters per plant (64 %) and seed number per pod (62 %) with the high genetic advance in per cent of the mean indicated the scope for improvement of these characters through selection.

Patel *et al*. (2016) experimented to estimate genetic variability and heritability studies of thirty-two genotypes of cowpea. The genotypic coefficient of variation, heritability and genetic advance were observed highest for the characters viz., number of pods per plant and green pod yield per plant. High heritability (77.44 %) coupled with high genetic advance (52.08) observed for green pod yield per plant and very high heritability (94.47 %) for plant height at final harvest indicate that phenotypic selection would be effective for genetic improvement in these traits.

Sarath and Reshma (2017) assessed 22 genotypes of cowpea. A high degree of variability was observed for all the characters. High magnitude of the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as 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 was found maximum in pod weight (30.15 %), followed by the number of pods per plant (18.12 %) and test weight (16.27 %).

Lokesh *et al*. (2017) studied the genetic variability generated from the IT-38956-1 x KBC-2 cross in F2 and F3 generation to make effective selections for improving productivity. The higher heritability and genetic advance per mean were recorded in F2 and F3 generation for secondary branches per plant, pods per plant, pod length and seeds per pod and seed yield per plant recorded the moderate values that implicate additive gene action in inheritance of these traits thus phenotypic selection would be effective in yield improvement.

Olunloyo *et al*. (2019) A line x tester analysis was undertaken using 4 lines (TVu3629, TVu1509, TVu14019 and TVu15687) and 1 tester (TVu1) resulting in 4 hybrids of cowpea to study genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance in four crosses of cowpea made. The high phenotypic and genotypic coefficient of variation was observed for days to flowering and seed yield per plant, while the lowest GCV and PCV were observed for pod length, number of seeds per pod and 100 seed weight. High magnitude of broad sense heritability along with moderate to high genetic advance as percentage of mean recorded for days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant obtained in crosses indicated that these characteristics can be improved through selection in advanced generations using line tester method.

Chaudhary *et al*. (2020) thirty accessions evaluated eleven agro-morphological traits at the agronomy instructional farm, C.P. College of Agriculture, S.D.A.U., Sardarkrushinagar. The genotypic coefficient of variation, heritability and genetic advance were observed highest for seed yield per plant followed by several pods per plant and leaf area per plant. A significant positive correlation was found between seed yield per plant and the number of pods per plant; several seeds per pod; the number of branches per plant; pod length and plant height. Whereas, a negative significant correlation was observed between seed yield per plant with days to flowering and days to maturity. In the present studies, pod length recorded the highest positive direct effect on seed yield per plant followed by several branches per plant and the number of pods per plant. While days to flowering had the highest negative direct effect on seed yield per plant. Both correlation and path analyses indicated that the number of pods per plant, number of seeds per pod, number of branches per plant and pod length were the major direct contributors to seed yield.

2.3 Correlation and Path Analysis

Sharma *et al*. (2016) studied correlation and path coefficients for ten quantitative characters among thirty cowpea germplasm. The number of pods per plant, number of flowers per plant, test weight, number of clusters per plant, harvest index and number of primary branches per plant had a direct high positive association with seed yield. The trait days to maturity had negative and non revealed that seed yield per plant can be improved by practicing selection for harvest index, number of pods per plant, number of primary branches per plant, test weight and plant height as they contributed directly to the seed yield per plant as revealed from path analysis. It indicated the possibilities of simultaneous improvement of traits by selection.

Khandait *et al*. (2016) experimented at Vegetable Research Farm, Collage of Agriculture, JNKVV, Jabalpur (Madhya Pradesh). These include 15 genotypes of cowpea. The present study resulted that, a significant positive phenotypic correlation of pod yield plant^{-1} was observed with pods plant^{-1} (0.589), days to first flowering (0.415), seeds pod^{-1} (0.395), number of flower cluster plant^{-1} (0.372) and pod length (0.304). Seed yield plant^{-1} resulted from a significant and positive correlation with pod yield plant^{-1} (0.395) indicating that these characteristics are the primary yield determinant in cowpea. Path coefficient analysis of different characters contributing towards pod yield plant^{-1} resulted from that number of pods plant^{-1} (2.108) had the highest positive direct effect followed by pod weight (2.054), number of flower cluster^{-1} (0.347), pod width (0.298), number of branches at 90 DAS (0.256), number of flower cluster plant^{-1} (0.154), days to first picking (0.128), plant height at 90 DAS (0.081) and pod length (0.033). Whereas, days to first flowering (-0.061) had the maximum negative direct effect on pod yield plant^{-1} followed by days to 50 % flowering (-0.121), number of seeds pod^{-1} (-0.563) and pod cluster^{-1} (- 0.712).

Baranda *et al*. (2017) conducted a field experiment to determine the correlation coefficient among 30 genotypes for twelve quantitative characters and one qualitative character i.e. protein content taken into consideration. The result revealed that seed yield per plant exhibited a significant positive correlation at both genotypic and phenotypic levels with biological yield, harvest index and 100-grain weight in (E1, E2, E3 and over pooled basis) and also with pods per plant and number of cluster per plant in at least two environments (E1, E2 and on pooled basis) and plant height in E2 only. However, seed yield per plant exhibited a positive correlation with plant height and pod length in at least two environments (E1, E3) both genotypically and phenotypically.

Sharma *et al*. (2017) revealed that differences between the estimates of GCV and PCV were found least 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 were found for test weight followed by plant height. Primary branches per plant, seed yield per plant and harvest index. These characters are governed by additive gene action and suggest selection for further improvement.

Dinesh *et al*. (2017) crossed two diverse parents i.e C-152 × V-16 and advanced to the F3 generation. The magnitude of variation, heritability, genetic advance, correlation and path coefficient analysis were estimated in a set of 194 F3 progenies. The traits having high heritability and significant positive correlation with the grain yield can be utilized for indirect selection for genetic improvement. A moderate phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates was recorded for plant height (15.75 and 12.91 %) and the number of pods per plant (16.29 and 11.42 %). High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for plant height (67.13 and 21.78 %) and moderate heritability and GAM were observed for the number of pods per plant (49.14% and 16.49 %). Path coefficient analysis revealed that seed yield was primarily influenced by the number of pods per plant, many seeds per pod and 100 seed weights which had the maximum direct effect on seed yield per plant. Information obtained in this study suggests that traits like plant height, number of pods per plant, number of seeds per pod and 100 seed weight could be used as selection criteria for grain yield improvement at segregating populations of cowpea.

Joghdhande *et al*. (2017) studied Correlation and path analysis of 30 genotypes of cowpea (*Vigna unguiculata (*L.) Walp.) The result on phenotypic and genotypic correlation coefficient revealed that pod yield per plot was significantly and positively correlated with some branches per plant (0.7659), number of nodes (0.5523), pod length (0.3960), number of seeds per pod (0.2815), number of cluster per plant (0.550), number of pods per plant (0.547), number of pods per cluster (0.524), plant height (0.437) and protein content (0.2871). Path coefficient analysis of different yield and yield contributing traits on the number of branches per plant, number of nodes per plant, number of clusters per plant, number of 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 these characters play a major role in recombination breeding and suggested that direct selection based on these traits will be rewarded for crop improvement of cowpea.

Lal *et al*. (2017) studied sixty-six bush type advanced breeding lines of vegetable cowpea at ICAR - Indian Institute of Vegetable Research (ICAR-IIVR) and revealed that pod yield per plant showed a strong positive correlation with the number of peduncles and pods per plant, pod weight, pod length, number of seeds per pod and number of primary branches per plant, while the negative correlation with days to 50 % flowering at genotypic and phenotypic levels. The maximum direct positive effect on pod yield per plant was found contributed by several pods per plant followed by pod weight.

Palve *et al*. (2018) carried out a field experiment on twenty genotypes of cowpea using a randomized block design with three replications at Main Garden, Department of Horticulture, Dr PDKV, Akola. The characters like number of pods per plant, number of pods per cluster, primary branches per plant, number of clusters per plant, pod length, pod diameter, average pod weight and leaf area had a highly significant positive correlation with pod yield per plot both genotypic and phenotypic levels, which indicates the dependence of these characters on each other. Path coefficient analysis reveals that the character's number of pods per plant, 100 seed weight, primary branches per plant, plant height, pod length and several seeds per pod positive direct effect on pod yield per plot. While traits like the number of pods per cluster, the 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 effects towards the yield.

Tsegaye *et al*. (2018) conducted a field experiment at Melkassa Agricultural Research Center. Thirty cowpea accessions with six standard checks were tested in a triple lattice design. Data for 13 agronomic traits were measured and statistically tested. Seed yield showed positive and significant phenotypic association with pod length, number of pods bearing cluster plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, 100-seed weight, harvest index and biomass yield. The Harvest index also showed a positive correlation with seed yield at the genotypic level. Therefore, any improvement in these traits may result in a substantial increase in seed yield. At the genotypic and phenotypic level, seed pod, number of pods plant^{-1}, 100-seed weight, harvest index, number of nods plant^{-1} and those traits exerted a positive direct effect on seed yield.

Walle *et al*. (2018) present study was conducted to determine the nature and extent of phenotypic and genotypic correlation and path coefficient analysis among 18 quantitative traits. A total of 324 cowpea landraces were tested in 18 × 18 simple lattice designs at Melkassa Agricultural Research Center and Miesso sub-centre during the 2016 cropping season. The magnitude of genotypic correlations was higher than phenotypic correlations in most traits at both locations; this implies that the traits under consideration were genetically controlled. Almost all traits' genotypic direct and indirect effects were higher than the phenotypic direct and indirect effects; this indicated that the other traits had a strong genetically inherited relationship with seed yield. Genotypic path coefficient analysis revealed that days to flowering, biomass and harvest index at Miesso and seed thickness, plant height, days to maturity and biomass at Melkassa had a relatively high positive direct effect on seed yield. However, seed width and hundred seed weight had exerted a negative direct effect on seed yield at each location. Phenotypic path coefficient analysis showed that biomass and harvest index had exerted a high positive direct effect on seed yield at both locations.

Paghadar *et al*. (2019) conducted an experiment using 60 genotypes of vegetable cowpea to find out the correlation coefficients and path coefficients. The observations were recorded on 12 characters. The pod yield per plant exhibited significant and positive correlations with the number of primary branches per plant, plant height, pod length, number of pods per plant and number of seeds per pod at both genotypic and phenotypic levels. The path coefficient analysis showed the high positive direct influences on pod yield per plant through the number of primary branches per plant and pod length hence, due emphasis should be placed on these characteristics while selecting high-yielding types in vegetable cowpea.

Kalambe *et al*. (2019) experimented on twenty-two genotypes including two checks of Cowpea (*Vigna unguiculata* L.) at a research farm, Department of Agril. Botany, VNMKV, Parbhani. The observations were recorded on twelve characters viz, plant height, number of primary branches per plant, days to 50 % flowering, number of pods per plant, number of seeds per pod, mean pod weight (g), pod length (cm), pod width (cm), days to first pod harvest, 100 seed weight (g), pod yield per plant (g) and pod yield per hectare (qt). It was observed that the magnitude of association varied among the genotypes. The character's plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, mean pod weight and 100 seed weight showed a positive and significant correlation with pod yield per plant.

Tambitkar *et al*. (2020) experimented with forty-one genotypes at a research and education farm, Department of Agriculture Botany, College of Agriculture, Dapoli. Observations were recorded on eleven characters. The correlation study revealed that the characters viz., dry matter yield per plant and harvest index showed a highly significant positive correlation with grain yield per plant at the phenotypic and genotypic levels. The path coefficient analysis revealed that the characters viz., days to fifty per cent flowering, number of pods per plant, number of seeds per pod, plant height at maturity, dry matter yield per plant and harvest index exhibited a positive direct effect on seed yield per plant. Based on path analysis and correlation study for grain yield, it is concluded that selection based on days to initiation of flowering, number of primary branches per plant, pods per plant and hundred seeds weight could help in genetic improvement of grain yield per plant in cowpea under study.

Patil *et al*. (2021b) experimented with assessing the genetic variability, correlation and path analysis in the F3 population of forty-five crosses of cowpea in a Randomized Block Design with two replications. A positive and highly significant correlation was reported between seed yield per plant and number of pods per plant (1.0080) followed by harvest index (0.8652), 100 seed weight (0.7685) at the genotypic level. A genotypically negative highly significant correlation was reported with days to maturity (-0.4294) and a negative nonsignificant correlation with days to 50 % flowering (-0.0413). Path coefficient analysis revealed a positive direct effect of several pods per plant, days to initiation of flowering and hundred seed weight at both genotypic and phenotypic levels. Whereas, characters viz., days to maturity, number of clusters per plant, number of pods per cluster and plant height at the genotypic level and characters viz., number of branches per plant and pod length at a phenotypic level were having a direct positive effect on seed yield per plant.

2.4 Genetic diversity

Nagalakshmi *et al*. (2010) studied sixty six genotypes of cowpea (*Vigna unguiculata (*L.) Walp) to understand the extent of genetic diversity through twelve quantitative traits. Mahalanobis's D^2 analysis established the presence of wide genetic diversity among these genotypes by the formation of 23 clusters. Intra-cluster distance analysis revealed that the minimum intra-cluster distance was observed in cluster II. The inter-cluster distance (D) was found to be the maximum between clusters XXII and XXIII and the same was minimum between clusters II and V. The results indicated that grain yield per plant contributed the maximum to the total divergence followed by 100 seed weight and days to 50 % flowering. The number of branches per plant had the least contribution to the total divergence followed by petiole length. In the present study, the variety Vellayani local had the maximum value for plant height and pod length and thereby distinguished from other varieties and it is present singly in cluster XXIII. Hence it is proved to be widely divergent, since its yield is high, it can be used for further crossing and yield improvement. Cluster XVIII had the highest cluster mean values for the number of clusters per plant and cluster XIV has the highest mean value for grain yield per plant. These two clusters may be utilized in the crossing programme.

Jogdhande *et al*. (2016) conducted a field experiment at Main Garden, Department of Horticulture, Dr PDKV, Akola. Thirty genotypes of cowpea [*Vigna unguiculata (*L.) Walp] were investigated to understand the extent of genetic diversity through sixteen traits. Cluster I was the largest and consisted of 21 genotypes followed by cluster III of 5 genotypes and clusters II, IV, V and VI consisting of only one genotype each. Maximum inter-cluster D2 value was observed between VI (6987.85) and III (4806.87), indicating that the genotypes included in these clusters had maximum divergence. The diversity among the genotypes measured by inter-cluster distance was adequate for the improvement of cowpea by hybridization and selection. The genotypes included in these diverse clusters may be used as promising parents for hybridization to obtain better segregants in cowpea.

Patel *et al*. (2017) accessed thirty-two cowpea [*Vigna unguiculata (*L.) Walp.] genotypes for 12 quantitative characters to estimate the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into eight clusters. The cluster strength varied from a single genotype (Clusters IV, V, VI, VII and VIII) to 12 genotypes (Cluster II). The maximum inter-cluster distance (D^2 = 35.43) was observed between cluster-VI and VIII. Clusters II, III and I had a maximum 100-seed weight, number of seeds per pod and seed yield respectively. Cluster VIII had the highest mean value for the characters viz., number of pods per plant, number of green pods per plant and green pod yield per hectare (kg/ha), while cluster III had the lowest mean value for days to 50 per cent flowering. Based on inter-cluster distances, cluster VIII was found to be more divergent. Therefore, it was concluded that the genotypes belonging to this cluster should be inter-crossed to generate more variability.

Mafakheri *et al*. (2017) studied 32 cowpea genotypes in which 17 morphological characters and multivariable statistical methods were studied followed by using a set of 22 Simple Sequence Repeat (SSR) primer pairs for molecular characterizations. The result revealed significant differences among accessions for all measured traits. In molecular analysis, a total of 186 alleles were detected with an average of two alleles for each locus and the genetic distance between genotypes was estimated at 0.0066. Results of factor analysis determined 5 and 6 factors in drought stress and normal irrigation condition explaining 81.17 and 88.20 per cent of the total variation respectively. The average genetic similarity observed across all the genotypes was 75.8 per cent.

