

**CHARACTERIZATION OF GERMPLASM FOR
YIELD AND IT'S ASSOCIATED
TRAITS IN COWPEA [*Vigna unguiculata* (L.)
Walp]**



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BANGALORE
2023**

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Thesis submitted to the
University of Agricultural Sciences, Bangalore
in partial fulfilment of the requirements
for the Degree of

Master of Science (Agriculture)

in

GENETICS AND PLANT BREEDING

By

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**UNIVERSITY OF AGRICULTURAL SCIENCES
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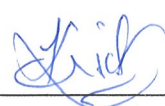
CERTIFICATE


This is to certify that the thesis entitled “Characterization of germplasm for yield and it’s associated traits in cowpea [*Vigna unguiculata* (L.) Walp]” submitted in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in Genetics and Plant Breeding to the University of Agricultural Sciences, Bangalore is a record of *bona fide* research work carried out by **Mr. MUBARAK A SALI, PAMB 0267**, during the period of his study in this University, under my guidance and supervision. The thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

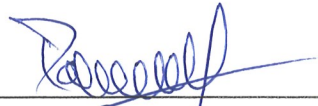
Bengaluru
February, 2023


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*Affectionately Dedicated
To My Beloved Parents,
Smt. Mahabubi A. Sali
Sri. AnwarBasha M. Sali
My sister Nisha & My
Family*

ACKNOWLEDGEMENT

With great memories...

It is my pleasure to glance back and recall the path travelled during the days of hard work and perseverance. This thesis is the result of two years of work whereby I have been accompanied, supported and guided by many people. It is my heart's turn to express my deepest sense of gratitude to all of those who directly and indirectly helped me in this endeavour.

My first debt of gratitude must go to the esteemed chairperson of my advisory committee **Dr. T. V. Krishna**, Assistant Professor, Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru. This work would not have been possible without his guidance, support and encouragement. His insightful comments at different stages of my research helped me focus my ideas. I'm grateful for his excellent guidance, valuable suggestions, everlasting patience and sustained encouragement throughout my studies, course of research work and during the preparation of the thesis. I consider myself lucky to have such an excellent perceiving, ever-cooperative and helpful personality as my guide.

I record sincerely, my profound sense of gratitude to **Dr. J. Shanthala**, Professor and Head, Department of Genetics and Plant Breeding, College of Agriculture, GKVK, Bengaluru, **Dr. H. C. Lohithaswa**, Senior scientist, Department of Genetics, College of Agriculture, GKVK, Bengaluru and **Dr. K. B. Palanna**, ZARS GKVK, Bengaluru and **Dr. M. Papireddy** Advisory Committee members of my research programme, for all the guidance, encouragement, valuable suggestions and critical evaluation of the manuscript.

I bow my head with overwhelming respect and thanks to the teachers of the Department of Genetics and Plant Breeding, **Dr. S. Ramesh**, **Dr. Uma Shannker**, **Dr. N. Marappa H. A. Mohan rao**, **Dr. J. Shanthala**, **Dr. K. Madhusudhan** and **Dr. D. L. Savithramma**.

I am very thankful to my guidemate, **Deeksha**.

My diction doesn't seem too rich enough to provide suitable words to articulate my sincere and heartfelt gratitude to thank my dear seniors especially, **Dr. L. Sanketh**, **L. Naveen**, **Dr. Basanagouda**, **Siddu**, **Mrs. Shilpa Rahul**, **Soumya**, **Kavya**, **Kalpna**, **Meena**, **Suma**, **Santoshi**, **Ranjitha**, **Ambika**, **Sahana** for their constant guidance, support, friendliness and helping me for management of my crop and also analysis of my data.

This record will be incomplete if I forget the valuable support extended to me by my lovely friends- **Samantha, Nimbu yateesh, Nagamma alias Cheta, Gouda alias pp, Boobayya, Mindri, Kiran, Jannya, Kaadu, Imrya, Manihal, Pajjya, Chutiya Avinash.**

A special mention of thanks to my friends cum classmates **Ram's, Kulli Sahana, Liger Hema, Pachchi Prashanth, Mouni, Chotabheem Satish, Ketto Aniket, Smiley Karthik, Laddu reddy alias Vinitha, Darshana Divya, Mika alias Premika, Gundamma alias Sinchana, Jyoshna, Shradhhu, Singara Siri, Mymmy alias Bidwan** and for their true friendship, love, help and care. I am very much privileged to get these buddies in my life because of them only this journey was enjoyable and more memorable in my whole life.

A special thanks to my dearest juniors, **Jaddu Mallu, Pramod, Sangu, Sunil, Kempa, Gundy, Sundra, Chinnu, First rank Raju, Murali sir** for their unconditional help, love and care.

I am overwhelmed with gratitude to all my respondents, without whose whole hearted co-operation, this study would not have been fruitful. Most of all, I thank ALLAH for the blessings showered and the helps received which enabled me to complete this thesis work.

..... Any omission in this brief acknowledgement doesn't mean lack of gratitude.

February, 2023

Bengaluru

(Mubarak A. Sali)

Characterization of germplasm for yield and it's associated traits in cowpea [*Vigna unguiculata* (L.) Walp]

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ABSTRACT

One hundred forty seven cowpea germplasm accessions were evaluated in Bengaluru, Pavagada and Mandya locations in α - lattice design to assess variability and Genotype \times Environment interaction in summer 2022. High heritability with high GAM was observed for plant height, primary branches per plant, pods per plant, average pod length, average seeds per pod and average grain yield per plant at all three locations. K- means clustering method was used to classify 147 genotypes, as a result 12 clusters were identified. Cluster 8 was largest with 22 genotypes and cluster 7 was smallest with four genotypes. Cluster 7 and cluster 6 had highest inter cluster distance and genotypes belonging to these clusters can be used as parents for further crop improvement programme. Additive Main effects and Multiplicative Interaction (AMMI) model was used to detect and characterize genotype \times environment interaction (GEI). GGE bi-plot was used to visually interpret GEI patterns of genotypes. Based on mean vs. stability pattern, genotypes KBC-2, IC-237422 and EC-170574- 6 were found to be highly stable with high mean grain yield per plant. Based on 'which won- where' pattern for average grain yield per plant, genotypes IC-402159 and CB-1024 were better in Bengaluru, and Pavagada location and genotypes IC-458492, NBC-51 and EC-472252 were better in Mandya location. Based on ASV, genotypes EC-458483, EC-394708, NBC-18 were found to be stable across three locations. Based on SI, genotypes IC-198355(45), EC-472271, EC-394708 were found stable with high mean grain yield per plant.

February, 2023

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T. V. KRISHNA
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ಅಲಸಂದೆಯ ವಂಶವಾಹಿರೂಪಗಳ ಇಳುವರಿ ಮತ್ತು ಇಳುವರಿಗೆ ಸಂಬಂಧಿಸಿದ ಗುಣಲಕ್ಷಣಗಳ
ವಿಶ್ಲೇಷಣೆ