Nameirakpam and Khanna (2018) studied genetic diversity among cultivated cowpea (*Vigna unguiculata*) varieties using RAPD markers and assessment of crossability within the species was taken up a total of 30 RAPD primers were randomly selected to assess the genetic diversity of 36 accessions of cowpea. Based on the PIC value, five primers (OPC 14, OPB 1, OPA 10, OPG 13 and OPA 4) were found to be more informative. The PIC value showed ranged from 0.597 to 0.885 with the primer OPC 14 having the highest PIC value of 0.885. Based on the Euclidean similarity matrix, a clustered dendrogram was made by following the ward's method (Ward, 1963), which indicated that PL-2 and CP-7 were found to be more distinct from IC-202826. Based on the PCA plot, the first component explained 18.56 per cent variation and the second and third components explained 16.85 and 12.77 per cent, respectively among the 36 accessions of cowpea. The first three components explained 48.21 per cent of the total variation.

Walle *et al*. (2019) studied morphological diversity by using 324 genotypes at Melkassa Agricultural Research Center. The cluster analysis based on quantitative traits revealed six distinct groups at a 90% similarity level. The clustering of genotypes did not follow patterns of geological origin, indicating no relationship between genetic and geographic distribution. The higher inter-cluster D^2 was recorded between cluster IV and cluster VI. Hence, the high genetic distance exhibited within and among clusters has to be exploited via crossing and selection of the most divergent parents for future cowpea breeding programmes.

Yadav *et al*. (2020) experimented at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad. Genetic diversity estimated in 30 cowpea genotypes using Mahalanobis's D^2 statistic showed that thirty genotypes were grouped into six clusters by Non- Hierarchical Euclidean cluster analysis. Cluster III was the largest comprising eleven genotypes followed by Cluster I with seven genotypes. The maximum inter-cluster distance was observed between cluster II and cluster IV. The maximum intra-cluster distance was observed in cluster V. Cluster VI showed the maximum cluster mean value for seed yield per plant followed by biological yield/plant, days to 50 % pod setting and days to maturity. The highest contribution in the manifestation of genetic divergence was exhibited by biological yield followed by days to maturity and seed yield per plant.

Gomes *et al*. (2020) assessed the genetic variation in 59 *Vigna unguiculata (*cowpea) accessions from 10 landraces spanning across six agro-ecological zones of Mozambique, based on nuclear microsatellite markers. The results revealed the existence of high genetic diversity between the landraces, even in comparison to other world regions. Four genetic groups were found, with no specific geographic pattern, suggesting the presence of gene flow between landraces. In comparison, the two commercial varieties had lower values of genetic diversity, although still close to the ones found in local landraces. The high genetic diversity found in Mozambique sustains the importance of local genetic resources and farm protection to enhance genetic diversity in modern varieties of cowpea worldwide.

Nkhoma *et al*. (2020) evaluated one hundred cowpea genotypes for agronomic traits in two selected sites in Zambia, using a 10 × 10 alpha lattice design with two replications. The results revealed that the number of pods $plant^{-1}$ (NPP), pod length (PDL) and some seeds pod^{-1} (NSP), were significantly ($p < 0.05$) affected by genotype × environment interaction effects. Genotypes such as CP411, CP421, CP645, CP732, Chimponongo and MS1-8-1-4 exhibited higher grain yield of > 1200 kg/ha with excellent performance in yield components such as NSP, PDL, HSW and GYD. Grain yield had significant ($p < 0.05$) associations with NPP ($r = 0.50$), NSP ($r = 0.46$) and PDL ($r = 0.42$) useful for simultaneous selection for yield improvement in cowpea. The SNP markers revealed gene diversity and polymorphic information content of 0.22 and 0.17, respectively, showing that the tested cowpea accessions were genetically diverse.

Patil *et al*. (2021) a studied Thirty-three seed cow genotypes (*Vigna unguiculata (*L.) Walp) collected from the different geographical regions and were assessed for their genetic divergence based on ten characters at Post Graduate Farm, MPKV, Rahuri. The genotypes were grouped into six clusters which indicated high genetic diversity among them. It indicated that genetic diversity and geographic diversity are not related. The present study revealed that days to 50 % flowering contributed a maximum (34.09 %) for divergence followed by plant height (32.58 %), number of pods per plant (10.98 %) and test weight (8.71 %). 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 a future breeding programme.

Gbedevi *et al*. (2021) accessed 255 cowpeas collected from five administrative regions and the Agricultural Research Institute of Togo were assessed using 4600 informative diversity array technology (DArT) markers. Among the regions, the polymorphic information content (PIC) ranged from 0.19 to 0.27 with a mean value of 0.25. The expected heterozygosity (He) varied from 0.22 to 0.34 with a mean value of 0.31, while the observed heterozygosity (Ho) varied from 0.03 to 0.07 with an average of 0.05. The average inbreeding coefficient (FIS) varied from 0.78 to 0.89 with a mean value of 0.83, suggesting that most of the accessions are inbred. Variation was highest (78 %) among accessions within populations and lowest between populations (7 %). These results revealed a moderate level of diversity among the Togo cowpea germplasm. The findings of this study constitute a foundation for the genetic improvement of cowpea in Togo.

3. MATERIAL AND METHODS

The present experiment, entitled "Variability studies in Cowpea (*Vigna unguiculata (*L.) Walp) genotypes." was conducted at All India Coordinated Research Project on Vegetable crops, Department of Horticulture, MPKV, Rahuri during Summer 2022.

The details of seed material used and methods adopted for the study of genetic variability, the experimental design adopted and the statistical procedures followed are mentioned under various sub-headings in this chapter.

3.1 Experimental Material

The twenty two germplasm lines and one check were obtained from All India Coordinated Research Project on Vegetable crops, Department of Horticulture MPKV Rahuri. The details of these total present twenty two Cowpea genotypes along with one check has given in table 3.1.

Table 3.1. Different cowpea genotypes and their sources

Sr. No.	Genotype	Geographical origin
1	RHRCP-1	AICRP on Vegetables, MPKV, Rahuri
2	RHRCP-2	AICRP on Vegetables, MPKV, Rahuri
3	RHRCP-3	AICRP on Vegetables, MPKV, Rahuri
4	RHRCP-4	AICRP on Vegetables, MPKV, Rahuri
5	RHRCP-5	AICRP on Vegetables, MPKV, Rahuri
6	RHRCP-6	AICRP on Vegetables, MPKV, Rahuri
7	RHRCP-7	AICRP on Vegetables, MPKV, Rahuri
8	RHRCP-8	AICRP on Vegetables, MPKV, Rahuri
9	RHRCP-9	AICRP on Vegetables, MPKV, Rahuri
10	RHRCP-16	AICRP on Vegetables, MPKV, Rahuri
11	RHRCP-17	AICRP on Vegetables, MPKV, Rahuri
12	RHRCP-18	AICRP on Vegetables, MPKV, Rahuri
13	RHRCP-19	AICRP on Vegetables, MPKV, Rahuri
14	RHRCP-20	AICRP on Vegetables, MPKV, Rahuri
15	RHRCP-21	AICRP on Vegetables, MPKV, Rahuri
16	RHRCP-22	AICRP on Vegetables, MPKV, Rahuri
17	RHRCP-25	AICRP on Vegetables, MPKV, Rahuri
18	RHRCP-26	AICRP on Vegetables, MPKV, Rahuri
19	RHRCP-27	AICRP on Vegetables, MPKV, Rahuri
20	RHRCP-28	AICRP on Vegetables, MPKV, Rahuri
21	RHRCP-29	AICRP on Vegetables, MPKV, Rahuri
22	RHRCP-31	AICRP on Vegetables, MPKV, Rahuri
23	Pooja (C)	AICRP on Vegetables, MPKV, Rahuri

3.2 Experimental Methods

3.2.1 Field Experiment

Field experiment consisting of twenty two cowpea genotypes with one check to study various quantitative and morphological characters was conducted at AICRP on vegetables, MPKV Rahuri. The details of the experiment were as follows :

1.	Crop	:	Cowpea
2.	Number of genotypes	:	22 Genotypes + 1 check (Pooja)
3.	Season	:	Summer 2022
4.	Design	:	Randomized Block Design (RBD)
5.	Replications	:	Two
6.	Plot size	:	2.4×2.7 m^2
7.	Spacing	:	45 cm × 30 cm
8.	Fertilizer dose	:	RDF 25:75:60 NPK (kg/ha)
9.	Location	:	AICRP on Vegetables, MPKV Rahuri

3.2.2 Sowing and cultural practices

The sowing of seeds was done on 22 February 2022 by Dibbling method. The recommended dose of 25:50:00 NPK (kg/ha) was applied at the time of sowing. The experimental plot was kept free from weeds. Other cultural practices were conducted to grow a good crop.

3.3 Observations Recorded

Five plants from each treatment in each replication were selected randomly to record the observations of cowpea for morphological characters except for days to 50 % flowering and days to maturity and an average of these five plants was worked out for the statistical analysis and further used for the study of genetic variability. Data of days to 50 % flowering and days to maturity was noted on a plot basis. The details of the observations are mentioned below.

3.3.1 Growth parameters

3.3.1.1 Vine length (m)

Five plants were selected randomly and height is measured with the help of tape and expressed in terms of average.

3.3.1.2 Number of primary branches per plant

Five plants are selected randomly and the total main branches are counted at the time of maturity and expressed in terms of average.

3.3.2 Flowering Parameters

3.3.2.1 Days to 50 % flowering (Days)

Days to 50 % flowering were recorded based on the date of sowing to the date on which 50 % of the plants in each genotype flowered were recorded and expressed in whole numbers.

3.3.2.2 Flower bud colour

Flower bud colours were recorded by visual appearance and three types of flower bud colour were observed i.e. Purple, Yellow and White.

3.3.2.3 Days to first pod harvest

The number of days required for the first pod harvesting from the date of flowering to the first pod harvesting was recorded.

3.3.3 Yield Parameters

3.3.3.1 Number of pods per plant (No)

Five plants were selected and total pods were counted for observation and expressed as average at the time of harvest.

3.3.3.2 Number of seeds per pod

Five well-filled pods which are undamaged are selected from each plant and seeds were counted from each pod then the average is calculated and observations were recorded.

3.3.3.3 Fresh pod length (cm)

Fresh pod length in centimetres of fresh pods was taken by randomly selecting five fresh pods at the time of harvesting of the plants and average of the plants was taken and observations were recorded.

3.3.3.4 Fresh pod width (cm)

Fresh pod width in centimetres of fresh pods was taken by randomly selecting five fresh pods at the time of harvesting of the plants and average of the plants was taken and observations were recorded.

3.3.3.5 Average pod weight (10 Pods) (g)

The ten pods are collected from each plant of each genotype for the respective replication and weighed in grams and the average was computed as average pod weight.

3.3.3.6 Yield per plant (g)

The pods are collected from each plant of each genotype for the respective replication and weighed in grams and the average was computed as yield per plant.

3.3.3.7 Crop duration (days)

The number of days required from the date of sowing to complete maturity at which plants are harvested was recorded.

3.3.3.8 Yield per plot (kg)

The pods collected from plants of each genotype for the respective replication were weighed in kilograms and the average was calculated as yield per plot.

3.3.3.9 Yield per hectare (q/ha)

Based on the plot yield per hectare in quintals was calculated.

3.3.4 Qualitative Parameters

3.3.4.1 Fresh pod colour (Green/Light Green/Purple)

Observation of pod colour was recorded by visual appearance.

3.3.4.2 Fresh pod shape (Straight/Slightly curved/Curved)

Observation of pod shape was recorded by visual appearance.

3.3.4.3 Cross section of the pod (Round/Flat/Oval)

Cross section of the pod is taken by cutting the pod horizontally and then observations were recorded by visual appearance.

3.3.4.4 Leaf area (cm^2)

Leaves of each genotype were selected that are not damaged and are clean and then leaf area was computed by using Leaf Area Meter instrument and observations were recorded.

3.3.4.5 Leaf shape (Hastate/Sub-Hastate/Globose/Sub-Globose)

Observation of leaf shape was recorded by visual appearance.

3.3.5 Biochemical

Crude Protein content (mg/100g)

A crude protein was estimated by Micro-kjeldal method as described by Sadashivam and Manikam (1992).

The proteins content was determined by Micro-kjeldahl's apparatus.

Protein content was calculated using following formula.

$$N\ (\%) = \frac{(S-B) \times N \times 14.007}{\text{Weight of sample (g)}} \times \frac{\text{Volume made (ml)}}{\text{Volume taken (ml)}} \times 100$$

Where,

S = ml of HCI required for sample titration

B = ml of HCI required for blank titration

N = Normality of HCI (0.02 N)

Protein (%) = Nitrogen (%) × 6.25

3.3.6 Incidence of Pest and Diseases

Pest and disease incidences of bean mosaic and pod borer were recorded.

3.3.6.1 Incidence of Bean mosaic

Number of plants infected by incidence of bean mosaic was counted and the per cent disease incidence worked out as per following formula.

$$\text{Per cent of bean mosaic incidence} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

3.3.6.2 Incidence of pod borer

At each harvesting, the healthy pods and borer infested pods were recorded. At the end of last harvesting sum up all healthy pods and infested pods in each genotype per replication and average incidence was worked out.

$$\text{Per cent of pod borer incidence} = \frac{\text{Number of infected pods}}{\text{Total number of pods}} \times 100$$

3.4 Statistical Analysis

The data were obtained for each parameter was subject to statistical analysis of variance (ANOVA) within the treatments. The comparison of mean was carried out by Randomized Block Design for significance of SE and CD at 5 per cent level as suggested by Panse and Sukhatme (1985).

3.4.1 Analysis of Variance (ANOVA)

The skeleton ANOVA table for RBD with t treatment and r replications.

Sr. No.	Source of variation	Degree of freedom	SS	MSS	T Variation
1	Replication	r-1	RSS	RMSS= RSS/ (r-1)	RMSS
2	Genotypes	t-1	TrSS	TrMSS= TrSS/ (t-1)	TrMSS
3	Error	(r-1)(t-1)	ESS	EMSS= ESS per (r-1) (t-1)	
4	Total	Rt-1	TSS		

Where,

r = Number of replications

n = Number of treatments

df = Degree of freedom SS = Sum of square

RSS = Replication sum of square

TSS = Treatment sum of square

ESS = Error sum of square

MSS = Mean sum of square

3.4.2 Test of Significance

If the variance ratio (MSSTrt/MSSE) was greater than the tabulated value of F, the difference were considered to be significant at 5% and 1% level of significance 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 Estimation of Mean

The mean values for each character were worked out by the following formula

$$\bar{X} = \frac{1}{N} \left(\sum_{i=1}^{n} X_i \right)$$

Where,

$\bar{X}$ = Mean of character

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

N = Number of observations

3.4.3.2 Estimation of Range

The difference between the highest and the lowest values, from mean of each character were recorded as range.

3.4.3.3 Variance

It is expressed 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

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

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 the 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 mean was calculated by the formula

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

3.5.3.5 Critical Difference

The following is the formula to calculate critical difference

Standard error of mean was calculated by the formula

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

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. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) in this study were calculated by formula given by Burton (1952).

Genotypic coefficient of variation (GCV)

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

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

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

Phenotypic coefficient of variation (PCV)

It was estimated as per the formula suggested by Burton (1952)

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

$\sigma^2 p = Vp$ = Phenotypic Variance

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).

The values of heritability are categorized as follows (Johnson *et al*, 1955)

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

$$h^2 \text{ (broad sense)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

3.4.3.8 Genetic Advance

3.5.3.8 Genetic Advance

The formula for genetic advance that means expected genetic gain was suggested by Lush (1949) and Johnson *et al.,* (1955) is presented below

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

$GA = k\,\sigma_p h^2\ (bs)$

Where,

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

h^2 (bs) = Heritability

σ_p = Phenotypic standard deviation

3.5.3.9 Genetic advance as % of mean (GAM)

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

Genetic advance as % of mean values are categorized as follows

High : More than 20 %

Medium : 10 – 20 %

Low : Less than 10 %

3.4.4 Correlation

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by adopting method described by Singh and Choudhary (1977).

3.4.4.1 Phenotypic correlation coefficients

$$\gamma_p = \frac{\text{Covariance } X,Y_{(p)}}{\sqrt{\text{Variance } X_{(p)}, \text{Variance } Y_{(p)}}}$$

Where,

r_p = Phenotypic correlation coefficient between character X and Y

p = Phenotypic

3.4.4.2 Genotypic correlation coefficient

$$\gamma_g = \frac{\text{Covariance } X,Y_{(g)}}{\sqrt{\text{Variance } X_{(g)}, \text{Variance } Y_{(p)}}}$$

Where,

r_g = Genotypic correlation coefficient between character X and Y

g = Genotypic

Significance of correlation coefficients were tested by'tʼ test (Panse and Sukhatme, 1985)

3.4.5 Path Analysis

The direct and indirect influence of components of flower yield path coefficient analysis was done by the methods employed by Dewey and Lu (1959) for the first time in plants. When the cause and effect relationship was well defined the whole systems of variables was represented by "Path Diagram" which was very helpful for solving the simultaneous equations directly. Path coefficient was obtained by solving a set of simultaneous equations as per Dewey and Lu (1959).

$Rn_y = Pn_y + rn_2. P_2y + en_3. P3x +$........

Where, rn_y = correlation coefficient between one component and yield

Pn_y = Path coefficient between character and yield

Rn_2 = correlation between that character and each of the other yield component.

Direct effect of the character was given by Pn_y

Indirect effect of a particular character through other characters was obtained by multiplication of direct paths and respected correlation coefficients between these characters respectively.

Indirect effect = rij × Pij

i = 1 to 10 and j = 1 to 10

$Pij = P_1y, p_2y, ...P_{10}y$

The Residual effect R was calculated as below,

$R^2 = 1- (P_1y.r_1y + P_2y.r_2y + ...+ P_ny.\ r_ny)$

Where,

$P_1y, P_2y,....., P_ny$ = Direct effects of respective characters on fruit yield.

$r_1y, r_2y,...., r_ny$ – Correlation coefficient between respective characters and yield.

The scales for path coefficient (Lenka and Mishra, 1973)

Values for Direct or Indirect effects	Rate or Scale
0.00 – 0.09	Negligible
0.1 – 0.19	Low
0.20 – 0.29	Moderate
0.30 – 0.99	High
More than 1.00	Very high

3.4.6 Genetic Divergence

3.5.6.1 D^2 analysis

The generalized distance between any two populations is defined as

$$\Delta^2 = \sum\sum\lambda_{ij}\,\sigma^i\,\sigma^j$$

Where,

λ_{ij} = Reciprocal matrix to the common dispersion matrix

σ^i = Difference between the mean values of the two populations for i^{th} character.

$$D^2 = \sum\sum S_{ij}\,\sigma^i\,\sigma^j$$

Where,

S_{ij} = sample estimates of σ_{ij}

σ^i = sample estimate of σ_i

This formula requires the inversion of 16^{th} order of determinant and the evaluation of 16 (16 +1/2) terms whose sum is D^2.

3.5.6.2 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)

Where,

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

$|E|$ = 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,

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

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 populations is lined by Mahalanobis (1936) as :

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^{th} character

Estimation of D^2 values from the above formula is very complicated in the present study. Since it requires the inversion of tenth order determinant and then the evaluation of 10 (10 +1)/2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters constructed from the original measurements D with such transformed variable is reduced to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Chaudhary, 1977). The coefficients for transformation were obtained by dividing the first row of the reduced matrix by the square root of corresponding pivotal condensation elements.

3.4.6.4 Determination of population constellation

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the cluster because a cluster is not a well defined term. The only criteria appears to be that any two groups belonging to the two different clusters. A simple device suggested by K. D. Tocher is to start with the two closely associated groups and find a third group which has the smallest D^2 from the first two. Similarly, the fourth group is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 of a group from those already listed appears to be high, then this group does not fit in the former groups and is therefore taken outside the formal cluster. The groups of the first cluster then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within the cluster due to the inclusion of an additional group. If the changes are appreciable, then the newly added group has to be considered as outside the cluster.

3.4.6.5 Average Intra and Inter-cluster D^2 and D values

3.4.6.5.1 Average Intra-cluster D^2 and D Values

$$D^2 = \frac{\Sigma Di^2}{N}$$

Where,

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

3.4.6.5.2 Average Inter-cluster D^2

$$D^2 = \frac{\Sigma \text{ distance between the population of cluster i and j}}{n_i n_j}$$

Where,

n_i = Number of populations in the cluster i

n_j = Number of populations in the cluster j.

3.5.6.5 Cluster mean

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

3.4.6.6 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. RESULT AND DISCUSSION

In order to achieve a superior genotype in plant breeding, it is necessary to select the best genotype combination with genetic variability present within it. A broad range of genetic variation is expected from progenies derived from a range of diverse crosses, which provides the breeder with enough scope for selecting segregates that produce high yield in advanced generations.

Based on the details mentioned above, the current inquiry was conducted to evaluate the genetic diversity of 23 cowpea genotypes that were collected from the AICRP on Vegetables, M.P.K.V., Rahuri. It also examined correlation coefficient and path efficiency. The findings are discussed using available research publications under the following subheadings.

4.1 Study of Qualitative Characters
4.2 Analysis of Variance
4.3 Mean Performance of Genotypes
4.4 Genetic Variability Studies
4.5 Correlation Coefficient Analysis
4.6 Path Coefficient Analysis
4.7 Genetic Divergence

4.1 Study of qualitative characters

Twenty-three Cowpea genotypes were studied for qualitative traits, which also aid to growth and yield, are equally important in terms of market and export. The qualitative characteristics that were recorded in this experiment are fresh bud colour, fresh pod colour, cross section of pod, leaf shape. These qualitative characteristics are further listed in table 4.1 and explained below.

4.1.1 Fresh bud colour

Based on the colour of the flower bud twenty-three cowpea genotypes were classified into purple, white and yellow coloured flower buds. All genotypes of the plant showed purple flower buds, however RHRCP-5, RHRCP-6, RHRCP-7 and RHRCP-9 had white flower buds, while RHRCP-1 had yellow flower buds.

Table 4.1. Qualitative characteristics of twenty-three cowpea genotype

Genotypes	Plant type	Flower bud colour	Fresh pod colour	Fresh pod shape	Cross section of pod	Leaf shape
RHRCP-1	Pole	Yellow	Green	Straight	Oval	Sub Globose
RHRCP-2	Pole	Purple	Green	Straight	Oval	Sub Hastate
RHRCP-3	Pole	Purple	Green	Straight	Oval	Sub Hastate
RHRCP-4	Pole	Purple	Green	Straight	Oval	Sub Globose
RHRCP-5	Pole	White	Green	Straight	Oval	Globose
RHRCP-6	Pole	White	Green	Straight	Oval	Sub Globose
RHRCP-7	Pole	White	Green	Straight	Oval	Sub Globose
RHRCP-8	Pole	Purple	Green	Straight	Oval	Sub Globose
RHRCP-9	Pole	White	Green	Straight	Oval	Sub Hastate
RHRCP-16	Pole	Purple	Green	Straight	Oval	Sub Globose
RHRCP-17	pole	Purple	Light Green	S.curved	Oval	Sub Hastate
RHRCP-18	Pole	Purple	Green	Straight	Oval	Sub Globose
RHRCP-19	pole	Purple	Light Green	S.curved	Oval	Sub Hastate
RHRCP-20	Bush	Purple	Green	Curved	Oval	Sub Globose
RHRCP-21	Bush	Purple	Green	Curved	Oval	Sub Globose
RHRCP-22	pole	Purple	Green	Curved	Oval	Sub Hastate
RHRCP-25	Bush	Purple	Green	Straight	Oval	Sub Globose
RHRCP-26	Pole	Purple	Green	Straight	Oval	Sub Globose
RHRCP-27	pole	Purple	Green	Curved	Oval	Globose
RHRCP-28	pole	Purple	Purple	S.curved	Oval	Sub Globose
RHRCP-29	Bush	Purple	Green	Curved	Round	Sub Hastate
RHRCP-31	Bush	Purple	Green	S.curved	Oval	Sub Hastate
Pooja (C)	Pole	Purple	Green	Straight	Round	Globose

4.1.2 Fresh pod colour

Twenty-three cowpea genotypes were classified into green, light Green and purple colour pods based on the colour of the pods, with RHRCP-17 and RHRCP-19 showing light green colour pods, RHRCP-28 showing purple colour pods and the rest showing green colour pods.

4.1.3 Fresh pod shape

Among all genotypes RHRCP-17, RHRCP-19, RHRCP-28 and RHRCP-31 showed slightly curved pod shape while, RHRCP-20, RHRCP-21, RHRCP-22, RHRCP-27 and RHRCP-29 showed curved shape and rest of all genotypes showed straight pod shape.

4.1.4 Cross section of pod

According to the visual observations, twenty-one genotypes had oval cross sections of pods, while two genotypes had round cross sections of pods.

4.1.5 Leaf shape

Based on the leaf shape twenty-three cowpea genotypes were classified into hastate, sub-hastate, globose and sub-globose leaf shape. Among all genotypes of the plant RHRCP-2, RHRCP-3, RHRCP-9, RHRCP-17, RHRCP-19, RHRCP-22, RHRCP-29, RHRCP-31 showed sub-hastate leaf shape while RHRCP-5, RHRCP-27 and Pooja showed globose leaf shape and rest of all showed sub-globose leaf shape.

4.2 Analysis of variance

Analysis of variance (Table 4.2) revealed significant variations among the twenty-three genotypes for all twelve characters tested, indicating significant variability among those genotypes.

As a result, the occurrence of a high degree of variability could be attributed to the varied sources of materials used in the current investigation. This showed that there is lots of opportunity for selecting promising lines.

Significant differences among the cowpea genotypes for pod yield and yield contributing characters were also reported by Sapra *et al*., (2014), Umesh Havaraddi and Deshpande (2018), Gupta *et al*., (2019), Koraddi and Basavraja (2019), Ugale *et al*. (2020) and Vinay *et al. (*2022).

Table 4.2. Analysis of variance for eleven characters of twenty-three cowpea genotypes

Sr. No.	Character	Replication	Treatment	Error
	DF	**2**	**22**	**44**
1	Days to 50 % flowering (Days)	241.49	63.71**	2.87
2	Days to first pod harvest (Days)	345.47	58.73**	3.60
3	Number of pods per plant (No.)	233.60	1548.14**	7.34
4	Number of Seeds per pod	18.65	5.85**	0.21
5	Fresh Pod Length (cm)	54.24	223.35**	1.11
6	Fresh Pod Width (cm)	0.06	0.03**	0.01
7	Average pod weight (10 Pods) (g)	398.36	3139.98**	11.45
8	Number of primary branches/plant	5.36	2.13**	0.06
9	Leaf Area (cm^2)	339.46	694.09**	4.44
10	Vine Length (m)	0.43	1.61**	0.07
11	Yield per plant (g)	3580.43	2375.36**	44.72

*, ** = significant at 5 % and 1 % levels, respectively.

4.3 Mean performance

4.3.1 Days to 50 % flowering (Days)

Days to 50 per cent flowering showed variation ranges from 34.38-53.70. In these genotypes, RHRCP-17 showed early flowering i.e. 34.38 DAS while, RHRCP-1 showed late flowering (53.70 DAS). RHRCP-17, RHRCP-19, RHRCP-20, RHRCP-21, RHRCP-22, RHRCP-28 and RHRCP-31 found significantly early than the general mean. Also, eight genotypes found significantly earlier flowering than the check Pooja.

4.3.2 Days to first pod harvest (Days)

Days to first pod harvest showed variation from 41.08-60.04. Out of these genotypes, RHRCP-17 genotype showed requirement of 41.08 DAS for first pod harvest while, RHRCP-1 requires 60.04 DAS for first pod harvest. RHRCP-17, RHRCP-19, RHRCP-20, RHRCP-21, RHRCP-22, RHRCP-28 showed significantly days required for early pod harvest than the population mean. Also, RHRCP-17, RHRCP-20, RHRCP-21 and RHRCP-22 showed significantly early maturity for days to first pod harvest than the check Pooja.

4.3.3 Number of pods per plant (Nos.)

Number of pods per plant showed variation ranges from 15.63-74.97. RHRCP-19 had lowest number of pods i.e. 15.63 while, RHRCP-26 had the highest number of pods i.e.74.97. RHRCP-1, RHRCP-2, RHRCP-3, RHRCP-4, RHRCP-5 and other eight genotypes had significantly higher number of pods than the general mean. RHRCP-2, RHRCP-9, RHRCP-18 and RHRCP-26 found significantly higher number of pods over check Pooja.

4.3.4 Number of Seeds per pod

Number of seeds per pod showed variation ranges from 7.11-13.68. RHRCP-1 had lowest number of seeds while RHRCP-7 had highest number of seeds when compared to other genotypes. RHRCP-2, RHRCP-6, RHRCP-7, RHRCP-9, RHRCP-17, RHRCP-19 and RHRCP-21 showed significantly more number of seeds per pod than the population mean (11.75) and seventeen genotypes show significantly higher number of seeds per pod than check Pooja.

4.3.5 Fresh Pod Length (cm)

Fresh pod length variation range 7.38-33.02 cm. RHRCP-1 had shortest pod length i.e. 7.38 cm while for RHRCP-29 pod length was 33.02 cm which is longest. Also, ten genotypes showed significantly longest length than the general mean (20.10 cm) and seventeen genotypes show significantly maximum fresh pod length than check Pooja (9.92 cm).

4.3.6 Fresh Pod Width (cm)

The variation in the pod width ranges from 0.51 to 0.87 cm. The genotype RHRCP-1 had shortest pod width (0.51 cm) while genotype RHRCP-9 had 0.87 cm width. Among all genotypes RHRCP-3, RHRCP-6, RHRCP-8, RHRCP-9, RHRCP-20 and RHRCP-29 showed significantly higher pod width over the population mean 0.65 cm and eighteen genotypes show significantly maximum fresh pod width than check Pooja (0.55 cm).

4.3.7 Average pod weight (10 Pods) (g)

Among all genotypes, RHRCP-28 showed highest average pod weight (10 pods) i.e. 105.17 g followed by RHRCP-20 (102 g), RHRCP-19 (100.02 g) while lowest average pod weight (10 pods) is of RHRCP-1 (19.33 g) followed by RHRCP-18 (20.69 g) and Pooja (21.44 g). The average pod weight ranges from 19.33 to 105.17 g. seventeen genotypes showed significantly higher average pod weight over Pooja (21.45 g).General mean for average pod weight was 54.50 g.

4.3.8 Number of primary branches/plant (Nos)

Number of primary branches per plant character showed variation ranges from 5.00 to 8.00. Highest number of primary branches was observed in RHRCP-8 (8.00) followed by RHRCP-26 (7.90) and RHRCP-18 (7.84). Lowest number of primary branches were present in RHRCP-31 (5.00). Twelve genotypes showed highest number of primary branches over the check Pooja.

4.3.9 Vine Length (m)

General mean for the vine length was 1.82 m and variation ranges from 0.92 to 2.84 m. Among all genotypes RHRCP-9 showed longer vine length i.e.2.84 m while RHRCP-31 showed shortest vine length (0.92 m). Twelve genotypes showed longest vine length over the general mean (1.82 m) and also, RHRCP-3, RHRCP-5, RHRCP-7, RHRCP-8, RHRCP-9 and RHRCP-18 genotypes showed significantly longest vine length over the check Pooja (2.41 m).

4.3.10 Leaf Area (cm^2)

The Leaf Area (cm^2) amongst all the genotypes ranges from 27.44 to 94.09 cm^2. Maximum leaf area (cm^2) was recorded for RHRCP-4 (94.09 cm^2), followed by RHRCP-27 (78.89 cm^2), RHRCP-28 (76.11 cm^2), RHRCP-25 (69.25 cm^2) and so on. The population mean for all the genotypes was 52.93 cm^2 to which RHRCP-4, RHRCP-25, RHRCP-27, RHRCP-28, RHRCP-29 and RHRCP-31 genotypes were found to be maximum and eleven genotypes were significantly maximum to standard check Pooja (49.43 cm^2).