ಮುಬಾರಕ್ ಎ. ಸಾಲ

ಸಾರಾಂಶ

ಅಲಸಂದೆಯ ೧೪೭ ವಂಶವಾಹಿರೂಪಗಳನ್ನು ೨೦೨೨ರ ಬೇಸಿಗೆಯಲ್ಲಿ ವ್ಯತ್ಯಯತೆ ಮತ್ತು ವಂಶವಾಹಿರೂಪಗಳು ಪರಿಸರಗಳ ಪರಸ್ಪರಕ್ರಿಯೆಯನ್ನು ಗುರುತಿಸಲು α -ಲ್ಯಾಟಿಸ್ ವಿನ್ಯಾಸದಲ್ಲಿ ಬೆಂಗಳೂರು, ಪಾವಗಡ ಮತ್ತು ಮಂಡ್ಯದ ಕೃಷಿ ಸಂಶೋಧನಾ ಕೇಂದ್ರಗಳಲ್ಲಿ ಮೌಲ್ಯಮಾಪನ ಮಾಡಲಾಯಿತು. ಎಲ್ಲಾ ಮೂರು ಸ್ಥಳಗಳಲ್ಲಿ ಸಸ್ಯದ ಎತ್ತರ, ಪ್ರಾಥಮಿಕ ಕೊಂಬೆಗಳ ಸಂಖ್ಯೆ, ಕಾಯಗಳ ಸಂಖ್ಯೆ, ಸರಾಸರಿ ಕಾಯಯ ಉದ್ದ, ಪ್ರತಿ ಕಾಯಯ ಸರಾಸರಿ ಬೀಜಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಸಸ್ಯದ ಸರಾಸರಿ ಧಾನ್ಯ ಇಳುವರಿಗೆ ಹೆಚ್ಚಿನ ಅನುವಂಶಿಕತೆ ಹಾಗೂ ಅನುವಂಶೀಯ ಮುನ್ನಡೆಯ ಶೇಕಡಾವಾರು ಸರಾಸರಿ (ಜಿ.ಎ.ಎಮ್.) ಕಂಡುಬಂದಿತು. ಕೆ-ಮೀನ್ಸ್ ಸಮೂಹಗಾರಿಕೆಯ ವಿಧಾನವನ್ನು ಬಳಸಿ ೧೪೭ ವಂಶವಾಹಿರೂಪಗಳನ್ನು ೧೨ ಸಮೂಹಗಳಾಗಿ ವಿಂಗಡಿಸಲಾಯಿತು. ೮ ನೇ ಸಮೂಹವು ೨೨ ವಂಶವಾಹಿರೂಪಗಳೊಂದಿಗೆ ಅತಿ ದೊಡ್ಡ ಸಮೂಹವಾಗಿ, ೭ ನೇ ಸಮೂಹವು ೪ ವಂಶವಾಹಿರೂಪಗಳೊಂದಿಗೆ ಅತಿ ಚಿಕ್ಕ ಸಮೂಹವಾಗಿ ಕಂಡುಬಂದಿರುತ್ತದೆ. ಸಮೂಹ ೭ ಮತ್ತು ಸಮೂಹ ೭ ರ ನಡುವಿನ ಪರಸ್ಪರ ಸಮೂಹ ಅಂತರವು ಹೆಚ್ಚಾಗಿರುವುದರಿಂದ, ಈ ಸಮೂಹಗಳಿಗೆ ಸೇರುವ ವಂಶವಾಹಿರೂಪಗಳನ್ನು ತಳಿ ಅಭಿವೃದ್ಧಿ ಯೋಜನೆಗಳಲ್ಲಿ ಪೋಷಕ ತಳಿಗಳಾಗಿ ಉಪಯೋಗಿಸಬಹುದು ಎಂದು ತಿಳಿದುಬಂದಿರುತ್ತದೆ. ವಂಶವಾಹಿರೂಪಗಳು ಪರಿಸರಗಳ ಪರಸ್ಪರಕ್ರಿಯೆಯನ್ನು ಗುರುತಿಸಲು ಹಾಗೂ ವಿಶ್ಲೇಷಿಸಲು ಸಂಯೋಜಕ ಮುಖ್ಯಪರಿಣಾಮಗಳು ಮತ್ತು ಗುಣಾತ್ಮಕ ಪರಸ್ಪರಕ್ರಿಯೆ (ಎ.ಎಮ್.ಎಮ್.ಐ.) ಮಾದರಿಯನ್ನು ಬಳಸಲಾಯಿತು. ವಂಶವಾಹಿಗಳ ಜಿ.ಇ.ಐ. ಮಾದರಿಯನ್ನು ದೃಷ್ಟಿಗೋಚರವಾಗಿ ಅಭ್ಯೇಷಿಸಿಕೊಳ್ಳಲು ಜಿ.ಜಿ.ಇ ಬೈ-ಪ್ಲಾಟ್‌ಗಳನ್ನು ಬಳಸಲಾಯಿತು. ಸರಾಸರಿ-ಸ್ಥಿರತೆಯ ಮಾದರಿಗಳ ಆಧಾರದ ಮೇಲೆ ಕೆಬಿಸಿ-೨, ಐಸಿ-೨೩೭೪೨೨ ಮತ್ತು ಇಸಿ-೧೭೦೫೭೪-೭ ಎಂಬ ವಂಶವಾಹಿಗಳು ಅತ್ಯಂತ ಸ್ಥಿರವಾಗಿರುವುದು ಮತ್ತು ಹೆಚ್ಚಿನ ಪ್ರಮಾಣದ ಸರಾಸರಿ ಧಾನ್ಯದ ಇಳುವರಿಯನ್ನು ಹೊಂದಿರುವುದು ಕಂಡುಬಂದಿರುತ್ತದೆ. 'ವಿಚ್ ವೋನ್ ವೆರ್' ಮಾದರಿಯ ಆಧಾರದ ಮೇಲೆ, ಪ್ರತಿ ಸಸ್ಯದ ಸರಾಸರಿ ಧಾನ್ಯದ ಇಳುವರಿಗಾಗಿ, ಬೆಂಗಳೂರು ಮತ್ತು ಪಾವಗಡದಲ್ಲಿ ಐಸಿ-೪೦೨೧೫೬ ಮತ್ತು ಸಿಬಿ-೧೦೨೪ ಗಳು ಹಾಗೂ ಮಂಡ್ಯದಲ್ಲಿ ಐಸಿ-೪೫೮೪೬೨, ಎನ್‌ಬಿಸಿ-೫೧ ಮತ್ತು ಇಸಿ-೪೭೨೫೨ ಗಳು ಉತ್ತಮ ವಂಶವಾಹಿರೂಪಗಳಾಗಿವೆ ಎಂದು ಕಂಡುಬಂದಿರುತ್ತದೆ. ಎ.ಎಸ್.ವಿ ಯ ಆಧಾರದ ಮೇಲೆ, ಇಸಿ-೪೫೮೪೬೩, ಇಸಿ-೩೬೪೭೦೮ ಮತ್ತು ಎನ್‌ಬಿಸಿ-೧೮ ಗಳು ಎಲ್ಲಾ ಮೂರು ಸ್ಥಳಗಳಲ್ಲಿಯೂ ಸ್ಥಿರವಾಗಿರುವುದು ಕಂಡುಬಂದಿತು. ಎಸ್‌ಐ ಆಧಾರದ ಮೇಲೆ, ಐಸಿ-೧೬೮೩೫೫(೪೫), ಇಸಿ-೪೭೨೨೭೧ ಮತ್ತು ಇಸಿ-೩೬೪೭೦೮ ಎಂಬ ವಂಶವಾಹಿರೂಪಗಳು ಅತ್ಯಂತ ಸ್ಥಿರತೆಯೊಂದಿಗೆ ಹೆಚ್ಚಿನ ಪ್ರಮಾಣದ ಸರಾಸರಿ ಧಾನ್ಯದ ಇಳುವರಿಯನ್ನು ಹೊಂದಿರುವುದು ಕಂಡುಬಂದಿರುತ್ತದೆ.

ಫೆಬ್ರವರಿ ೨೦೨೩

ಅನುವಂಶೀಯ ಮತ್ತು ಸಸ್ಯತಳಿ ಅಭಿವೃದ್ಧಿ ಶಾಸ್ತ್ರ ವಿಭಾಗ

(ಉ. ವಿ. ಕೃಷಿ)

ಕೃಷಿ ಮಹಾವಿದ್ಯಾಲಯ, ಗಾ.ಕೃ.ವಿ.ಕೆ., ಬೆಂಗಳೂರು- ೫೬೦೦೭೫

ಪ್ರಮುಖ ಸಲಹೆಗಾರರು



Assessment of trait-specific accessions in cowpea [*Vigna unguiculata* (L.) W.] germplasm



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Introduction

- Cowpea is an annual self-pollinated crop belonging to family Fabaceae, which is known for its drought tolerance and inherent capacity of fixing soil nitrogen
- In Karnataka, cowpea is grown over 0.45 lakh hectares with a production of 0.15 lakh tonnes and lower productivity of 330 kg/ha
- Identification of superior accessions in the germplasm collection is required for using them in crop improvement programmes and increasing the productivity levels of cowpea



Objective

- To identify superior cowpea germplasm accessions based on selected quantitative traits

Material and Methods

- Material consisted 147 germplasm accessions maintained in AINP on Arid Legumes, ZARS, GKVK, Bengaluru
- 147 accessions along with two checks (C-152 and KBC-9) evaluated in alpha lattice design with two replications at ZARS, GKVK, Bengaluru

147 germplasm accessions

Documentation of selected quantitative traits

Identification of promising germplasm accessions based on superior quantitative traits



Picture 1: General field view

Statistical Analysis

- Descriptive statistics - Mean, Standard Error, Range
- $SE = \frac{\sigma}{\sqrt{n}}$, σ = Population standard deviation and n = size of population

Results and Discussion

- Based on early flowering time (<45 days from date of sowing) and higher expression than that of check entries, the promising accessions for each of the traits and combination of traits were identified
- Germplasm accession NBC-30 was found to be superior for Days to 50% flowering, primary branch plant⁻¹ pods plant⁻¹ and mean grain yield plant⁻¹
- EC-488480 and V-585 were found to be superior for Days to 50% flowering, pods plant⁻¹ and mean grain yield⁻¹

Sl. no	Traits	Mean ± SE	Range	
			Min	Max
1	Days to 50% flowering	53.07 ± 0.37	46	65
2	Primary branch	1.33 ± 0.059	0	3.2
3	Pods plant ⁻¹	18.79 ± 0.764	5.6	57.08
4	Mean grain yield ⁻¹ (g)	12.52 ± 0.725	9.95	57.05

Table 1: Descriptive statistics for four quantitative traits in cowpea germplasms

Traits	Selection Criterion	Range	Germplasm accession
Days to 50% flowering	Early	<45 days	NBC-30, V-585, EC-458480, NBC-36, IC-402098, VCP-17-019
Primary branch	High	>3	IC-202867(99), IC-402125, IC-402135, IC-402175, NBC-30
Pods plant ⁻¹	High	>40	NBC-30, EC-458480, V-585, EC-472271, PMCP-1131, IC-107120
Mean yield plant ⁻¹ (g)	High	>40	NBC-30, V-585, EC-458480, NBC-36

Table 2: Promising traitspecific accessions in cowpea germplasm

Name of accession	Traits
NBC-30	Days to 50% flowering, primary branch plant ⁻¹ , pods plant ⁻¹ , average grain yield plant ⁻¹
V-585	Days to 50% flowering, pods plant ⁻¹ , average grain yield plant ⁻¹
EC-458480	Days to 50% flowering, pods plant ⁻¹ , average grain yield plant ⁻¹
NBC-36	Days to 50% flowering, average grain yield plant ⁻¹

Table 3: Promising accessions identified for multiple traits in cowpea germplasm

Summary

> Germplasm accessions NBC-30, V-585, EC-458480 and NBC-36 were found to be superior in terms of days to 50% flowering, primary branch plant⁻¹, pods plant⁻¹, average grain yield plant⁻¹ data and these germplasm accessions can preferably suggested for further utilization in breeding programmes

Advisory Committee

Chairman
Dr. Krishna. T. V
Members
Dr. Lohithaswa. H.C
Dr. Papireddy. M
Dr. Palanna. K. B

Reference:

VAIJAYANTHI, P.V., RAMESH, S., BYRE GOWDA, M., RAO, A.M., KEERTHI, C.M. AND CHANDRAKANT, N., 2016, Identification of Trait-Specific Accessions from a Core Set of Dolichos Bean Germplasm. *J. Crop. Sci.* 30(2):244-257.