4.3.11 Yield per plant (g)

General mean for yield per plant (g) is 164.57 g. Variation ranges from 114.40 to 222.63 g. RHRCP-8 recorded highest yield per plant i.e. 222.63 g followed by RHRCP-5 (202.75 g), RHRCP-29 (194.14 g), RHRCP-6 (189.84 g), RHRCP-3 (184.94 g) while lowest yield per plant was recorded for RHRCP-1 (114.40 g). Ten genotypes found significantly maximum to general mean 164.57 g and also, except three genotypes all other genotypes found significantly maximum over standard check Pooja (124.52 g).

4.3.12 Yield per plot (kg/plot)

The mean performance of the genotypes for yield per plot ranges from 5.49 kg/plot (RHRCP-1) to 10.69 kg/plot (RHRCP-8). Except five genotypes all other genotypes were maximum to standard check Pooja (5.98 kg/plot) and RHRCP-08 (10.69 kg/plot), RHRCP-05 (9.73 kg/plot) and RHRCP-29 (9.32 kg/plot) were found significantly maximum to general mean 7.90 kg/plot.

4.3.13 Yield per hectare (q/ha)

The mean performance of the genotypes for yield per hectare was 121.90 q/ha and variation ranges from 84.74 to 164.91 q/ha. Lowest yield per hectare was calculated for RHRCP-1 (84.74 q/ha) while highest yield was calculated for RHRCP-08 164.91 q/ha. Among all genotypes three genotypes showed significantly higher yield per hectare over general mean (121.90 q/ha) and also fifteen genotypes showed significantly higher yield per hectare over standard check Pooja.

Table 4.3. Mean performance of all the genotypes for the following characters

Genotypes	Days to 50 % flowering (Days)	Days to first pod harvest (Days)	Number of pods per plant (No.)	Number of seeds per pod	Fresh pod length (cm)	Fresh pod width (cm)	Average pod weight (10 Pods)	Number of primary branches/ plant	Vine length (m)
RHRCP-1	53.70	60.04	59.17	7.11	7.38	0.51	19.33	6.00	1.91
RHRCP-2	42.67	50.68	69.39	13.41	14.32	0.58	21.83	6.00	2.31
RHRCP-3	45.19	52.99	62.79	11.17	13.79	0.69	29.73	6.93	2.51
RHRCP-4	41.67	49.36	54.40	11.67	13.49	0.51	32.92	7.48	2.42
RHRCP-5	44.61	52.71	61.32	11.94	14.75	0.62	33.05	7.00	2.47
RHRCP-6	47.85	55.07	59.88	13.66	15.83	0.71	31.27	6.08	2.42
RHRCP-7	45.06	53.09	53.99	13.68	13.31	0.54	32.87	6.34	2.62
RHRCP-8	47.06	55.07	59.61	11.61	13.26	0.69	37.34	8.00	2.49
RHRCP-9	50.93	57.38	65.79	12.83	19.63	0.87	24.91	6.93	2.84
RHRCP-16	45.06	53.10	54.36	11.47	13.61	0.64	33.07	6.68	2.42
RHRCP-17	34.38	41.08	17.16	12.52	26.77	0.66	86.15	6.05	1.10
RHRCP-18	44.15	52.24	67.44	9.36	8.91	0.59	20.69	7.84	2.53
RHRCP-19	38.99	46.63	15.63	12.36	27.15	0.63	100.02	6.70	1.12
RHRCP-20	36.00	43.63	16.63	11.39	27.75	0.83	102.00	6.20	0.98
RHRCP-21	35.99	44.25	20.56	12.31	31.44	0.68	73.90	5.85	0.99
RHRCP-22	35.80	42.70	16.19	11.28	25.45	0.68	79.75	5.39	1.03
RHRCP-25	40.41	49.17	16.02	11.71	29.37	0.64	75.27	5.41	0.97
RHRCP-26	45.62	53.40	74.97	11.93	12.17	0.59	21.75	7.90	2.36
RHRCP-27	40.05	47.42	19.03	11.79	28.12	0.64	95.43	6.00	1.02
RHRCP-28	38.70	46.37	17.00	11.72	30.35	0.68	105.17	6.20	1.07
RHRCP-29	39.76	47.85	21.70	12.83	33.02	0.78	87.84	5.40	1.02
RHRCP-31	39.58	47.29	20.47	11.72	32.48	0.60	87.79	5.00	0.92
POOJA (C)	42.84	47.45	60.78	10.70	9.92	0.55	21.45	5.73	2.30
Mean	42.45	50.13	42.79	11.75	20.10	0.65	54.50	6.40	1.82
S.E.	0.98	1.10	1.56	0.26	0.61	0.01	1.95	0.15	0.05
C.D. 5 %	2.79	3.12	4.46	0.75	1.74	0.04	5.57	0.42	0.15
C.V.	3.99	3.79	6.33	3.91	5.25	3.91	6.21	3.95	4.88

Table 4.3 contd…

Genotypes	Leaf area (cm^2)	Yield per plant (g)	Yield per plot (kg)	Yield per hectare (q/ha)	Crop duration (days)	Protein content (%)	Incidence of Bean mosaic (%)	Incidence of pod borer (%)
RHRCP-1	51.14	114.40	5.49	84.74	180.66	15.86	13.49(21.55)	9.07(17.53)
RHRCP-2	46.94	151.47	7.27	112.20	151.33	23.61	8.13(16.57)	8.12(16.56)
RHRCP-3	54.45	184.94	8.88	136.99	167.70	21.22	7.20(15.56)	6.24(14.47)
RHRCP-4	94.09	170.32	8.18	126.16	142.08	21.87	6.89(15.22)	5.08(13.03)
RHRCP-5	41.13	202.75	9.73	150.19	156.49	20.56	6.94(15.27)	6.00(14.18)
RHRCP-6	53.79	189.84	9.11	140.62	174.91	23.19	7.23(15.60)	7.14(15.50)
RHRCP-7	37.20	177.60	8.52	131.55	161.18	17.50	7.83(16.25)	8.08(16.51)
RHRCP-8	52.41	222.63	10.69	164.91	174.05	18.81	5.16(13.13)	5.00(12.92)
RHRCP-9	52.48	166.93	8.01	123.65	176.30	19.68	8.21(16.65)	8.30(16.74)
RHRCP-16	41.92	179.98	8.64	133.32	159.95	21.87	7.56(15.96)	7.83(16.25)
RHRCP-17	43.04	141.29	6.78	104.66	78.66	20.34	9.15(17.61)	10.00(18.43)
RHRCP-18	37.33	138.46	6.65	102.56	153.77	20.12	8.83(17.29)	9.03(17.49)
RHRCP-19	46.68	156.33	7.50	115.80	94.33	16.84	9.12(17.58)	9.15(17.61)
RHRCP-20	54.58	169.62	8.14	125.65	82.33	17.50	8.84(17.30)	9.04(17.50)
RHRCP-21	41.38	150.55	7.23	111.52	82.98	18.59	13.23(21.33)	12.44(20.65)
RHRCP-22	46.34	122.76	5.89	90.93	88.17	19.90	12.43(20.64)	12.23(20.47)
RHRCP-25	69.25	120.68	5.79	89.39	116.82	17.50	13.67(21.70)	15.00(22.79)
RHRCP-26	27.44	165.27	7.93	122.42	159.14	19.46	8.17(16.61)	8.21(16.65)
RHRCP-27	78.89	181.74	8.72	134.62	104.15	19.03	12.36(20.58)	11.90(20.18)
RHRCP-28	76.11	178.85	8.58	132.48	89.70	16.44	9.07(17.53)	9.10(17.56)
RHRCP-29	64.26	194.14	9.32	143.81	96.69	17.57	9.91(18.35)	11.16(19.52)
RHRCP-31	57.06	179.94	8.64	133.29	103.58	20.78	8.90(17.36)	13.37(21.45)
POOJA (C)	49.43	124.52	5.98	92.24	143.11	19.68	8.45(16.90)	8.51(16.96)
Mean	52.93	164.57	7.90	121.90	132.09	19.47	17.50	9.13
S.E.	1.22	3.86	0.50	7.70	6.76	0.96	0.86	0.45
C.D. 5 %	3.47	11.01	1.42	21.94	19.26	2.72	2.46	1.29
C.V.	3.98	4.06	10.94	10.94	8.86	8.56	8.61	8.63

4.3.14 Protein content (%)

The general mean for protein content was 19.47 per cent and variation ranges from 15.86 to 23.61 per cent. RHRCP-02 showed highest protein content i.e. 23.61 per cent while RHRCP-01 showed lowest protein content i.e. 15.86 per cent among all genotypes.

4.3.15 Crop duration (days)

General mean for the days to first pod harvest was 132.09 days. All genotypes showed variation of 78.66-180.66 days for crop duration. Out of these genotypes, RHRCP-17 genotype showed requirement of 78.66 days and RHRCP-01 requires 180.66 days for complete its crop period. Ten genotypes showed significantly maximum days required to complete its crop period than the population mean. RHRCP-1, RHRCP-3, RHRCP-6, RHRCP-8 and RHRCP-9 genotypes required significantly maximum days than the check Pooja (143.11).

4.3.16 Disease and pest incidence :

4.3.16.1 Incidence of Bean mosaic

The genotypes showed very mild symptoms of infestation of bean mosaic ranges from 5.16 per cent (RHRCP-08) to 13.68 (RHRCP-25) per cent.

4.3.15.2 Incidence of Pod borer

The fruit borer incidence for all the cowpea genotypes ranges from 4.83 per cent (RHRCP-04) to 15.01 per cent (RHRCP-25). The fourteen genotypes had significantly less pest incidence than the population mean (9.13). Eight genotype had significantly lower pest incidence than the standard check Pooja.

4.4 Parameters of Genetic Variability

Genetic variability is the basis of any crop improvement programme. Testing the variability parameters is of fundamental importance for the development of high-quality varieties. High variability offers more scope for improvement. Variability is estimated at the genotypic and phenotypic levels using the genotypic and phenotypic correlation coefficient, heritability (h^2 in the broad sense) and genetic advance.

The range of average values does not reflect the total variation in the studied material; therefore, it is necessary to estimate the actual variation in order to know the externality of the existing variation. Therefore, the coefficients of variation calculated by taking into account the respective means (PCV and GCV) are used for comparison. The estimates of variance, variation coefficients, heritability and genetic advance for all 12 traits studied (Table 4.4) are explained below.

4.4.1 Variance

In this experiment, variance (σ^2g) estimated genotypic and phenotypic variances (Vp and Vg) for twelve characters of cowpea, Average pod weight (10 pods) (g) had highest values of genotypic and phenotypic variances (1042.84 and 1054.29) followed by yield per hectare (q/ha) had genotypic (530.05) and phenotypic (548.15) variances whereas lowest for Fresh pod width (0.07 and 0.08) respectively.

4.4.2 Coefficient of variation

The estimation of genotypic coefficient of variation and phenotypic coefficient variation for all the traits were presented in (Table 4.4). The high GCV and PCV (>20 %) were estimated for Average pod weight (10 pods) (59.25 and 59.58), number of pods per plant (52.96 and 53.33), fresh pod length (42.82 and 43.15), vine length (40.18 and 40.48), leaf area (cm^2) (28.65 and 28.92). Moderate GCV and PCV values (10-20 %) were observed for fresh pod width (cm) (14.10 and 14.63), number of primary branches per plant (12.99 and 13.58), number of seeds per pod (11.68 and 12.32). However, days to 50 % flowering (Days) (10.61 and 11.33) and days to first pod harvest (Days) (8.55 and 9.35) showed low GCV and PCV (<10 %).

The high GCV and PCV values were found for average pod weight (10 pods), number of pods per plant, fresh pod length, vine length, leaf area (cm^2) and yield per plot (kg). The genotypic and phenotypic coefficient of variation estimate indicates the extent of genetic and nongenetic variation that exists for various desirable traits. Higher GCV and PCV values for these traits indicated a high level of variability and better selection.

The magnitude of PCV was higher than GCV was also observed by the scientists Magashi *et al*. (2018), Panchta *et al*. (2020). Krishnan *et al*. (2019) also found high PCV for all yield paramters i.e. seed yield per plant, hundred seed weight and number of pods per plant than GCV. Umesh Havaraddi and Deshpande (2018) observed high GCV and PCV values for the traits seed yield per plot and number of pods per plant. Panchta *et al*. (2020) observed high GCV and PCV values for seed yield per plot, days to

50 % flowering, days to maturity and plant height. Wadghane *et al*. (2022) observed high values for Days to 50 % flowering. Sharma *et al.* (2017) observed high GCV and PCV values for plant height, primary branches per plant, seed yield per plant and test weight. Meena *et al*. (2015), Sharma *et al*. (2017), Havaraddi and Deshpande (2018), Devi and Jayamani (2018), Koraddi and Basavaraja (2019) reported high GCV and PCV values for plant height, green pod yield per plant, primary branches per plant, number of pods per plant. Sapara *et al*. (2014) observed high genotypic and phenotypic coefficient of variation for several pods per plant, 100 fresh seed weights, plant height, 10 pod weights and green pod yield per plant.

4.4.3 Heritability (b.s.)

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. In order to achieve effective improvement in the trait for which selection is made, heritability has been adopted as a reliable indicator by a large number of workers. The proportion of genetic variability that is passed on from parents to offspring is reflected in heritability. According to Lush (1949), heritability in the broadest sense is the ratio of total genotypic variance to phenotypic variance, expressed as a percentage.

All characters showed high heritability (b.s.) estimates ranged between 83.6 to 98.9 per cent. Average pod weight (10 pods) showed high heritability i.e. (98.90 %) followed by number of pods per plant (98.60 %), Leaf Area (cm^2) (98.10 %), for both fresh pod length and vine length (m) (98.50 %), for yield per plot and yield per hectare (96.70 %), fresh pod width (cm) (92.90 %), number of seeds per pod (89.90 %), days to 50 % flowering (days) (87.60 %), days to first pod harvest (days) (83.60 %). Presence of high heritability for the above characters studied indicates the better scope for the improvement of these characters through selection.

For the high values of heritability (b.s.), the resulted values are in accordance with Rambabu *et al. (*2016), Patel *et al*. (2016), Sarth and Reshma (2017). Rambabu *et al. (*2016), observed high heritability for the characters pod length, pod girth, plant height, pod yield per plant, seed protein content and seed number per pod. Patel *et al*. (2016) observed high heritability for the characters green pod yield per plant and plant height. Sarth and Reshma (2017) recorded high heritability for the characters plant height, grain yield per plant and length of pods.

4.4.4 Genetic Advance

The combined application of heritability and genetic advance was emphasized because without genetic advance, heritability estimates would not be of useful values. To achieve adequate improvements through selection in genetic advance generation, high heritability alone is inadequate.

The magnitude of genetic advance ranges from 66.162 (Average pod weight of 10 pods) to 0.182 (Fresh pod width) genetic advance was highest for the average pod weight of 10 pods (66.162) followed by yield per plant (55.83), number of pods per plant (46.36), whereas lowest genetic advance was estimated for Fresh pod width (0.182).

4.4.5 Genetic advance as per cent of mean (%)

Highest genetic advance as per cent mean (> 20 %) was observed for yield per plant (71.55 %), Vine length (82.17 %), Average pod weight (121.39 %) whereas Days to first pod harvest (16.11 %) and days to 50 % flowering (20.45 %) had moderate value of genetic advance as per cent mean (10-20 %).

For the high genetic advance as of mean values, the result is in accordance with Vavilapalli *et al*. (2013), Shanko *et al*. (2014), Santos *et al*. (2014), Khanpara *et al*. (2015), Rambabu *et al*. (2016), Patel *et al*. (2016), Sarath and Reshma (2017), Lokesh *et al*. (2017), Olunloyo *et al*. (2019), Chaudhary *et al*. (2020). High GAM values for fruit yield per plant and plant height was also observed by Vavilapalli *et al*. (2013), Rambabu *et al*. (2016), Patel *et al*. (2016). Krishnan *et al.* (2019) showed high heritability coupled with high genetic advance as per cent has been noticed in the parameters like plant height, seed yield per plant, number of pods per plant, pod length and hundred seed weight. Meena *et al.* (2015) showed high estimates of heritability along with high genetic advance as per cent of mean for the characters 100-seed weight and plant height. Sharma *et al.* (2017) found maximum heritability and maximum genetic gain for test weight followed by plant height, primary branches per plant, seed yield per plant and harvest index. Vavilapalli *et al.* (2013) observed high heritability coupled with high genetic advance for all characters studied, except days to first flowering and days to the first

Table 4.4 Genetic variability parameters of twenty-three genotypes of cowpea

Sr. No.	Character	General Mean	Range	GV	PV	GCV (%)	PCV (%)	ECV (%)	H^2 (bs)	GA	GA as 5 % Mean
1	Days to 50 % flowering (Days)	42.45	35.98-53.70	20.28	23.15	10.61	11.33	3.99	87.60	8.68	20.45
2	Days to first pod harvest (Days)	50.13	43.00-60.04	18.38	21.98	8.55	9.35	3.79	83.60	8.08	16.11
3	Number of pods per plant (No.)	42.79	15.6-75.0	513.60	520.94	52.96	53.33	6.33	98.60	46.36	108.32
4	Number of Seeds per pod	11.75	7.11-13.68	1.88	2.09	11.68	12.32	3.91	89.90	2.68	22.82
5	Fresh Pod Length (cm)	20.10	7.38-33.03	74.08	75.20	42.82	43.15	5.25	98.50	17.60	87.56
6	Fresh Pod Width (cm)	0.65	0.51-0.88	0.01	0.01	14.10	14.63	3.91	92.90	0.18	27.99
7	Average pod weight (10 Pods)	54.50	19.33-105.17	1042.84	1054.30	59.25	59.58	6.21	98.90	66.16	121.39
8	Number of primary branches/plant	6.40	5.01-8.00	0.69	0.75	12.99	13.58	3.95	91.50	1.64	25.60
9	Vine Length (m)	1.82	0.92-2.79	0.53	0.54	40.18	40.48	4.88	98.50	1.50	82.17
10	Leaf Area (cm^2)	52.93	27.07-28.94	229.88	234.33	28.65	28.92	3.98	98.10	30.94	58.45
11	Yield per plant (g)	164.57	114.4-222.63	776.88	821.61	16.94	17.42	4.06	94.56	55.83	71.55

harvest. Ugale *et al.* (2020) recorded high heritability coupled with high genetic advance as per cent of mean for all growth, flower attributes, earliness attributes and pod attributes except days to 50 % flowering and pod width. Pandiyan *et al.* (2020) recorded high heritability and low genetic advance as a percentage of the mean for days to 50 % flowering, days to maturity and plant height.

4.5 Correlation Coefficient Analysis

A tool used in statistics for determining the strength and direction of a relationship between two or more variables is the correlation coefficient. Characters may be linked by linkage, the pleiotropic effect of genes, physiological and developmental interactions, environmental factors, or a combination of all of characteristics.

When the breeder has to combine high yield potential with desirable features, correlation studies would offer reliable data about the nature of the selection and its direction. The genotypic and phenotypic correlation coefficients of several characteristics with pod yield per plant and their interactions are provided in Table 4.5 and are covered in the sections that follow.

4.5.1 Association of yield per plant with other characters

According to correlation studies, genotypic correlation coefficients were generally higher than phenotypic correlation coefficients. The following Table 4.5 shows the correlation coefficient between the eleven characters at the genotypic and phenotypic levels.

The yield per plant had significant positive association with number of seeds per pod (rg= o.444 and rp=0.479), number of primary branches per plant (rg=0.337 and rp=0.376), fresh pod width (rg=0.301 and rp=0.340), vine length (rg=0.236 and rp=0.249). Also yield per plant had non-significant association with days to 50 % flowering, days to first harvest, number of pods per plant, fresh pod length, average pod weight and leaf area (cm^2).

Khandait *et al*. (2016) showed a significant positive phenotypic correlation of pod yield $plant^{-1}$ with pods $plant^{-1}$, days to first flowering, seeds pod^{-1}, number of flower cluster $plant^{-1}$ and pod length. Joghdhande *et al*. (2017) found significant positive association with some branches per plant, number of nodes, pod length, 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. Lal *et al*. (2017) found strong positive correlation with the number of peduncles and pods per plant, pod weight, pod length, number of seeds per pod and number of primary branches per plant. Paghadar *et al*. (2019) showed significant and positive correlations with the number of primary branches per plant, plant height, pod length, number of pods per plant and number of seeds per pod. Patil *et al*. (2021) reported positive and highly significant correlation between seed yield per plant and number of pods per plant followed by harvest index, 100 seed weight. Lal *et al*. (2017) also found negative correlation with days to 50 % flowering.

4.5.2 Association among yield component traits

4.5.2.1 Days to 50 per cent flowering

Among inter correlation, there is significant positive relationship with days to first pod harvest (rg=0.986 rp=0.983), leaf area (cm^2) (rg= 0.301 and rp= 316). Number of primary branches per plant had significant negative relationship (rg= -0.307) at genotypic level and non significant relationship at phenotypic level. Days to 50 per cent flowering had non-significant relationship with number of pods per plant, number of seeds per plant, fresh pod length, fresh pod width, average pod weight and vine length.

4.5.2.2 Days to first pod harvest

Among inter correlation, there is significant positive relationship with days to 50 per cent flowering (rg=0.986 rp=0.983), leaf area (cm^2) (rg= 0.356 and rp= 367).Number of primary branches per plant had significant negative relationship (rg= -0.307) at genotypic level and non significant relationship at phenotypic level. Days to first pod harvest had non-significant relationship with number of pods per plant, number of seeds per plant, fresh pod length, fresh pod width, average pod weight and vine length.

4.5.2.3 Number of pods per plant

Among inter correlation, there is significant positive relationship with Number of primary branches per plant (rg= 0.629 and 0.621), vine length (rg=0.954 and rp= 953). Also fresh pod length (rg= -0.917, rp= -0.904), fresh pod width (rg= -0.299 and rp = -0.269), average pod weight (rg= -0.968 and rp= -0.958) and leaf area (cm^2) (rg= -0.352 and rp= -0.339) had significant negative relationship with number of pods per plant. Number of pods per plant had non-significant relationship with days to 50 per cent flowering, number of seeds per pod and yield per plant.

4.5.2.4 Number of seeds per pod

Among inter correlation, there is significant positive relationship with fresh pod length (rg=0.349 and rp= 0.357), fresh pod width (rg=0.321 and rp=0.373) and yield per plant (rg=0.444 and rp=0.479). Days to 50 per cent flowering, days to first pod harvest, number of pods per plant, average pod weight, vine length and leaf area had non-significant relationship with number of seeds per pod.

4.5.2.5 Fresh pod length (cm)

There is significant positive relationship with number of seeds per pod (rg=0.349 and 0.357), fresh pod width (rg= 0.480 and rp = 0.485), average pod weight (rg= 0.924 and rp = 0.924) and leaf area (cm^2) (rg = 0.331 and rp= 0.336). Also showed negative significant association with number of pods per plant (rg= -0.917 and rp= -0.904), number of primary branches per plant (rg= -0.623 and rp= -0.571) and vine length (rg= -0.891 and rp= -0.876). Days to 50 per cent flowering, days to first pod harvest and yield per plant had non-significant relationship with fresh pod length.

4.5.2.6 Fresh pod width (cm)

There is significant positive relationship with number of seeds per pod (rg=0.321 and 0.373), fresh pod length (rg= 0.480 and rp = 0.485), average pod weight (rg= 0.368 and rp = 0.370) and yield per plant (rg = 0.301 and rp= 0.340). Also showed negative significant association with number of pods per plant (rg= -0.299 and rp= -0.269). Days to 50 per cent flowering, days to first pod harvest, number of primary branches per plant, vine length and leaf area had non significant relation with fresh pod width.

4.5.2.7 Average pod weight (10 pods)

There is significant positive relationship with number of fresh pod length (rg = 0.924 and rp = 0.924), fresh pod width (rg= 0.368 and rp = 0.370) and leaf area (rg = 0.352 and rp = 0.355). Also showed negative significant association with number of pods per plant (rg = -0.968 and rp = -0.958), Number of primary branches per plant number (rg = -0.527 and rp = -0.488) and vine length (rg = -0.929 and rp = -0.918). Days to 50 per cent flowering, days to first pod harvest, number of seeds per pod and yield per plant had non significant relation with average pod weight (10 Pods).

4.5.2.8 Number of primary branches per plant

Number of branches per plant has significant positive relationship with number of pods per plant (rg=0.629 and rp=0.621), vine length (rg=0.669 and rp=0.664) and yield per plant (rg=0.337 and rp=0.376). Days to 50 per cent flowering (rg= -0.307) and days to first pod harvest (rg= -0.307) had negative relationship at genotypic level and non significant relationship at phenotypic level. Fresh pod length (rg= -0.623 and rp= -0.571) and average pod weight (rg= -0.527 and rp= -0.488) showed negative significant relationship with number of primary branches per plant. Number of seeds per pod, fresh pod width and leaf area (cm^2) had non significant relationship with number of primary branches per plant.

4.5.2.9 Vine length (m)

Among inter correlation, there is significant positive relationship with number of pods per plant (rg=0.954 and rp= 953), number of primary branches per plant (rg=0.669 and rp=0.664) and yield per plant (rg=0.236 and rp=0.249). Also showed negative significant association with fresh pod length (rg= -0.891 and rp= -0.876), average pod weight (rg= -0.929 and rp= -0.918) and leaf area (rg= -0.295 and rp= -0.281). Days to 50 per cent flowering, days to first pod harvest, number of seeds per pod and fresh pod width had non significant relationship with vine length.

4.5.2.10 Leaf area (cm^2)

Leaf area showed significant positive relationship with days to 50 per cent flowering (rg= 0.301 and rp= 316), days to first pod harvest (rg= 0.356 and rp= 367), fresh pod length (rg = 0.331 and rp= 0.336) and average pod weight (rg = 0.352 and rp=0.355). Also showed negative significant relationship with vine length (rg= -0.295 and rp= -0.281).

4.5.2.11 Yield per plant (g)

Yield per plant showed significant positive relationship with number of seeds per pod (rg=0.444 and rp=0.479), fresh pod width (rg = 0.301 and rp= 0.340), number of primary branches per plant (rg=0.337 and rp=0.376) and vine length (rg=0.236 and rp=0.249). All other remaining characters showed non significant relationship with yield per plant.

Table 4.5. Estimates of Genotypic (Above Diagonal) and Phenotypic (below Diagonal) Correlation for eleven Characters of cowpea

Sr. No.	Characters	Days to 50 % flowering (Days)	Days to first pod harvest (Days)	Number of pods per plant (No.)	Number of seeds per pod	Fresh pod length (cm)	Fresh pod width (cm)	Average pod weight (10 Pods)	Number of primary branches/ plant	Vine length (m)	Leaf area (cm^2)	Yield per plant (g)
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
1	Days to 50 % flowering (Days)	**1.0000**	0.986**	-0.03	-0.145	0.097	0.035	-0.032	-0.307*	-0.083	0.301*	-0.078
2	Days to first pod harvest (Days)	0.983**	**1.0000**	-0.051	-0.099	0.127	0.059	0.007	-0.307*	-0.086	0.356**	0.015
3	Number of pods per plant (No.)	-0.001	-0.014	**1.0000**	-0.135	- 0.917**	-0.299*	- 0.968**	0.629**	0.954**	- 0.352**	0.138
4	Number of Seeds per pod	-0.032	0.03	-0.106	**1.0000**	0.349**	0.321**	0.187	-0.145	-0.013	-0.014	0.444**
5	Fresh Pod Length (cm)	0.116	0.147	- 0.904**	0.357**	**1.0000**	0.480**	0.924**	-0.623**	- 0.891**	0.331**	0.038
6	Fresh Pod Width (cm)	0.112	0.149	-0.269*	0.373**	0.485**	**1.0000**	0.368**	-0.12	-0.221	0.038	0.301*
7	Average pod weight (10 Pods)	-0.013	0.027	- 0.958**	0.196	0.924**	0.370**	**1.0000**	-0.527**	- 0.929**	0.352**	0.019
8	Number of primary branches/plant	-0.186	-0.162	0.621**	-0.048	- 0.571**	-0.04	- 0.488**	**1.0000**	0.669**	-0.207	0.337**
9	Vine Length (m)	-0.047	-0.042	0.953**	0.014	- 0.876**	-0.191	- 0.918**	0.664**	**1.0000**	-0.295*	0.236**
10	Leaf Area (cm^2)	0.316**	0.367**	- 0.339**	0.018	0.336**	0.064	0.355**	-0.168	-0.281*	**1.0000**	0.133
11	Yield per plant (g)	-0.001	0.098	0.15	0.479**	0.056	0.340**	0.032	0.376**	0.249*	0.153	**1.0000**

*, **significance at 1 and 5 % level, respectively

4.6 Path Analysis Study

The information on the actual impact of a character on the yield is offered by path coefficient analysis, a reliable statistical technique that has been developed exclusively to divide the correlation coefficients into direct and indirect effects. When the decisive component characters are correlated, this approach becomes even more important to understanding the genetic make-up of a dependent character. The estimations of other characters under study direct and indirect effects on yield per plant are provided in Table 4.6.

The direct effect of any component characteristic on pod yield shows the certainty of indirect selection to be done through that trait to improve pod yield. Correlation explains the genuine relationship between two variables, therefore a choice for that character will perform well if both the correlation coefficient and the direct effect are positive and high. When the correlation coefficient is negative but the direct effect is high and positive, direct selection for those traits should be used to minimize the undesirable indirect effect. On the contrary, when the correlation coefficient is negative but the direct effect is high and positive, direct selection for those traits is recommended. The remaining effect determines how the causal factor best explains the variation in the dependent factor, fruit yield per tree. In this case, if the value of the residual effect is medium or high, this indicates that in addition to the studied traits, there are other attributes that contribute to yield.

4.6.1 Direct effects

According to the data estimated, the character average pod weight (1.5855) showed very high positive direct effect on pod yield per plant followed by days to first pod harvest (1.4475) and number of pods per plant (1.2888). High positive direct effect was shown by vine length (0.7858) and fresh pod length (0.4532). The characters such as number of primary branches per plant (0.1836) and number of seeds per pod (0.1541) exhibit low positive direct effect whereas leaf area exhibit negligible direct effect on pod yield per plant whereas, days to 50 per cent flowering exhibit negative very high direct effect on yield per plant.

Direct selection of characters depends on positive and highest value of path correlation coefficient. Hence, Path correlation coefficient of average pod weight, days to first pod harvest and number of pods per plant indicated direct selections of these characters.

4.6.2 Indirect effect

4.6.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering exhibited negligible negative direct effect of magnitude (-1.3262) on pod yield per plant. Its genotypic correlation with pod yield per plant (-0.078) was negative and non significant. It was due to very high indirect effect via days to first pod harvest (1.4270), negligible positive indirect effect by fresh pod length (0.0439) and leaf area (0.0102), negligible negative indirect effect by number of pods per plant (-0.0381), number of seeds per pod (-0.224), fresh pod width (-0.0003), average pod weight (-0.0509), number of primary branches per plant (-0.0564) and vine length (-0.0648).

4.6.2.2 Days to first pod harvest

Days to first pod harvest exhibited very high positive direct effect of magnitude (1.4475) on pod yield per plant. Its genotypic correlation with pod yield per plant (0.015) was positive and non significant. It was due to negative very high indirect effect by days to 50 per cent flowering (-1.3075), negligible positive indirect effect by fresh pod length (0.0576), average pod weight (0.0106) and leaf area (0.0120), negative negligible indirect effect by number of pods per plant (-0.0654), number of seeds per pod (-0.0152), fresh pod width (-0.0005), number of primary branches per plant (-0.0563) and vine length (-0.0676).