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4	IC- 198355(45); Best identified accession	27-28
5	EC- 472271; Best identified accession	27-28
6	EC- 394708; Best identified accessions	27-28

INTRODUCTION

I. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important legume grown in India. Vavilov (1951) recognized India and Africa as the origin of cowpea. China is considered a secondary centre of origin. It contains a high amount of quality protein (23.4%), carbohydrate (60.3%), fat (1.8%), sufficient amount of calcium (76mg / 100 gm), iron (57 mg / 100 gm) and vitamins such as thiamine (0.92mg / 100 g), riboflavin (0.18mg / 100 g) and nicotinic acid (1.9 mg / 100 g) (Chatterjee and Bhattacharya, 1986).

Cowpea is a diploid with chromosome number $2n= 22$ and it belongs to the family Fabaceae. The name cowpea was given due to its use as fodder for cows (Timko *et al.*, 2007). Annual cowpea has two botanical variants, the cultivated *Vigna unguiculata* var. *unguiculata* and the wild form *Vigna unguiculata* var. *spontanea*. Cultivated cowpeas have been divided into five cultivar groups based mainly on pod, seed and ovule characteristics (Pasquet, 1999).

Cultivated cowpeas are grown as warm season annuals in tropical and subtropical zones in all countries in sub-Saharan Africa and in Asia, South America, Central America, the Caribbean, the United States and around the Mediterranean Sea. In subtropical zones temperatures are only suitable for cowpea in the summer whereas, temperatures are suitable year-round in tropical zones. About 6.5 million metric tons of cowpea was produced annually on about 14.5 million hectares worldwide. In Sub-Saharan Africa, West Africa is regarded as the major cowpea producing region with 80% of the total regional production reported from Nigeria and Niger at first and second positions, respectively for 14 years in a row (Horn *et al.*, 2022). India has an area of 0.19 million hectares and production of 0.12 million metric tonnes. In India, it is cultivated mainly in Karnataka, Maharashtra and Gujarat.

Cowpea is widely adapted and capable of producing seeds even in low land and semi-arid regions. However, grain yield of this legume varies widely when grown at different locations. It can be grown in a wide range of soil types and environmental conditions. As a pulse crop, it plays a key role in maintaining soil health and sustainability in the production from different cropping systems as it fixes atmospheric nitrogen. On an average, the grain legumes fix 250 to 312 kg nitrogen per hectare per year. In case of cowpea, it fixes about 70 to 240 kg of nitrogen per hectare per year. This ensures the soil fertility as well as reduces the financial burden on poor farmers. It is also considered as a versatile pulse crop because of its smothering nature, drought tolerant characteristics and soil restoring properties.

The majority of present-day cultivars are characterized by lower productivity, non-synchronous flowering and fruiting, non-response to high doses of inputs like fertilizers, irrigation, tillage etc., non-suitability for various cropping systems, lodging, shattering susceptible, long duration, complete or partial absence of genetic resistance to major pests and diseases like mosaics, rust, powdery mildew and bacterial blight, which cause considerable damage and very poor harvest indices. However, some cultivars with early maturity, acceptable grain quality, resistance to some important diseases and pests have significantly increased the yield and cultivated area (Ehlers and Hall, 1997). Collection and evaluation of genotypes of cowpea is a pre-requisite for breeding programme, which provides better scope for exploiting genetic diversity. Information on nature and degree of genetic diversity would assist plant breeders in choosing the best genotypes as parents for hybridization. Yield being a complex trait is influenced by many other important yield contributing characters controlled by polygenes and environmental factors. The necessity for estimating the genetic divergence among the genotypes is more evident because of following two reasons: i) High heterotic effect can be observed if the parents involved in hybridization are diverse. ii) A wide spectrum of variability could be expected in the segregating generation of crosses involving distantly related parents. The magnitude of genetic variance denotes how much of the variability of the characters is heritable and how genetic advance can be achieved. Hence, estimation of genetic variability parameters becomes the initial step in cowpea improvement programmes. It is also important to study the performance of genotypes in more than one environment to estimate the extent of environmental effect on the performance of genotype. Genotype \times environment interaction certainly plays an important role in the evaluation and execution of breeding programmes. Allard and Bradshaw (1964) have critically reviewed this phenomenon and brought out its implications in applied plant breeding. Moreover, multi environment evaluation is important to identify genotypes, which are highly productive over a wide range of environments. Such genotypes will be very useful for utilizing their potentials for the development of high yielding and stable varieties.

With this background the current research was framed with the following objectives,

1. To study the genetic variability for yield and its associated traits
2. To work out the G x E interaction for yield and yield attributes
3. Identification of high yielding cowpea lines

REVIEW OF LITERATURE

II. REVIEW OF LITERATURE

The success of crop improvement depends on the formulation of clear cut objectives and minimizing the errors in the experiment. Information on experiments carried out will aid in conducting research and bringing out the novelty in the present work. The thorough review of the research work already carried out in the proposed area of research is presented under the following heads.

2.1. Genetic variability studies

2.2. Heritability and genetic advance studies

2.3. Clustering studies

2.4. Studies on genotype and environment interactions and stability

2.1. Genetic variability studies

Imran *et al.* (2010) evaluated fourteen lines of cowpea and reported significant variability among the lines. High genetic variability was observed for green fodder yield, leaf area and tendril length, whereas low to medium variability was observed for the rest of the traits studied. Three lines were found to be suitable for obtaining higher green fodder yield, twelve lines were found to be suitable for getting maximum seed yield and two lines could be used for both fodder and seed yield and one line proved to be suitable exclusively for green fodder yield under rainfed conditions of Islamabad.

Adeigbe *et al.* (2011) evaluated ten genotypes of cowpea in different environments to assess their variability and stability and reported that the genotypes differed significantly concerning all the eight phenotypic traits studied. In all three conditions, the number of branches per plant has consistently had the highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The mean proportion of the phenotypic variation due to its genotype was 92.9 *per cent*.

Inuwa *et al.* (2012) studied genetic variability in cowpea germplasm and reported considerable variations among the lines for the duration of the vegetative and reproductive phase and yield characters such as number of pods per plant, pod yield per plant, number of seeds per pod and hundred seed weight.

Manggoel *et al.* (2012) evaluated ten cowpea accessions and observed significant variability for number of days to 50 *per cent* flowering, number of clusters per plant, number of flowers per plant, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and seed yield per plant. The PCV and GCV were high for all the traits studied, except for pod length and the number of seeds per pod.

Vavilapalli *et al.* (2013) studied the genetic variability in 22 bush type cowpea genotypes and the analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all the characters studied. The high PCV and GCV were observed for plant height and pod length. Among the genotypes, VU 6 was the highest seed yielder, whereas the number of pods per plant was highest in VU 8.

Kharde *et al.* (2014) studied the genetic variability in twenty genotypes of cowpea and reported significant differences among the genotypes evaluated for all the characters. The PCV and GCV were higher for plant height, pod length, pod yield per plant and the number of seeds per pod.

Olayiwola and Soremi (2014) evaluated eleven cowpea genotypes and the traits *viz.*, the number of pods per plant, pod yield per plant, seed yield per plant and dry fodder yield per plant showed high PCV and GCV.

Sapara and Javia (2014) investigated 12 traits among 40 genotypes of cowpea and reported significant differences among the genotypes for all the characters studied except pod width, indicating ample variability in the experimental material for all the characters. The estimates of GCV and PCV were high for the number of pods per plant, hundred fresh seed weight, plant height, ten pod weights and green pod yield per plant and the values of PCV were higher than their GCV for all the characters indicating the influence of environmental factors.

Shanko *et al.* (2014) studied 49 cowpea accessions and reported significant variation for all the characters studied. The difference between PCV and GCV values were high for plant height, number of secondary branches per plant, seed yield per plant and the number of pods per plant indicating the influence of the environment on these characters. The difference was low for the number of days to 50 *per cent* flowering, number of days to maturity, number of seeds per pod, number of primary branches, pod length and hundred seed weight, clearly indicating the negligible influence of the environment on expression of these characters.

Vir and Singh (2014) experimented on 33 cowpea accession in two seasons viz. Summer and Kharif of the year 2012. They reported a high degree of genetic variability during both seasons for seed yield per plant, hundred seed weight, pod length, number of seeds per pod, number of pods per plant, number of pods per cluster, number of branches per plant, number of clusters per plant, plant height, number of days to 50 *per cent* flowering and number of days to maturity.

Animasaun *et al.* (2015) experimented on ten cultivars of cowpea and results showed considerable variations in growth and yield characters. Principal components analysis revealed that fruiting and seed characters accounted for 26.63 *per cent* of the observed variation, followed by the vegetative parameters (23.05%) and nutritional variations (13.82%). Proximate results indicated that the crude protein content of seeds varied from 23.42 to 26.78 *per cent*.

Khan *et al.* (2015) conducted a variability study with a set of 196 cowpea genotypes and reported significant differences among the genotypes, PCV values were of higher magnitude than GCV for all the characters studied, the estimates of PCV and GCV were high for the number of pods per plant, pod length, plant height, number of branches per plant, test weight and seed yield per plant.

Udensi and Edu (2015) experimented on thirty accessions of cowpea and revealed that the number of seeds per pod, hundred seed weight, pod length, number of days to 50 *per cent* maturity, seed yield per plant and number of leaves per plant contributed significantly to the total genetic variability.

Khanpara *et al.* (2016) studied sixty diverse genotypes of vegetable cowpea. Higher values of PCV and GCV were observed for green pod yield per plant followed by ten pod weight, the number of pods per plant, plant height, pod length and the number of seeds per pod.

Dinesh *et al.* (2017) conducted a study on a set of 194 F₃ generation genotypes of cowpea and reported moderate PCV and GCV estimates for plant height (15.75% and 12.91%) and number pods per plant (16.29% and 11.42%), respectively.

Lovely and Radhadevi (2017) studied fifty diverse genotypes of vegetable cowpea and reported high GCV for number of pods per cluster, seed yield per plant, number of pods per plant and number of clusters per plant.

Sharma *et al.* (2017) investigated the genetic parameters of ten traits among thirty genotypes of cowpea and reported the least difference between the estimates of GCV and PCV for most of the traits. Higher estimates of GCV and PCV were observed for plant height, the number of primary branches per plant, seed yield per plant and test weight.