4.6.2.3 Number of pods per plant

Number of pods per plant exhibited very high positive direct effect of magnitude (1.2888) on pod yield per plant. Its genotypic correlation with pod yield per plant (0.138) was positive and non significant. It was due to high positive indirect effect by vine length (0.7493), low positive indirect effect by number of primary branches per plant (0.1154), negligible positive indirect effect by days to 50 per cent flowering (0.0392), negative very high indirect effect by average pod weight (-1.5352), negative high indirect effect by fresh pod length (-0.4158), negligible negative indirect effect via days to first pod harvest (-0.0735), number of seeds per pod (-0.0209) and leaf area (-0.0120).

4.6.2.4 Number of seeds per pod

Number of seeds per pod exhibited low positive direct effect of magnitude (0.1541) on pod yield per plant. Its genotypic correlation with pod yield per plant (0.444**) was positive and significant. It was due to moderate positive indirect effect by average pod weight (0.2965), low positive indirect effect by days to 50 per cent flowering (0.1928) and fresh pod length (0.1580), low negative indirect effect by days to first pod harvest (-0.1429) and number of pods per plant (-0.1743), negligible negative indirect effect by leaf area (-0.0005), fresh pod width (-0.0028), number of primary branches per plant (-0.0267) and vine length (-0.0104).

4.6.2.5 Fresh pod length (cm)

Fresh pod length exhibited high positive direct effect of magnitude (0.4532) on pod yield per plant. Its genotypic correlation with yield per plant (0.038) was positive and non significant. It was due to very high positive indirect effect by average pod weight (1.4650), low positive indirect effect by days to first pod harvest (0.1840), negligible positive indirect effect by leaf area (0.0112) and number of seeds per pod (0.0538), very high negative indirect effect by number of pods per plant (-1.1824), high negative indirect effect by vine length (-0.6998), low negative indirect effect by days to 50 per cent flowering (-0.1285) and number of primary branches per plant (-0.1144), negligible negative indirect effect by fresh pod width (-0.0042).

4.6.2.6 Fresh pod width (cm)

Fresh pod width exhibited negligible negative direct effect of magnitude (-0.0087) on pod yield per plant. Its genotypic correlation with yield per plant (0.301*) was positive and significant. It was due to high positive indirect effect by days to first pod harvest (0.0853) and average pod weight (0.5828), moderate positive indirect effect by fresh pod length (0.2177), negligible positive indirect effect by number of seeds per pod (0.0496) and leaf area (0.0013), high negative indirect effect by number of pods per plant (-0.3849), low negative indirect effect by vine length (-0.1739), negligible negative indirect effect by days to 50 per cent flowering (-0.0464) and number of primary branches per plant (-0.0219).

4.6.2.7 Average pod weight (10 pods)

Average pod weight exhibited very high positive direct effect of magnitude (1.5855) on pod yield per plant. Its genotypic correlation with yield per plant (0.019) was positive and non significant. It was due to high positive indirect effect by fresh pod length (0.4187), negligible positive indirect effect by days to 50 per cent flowering (0.0426), days to first pod harvest (0.0096), number of seeds per pod (0.0288) and leaf area (0.0120), very high negative indirect effect by number of pods per plant (-1.2479), high negative indirect effect by vine length (-0.7299), negligible negative indirect effect by fresh pod width (-0.0032) and number of primary branches per plant (-0.0968).

4.6.2.8 Number of primary branches per plant

Number of primary branches per plant exhibited low positive direct effect of magnitude (0.1836) on pod yield per plant. Its genotypic correlation with yield per plant (0.337**) was positive and significant. It was due to high positive indirect effect by days to 50 per cent flowering (0.4077), number of pods per plant (0.8104) and vine length (0.5259), negligible positive indirect effect by fresh pod width (0.001), high negative indirect effect by days to first pod harvest (-0.4441) and average pod weight (-0.8361), moderate negative indirect effect by fresh pod length (-0.2823), negligible negative indirect effect by number of seeds per pod (-0.0224) and leaf area (-0.0070).

4.6.2.9 Vine length (m)

Vine length exhibited high positive direct effect of magnitude (0.7858) on pod yield per plant. Its genotypic correlation with yield per plant (0.236**) was positive and significant. It was due to very high positive indirect effect by number of pods per plant (1.2290), low positive indirect effect by days to 50 per cent flowering (0.1094) and number of primary branches per plant (0.1229), negligible positive indirect effect by fresh pod width (0.0019), very high negative indirect effect by average pod weight (-1.4729), high negative indirect effect by fresh pod length (-0.4036), low negative indirect effect by days to first pod harvest (-0.1246), negligible negative indirect effect by number of seeds per pod (-0.0020) and leaf area (-0.0100).

4.6.2.10 Leaf area (cm^2)

Leaf area exhibited negligible positive direct effect of magnitude (0.0340) on pod yield per plant. Its genotypic correlation with yield per plant (0.133) was positive and non significant. It was due to high positive indirect effect by days to first pod harvest (0.5155) and average pod weight (0.5586), low positive indirect effect by fresh pod length (0.1501), high negative indirect effect by number of pods per plant (-0.4542) and days to 50 per cent flowering (-0.3987), moderate negative indirect effect by vine length (-0.2316), negligible negative indirect effect by number of seeds per pod (-0.0022), number of primary branches per plant (-0.0380), fresh pod width (-0.0003)

Sharma *et al*. (2016) observed direct high positive effect of number of pods per plant, number of flowers per plant, test weight, number of clusters per plant, harvest index and number of primary branches per plant with seed yield. Khandait *et al*. (2016) resulted a significant positive phenotypic correlation of pod yield plant^{-1} with pods plant^{-1}, days to first flowering, seeds pod^{-1}, number of flower cluster plant^{-1} and pod length. Dinesh *et al*. (2017) revealed that seed yield was primarily influenced by the number of pods per plant, many seeds per pod and 100 seed weights which had the maximum direct effect on seed yield per plant. Joghdhande *et al*. (2017) revealed that pod yield per plot was significantly and positively correlated with some branches per plant, number of nodes, pod length, 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. Palve *et al*. (2018) studied the characters like number of pods per plant, number of pods per cluster, primary branches per plant, number of clusters per plant, pod length, pod diameter, average pod weight and leaf area which had a highly significant positive correlation with pod yield per plot both genotypic and phenotypic levels. Tsegaye *et al*. (2018) observed that seed yield showed positive and significant phenotypic association with pod length, number of pods bearing cluster plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, 100-seed weight, harvest index and biomass yield. The Harvest index also showed a positive correlation with seed yield at the genotypic level. Paghadar *et al*. (2019) showed high positive direct influences on pod yield per plant through the number of primary branches per plant and pod length.

Table 4.6. Estimates of Genotypic direct (Diagonal) and indirect effects (above and below diagonal) of various yield and yield components

Sr. No.	Characters	Days to 50 % flowering (Days)	Days to first pod harvest (Days)	Number of pods per plant (No.)	Number of seeds per pod	Fresh pod length (cm)	Fresh pod width (cm)	Average pod weight (10 Pods)	Number of primary branches/ plant	Vine length (m)	Leaf area (cm^2)	Correlation value of yield per plant (g) at genotypic level
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
1	Days to 50 % flowering (Days)	-1.3262	1.4270	-0.0381	-0.0224	0.0439	-0.0003	-0.0509	-0.0564	-0.0648	0.0102	-0.078
2	Days to first pod harvest (Days)	-1.3075	1.4475	-0.0654	-0.0152	0.0576	-0.0005	0.0106	-0.0563	-0.0676	0.0121	0.015
3	Number of pods per plant (No.)	0.0392	-0.0735	1.2888	-0.0209	-0.4158	0.0026	-1.5352	0.1154	0.7493	-0.0120	0.138
4	Number of Seeds per pod	0.1928	-0.1429	-0.1743	0.1541	0.1580	-0.0028	0.2965	-0.0267	-0.0104	-0.0005	0.444**
5	Fresh Pod Length (cm)	-0.1285	0.1840	-1.1824	0.0538	0.4532	-0.0042	1.4650	-0.1144	-0.6998	0.0112	0.038
6	Fresh Pod Width (cm)	-0.0464	0.0853	-0.3849	0.0496	0.2177	-0.0087	0.5828	-0.0219	-0.1739	0.0013	0.301*
7	Average pod weight (10 Pods)	0.0426	0.0096	-1.2479	0.0288	0.4187	-0.0032	1.5855	-0.0968	-0.7299	0.0120	0.019
8	Number of primary branches/plant	0.4077	-0.4441	0.8104	-0.0224	-0.2823	0.0010	-0.8361	0.1836	0.5259	-0.0070	0.337**
9	Vine Length (m)	0.1094	-0.1246	1.2290	-0.0020	-0.4036	0.0019	-1.4729	0.1229	0.7858	-0.0100	0.236**
10	Leaf Area (cm^2)	-0.3987	0.5155	-0.4542	-0.0022	0.1501	-0.0003	0.5586	-0.0380	-0.2316	0.0340	0.133

*, ** = Significant at 5% and 1% levels, respectively.

Residual effect (R) = 0.58 Bold figures indicate direct effect

4.7 Genetic divergence

One important quality to consider when selecting as a parent within the hybridization program is divergence of genotypes. In order to develop new improved varieties with high hematopoietic potential, such parents should be used in the breeding programme. Hence, it is common practice to use statistical data developed by Mahalonobis for the determination of divergence between genotypes.

In the presented study, the divergence is studied among thirty-two genotypes of okra with the help of Mahalonobis D^2 Statistics considering yield and yield contributing characters.

4.7.1 Mahalonobis D^2 Values

Using Mahalonobis D^2, the twenty three genotypes including the standard check Pooja were assessed for the genetic diversity present in them. The mean values of twenty three genotypes [(X1) (X2)] were converted into unstandardized in correlated mean values [(Y1) (Y2)]. The values of D^2 were calculated for all the possible combinations i.e. 23 (23-1)/2, is equal to 253 pairs of genotypes.

4.7.2 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 'χ2' at 264 degrees of freedom. The 'λ' (Statistics) value was 2410.924**, suggesting that the genotypes differed significantly when all characters were considered simultaneously. The ANOVA of dispersion of thirty three genotypes is presented in Table 4.7.

Table 4.7. Analysis of variance for dispersion in twenty three cowpea genotypes

Source of variation	Degree of freedom (df)	Mean sum of squares
Genotype	22	2.9360E+13**
Error	43	9.7463E-09
Total	65	9.9372E+12

**** Significant at 1% level** V statistics at 242 df = 2341.77

4.7.3. Cluster Pattern

All the twenty three genotypes were clustered into four groups which was done using Tocher's method, as suggested by Rao (1952). The clusters I, II, III and IV includes genotypes in it and are presented in the table 4. The source of all the genotypes is AICRP on Vegetables, MPKV, Rahuri. The Cluster I was the largest consisting of twenty genotypes. Rest of the clusters i.e. II, III and IV are monogenotypic in nature.

In the research findings of Nagalakshmi *et al*. (2010) Sixty six genotypes of cowpea were clustered into twenty three clusters, Srinivas *et al*. (2016) grouped thirty genotypes of cowpea into six clusters, Patel *et al*. (2017) accessed Thirty-two cowpea which are grouped into eight clusters, Walle *et al*. (2019) grouped three hundred twenty-four genotypes into six clusters, Yadav *et al*. (2020) grouped thirty cowpea genotypes into six clusters, Patil *et al*. (2021) accessed Thirty-three seed cowpea genotypes which are grouped into six clusters.

4.7.4 Intra-cluster and inter cluster distances

The intra and inter cluster distances were worked out by D^2 statistics. The mean D^2 values of cluster elements were used as a measure of intra and inter cluster distances which is given in Table 4.8.

The maximum intra cluster distance were found in cluster I (D^2=565.01).The clusters II, III and IV are monogenotypic and recorded as the least values (D^2 =0). The maximum inter cluster distance is between cluster III and cluster IV (D^2= 1942.16) followed by cluster I and cluster IV (D^2 = 1288.81).

Cluster I had maximum inter cluster distance with cluster IV (D^2= 1288.81). Cluster II had maximum inter cluster distances with cluster IV (D^2= 1278.06). Cluster III had maximum inter cluster distance (D^2= 1942.16).

Table 4.8. Distribution of twenty three genotypes of cowpea into different clusters

Sr. No.	Cluster	Number of genotypes	Source	Genotypes
1.	I	20	AICRP on Vegetables, MPKV, Rahuri	RHRCP-3, RHRCP-16, RHRCP-5, RHRCP-8, RHRCP-26, RHRCP-6, Pooja, RHRCP-2, RHRCP-17, RHRCP-7, RHRCP-22, RHRCP-19, RHRCP-21, RHRCP-28, RHRCP-27, RHRCP-29, RHRCP-20, RHRCP-31, RHRCP-1, RHRCP-25
2.	II	1	AICRP on Vegetables, MPKV, Rahuri	RHRCP-18
3.	III	1	AICRP on Vegetables, MPKV, Rahuri	RHRCP-9
4.	IV	1	AICRP on Vegetables, MPKV, Rahuri	RHRCP-4

Table 4.9. Average intra (Bold) and inter cluster distance D and D^2 values four clusters in twenty three genotypes

Clusters	I	II	III	IV
I	**23.77 (565.0129)**	27.99 (783.44)	35.44 (1255.99)	35.9 (1288.81)
II		**0.00**	27.31 (745.84)	35.75 (1278.06)
III			**0.00**	44.07 (1942.16)
IV				**0.00**

4.7.5 Cluster Means

The cluster means for all the eleven characters presented in the table 4.9.

4.7.5.1 Days to 50 % flowering (Days)

Minimum days required for 50 per cent flowering was shown by cluster IV (38.99 DAS) followed by cluster IIs (39.03 DAS) whereas cluster I and cluster III required maximum days for 50 percent flowering.

4.7.5.2 Days to first pod harvest (Days)

Minimum days required to first pod harvest was shown by cluster II (46.97 DAS) while, maximum days to first pod harvest was shown by cluster III (54.32 DAS).

4.7.5.3 Number of pods per plant (No.)

On the basis of cluster means it was found that the cluster II (67.44) had large number of pods per plant followed by cluster III (65.79), cluster IV (54.40) and cluster I (39.83).

4.7.5.4 Number of Seeds per pod

The cluster means value estimated was maximum for Cluster III (12.83) followed by cluster I, cluster IV and minimum for Cluster II (9.36).

4.7.5.5 Fresh Pod Length (cm)

Cluster means for fresh pod length ranges from cluster II (8.91 cm) to cluster I (21.01 cm).

4.7.5.6 Fresh Pod Width (cm)

Fresh pod width was maximum for cluster III (0.87 cm) followed by cluster I (0.65 cm), cluster II (0.59 cm) and cluster IV (0.51 cm).

4.7.5.7 Average pod weight (10 Pods) (g)

Cluster I (58.75 g) showed highest average pod weight followed by cluster IV (32.92 g), cluster III (24.91 g) and cluster II (20.69 g).

4.7.5.8 Number of primary branches/plant

Number of primary branches/plant was high for cluster II (7.84) and low in cluster I (6.24).

Table 4.10. Cluster mean Performance of various characters of cowpea

	Days to 50 % flowering (Days)	Days to first pod harvest (Days)	Number of pods per plant (No.)	Number of Seeds per pod	Fresh pod length (cm)	Fresh pod width (cm)	Average pod weight (10 Pods)	Number of primary branches/ plant	Vine length (m)	Leaf area (cm^2)	Yield per plant (g)
I	42.56	50.22	39.83	11.82	21.01	0.65	58.75	6.24	1.70	51.67	165.47
II	39.03	46.97	67.44	9.36	8.91	0.59	20.69	7.84	2.53	37.33	138.46
III	47.20	54.32	65.79	12.83	19.63	0.87	24.91	6.93	2.84	52.48	166.93
IV	38.99	47.23	54.40	11.67	13.49	0.51	32.92	7.48	2.42	94.09	170.32

4.7.5.9 Vine Length (m)

Cluster III (2.84 m) showed maximum vine length while, cluster I (1.70 m) showed minimum vine length.