Surpura and Sharma (2017) studied variability parameters of 16 traits in 25 genotypes of cowpea and reported significant differences among all the genotypes for all the traits studied. The high GCV and PCV were recorded for traits *viz.*, the number of pods per plant, seed yield per plant, biological yield per plant, hundred seed weight, seedling vigor index, plant height and germination stress index.

Devi and Jayamani (2018) evaluated 180 genotypes of cowpea for 13 biometrical traits. Analysis of variance revealed a significant difference among the genotypes for all the traits studied. The PCV was higher than the GCV for all the traits studied. The high estimates of GCV were found for the traits *viz.*, number of pods per plant, number of clusters per plant, hundred seed weight and seed yield per plant.

Sabale *et al.* (2018) conducted an experiment with 23 F₂ generation genotypes of cowpea and revealed that the PCV was higher than the GCV for all the traits studied. GCV and PCV were high for seed yield per plant, number of pods per plant, number of clusters per plant and number of primary branches per plant, while lowest GCV and PCV were observed for the number of days to first flowering and number of days to maturity.

Nkoana *et al.* (2019) experimented on cowpea accessions reported highly significant differences for the traits *viz.*, number of days to 50 *per cent* maturity and 95 *per cent* maturity, hundred seed weight, leaf area index, number of branches per plant, number of internodes, plant height, number of pods per plant, pod length, dry biomass weight per plant and seed yield per plant.

Verma *et al.* (2019) carried out an investigation to assess the genetic variability of growth and yield traits in the F₂ generation genotypes of 24 hybrids of cowpea. A broad range of variability was reported for all traits except the number of branches per plant and the width of the pod. The high GCV was recorded for the number of pods per plant, the number of pods per cluster and hundred seed weight.

Mofokeng *et al.* (2020) conducted a study to determine the variability among hundred cowpea genotypes and reported that the GCV was relatively higher, while the PCV was

moderate for the total number of branches, the number of seeds per pod and pod yield per plant.

Singh *et al.* (2020) conducted genetic variability studies using 38 accessions of cowpea in two environments *i.e.*, Kharif 2013 and Kharif 2014. Analysis of variance revealed significant differences among the genotypes for all the traits studied. GCV was highest for the number of clusters per plant, followed by the number of pods per plant in both the environments.

Owusu *et al.* (2021) conducted a study on genetic variability and heritability by using 16 advanced breeding lines of cowpea. Among the variance components computed, the σ^2_e , σ^2_g and σ^2_p ranged from 0.02-16.68, 0.13-60.92 and 0.15-77.60, respectively. The broad sense heritability (h^2) had the minimum and maximum estimates of 55.03 % (number of seeds per pod) and 91.52 % (100- seed weight).

Vinay *et al.* (2022) conducted studies on 32 cowpea germplasm and reported high estimates of GCV and PCV 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.

2.2. Heritability and genetic advance studies

Idahosa *et al.* (2010) reported a high broad-sense heritability percentage for all the characters studied except for pod weight, which revealed low estimates of 25.5 *per cent*. The expected genetic advance was relatively high for pod length, the number of seeds per pod and hundred seed weight.

Inuwa *et al.* (2012) experimented on cowpea germplasm and reported that the broad sense heritability estimate (h^2) was 83 *per cent* for hundred seed weight, 53 *per cent* for the number of seeds per pod, 48 *per cent* for the number of days to first flowering and 46 *per cent* for the number of root nodules.

Nwosu *et al.* (2013) studied genetic variability, heritability and genetic advance in five genotypes of cowpea. They reported high heritability along with high GAM for number of pods per plant, peduncle length, pod length, dry pod weight, hundred seed weight, number of seeds per pod and seed yield per plant indicating that these traits were controlled by additive gene action and could be dependable for seed yield improvement.

Thorat and Gadewar (2013) experimented on 30 genotypes of cowpea and reported high heritability coupled with high genetic advance for the characters *viz.*, plant height, number of pods per plant and number of branches per plant.

Vavilapalli *et al.* (2013) experimented on 22 diverse genotypes of bush cowpea and reported high heritability coupled with high genetic advance for all the characters studied, except for the number of days to first flowering and number of days to first harvest.

Ajayi *et al.* (2014) conducted a study on ten genotypes of cowpea for 20 quantitative traits. Results revealed high broad-sense heritability values for all the traits studied and moderate values for plant height, indicating that these traits are less influenced by environmental effects.

Chattopadhyay *et al.* (2014) studied sixty genotypes of vegetable cowpea and reported high to moderate GCV and PCV values and higher estimates of broad-sense heritability coupled with higher genetic advance for the traits *viz.*, the number of pods per plant, pod yield per plant, pod length and the number of seeds per pod.

Olayiwola and Soremi (2014) evaluated eleven cowpea genotypes and recorded high heritability values for the number of pods per plant, hundred seed weight and dry fodder yield per plant. The genetic advance was high for seed yield per plant, pod yield per plant and dry fodder yield per plant. All traits had high GAM except for the number of days to 50 *per cent* flowering and the number of seeds per pod.

Sapara *et al.* (2014) investigated 12 traits among 40 genotypes of cowpea and reported high heritability along with high GAM for the number of pods per plant, hundred fresh seeds weight, ten pod weight, green pod yield per plant and plant height indicating scope for improvement by selection.

Shanko *et al.* (2014) experimented on 49 accessions of cowpea and reported high estimates of broad-sense heritability and high genetic advance for the characters *viz.*, seed yield per plant, number of pods per plant and hundred seed weight.

Vir and Singh (2014) evaluated 33 indigenous and exotic accessions of cowpea. The moderate to high heritability coupled with moderate to high expected genetic advance were observed for the traits *viz.*, seed yield per plant, hundred seed weight, pod length, number of seeds per pod, number of pods per plant, number of pods per cluster, number of branches per

plant, number of clusters per plant, plant height, number of days to 50 *per cent* flowering and number of days to maturity.

Khan *et al.* (2015) conducted a study on 196 cowpea genotypes and reported high heritability and high GAM for number of pods per plant, number of seeds per pod, pod length, plant height, number of branches per plant, test weight and seed yield per plant.

Kumar *et al.* (2015) investigated 49 genotypes of cowpea and reported high heritability and high GAM for the traits *viz.*, plant height, number of secondary branches per plant, number of clusters per plant, number of pods per plant and hundred seed weight.

Meena *et al.* (2015) experimented on 72 genotypes of cowpea for ten quantitative characters. High estimates of heritability and high GAM were recorded for hundred seed weight and plant height, while high heritability and moderate GAM were recorded for pod wall proportion, seed yield per plant and pod length.

Khanpara *et al.* (2016) experimented on sixty diverse genotypes of vegetable cowpea and reported high heritability along with high genetic advance for the characters *viz.*, plant height, green pod yield per plant, 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.

Dinesh *et al.* (2017) conducted a study on a set of 194 F₃ generation genotypes of cowpea and reported high heritability coupled with high genetic advance as *per cent* of the mean (GAM) for plant height (67.13% and 21.78%) and moderate heritability and GAM for number pods per plant (49.14% and 16.49 %), respectively.

Lovely and Radhadevi (2017) studied fifty diverse genotypes of vegetable cowpea. They revealed that the characters *viz.*, number of clusters per plant, number of pods per cluster, number of pods per plant, number of primary branches per plant, pod yield per plant, pod weight, pod length, number of seeds per pod and main stem length had high heritability coupled with high genetic advance. In contrast, high heritability and the low genetic advance was noted for the number of days to 50 *per cent* flowering and pod width.

Phogat *et al.* (2017) conducted a study on thirty fodder cowpea genotypes and reported high heritability coupled with high GAM for dry fodder yield per plant, number of days to 50 *per cent* flowering, number of branches per plant, leaf to stem ratio and green fodder yield per plant.

Sharma *et al.* (2017) investigated sixty genotypes of cowpea to study genetic parameters of sixteen traits and reported high heritability with high genetic advance for hundred seed weight followed by plant height, biological yield per plant, seed protein content, number of primary branches per plant and number of pods per plant.

Devi and Jayamani (2018) evaluated 180 genotypes of cowpea for thirteen quantitative traits and reported high heritability values for plant height, number of days to 50 *per cent* flowering, number of racemes per plant, peduncle length, number of pods per plant, number of clusters per plant, pod length, hundred seed weight and seed yield per plant.

Sabale *et al.* (2018) observed high heritability coupled with high genetic advance for the traits *viz.*, seed yield per plant, number of pods per plant, plant height, number of primary branches per plant, hundred seed weight and harvest index in 23 genotypes of cowpea which represents the additive gene action and can be effectively used for selection.

Verma *et al.* (2019) carried out an investigation to assess the heritability and expected genetic advance for growth and yield traits in the F₂ generation of 24 hybrids of cowpea. Higher heritability estimates coupled with high GAM were observed for plant height, number of branches per plant, number of flowers per cluster, number of pods per cluster, *per cent* of pod set, number of days to final harvest, pod length, number of seeds per pod, hundred seed weight and pod yield per plant.

Mofokeng *et al.* (2020) conducted a study to determine the heritability and genetic advance among a hundred cowpea genotypes, and the results revealed that the heritability and genetic advance values ranged from 37.27 to 97.2 *per cent* and 73.3 to 2242.6 *per cent*, respectively, for the traits studied.

Singh *et al.* (2020) conducted a study on 38 accessions of cowpea and reported high broad-sense heritability along with high genetic advance for seed yield per plant, hundred seed weight, pod length, peduncle length, number of clusters per plant, number of pods per plant and plant height.

Moderate to high narrow sense heritability and broad sense heritability coupled with high genetic advance were observed in GDVC-2 × LC-1 and GC-6 × LC-1 crosses of cowpea for seed yield per plant, harvest index, number of pods per plant and plant height was reported by Shinde *et al.* (2021).

Singh *et al.* (2022) reported that on the basis of the performance of 36 genotypes of cowpea, the trait like TSS (⁰Brix), pod yield (q/ha), pod yield per plot (kg), pod yield (gm) per plant, pod weight (g), 100 seed weight, number of seeds per plant, length of the pod (cm), no. of nodes per plant on the main stem, number of pods per plant and number of branches per plant were found with high heritability coupled with high genetic advance.

2.3. Clustering studies

Vishwanathan *et al.* (1998) grouped 72 cowpea genotypes into 5 clusters with the highest inter cluster distance between cluster III and IV (2818.82). Out of seven traits studied, 100 seed weight contributed maximum (33.5%) to the divergence.

Ushakumari *et al.* (2000) studied fifty genotypes of cowpea and grouped into thirteen clusters by Mahalanobis D² statistics. The genotypes IT-86-F-310-6 and IT-87-0-272 had distinct identity with respect to yield attributes. Among the yield attributing characters, seeds per pod, number of branches, number of pods per cluster and pod length were the important traits responsible for the divergence recorded.

Borah and Khan (2001) grouped 60 cowpea cultivars into 10 clusters and noticed that based on inter cluster distance and cluster means for 13 characters, cluster I, cluster II, IX and X were the most genetically diverse. Dry matter yield, green fodder yield and plant height recorded the highest contribution to the total divergence, suggesting that these traits are good criterion for the selection of parents in hybridization programme.

Venkatesan *et al.* (2004) reported clusters per plant, pods per clusters, pods per plant and seed yield per plant contributed maximum towards the total divergence.

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

Sulnathi *et al.* (2007) assessed 56 genotypes of cowpea for thirteen yield contributing characters showed grouping of genotypes into nine clusters. Cluster I had the maximum number of genotypes. Characters *viz.*, days to maturity, 100-seed weight and days to

flowering were the highest contributors to D^2 values. The geographical diversity was not related to genetic diversity.

Dalsaniya *et al.* (2009) grouped 60 genotypes of cowpea into 12 clusters. Inter cluster distance and mean cluster character values indicated that hybridization of cluster X variety (JCPL-134) with cluster IV varieties (JCPL-1, JCPL-13 and JCPL-21) and cluster V varieties (JCPL-50 and JCPL-133) with cluster III varieties (JCPL-26 and JCPL-131) would exhibit high heterosis and also results in transgressive segregants with higher yield. The characters like plant height, green pod yield per plant, protein content and leaf area were found to contribute much to the total genetic divergence in cowpea.

Nagalakshmi *et al.* (2010) studied 66 genotypes of cowpea that formed 23 clusters. Cluster I had the maximum number of genotypes *i.e.* 22 and cluster XXIII had only one genotype. Intra cluster distance analysis revealed that the minimum intra cluster distance was observed in the cluster II. The inter-cluster distance (D) was found to be the maximum between the clusters XXII and XXIII and the same was minimum between clusters II and V. The results indicated that grain yield per plant contributed maximum to the total divergence followed by 100 seed weight and days to 50% flowering. Number of branches per plant had least contribution to the total divergence followed by petiole length. The existence of wide genetic diversity among the types chosen from the same geographical location was obviously seen. The cluster XVIII had the highest cluster mean values for number of clusters per plant and the cluster XIV had the highest mean value for grain yield per plant. These two clusters may be utilized in crossing programme which may yield in a wide spectrum of variability and for selection for seed yield in the subsequent generations. The clustering pattern of the varieties in the present study clearly indicated that there was no parallelism between genetic and geographic diversities.

Huque *et al.* (2012) determined genetic divergence among 13 commercial yard long bean cowpea genotypes to select the parents for hybridization using Mahalanobis D^2 statistics. Cluster analysis was used for grouping 13 yardlong bean genotypes. The genotypes fall into four clusters. Cluster III had the maximum (5) and cluster I had the minimum (1) number of genotypes. Cluster III ($D^2 = 1.439$) had highest intra-cluster distance and the lowest in cluster I ($D^2 = 0.000$). The inter-cluster divergence ranged from 4.160 to 15.515 between clusters II and III and clusters I and II, respectively. The characteristics *i.e.* number of pods per plant, number of pods per cluster, days to first flowering, and vegetable pod yield per plant contributed maximum towards divergence among yardlong bean genotypes.

Tigga and Tandekar (2013) revealed the genotypes were grouped into four non overlapping clusters showed genetic diversity rather geographical diversity. The maximum intra cluster distance (3.377) was obtained for cluster I followed by cluster III (2.795) and cluster II (2.014). The lowest intra cluster D^2 value was shown by cluster IV (0.000) which had only one genotype belonging to the cluster. The highest inter cluster D^2 values were observed between cluster I and cluster IV (8.045) followed by cluster III and IV (7.925), cluster II and cluster IV (7.086) and cluster II and cluster III (4.864). The lowest inter cluster was found between cluster I and cluster III (3.548) followed by cluster I and cluster II (4.151). Thus, inter-crossing of genotypes from different clusters showing superior mean performance may help in obtaining higher yields. Genotypes belonging to cluster I may produce better heterosis and segregants with the genotypes of cluster III and IV.

Ahamed *et al.* (2014) carried out multivariate analysis to assess genetic diversity among 11 genotypes of cowpea. Considering the mean values, the germplasm was grouped into 4 clusters. Cluster III included maximum number of genotypes (4), whereas clusters II and IV included minimum number of genotypes (2). Highest inter-cluster distance was obtained in between cluster IV and II, while lowest cluster distance was obtained between cluster II and I. Maximum value of cluster distance indicated greater divergence among the cluster IV and II.

Meena *et al.* (2015) evaluated 72 genotypes of cowpea for exploitation in a breeding programme aimed at improving yield potential of cowpea by using D^2 statistics. The intra cluster D^2 value ranged from 0.00 to 43.96 while Inter cluster D^2 value ranged from 30.9 to 375.97 indicated that the selected genotypes were highly divergent. The maximum intra cluster distance was recorded for cluster IV (43.96) while cluster III and IX (0.00) showed no intra-cluster distance values revealed homogenous nature of the genotype within the cluster. The genetically more divergent genotypes present in cluster V and VIII as indicated by inter cluster distance value (375.97). Inter cluster D^2 value and mean cluster values for characters indicated that hybridization of clusters VIII with clusters V genotypes would result in marked heterosis and produce better segregants with improved yield. Among the characters studied, seed yield per plant (38.81%) contributed highest towards genetic divergence followed by 100 seed weight (29.07%). Selecting parents of these clusters probably provide promising recombinants and better segregants for future breeding strategy.

Chandrakar *et al.* (2016) studied genetic diversity among 21 genotypes of vegetable cowpea. The genotypes showed low quantum of divergence and grouped into five clusters.

Maximum number of genotypes (9) was accommodated in cluster - II. The average inters and intra cluster divergence (D) values had also been calculated. The intra-cluster distance varied from 0.00 to 5.04. The maximum intra cluster distance was shown by cluster I (5.04) followed by cluster V, cluster II, cluster III and cluster IV. The maximum inter cluster distance was observed in between cluster I and V (5.04). The cluster III showed maximum value for mean green pod yield (146.820g.) followed by cluster IV (146.156g). Crossing between the genotypes of maximum two clusters appeared to be most promising to combine the desirable characters.

Patel *et al.* (2017) evaluated 32 cowpea genotypes to estimate the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into eight clusters. The cluster strength varied from 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 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 the cluster III had a lowest mean value for days to 50 *per cent* flowering. On the basis of inter cluster distances, cluster VIII was found to be more divergent. Therefore, it was concluded that the genotypes belonging to these cluster should be inter-crossed in order to generate more variability.

Singh *et al.* (2018) evaluated 38 accessions of cowpea during kharif 2013 (E1) and Kharif 2014 (E2). The genotypes were grouped into ten clusters in E1 and into five clusters in E2 environment. In E1 environment, the cluster strength varied from single genotype (Cluster III, IV, V VI, VIII, IX and X) to 16 genotypes (Cluster II), while in E2 environment, it varied from single genotype (Cluster III, IV and V) to 19 genotypes (cluster I). Clusters VII and X had highest inter cluster distance in E1 and cluster II and III had highest inter-cluster distance in E2 environment. The maximum mean value for seed yield per plant, number of pods per plant and number of clusters per plant was showed by genotypes of clusters VII in E1 environment and by genotypes of cluster IV for the traits number of seeds per pod, pod length and plant height in E2 environment. On the basis of inter-cluster distances, cluster VII and X in E1 environment and cluster II and III in E2 environment were found to be most divergent. Cluster VII had the genotype with the highest

Purohit *et al.* (2020) studied 42 genotypes including five checks, Pant Lobia 1, Pant Lobia 2, Pant Lobia 3, Pant Lobia 4 and Pant Lobia 5 of grain cowpea at Breeder Seed Characterization of germplasm for yield and it's associated traits in cowpea [*Vigna unguiculata* (L.) Walp] 14

Production Centre to estimate genetic divergence. Analysis of variance showed the presence of significant amount of variability in all the characters studied. Genetic divergence was performed by D^2 statistics. Genotypes were divided into 8 clusters. Maximum inter-cluster distance was observed between cluster VI and VII while maximum intra-cluster distance was observed in cluster V. Mean values of different characters between different clusters was observed maximum for number of seeds per pod. Inter-cluster distance was higher than intra-cluster distance. Three genotypes were identified as the most diversified and could be utilized in future crop improvement programmes.

2.4. Studies on genotype and environment interactions and stability

A specific genotype does not exhibit the same genotypic characters including yield in all environment. The failure of genotype to give the same phenotypic performance when tested under different environment is the reflection of genotype environmental interaction. $G \times E$ interaction are of major importance to the plant breeder to develop stable variety (Eberhart and Russel, 1966).

Yield in cowpea is the result of many interacting yield components such as number of clusters per plant, pods per plant, and mean seed weight. Yield and its components are affected by various factors including phenological development, planting date, genotypic differences and the environment (Gardener *et al.*, 1985).