4.7.5.10 Leaf Area (cm^2)

Cluster IV (94.09 cm^2) recorded highest cluster mean value followed by cluster III (52.48 cm^2), cluster I (51.67 cm^2). Lowest Leaf Area was observed for Cluster II (37.33 cm^2).

4.7.5.11 Yield per plant (g)

Cluster IV (170.32 g) recorded highest cluster mean value followed by Cluster III (166.93 g), cluster I (165.47 gm) lowest number of fruits per plant was observed for Cluster II (138.46 g).

4.7.6 Per cent Contribution of eleven Characters for Divergence

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

There were maximum contribution by yield per plant (21.34 %) followed by number of pods per plant (18.58 %), vine length (13.83 %), leaf area (11.46 %), average pod weight (10.67 %), number of seeds per pod (9.09 %), fresh pod width (7.91 %), number of primary branches per plant (3.95 %) and fresh pod length (3.16 %).

4.7.7 Identification of Diverse genotypes for future Hybridization

The significant amount of variability is proved by the pattern of group constellation proved. 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 performance and cluster mean for characters. Based on inter-cluster and intra cluster distance, cluster mean and per se performance, the genotypes viz., RHRCP-18 RHRCP-09 and RHRCP-04 are suggested to utilize for future breeding programme.

Table 4.11. Per cent contribution of eleven characters of cowpea

Sr. No.	Source	Times Ranked 1st	Contribution (%)
1	Days to 50 % flowering (Days)	0	0.00
2	Days to first pod harvest (Days)	0	0.00
3	Number of pods per plant (No.)	47	18.58
4	Number of Seeds per pod	23	9.09
5	Fresh Pod Length (cm)	8	3.16
6	Fresh Pod Width (cm)	20	7.91
7	Average pod weight (10 Pods)	27	10.67
8	Number of primary branches/plant	10	3.95
9	Vine Length (m)	35	13.83
10	Leaf Area (cm square)	29	11.46
11	Yield per plant (g)	54	21.34

5. SUMMARY AND CONCLUSION

The research investigation was carried out under the title "Variability studies in cowpea (*Vigna unguiculata (*L.) Walp) genotypes" while keeping following objectives in mind.

1. To study the nature and extent of variability present in the different cowpea genotypes.
2. To study the correlation of yield and yield contributing characters.
3. To identify the most suitable and best-performing elite genotype.
4. To identify the elite genotypes for disease resistance.

The twenty three genotypes studied in this investigation along with the standard check Pooja were received from AICRP on vegetable crops, Mahatma Phule Krishi Vidyapeeth, Rahuri (Maharashtra). These genotypes were assessed in Randomized Block Design with three replication. It was carried out in the season of Summer during the year 2022.

The genotypes were studied for the variability, heritability, genetic advance, association studies, path analysis along with divergence for various growth and yield contributing characters viz. Days to 50 % flowering (Days), days to first pod harvest (Days), number of pods per plant (No.), number of seeds per pod, fresh pod length (cm), fresh pod width (cm), average pod weight (10 Pods) (g), number of primary branches/plant, leaf area (cm^2), vine length (m), yield per plant (g). Also qualitative characters and incidence of disease and pests were studied.

5.1 Qualitative characters

All the twenty three genotypes are classified according to pod colour, flower bud colour and pod shape. Except for genotypes RHRCP-17 and RHRCP-19 showing light green colour pods, RHRCP-28 showing purple colour pods, the rest showed green colour pods. All genotypes of the plant showed purple flower buds, except RHRCP-5, RHRCP-6, RHRCP-7 and RHRCP- 9 had white flower buds, while RHRCP-1 had yellow flower buds. Based on the leaf shape genotypes were classified into hastate, sub-hastate, globose and sub-globose leaf shape. All genotypes show above mentioned leaf shape viz., RHRCP-2, RHRCP-3, RHRCP 9, RHRCP- 17, RHRCP-19, RHRCP-22, RHRCP-29, RHRCP-31 showed sub-hastate leaf shape while RHRCP-5, RHRCP-27 and Pooja(C) showed globose leaf shape and rest of all showed sub-globose leaf shape.

5.2 Variability, Heritability and Genetic Advance

Significant variability was observed among all genotypes for all the eleven characters taken for study which showed significant differences in the mean sum of squares values. Among all the characters studied, the average pod weight (10 pods)(g), number of pods per plant, fresh pod length, vine length, leaf area (cm^2) and yield per plot (kg) had high estimate of gcv and pcv, while moderate GCV and PCV values showed by yield per hectare (q/ha), fresh pod width (cm), number of primary branches per plant, number of seeds per pod. While regarding, days to 50 % flowering (Days) and days to first pod harvest (Days) showed least GCV and PCV values.

The estimates of high heritability (broad sense) per cent values were high for average pod weight of 10 pods (g), number of pods per plant, leaf area (cm^2), fresh pod length and vine length (m), for yield per plot and yield per hectare (q/ha), fresh pod width (cm), number of seeds per pod, days to 50 % flowering (Days), days to first pod harvest (Days).

5.3 Correlation and Path Analysis

The yield per plant had significant positive association with number of seeds per pod, number of primary branches per plant, fresh pod width, vine length. While, yield per plant had non-significant association with days to 50 % flowering, days to first pod harvest, number of pods per plant, fresh pod length, average pod weight and leaf area (cm^2).

The character average pod weight showed very high positive direct effect on pod yield per plant followed by days to first pod harvest and number of pods per plant. High positive direct effect was shown by vine length and fresh pod length. The characters such as number of primary branches per plant and number of seeds per pod exhibit low positive direct effect whereas leaf area exhibit negligible direct effect on pod yield per plant whereas, days to 50 per cent flowering exhibit negative very high direct effect on yield per plant.

5.4 Genetic Divergence

Tocher's method which is described by Rao (1952) is used to formed clusters. The clusters I, II, III and IV includes genotypes in it. The source of all the genotypes was AICRP on Vegetables, MPKV, Rahuri. The Cluster I was the largest consisting of twenty genotypes. Rest of the clusters i.e. II, III and IV are monogenotypic in nature.

The maximum intra cluster distance were observed in cluster I (565.01). The clusters II, III and IV are monogenotypic and recorded as the least values.

The maximum inter cluster distance is in between cluster III and cluster IV (1942.16) followed by cluster I and cluster IV (1288.81). The cluster I had maximum inter cluster distance with cluster IV (1288.81). Cluster II had maximum inter cluster distances with cluster IV (1278.06). Cluster III had maximum inter cluster distance (1942.16).

Maximum contribution in diversity by yield per plant (21.34 %) followed by number of pods per plant (18.58 %), vine length (13.83 %), leaf area (11.46 %), average pod weight (10.67 %), number of seeds per pod (9.09 %), fresh pod width (7.91 %), number of primary branches per plant (3.95 %) and fresh pod length (3.16 %).

Conclusion:

From above discussion we can conclude that,

1. As per the analysis of variance table, for all the twenty three genotypes the eleven selected characters had significant differences in it, which means these characters should be considered while exploitation.
2. Based on mean performances of all the yield contributing and growth characters in general, the genotypes viz. RHRCP-8, RHRCP-04, RHRCP-05 and RHRCP-03 were found superior for most of the characters. Also in terms of yield, the estimates for these genotypes are superior to standard check Pooja.
3. The genotypes from the above conclusion, viz., RHRCP-08, RHRCP-03, RHRCP-04, RHRCP-05 and RHRCP-06 were highly resistant to bean mosaic virus and rest of all the genotypes had negligible incidence of it and also RHRCP-04 had comparatively lower pod borer incidence hence should be considered for resistance breeding.

4. Protein content was found highest in the genotypes viz. RHRCP-02, RHRCP-06, RHRCP-04, RHRCP-16 and RHRCP-03.
5. The magnitude of phenotypic variance as well as phenotypic coefficient of variation is slightly higher than genotypic variance and coefficient of variation.
6. In the present investigation, the average pod weight (10 pods), number of pods per plant, fresh pod length, vine length, leaf area (cm^2) and yield per plot (kg) had high estimate of GCV and PCV and moderate GCV and PCV values showed by yield per hectare (q/ha), fresh pod width (cm), number of primary branches per plant, number of seeds per pod which shows that these characters should be improve through selection.
7. The characters such as yield per plant, vine length and average pod weight, high heritability along with high genetic advance as per cent means was observed which means these characters are predominantly governed by additive gene action and it would be more effective to select these traits for genetic improvement.
8. The yield per plant had significant positive association with number of seeds per pod, number of primary branches per plant, fresh pod width, vine length at both genotypic and phenotypic levels.
9. In path analysis study, the character average pod weight showed very high positive direct effect on pod yield per plant followed by days to first pod harvest and number of pods per plant. High positive direct effect was shown by vine length and fresh pod length. The characters such as number of primary branches per plant and number of seeds per pod exhibit low positive direct effect whereas, leaf area exhibit negligible direct effect on pod yield per plant and days to 50 per cent flowering exhibit negative very high direct effect on yield per plant.
10. The twenty three genotypes were grouped into four clusters. From which cluster I is the largest and the smallest ones are II, III and IV which are monogenotypic in nature.
11. Out of eleven characters studied, maximum contribution in diversity by yield per plant (21.34 %) followed by number of pods per plant (18.58 %), vine length (13.83 %), leaf area (11.46 %), average pod weight (10.67 %), number of seeds per pod (9.09 %), fresh pod width (7.91 %), number of primary branches per plant (3.95 %) and fresh pod length (3.16 %).

12. Based on inter-cluster and intra cluster distance, cluster mean and per se performance, the genotypes viz., RHRCP-18 RHRCP-09 and RHRCP-04 are suggested to utilize for future breeding programme.

6. LITERATURE CITED

Anonymous, 2021. https://agriinfo.in, Statistics of Area and Production of Vegetable in India.

Anonymous, NHB data, Horticultural Statistics at a Glance (2018), https://agricoop.nic.in, Horticulture Statistics Division, Department of Agriculture, Cooperation & Farmers' Welfare, Ministry of Agriculture & Farmers' Welfare Government of India.

Arya, R.K., Panchta, R., Nguyen, N.V. and Pahuja, S.K. 2019. Meteroglyph analysis of cowpea (*Vigna unguiculata* L. Walp) elite genotypes. *Ekin Journal*. **5**(2) : 97-102.

Baranda Bhagwati, Sharma, P.P. and Meghawal Deva Ram. 2017. Correlation coefficient analysis for various quantitative traits in cowpea [*Vigna unguiculata (*L.) Walp] genotypes under different environments (E1, E2, E3 and pooled basis): *Journal of Pharmacognosy and Phytochemistry.,* **6**(5) : 1994-2001.

Burton, G.W. 1952. Quantitative inheritance in grasses Proc. Sixth International Grassland Cong. **1** : 277-283

Burton, G.W. and Devane, E.H. 1953. Estimating heritability fall fescue (*Festuca arundanaceae*) from replicated conial material. *Agronomy Journal*, **45** : 478-481.

Chaudhary, A.R, Solanki, S.D., Rahevar, P.M. and Patel, D.A. 2020. Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in cowpea [*Vigna unguiculata (*L.) Walp] Accessions: *International Journal of Current Microbiology and Applied Sciences.* **9**(2) : 1281-1293.

Devi, S.M. and Jayamani, P. 2018. Genetic variability, heritability, genetic advance studies in cowpea germplasm [*Vigna unguiculata (*L.) Walp.]. *Electronic Journal of Plant Breeding*, **9(**2) : 476-481

Dewey, D.I. and Lu, K.H. 1959. A Correlation and path-Coefficient Analysis of components of created wheat grass seed production. *Agronomy Journal.* **5**(1) : 515-518.

Dinesh, H.B, Viswanatha, K.P, Lohithaswa, H.C, Pavan, R. and Poonam Singh. 2017. Variability, correlation and path analysis studies in F_3 generation of cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of Current*

Microbiology and Applied Sciences. **6**(9) : 1420-1428.

Gbedevi, K.M., Boukar, O.I., Shikawa, H., Abe, A., Ongom, P.O., Unachukwu, N., Rabbi, I. and Fatokun, C.G. 2021. Diversity and Population Structure of Cowpea [Vigna unguiculata (L.) Walp.] Germplasm Collected from Togo Based on DArT Markers. Genes **12**(9), 1451. https://doi.org/10.3390/genes12091451.

Gomes Ana Maria Figueira, Draper David, Talhinhas Pedro, Santos Paula Batista, Simões Fernanda, Nascimento Nhantumbo, Rafael Massinga, José C. Ramalho, Isabel Marques and Ana I. Ribeiro-Barros. 2020 Genetic diversity among cowpea (*Vigna unguiculata (*L.)Walp.) Landraces Suggest Central Mozambique as an Important Hotspot of Variation: Agronomy 2020, **10**(12) **:** 1893. www.mdpi.com/journal/agronomy

Gupta Ramesh Kumar, Parmila, Madhuri Arya, Ashutosh Kumar and Preeti Kumari. 2019. Study on Genetic Variability in Cowpea [*Vigna unguiculata* (L.) Walp]. *Current Journal of Applied Sciences and Technology.* **33**(2) : 1-8.

Havaraddi Umesh and Deshpande, S.K. 2018. Genetic variability studies in advanced stabilized lines of cowpea (*Vigna unguiculata (*L.) Walp.). *International Journal of Pure and Applied Bioscience.* **6**(6) : 221-226.

Jogdhande, S., Kale, V.S., Nagre, P.K. and Meshram, S. 2016. Genetic divergence studies in cowpea. *International Journal of Agricultural Science and Research.* **6**(3) : 97-104.

Jogdhande, S., Kale, V.S. and Nagre, P.K. 2017. Correlation and Path Analysis Study in Cowpea [*Vigna unguiculata (*L.) Walp.] Genotypes : *International Journal of Current Microbiology and Applied Sciences.* **6**(6) : 3305-3313.

Johnson, H.W., Robinson, H.E. and Comstock, R.E. 1955 Estimation of genetic and environmental variability in soybean. *Agronomy Journal.* **47**(7) : 314-318.

Kalambe, A.S., Wankhade, M.P., Deshmukh, J.D., Chavan, B.R. and Shinde, A.V. 2019. Correlation studies in cowpea (*Vigna unguiculata (*L) Walp). *Journal of Pharmacognosy and Phytochemistry.* **8**(3) : 321-323.

Khandait Ramnarayan, Jain, P.K., Prajapati, S. and Dangi Avtar Singh. 2016. Correlation and Path Co- efficient analysis for yield and its attributing traits in diverse genotypes of cowpea (*Vigna unguiculata* L.). *International Journal of*

Bio-resource and Stress Management, **7**(1) : 008-017.

Khanpara, S.V., Jivani, L.L., Vachhani, J.H. and Kachhadia V.H. 2015. Genetic variability, heritability and genetic advance studies in vegetable cowpea (*Vigna Unguiculata* (L.) Walp.). *Electronic Journal of Plant Breeding*., **7**(2) : 408-413

Koraddi Shruti and Basavaraja, G.T. 2019. Genetic variability studies on yield and yield component traits of soybean : *International Journal of Current Microbiology and Applied Sciences.* **8**(2) : 1269-1274

Krishnan, M.R., Lovely, B. and Suga, G. 2019 Genetic variability and heritability studies in cowpea (*Vigna unguiculata* (L.) Walp). *International Journal of Agricultural Science and Research.* **9**(4) : 311–316.

Lal Hira, Reddy B. Rajasekhar and Vishwa Nath. 2017. Biometrical studies of yield and related traits in advance breeding lines of bush type vegetable cowpea [*Vigna unguiculata* (L.) Walp.]: *Legume Research*, Online ISSN:0976-0571.

Lenka, D. and Mishra, B. 1973. Path coefficient analysis of yield in rice varieties. *Indian Journal of Agricultural Science.* **43** : 376-379.

Lokesh, G.Y. and Niranjana Murthy. 2017 Genetic variability for yield and yield component traits in advanced F_2 and F_3 generations of cowpea [*Vigna unguiculat*e (L). Walp]. *International Journal of Pure and Applied Bioscience.* **5**(5) : 1156-1160.