Hanumanthraya (2003) evaluated twenty elite lines of cowpea over three locations and concluded that the genotype C-232 was the only genotype found suitable with higher mean value for grain yield. The genotype C-120 showed higher mean value for yield and stability along with adaptability to favourable environments ($b_i > 1$) whereas C-203 possessed stability with lower mean yield and significantly lower b_i value indicating its adaptability to less favourable environments.

Similar results were obtained by Ali *et al.* (2004) based on evaluation of five cowpea genotypes at five different locations. The results showed that varieties, environment and varieties \times environment showed significant differences. Significant and highest seed yield (880 kg ha⁻¹) was observed in NIAB cowpea mutant-1 followed by Elite (729 kg ha⁻¹). The highest yielding genotypes *i.e.*, NIAB cowpea mutant-1 and Elite showed non-significant differences of regression coefficient from unity. These genotypes also exhibited non-significant difference of standard deviation to regression from zero. Based on three

parameters *i.e.*, high mean seed yield, regression coefficient and standard deviation to regression, these genotypes showed excellent and trustworthy stable performance over different environment.

Akande (2007) studied the grain yield and number of days to 50 *per cent* flowering of nine cowpea varieties over four locations within the forest and southern guinea savanna agro-ecologies of Nigeria. Five cowpea varieties were identified to be stable for grain production across locations.

Aremu *et al.* (2007) assessed the $G \times E$ interaction of ten genotypes of cowpea which were grown in four environments comprising the early and late seasons of Ogbomoso and Abeokuta locations. The results showed that regression coefficient for each genotype differed significantly from each other suggesting that the genotypes responded differently to the seasons and the locations. The regression coefficient revealed that IT 97K-499-39, TVX-3236, AGRIBVI, Owode and Ife-brown were environment insensitive and could be cultivated in the early and late seasons.

The grain yield components of eleven cowpea genotypes were studied in 2006 and 2007 by Adewale *et al.* (2010) to understand the sensitivity of the quantitative traits to heterogeneous environments. Results revealed that days to 50 *per cent* flowering, 100 seed weight and pod yield were significantly ($p \leq 0.05$) influenced by the effect of genotype, year and their interactions. IT 97K-499-35, IT 97-568-18 and IT 95K-2011-11 were identified as the genotypes with high productivity and good genetic stability for pod yield, number of seeds per pod and 100 seed weight, respectively.

Nelia (2013) reported that there were no significant interactions among the genotypes and the environments ($G \times E$), indicating that genotypes did not respond differently to varying environmental conditions. However, there was variability in the main effects which are genotypes (G) and environments (E).

El-Shaieny *et al.* (2015) concluded that the interaction between genotypes and environments ($G \times E$) were non-significant for pod length, hundred seed weight and weight of pods per plant, indicates stability of the studied genotypes for these characters across the environments.

Gabriel *et al.* (2015) evaluated twenty nine cowpea genotypes, including four Ugandan genotypes for grain yield and adaptability under diverse environments. The analysis

showed that cowpea grain yield was significantly ($p < 0.01$) affected by genotypes (G), environments (E), and interaction ($G \times E$). Genotype C-2T has the highest grain yield but it was adapted to specific environment. Genotypes C-1J, C-1V, C-2A, C-2O, and C-2R were adapted to three environments with high yield which was stable.

Similar results were obtained by Olayiwola *et al.* (2015) based on evaluation of seven improved cowpea genotypes in four environments during the late seasons of 2009, 2010, 2011 and 2012. Results revealed that there was highly significant genotype \times environment interaction on seed yield ($p < 0.001$) indicating the need for $G \times E$ interaction analysis. Genotypes IT 04K-227-4, IT 04K-333-2, IT 98K-573-1-1 and IT 98K-573-2-1 were identified to have performed above average while IT99K-1060, LDP10-OBR1 and IFE-98-12 yielded below average. LDP10-OBR1 was the most stable genotype but was low yielding.

Olawale and Bukola (2016) reported that twenty-one cowpea breeding lines were evaluated for phenotypic stability for seed yield components for two years (2013 and 2014). Results confirmed that all the yield components exhibited significant genotypic variation, while flowering, pod maturity and seed yield traits recorded significant variation for years and its interactions. The genotypes exhibited relative phenotypic stability for the yield components across years except for seed yield. Six cowpea lines (IT 10K-837-1, IT 07K-299-6, IT 10K-815-5, IT 10K-817-7, IT 08K-150-24 and IT 11K-61-82) with multiple quality yield traits were identified as stable genotypes over two years.

Torres *et al.* (2016) conducted six trials of different cowpea genotypes in 2005 and 2006 with the aim of selecting erect cowpea genotypes simultaneously for high adaptability, stability and grain yield. Results confirmed that MNC99542F-5 and MNC99-537F-4 genotypes could be grown in various environments, as they exhibited high grain yield, adaptability and stability.

Agbahoungba *et al.* (2017) assessed 72 cowpea genotypes for yield in three locations and two seasons and assesses the extent of genotype \times environment interaction and selected the stable cowpea genotypes. The yield data were subjected to analysis of variance and additive main effects and multiplicative interactions (AMMI) analysis. The results showed a highly significant ($P < 0.001$) genotype by location and by year (season) interaction effects for grain yield, with 69.16% of the total variation attributable to environmental effects, 5.36% to genotypic effects and 12.74% to $G \times E$ interactions effects.

Tariku *et al.* (2018) conducted a study to evaluate the stability of cowpea genotypes and to estimate the magnitude of genotypes by environment interaction (GEI) effect on grain yield using 16 genotypes in 7 environments. Considering all stability parameters, viz; deviation from regression ($S^2 d_i$), coefficient of regression (b_i) from ER's model, IPCA1, IPCA2 and AMMI stability value (ASV) from AMMI model, GGE biplot and variety TVU was identified as the most stable with mean yield above the mean grain yield of genotypes.

The study conducted in 3 locations over 2 years by Kuruma *et al.* (2019) showed that, genotypes G5, G7 and G3 high stability while G10 and G1 depicted least stability with poor performance.

Gerrano *et al.* (2020) evaluated fifteen cowpea accessions at three locations during 2016 and 2017 growing seasons. The analysis of variance showed significant effects for genotype, location and season on grain yield. The genotype \times location interaction effects were not significant for grain yield. The three-way interaction involving genotype, location and season was significant for grain yield.

Kindie *et al.* (2021) conducted the study at six environments, twenty-four cowpea landraces and one check were evaluated in a 5×5 triple lattice during the 2019 cropping season. The analysis of variance for each environment and across environments showed significant differences among genotypes, environments, and genotype environment interaction for most traits including yield. Environment, genotype, and genotype environment interaction showed 27.45%, 20.9%, and 49.55% contribution to the total sum of squares, respectively, for grain yield. This indicated that the environments were diverse and most of the variation in grain yield was caused due to interaction and environmental means.

MATERIAL AND METHODS

III. MATERIAL AND METHODS

Detailed information about the materials used in the current investigation, the site of the experiment, methods followed for recording observation of various characters, statistical tools used for the analysis of data is discussed in this chapter.

3.1 Experimental site

All the experiments of the research work were carried out in the experimental blocks situated at Zonal Agricultural Research Station (ZARS), GKVK, Bengaluru (E1), Agriculture Research Station, Pavagada (E2) and ZARS, V.C. Farm Mandya (E3) which belongs to zone 5 (eastern dry zone), zone 4 (central dry zone) and zone 6 (southern dry zone) of Karnataka. ZARS, GKVK is located at an altitude of 930 meters above mean sea level (MSL), 12° 58' North latitude and 77° 35' East longitude; ARS, Pavagada is located at 14° 5' N latitude, 77° 05' E longitude and Altitude of 768 meters from MSL and ZARS, V.C. Farm Mandya is situated at 19° N latitude and 76° E, longitude and at an altitude of 695 meters above MSL.

3.2 Experimental material

The experimental material consisted of 147 Cowpea [*Vigna unguiculata* (L.) Walp.] germplasm including two checks [KBC-9 and C-152]. The cowpea germplasm was collected from All-India Network Research Project on Arid Legumes (AINP on Arid Legumes) at the Zonal Agricultural Research Station, GKVK, Bengaluru. The details of the genotypes used in the present investigation are presented in Table 1.

Table 1: List of the 147 germplasm accessions.

Sl. No.	Accession name	Sl. No.	Accession name	Sl. No.	Accession name
1	VCP-17-019	16	IC-1070	31	IC-206240
2	IC-253251	17	IC-402164	32	IC-202792(72)
3	GC-3	18	IC-198355(45)	33	IC-402135
4	EC-458511	19	IC-402106	34	IC-402104
5	NBC-8	20	IC-1071	35	IC-249588
6	IC-202867(99)	21	IC-25105	36	IC-202781
7	IC-603187	22	IC-402172	37	IC-202777
8	IC-462099	23	IC-458430	38	IC-402162
9	IC-402048	24	IC-58905	39	IC-402175
10	IC-249141	25	IC-330996	40	IC-202711(58)
11	IC-422174	26	IC-202325	41	IC-10171
12	IC-249593	27	IC-237422	42	IC-202290
13	IC-4506	28	IC-45061	43	IC- 2574422(7)
14	IC-198326-38	29	IC-219489	44	IC-402161
15	IC-402125	30	IC-402159	45	IC-402101

Sl. No.	Accession name	Sl. No.	Accession name	Sl. No.	Accession name
46	IC-402098	80	EC-458473	114	KBC-2
47	IC-402114	81	EC-075180	115	CPD-331
48	IC-107120	82	V-16	116	PMCP-1016
49	IC-202521(93)	83	EC-472250	117	PCD-1124-1
50	IC-27749(20)	84	EC-458490	118	KM-5
51	IC-201095(32)	85	EC-458483	119	NBC-40
52	IC-202854(97)	86	EC-458411	120	NBC-43
53	IC-202329-89	87	EC-390287	121	GWHOPE
54	EC-394838	88	EC-458425	122	GC-1801
55	EC-458469	89	EC-170604	123	NBC-41
56	EC-458505	90	EC-472267	124	GC-1805
57	EC-458470	91	EC-394839	125	NBC-4716
58	EC-458440	92	NBC-51	126	C-457
59	EC-170574-6	93	NBC-391	127	CPD-15
60	EC-458485	94	NBC-30	128	GC-1602
61	EC-271040	95	NBC-23	129	CB-10
62	EC-472252	96	NBC-32	130	C-33
63	EC-458442	97	NBC-98	131	IT-9715499-38
64	V-604-7-29-3	98	NBC-68	132	NBC-25
65	EC-472257	99	NBC-36	133	C-157
66	EC-458489	100	NBC-6	134	C-24-1
67	EC-170584-1.1	101	NBC-38	135	CP-98
68	EC-472271	102	NBC-33	136	CPD-340
69	EC-402159	103	TPTC-29	137	SKUA-WCP-49
70	EC-492292	104	NBC-18	138	NBC-44
71	V-578	105	NBC-27	139	NBC-24
72	V-585	106	NBC-29	140	EC-394779
73	V-589	107	NBC-19	141	IC-2591054
74	VCP-18-032	108	TOME-774	142	IC-402090
75	CB-1024	109	PCP-0306-1	143	NBC-7
76	IC-458492	110	PMCP-1131	144	EC-458438
77	V-240	111	NBC-14	145	EC-458418
78	IC-402166	112	NBC-016	146	EC-458480
79	EC-394708	113	SUPER-30	147	IC-202804(83)

3.3 Experimental plot layout

A total of 147 germplasm accessions were evaluated along with two checks, which were repeated to fit in α -lattice design with two replications with 13 blocks and 12 entries in each block. Spacing of 0.15m between plants and 0.45m between the rows was followed. Evaluation was carried out during summer 2022 at ZARS, Bengaluru; ARS, Pavagada and ZRAS, V.C. Farm Mandya

3.4 Observations recorded

Observations on different yield and yield contributing traits were recorded on five randomly selected plants. Five plants in each line of the checks excluding the border plants in each row were considered. The procedure carried out for recording observations on these plants is described below.

1. **Days to 50 per cent flowering:** The number of days taken for the flowering of 50 per cent plants in a genotype from the day of sowing was recorded.
2. **Plant height (cm):** The height of the plant from the ground level of the main axis to the apical leaflet was measured before harvesting and expressed in centimetres.
3. **Primary Branches:** Total number of branches arising from the main stem was recorded as primary branches.
4. **Clusters plant⁻¹:** The number of clusters in each plant was counted and expressed as the total number of clusters per cluster.
5. **Pods cluster⁻¹:** Total number of pods produced in each cluster were counted and the average was considered as pods per plant.
6. **Pods plant⁻¹:** Total number of pods in each plant was counted and recorded as pods per plant.
7. **Average pod length (cm):** Mean of five randomly selected mature pods were measured in centimetres and noted as average pod length.
8. **Average seeds pod⁻¹:** Seeds present in five randomly selected pods in each plant were counted and the average was noted as average seeds per pod.
9. **100 seeds weight (g):** Randomly selected 100 seeds were weighed in grams and recorded.
10. **Average grain yield plant⁻¹ (g):** Seeds from five randomly selected plants were weighed in grams, averaged and recorded as average grain yield per plant.

3.4 Statistical analysis:

The mean values of observations recorded on five plants were computed and mean values for each germplasm were used in statistical analysis through the computer using Microsoft excel and R software version 4.0.5 program at the Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru. Statistical methods used for different analysis are explained below

3.4.1. Estimates of descriptive statistics and genetic variability parameters:

- **Mean** = $\sum \frac{X_i}{n}$

Where, x_i = i^{th} observation of a population; n = number of observations

- **Range:** Range was calculated as difference between minimum and maximum value recorded for each character on individual plant.

- **Standard Error (SE)** = $\frac{SD}{\sqrt{n}}$

Where, SD = standard deviation; n = number of observations.

- **Genotypic coefficient of variation (GCV):** $\sigma_g / \bar{x} \times 100$
- **Phenotypic co-efficient of variation (PCV):** $\sigma_p / \bar{x} \times 100$

Where,

σ_p = phenotypic standard deviation

σ_g = genotypic standard deviation

\bar{x} = mean

PCV and GCV were classified as follows (Robinson *et al.*, 1949)

0-10	Low
10.1-20	Medium
>20	High

- **Heritability in broad sense ($h^2_{(bs)}$)** (Lush, 1945).

$$h^2_{(bs)} = \frac{\sigma_g^2}{\sigma_p^2}$$

Where,

$h^2_{(bs)}$ = heritability (Broad sense) expressed in *per cent*

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

As given by Robinson *et al.* (1949), heritability was categorized as

0-30	Low
30.1-60	Medium
>60	High

- **Genetic Advance** (Allard, 1960)

$$GA = H \times \sqrt{\sigma_p^2} \times K$$

H = Heritability coefficient

σ_p = Phenotypic standard deviation

K = Selection differential in the standard units which is 2.06 at 5 *per cent* selection intensity

- **Genetic Advance as *per cent* mean (GAM)** (Johnson *et al.*, 1955)

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

GA = genetic advance

\bar{X} = mean of trait

GAM will be categorized as follows:

0-10	Low
10.1-20	Medium
>20	High

3.4.2. α – lattice design analysis

Patterson and Williams (1976) described a new way to construct cyclic, resolvable incomplete block designs, (α -designs) available for many (r,k,s) combinations. This design allows the adjustment of treatment means for block effects. This helps in varietal comparison under mere homogeneous conditions. It also provides effective control within replicate variability.

Table 2. Structure of alpha lattice ANOVA:

Source of variation	Degrees of freedom (df)	Sum of squares (SS)	Mean sum of squares (MSS)	F-ratio
Replication	(r-1)	RSS	RMSS	RMSS/EMSS
Blocks	(rs-r)	BSS	BMSS	BMSS/EMSS
Treatments	(t-1)	Tr.SS	Tr. MSS	Tr. MSS/EMSS
Error	rt-rs-t+1	ESS	EMSS	-
Total	(tr-1)	TSS	-	-

t - number of treatments, r - number of replications, s - number of blocks

3.4.3. Clustering of genotypes using k-means clustering

The inbred lines were classified following model-based ‘k means’ clustering approach (Macqueen, 1967) to unravel organization of variability using “*Factoextra*” package in R software programme *Ver 4.1.1*. The trait means were estimated in each cluster using the formula,

$$J = \sum_{i=1}^m \sum_{k=1}^k \omega_{ik} \|X^2 - \mu_k\|^2$$

Where,

$\|X^2 - \mu_k\|^2$ – indicator of distance between n data point from their respective cluster centre.

x_i - number of data points

μ_k - number of cluster center

3.4.4. Stability analysis using Additive main effects and multiplicative interaction (AMMI) model

The quantitative traits mean of each genotype were also subjected to ANOVA following additive main effects and multiplicative interaction (AMMI) model (Gauch and Zobel, 1988) to detect and characterize the patterns of genotype and environment interaction. The additive main effects of genotypes and environment were fitted by univariate ANOVA followed by fitting genotype and environment interaction by principal component (PC) analysis by the following AMMI II model (Table 5).

$$y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where, Y_{ij} is the quantitative trait value of i^{th} genotype in the j^{th} environment, μ is the experimental quantitative trait mean value, g_i and e_j are the i^{th} genotype and j^{th} environment mean deviation from experimental quantitative trait mean values respectively. λ_k is the square root of eigen value of the k^{th} IPC axis, α_{ik} and γ_{jk} are the interaction principal component (IPC) scores for k^{th} IPC of the i^{th} genotype and j^{th} environment, respectively and ε_{ij} is the residual. The parameters of AMMI II model were estimated using the least square principle implemented by R software.

Table 3. Structure of AMMI ANOVA

Sources of variation	Degrees of Freedom	Mean sum of squares	'F' Ratio	% Variation
Genotype (G)	G-1	GMSS	GMSS/eMSS	(GSS/TSS) *100
Environment(E)	E -1	EMSS	EMSS/eMSS	(ESS/TSS) *100
G × E	(G-1) (E -1)	GEMSS	GEMSS/eMSS	(GESS/TSS) *100
IPC 1	G + E – 1-2n	IPCA1MSS	IPCA1MSS/eMSS	(IPCA1SS/GESS) *100
IPC 2	G+ E – 1-2n	IPCA2MSS	IPCA2MSS/eMSS	(IPCA2SS/GESS) *100
Residual	(G-1) (E-1)- {df PCA1 + df PCA2 +... + PCAn}	RMSS	RMSS/eMSS	(RSS/TSS) *100
Error	-	eMSS	eMSS	eSS

Visual and objective criteria were used to interpret GEI patterns of a genotype and their specific/wide adaptation. The visual criterion was based on Genotype + Genotype × Environment (GGE) bi-plot (Yan *et al.*, 2000). The objective criterion was based on the estimates of AMMI stability value (ASV) (Purchase, 2000) and Stability Index (SI). These two criteria are described in the following sections.

- **GGE bi-plot analysis**

GGE bi-plot methodology, which is a combination of AMMI bi-plot and GGE concepts (Yan *et al.*, 2000) was used for visual interpretation of patterns of GEI. The GGE bi-plot is based on the following model.

$$Y_{ij} - Y_i = \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}$$

Where, Y_{ij} = quantitative trait means of i^{th} genotype in the j^{th} environment; Y_j = quantitative traits mean of all the genotypes in the j^{th} environment; λ_1 and λ_2 are the square root of eigen values of first and second genotype-by-environment interaction principal components (IPC) axes, respectively; α_{i1} and α_{i2} are the scores of the first and second IPC, respectively for the i^{th} genotype, γ_{j1} and γ_{j2} are the first and second IPCs respectively for its environment.