Lush, J.L. 1949. Heritability of quantitative character in farm animals. Proc. 8th Int. Cong. Genet. Heredita (Suppl. 217-367).

Mafakheri Khosro, Bihamata, M.R. and Abbasi, A.R. 2017. Assessment of genetic diversity in cowpea (*Vigna unguiculata* L.) germplasm using morphological and molecular characterization. *Cogent Food and Agriculture.* **3** : 1327092.

Magashi, A.I., Shawai, R.S., Muhammad, A. and Tijjani, S.S. 2018. Genetic variability and heritability of growth and yield characters of cowpea germplasm under Gaya Sudan Savannah. *International Journal of Innovative Research & Development.* **7**(7) : 309-312.

Sharma Mahesh, Sharma, P.P., Sharma Hemlata and Meghawal, D.R. 2017. Genetic variability in cowpea [*Vigna unguiculata (*L.) Walp.] Germplasm lines: *Journal of Pharmacognosy and Phytochemistry.* **6**(4) : 1384-1387.

Manggoel, W., Uguru, M.I., Ndam, O.N. and Dasbak, M.A. 2012. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpeas [*Vigna unguiculata (*L.) Walp] accessions. *Journal of Plant Breeding and Crop Science.* 4(5) : 80-86

Meena, H.K., Ram Krishna, K. and Singh Bhuri. 2015. Genetic Variability, Heritability and Genetic Advance in Cowpea (*Vigna unguiculata* (L.) Walp.). *Journal of Plant Science and Research.* **31**(1) : 13-16.

Nagalakshmi, R.M., Usha Kumari, R. and Boranayaka, M.B. 2010. Assessment of genetic diversity in cowpea (*Vigna unguiculata*). *Electronic Journal of Plant Breeding*, **1**(4) : 453-461.

Nair Reena and Mehta, A.K. 2014. Induced genetic variability in cowpea [*Vigna unguiculata* (L.) Walp] var. Pusa Komal: *An International Quarterly Journal of Life Science.* **9**(2) : 829-833.

Nameirakpam, B. and Khanna, V.K. 2018. Studies on Crossability and Genetic Diversity in Cowpea (*Vigna unguiculata* L. Walp.). *International Journal of Environmental Science & Natural Resources.* **13**(1) : 45-48.

Nguyen, N.V., Arya, R.K., Panchta, R. and Tokas, J. 2017. Studies on genetic divergence in Cowpea (*Vigna unguiculata*) by using D^2 statistics under semi-arid conditions. *Forage Res*., **43**(3) : 197-201.

Nkhoma Nelia, Shimelis Hussein, Mark D. Laing, Admire Shayanowako and Isack Mathew. 2020. Assessing the genetic diversity of cowpea [*Vigna unguiculata* (L.) Walp.] germplasm collections using phenotypic traits and SNP markers: *BMC Genetics.* **21** : 110.

Olunloyo, A.A., Aderemi, F.T., Adedokun, S.A., Alarape, A.B., Sulaiman, O.N. and Aderemi, A.M. 2019. Genetic Advance and Heritability Analysis of line x tester of four cowpea crosses IOSR. *Journal of Agriculture and Veterinary Science.* **12**(9) : 06-10.

Paghadar, P.J., Vachhani, J.H., Gajera, K.P. and Chovatiya, S.J. 2019. Evaluation of correlation and path analysis in vegetable cowpea [*Vigna unguiculata (*L.) Walp.]. *International Journal of Chemical Studies.* **7**(4) : 628-630.

Palve, M.R., Kale, V.S., Bhaladhare, M.B. and Jadhav, R.D. 2018 Correlation and Path Analysis Study in F_5 Generation of Cowpea*: International Journal of Current Microbiology and Applied Science.* Special Issue **6** : 1529-1537.

Panchta Ravish, Satyawan Arya, Dalvinder Pal Singh, Satpal, Preeti and Rajender Kumar 2020. Genetic variability and association studies in cowpea [*Vigna unguiculata* (L.) Walp] for seed yield and related traits. *Forage Research*. **46**(3) : 232-235.

Pandiyan, M., Vaithilingan, M., Krishnadevi, A., Sivakumar, P., Sivakumar, C., Jamuna, E., Sivakumar, B., Sivaji, M., Yuvaraj, M. and Senthilkumar 2020. Genetic variability studies on cowpea genotypes. *International Journal of Current Microbiology and Applied Science.* **9**(6) : 3794-3797.

Panse, V.G. and Sukhatme, P.V. 1985. Statistical methods for agricultural workers. Publication and Information Division, ICAR, New Delhi.

Patel, U.V., Parmar, V.K., Patel, A.I., Jadav, N.K. and Patel, N.M. 2016. Genetic Variability and Heritability Study in Cowpea (*Vigna unguiculata* (L.) Walp.) : *Advances in Life Science.* **5**(19) : 8636-8640.

Patel, U.V., Parmar, V.K., Tandel, Y.N. and Patel, H.R. 2017. Genetic divergence in cowpea [Vigna *unguiculata* (L.) Walp.] for yield components parameters. *Electronic Journal of Plant Breeding.* **8**(1): 331-335.

Patil Snehal, Pethe, U.B., Mahadik, S.G., Dalvi, V.V. and Joshi, M.S. 2021b. Correlation and path analysis studyin F_3 generation of cowpea [*Vigna unguiculata (*L.) Walp.] genotypes. *Journal of Pharmacognosy and Phytochemistry.* **10**(1) : 203-207.

Patil, A.R., Shinde, G.C., Awari, V.R. and Tambe, S.I. 2021. A genetic diversity studies in seed cowpea (*Vigna unguiculata* L. Walp) genotypes *: International Journal of Current Microbiology and Applied Science.* **10**(10) : 533-538.

Rambabu, E., Reddy, K., Ravinder, Kamala V., Saidaiah, P. and Pandravada, S.R. 2016. Genetic variability and heritability for quality, yield and yield components in Yardlong bean (*Vigna unguiculata* (L.) Walp. sesquipedalis Verdc.): *Green Farming.* **7**(2) : 311-315.

Rao, C.R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons, New York.

Sabale, G.R., Bhave, S.G., Desai, S.S., Dalvi, M.B. and Pawar, P.R. 2018. Variability, heritability and genetic advance studies in F_2 generation of cowpea (*Vigna unguiculata* sub sp. Unguiculata). *International Journal of Current Microbiology and Applied Science.* **7**(9) : 3314-3320.

Sadashivam, S. and Manikam, A. 1992. Biochemical method for Agriculture Science. Wiley Eastern Ltd. New Delhi.

Santos Adriano dos, Ceccon Gessí, Livia Maria Chamma Davide, Agenor Martinho Correa and Valdecir Batista Alves. 2014. Correlations and path analysis of yield components in cowpea: *Crop Breeding and Applied Biotechnology.* **14** : 82-87

Sapara, G.K., Javia, R.M. and Pokar, M.V. 2014. Genetic Variability, heritability and genetic advance in vegetable cowpea (*Vigna unguiculata* (L.) Walp). *International Journal of Plant Science.* **9**(2) : 326-329.

Sarath, P.S. and Reshma, T. 2017. Genetic Variability Studies in Cowpea [*Vigna Unguiculata* (L.) Walp]. *International Journal of Agriculture Science and Research.* **7**(3) : 129-132.

Shanko Diriba, Andargie Mebeaselassie and Zelleke Habtamu. 2014. Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.) *Research in Plant Biology.* **4**(2) : 21-26.

Sharma, M., Sharma, P.P., Sharma, H. and Meghawal, D.R. 2017. Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp] Germplasm lines. *Journal of Pharmacognosy and Phytochemistry*. **6**(4) : 1384-1387.

Sharma, P.P., Mahesh Sharma and Mukesh Vyas. 2016. Correlation coefficient and path analysis components traits in cowpea (*Vigna unguiculata* (L.) Walp.] *International Journal of Current Research.* **8**(8) : 35783-35786.

Singh, R.K. and Chaudhary, B.D. 1977. “Biometrical Methods In Quanitative Genetic Analysis” Kalyani Publishers, New Delhi, pp. 1-318.

Tambitkar, N.B., Pethe, U.B., Desai, S.S., Dhopavkar, R.V. and Kadam, J.J. 2020. Correlation and path analysis studies in cowpea : *The Pharma Innovation*

Journal. **9**(12) : 314-316.

Tsegaye Dagmawit, Mohammed Hussein and Amsalu Berhanu. 2018. Correlation and path coefficient analysis of yield and yield related traits interactions in Ethiopian Cowpea (*Vigina Unguiculata* Walp L.) Accessions. *Academic Research Journal of Agricultural Science and Research.* **6**(9) : 526-530.

Ugale, P.N., Wankhade, M.P. and Bagade, A.B. 2020. Genetic variability studies in cowpea (*Vigna unguiculata* L.). *Journal of Pharmacognosy and Phytochemistry.* **9**(6) : 476-479.

Vavilapalli Sivakumar, Celine, V.A., Duggi Shrishail, Padakipatil Sanjeev and Magadum Santoshkumar. 2013. Genetic Variability and Heritability Studies in Bush Cowpea (*Vigna unguiculata (*L.) Walp.) *Legume Genomics and Genetics.* **4**(4) : 27-31.

Vinay, K., Jagan Mohan Rao, P., Sandhya Kishore, N. and Hari, Y. 2022. Genetic variability studies for seed yield and yield component traits in cowpea [*Vigna unguiculata (*L.) Walp.]. *Electronic Journal of Plant Breeding.* **13**(2) : 544-548.

Wadghane Shrikant, Aher Adhir, Dhandore Rajesh, Sargar Yogesh and Jadhav Sonali. 2022 Genetic variability for quantitative and quality traits in cowpea (*Vigna unguiculata (*L.) Walp). *Electronic Journal of Plant Breeding.* **13**(3) : 1144-1149.

Walle Tesfaye, Mekbib Firew, Amsalu Berhanu and Gedil Melaku. 2019. Genetic Diversity of Ethiopian Cowpea [*Vigna unguiculata* (L) Walp] Genotypes Using Multivariate Analyses : *Ethiopian Journal of Agricultural Sciences.* **29**(3) : 89-104.

Walle Tesfaye, Mekbib Firew, Amsalu Berhanu and Gedil Melaku. 2018. Correlation and Path Coefficient Analyses of Cowpea (*Vigna unguiculata* L.) Landraces in Ethiopia. *American Journal Plant Sciences.* **9** : 2794-2812.

Wilk, S.S. 1932. Certain generalization in the analysis of variance Biometerics., **24** : 471-494.

Yadav, N.P., Rajasekhar D., Blessy, V. and Yadav, B. 2020. Genetic diversity studies in cowpea (*Vigna unguiculata* L.Walp). *International Journal of Agriculture Science.* **12**(15) : 10118-10120.

7. APPENDICES

Appendix-I: Details of Meteorological Data During Experimental Period

Week No.	Date	Temperature (^{0}C)		Humidity (%)		Wind Speed (km/hr)	Daily rain (mm)	Bright sunshine Hours	Open pan evaporation (mm)
		Max.	Min.	RH-I	RH-II				
8	19.02.2022 - 25.02.2022	33.03	16.06	73.14	23.29	0.96	0.00	9.71	5.46
9	26.02.2022 - 04.03.2022	33.14	18.07	65.43	21.29	0.59	0.00	9.01	5.69
10	05.03.2022 - 11.03.2022	32.26	19.66	72.86	29.57	1.37	0.00	7.01	5.57
11	12.03.2022 - 18.03.2022	35.66	21.07	59.43	17.57	1.99	0.34	9.04	6.77
12	19.03.2022 - 25.03.2022	37.63	22.47	55.29	16.00	2.06	0.00	7.11	7.63
13	26.03.2022 - 01.04.2022	38.20	22.29	55.29	14.14	1.77	0.00	8.99	8.77
14	02.04.2022 - 08.04.2022	39.74	23.44	52.43	12.14	1.91	0.00	9.36	9.43
15	09.04.2022 - 15.04.2022	38.86	24.49	59.29	17.43	2.19	0.00	8.57	8.91
16	16.04.2022 - 22.04.2022	38.83	24.94	51.86	15.57	1.87	0.00	9.24	10.03
17	23.04.2022 - 29.04.2022	39.40	27.50	45.43	17.00	1.96	0.00	8.73	10.11
18	30.04.2022 - 06.05.2022	39.94	26.36	49.86	16.71	3.16	0.00	10.23	11.49
19	07.05.2022 - 13.05.2022	40.94	28.13	49.57	20.57	3.64	0.00	7.00	12.11
20	14.05.2022 - 20.05.2022	39.14	26.96	60.43	22.71	4.93	0.23	7.34	11.11
21	21.05.2022 - 27.05.2022	37.51	26.97	60.71	25.00	5.91	0.00	8.39	9.94
22	28.05.2022 - 03.06.2022	38.31	26.34	65.29	25.29	6.00	0.00	8.27	11.17
23	04.06.2022 - 10.06.2022	38.14	26.01	65.14	30.86	3.83	1.23	6.51	10.03
24	11.06.2022 - 17.06.2022	35.83	26.16	71.71	38.86	3.43	1.29	7.76	8.11
25	18.06.2022 - 24.06.2022	33.37	24.90	79.57	51.71	3.46	13.80	6.10	6.80
26	25.06.2022 - 01.07.2022	31.06	24.34	83.71	57.71	2.34	8.31	4.50	5.00
27	02.07.2022 - 08.07.2022	30.54	24.53	84.29	63.29	4.39	2.17	3.27	4.77
28	09.07.2022 - 15.07.2022	26.23	23.36	89.43	79.86	2.41	5.37	0.00	2.57
29	16.07.2022 - 22.07.2022	29.31	24.01	86.14	63.00	4.49	1.06	2.83	4.09
30	23.07.2022 - 29.07.2022	29.14	23.47	86.71	65.29	2.37	9.77	1.64	3.43
31	30.07.2022 - 05.08.2022	30.74	23.50	88.86	62.43	0.99	17.14	5.21	3.80
32	06.08.2022 - 12.08.2022	28.29	24.07	84.43	71.14	3.11	8.03	2.11	2.80
33	13.08.2022 - 19.08.2022	28.34	24.11	81.29	70.00	5.44	0.37	3.80	3.66
34	20.08.2022 - 26.08.2022	29.83	24.13	81.29	64.14	3.96	0.23	5.19	4.71
35	27.08.2022 - 02.09.2022	31.57	23.19	86.86	55.29	1.54	3.40	7.63	5.71
36	03.09.2022 - 09.09.2022	30.77	23.46	91.00	65.00	1.30	21.43	5.40	5.03
37	10.09.2022 - 16.09.2022	28.97	23.60	91.43	74.43	1.83	10.83	2.61	3.74
38	17.09.2022 - 23.09.2022	27.49	22.24	90.14	70.43	2.69	14.00	2.27	2.49
39	24.09.2022 - 30.09.2022	29.63	22.69	90.14	62.71	1.04	4.66	4.89	4.23

8. VITAE

MISS. BANKAR VARSHA POPAT

Candidate for the degree

of

MASTER OF SCIENCE (HORTICULTURE)

IN

HORTICULTURE
(VEGETABLE SCIENCE)

2024

Title of thesis		:	"Variability studies in cowpea (*Vigna unguiculata* (L.) Walp) genotypes"
Major field		:	Horticulture (Vegetable Science)
Biographical information		:	
Personal	**Date of Birth**	:	12^{th} July 1999
	Place of Birth	:	Rahuri, Tal. Rahuri, Dist. Ahmednagar
	Father's Name	:	Late. Popat Gopinath Bankar
	Mother's Name	:	Smt. Kanchan Popat Bankar
Educational	**Bachelor Degree**	:	B.Sc. (Agri.) degree from College of Agriculture, Sonai
	Class	:	First Class with Distinction
	Name of the University	:	Mahatma Phule Krishi Vidyapeeth, Rahuri.
Address		:	A/P. Bramhani, Tal. Rahuri, Dist. Ahmednagar, Pin code : 414105
	Email-id	:	varshabankar127@gmail.com
	Contact No.	:	9545790903