There are numerous ways to use a GGE bi-plot. However, four views of the GGE bi-plot are most relevant (Segherloo *et al.*, 2010). These are (1) Polygon view of GGE bi-plot based on symmetrical scaling for determining ‘which-won-where’ pattern of genotypes with test environments, (2) Discriminative and representativeness of test environments view of GGE bi-plot, (3) Average-environment coordination (AEC) view of GGE bi-plot based on genotype-focused scaling for ranking of the test genotypes relative to ideal genotype; the ideal genotype is the one whose point is located in the center of concentric circles in the GGE bi-plot and (4) AEC view of bi-plot based on environment-focused scaling for interpreting the mean performance of the genotypes vs. their adaptability patterns.

- **AMMI stability value (ASV)**

To facilitate an objective method of identifying genotypes with stable performance across different locations, the ASV was estimated (Purchase *et al.*, 2000).

$$ASV = \sqrt{\frac{SSIPCA1}{SSIPCA2} (IPCA1)^2 + (IPCA2)^2}$$

Where, the sum of squares (SS) attributable to the first two IPCs are SSIPCA 1 and SSIPCA 2. ASV is conceptually defined as the distance from zero on a two-dimensional scatter diagram of IPCA 1 vs. IPCA 2 scores (Purchase., 2000). Because the IPCA 1 score contributes more proportionately to GEI, it is weighted by the proportional difference between the IPCA 1 and IPCA 2 scores to account for the relative contribution of the IPCA 1 and IPCA 2 scores to the total GEI sum of squares. A lower magnitude of ASV estimates indicates wider adaptation, whereas a higher magnitude of ASV indicates specific adaptation (Purchase., 2000).

- **Stability Index (SI)**

To facilitate simultaneous selection of genotypes for different quantitative traits and stability, the stability index (SI), which incorporates both quantitative traits mean and stability in a single criterion, was estimated as $SI = RASV + RY$ where RASV is the rank of the genotypes based on ASV and RY is the rank of the genotype-based on quantitative trait mean (Farshadfar, 2011) across three different locations. The genotypes with low SI were regarded as those with high trait expression and high stability.



Plate 1: Field view of cowpea at Bengaluru



Plate 2: Field view of cowpea at Mandya



Plate 3: Field view of cowpea at Pavagada



Plate 4: IC- 198355(45); Best identified accession



Plate 5: EC- 472271; Best identified accession



Plate 6: EC- 394708; Best identified accessions

RESULTS AND DISCUSSION

IV. RESULTS AND DISCUSSION

The present investigation entitled “Characterization of germplasm for yield and its associated traits in cowpea (*Vigna unguiculata* (L.) Walp)” was conducted to study the variability, divergence and stability of cowpea germplasm over the three different locations. The results obtained are presented below under following headings.

4.1 Analysis of variance

4.2 Descriptive statistics

4.3 Estimation of genetic variability parameters for yield and its components

4.4 *k*-means clustering analysis

4.5 Stability analysis

4.1 Analysis of variance

The analysis of variance indicated significance of genotypes for all the traits (Table 4).

Pooled analysis of variance also showed significant differences among genotypes for all traits under study. Mean squares due to genotype \times location significance was found for all traits indicating environmental role in expression of these traits (Table 5).

4.2 Descriptive statistics

Mean, standard error and range of ten traits is given in table 6

4.2.1 Days to 50 % flowering

For days to 50 % flowering, mean values of 53.30, 53.28 and 47.12 days were observed at Bengaluru, Pavagada and Mandya locations, respectively. Bengaluru location recorded a range of 40 to 58 days for this trait. It was 41 to 66 days for Pavagada and 40 to 60 days for Mandya location.

4.2.2 Plant Height (cm)

At Bengaluru, Pavagada and Mandya locations, mean plant height of 59.87, 38.32 and 47.44 cm were observed. maximum height recorded was 88.65, 87.85 and 85.12 cm and minimum height recorded was 20.00, 22.14 and 25.78 cm at Bengaluru, Pavagada and Mandya locations, respectively.

Table 4. ANOVA for yield and yield related traits in cowpea

Source of variation	Degrees of freedom	Mean sum of squares											
		Days to 50% flowering			Plant Height (cm)			Primary branches plant ⁻¹			Clusters plant ⁻¹		
		Bengaluru	Pavagada	Mandya	Bengaluru	Pavagada	Mandya	Bengaluru	Pavagada	Mandya	Bengaluru	Pavagada	Mandya
Genotypes	155	39.49***	38.45***	21.16***	652.98***	208.06***	277.32***	1.03***	0.36***	0.71***	42.72***	25.97**	80.07***
Replication	1	2.69	22.61*	10.41*	25.67**	12.44	0.65	1.02**	0.12	0.25	59.89***	0.05	0.42
Block	12	1.48	1.72	2.15*	1.23	13.10	3.66	0.10	0.06	0.11	2.9	25.89	1.86
Error	143	1.23	1.45	1.16	3.40	19.73	6.10	0.10	0.10	0.13	1.9	16.27	1.79
Source of variation	Degrees of freedom	Mean sum of squares											
		Pods cluster ⁻¹			Pods plant ⁻¹			Average pod length (cm)			Average seeds pod ⁻¹		
		Bengaluru	Pavagada	Mandya	Bengaluru	Pavagada	Mandya	Bengaluru	Pavagada	Mandya	Bengaluru	Pavagada	Mandya
Genotypes	155	0.50***	0.59***	0.26***	191.54***	220.63***	310.58***	17.99***	12.47***	15.37***	12.83***	19.50***	9.89***
Replication	1	0.01	0.28	0.08	28.44**	125.33	0.08	2.00	18.10	2.69	1.22	2.23	7.76**
Block	12	0.08	0.09	0.04	6.10*	55.20	2.49	3.31	5.30	0.84	2.29	3.89	1.26
Error	143	0.07	0.12	0.05	2.84	65.01	1.79	1.91	5.29	0.81	1.34	3.61	0.98
Source of variation	Degrees of freedom	Mean sum of squares											
		Average grain yield plant ⁻¹ (g)			100 seed weight (g)								
		Bengaluru		Pavagada	Mandya			Bengaluru		Pavagada	Mandya		
Genotypes	155	139.01***		161.76***	780.34***			9.52***		4.64*	7.71***		
Replication	1	0.64		300.53*	0.91			2.23*		1.87	3.12**		
Block	12	1.00		23.92	0.80			0.83*		2.98	0.14		
Error	143	1.81		50.34	3.15			4.33		3.38	0.43		

* significance at 5%; ** significance at 1%; *** significance at 0.1%

Table 5. Pooled ANOVA for yield and yield related traits in cowpea

Source of variation	Degrees of freedom	Mean sum of squares									
		Days to 50% flowering	Plant height (cm)	Primary branches plant ⁻¹	Clusters plant ⁻¹	Pods cluster ⁻¹	Pods plant ⁻¹	Average pod length (cm)	Average seed plant ⁻¹	Average grain yield plant ⁻¹ (g)	100 seed weight (g)
Genotypes	155	47.20***	364.25***	1.69***	42.05***	4.59***	1.98***	16.45***	17.53***	230.71***	9.45***
Environment	2	1645.2**	16324.2**	26.18**	90.24***	10.59*	22.18**	20.58***	122.45***	3698.2***	6.48**
Genotype × Environment	310	32.52***	396.08***	0.60***	47.78***	0.44***	22.30***	15.21***	14.03***	348.7***	5.06***
Replication	1	33.61**	245.48*	2.34*	26.46*	4.1	2.45**	50.15	27.21**	256.58	56.85
Block	12	6.48*	20.9	0.58	14.15	1.97	0.99	3.68*	2.47*	75.15	13.55
Pooled error	454	1.69	32.05	0.9	15.17	2.94	0.84	5.17	4.14	120.42	5.69

* significance at 5%; ** significance at 1%; *** significance at 0.1%

4.2.3 Primary branches per plant

The mean values of primary branches per plant were 1.81, 1.94 and 1.54 at Bengaluru, Pavagada and Mandya locations. Minimum of one primary branch was found at three locations and maximum of 5.00, 2.60, 3.45 were found at Bengaluru, Pavagada and Mandya location, respectively.

4.2.4 Clusters per plant

Bengaluru had a mean of 13.13, Pavagada had a mean of 14.13 and Mandya had mean of 14.44 clusters per plant. Range was 4.2 to 53.24 cluster in Bengaluru, 5 to 32.6 clusters in Pavagada and 4.00 to 42.15 in Mandya.

4.2.5 Pods per cluster

Mean values of pods per cluster were 2.13, 1.77 and 1.98 at Bengaluru, Pavagada and Mandya location with a range of 1 to 4 pods per cluster at three locations.

4.2.6 Pods per plant

Mean pods per plant recorded was 19.17 at Bengaluru 25.12 at Pavagada and 23.89 at Mandya. Pods per plant ranged from 6.54 to 101.20 at Bengaluru, 7.40 to 86.7 at Pavagada and 7.25 to 99.8 at Mandya.

4.2.7 Average pod length (cm)

Bengaluru, Pavagada and Mandya had a mean of 15.77, 13.60 and 14.73 respectively, with a range of 8.52 to 25.00, 6.20 to 26.4 and 7.56 to 24.26 respectively.

4.2.8 Average seeds per pod

Average seeds per pod had a mean of 13.43, 11.95 and 12.41 with a range of 7.41 to 25.00, 9.8 to 25.50 and 6.56 to 23.42 at Bengaluru, Pavagada and Mandya locations respectively.

4.2.9 Average Grain yield per plant (g)

Range of 7.69 to 142.00, 6.50 to 79.30 and 7.14 to 150.80 was observed for grain yield per plant with mean of 26.75, 20.02 and 19.43 at Bengaluru, Pavagada and Mandya locations, respectively.

Table 6. Descriptive statistics of the ten traits

Characters	Mean \pm S.Em			Range					
				Bengaluru		Pavagada		Mandya	
	Bengaluru	Pavagada	Mandya	Minimum	Maximum	Minimum	Maximum	Minimum	Maximum
Days to 50% flowering	53.30 \pm 0.79	53.28 \pm 0.85	47.12 \pm 0.78	40.00	58.00	41	66.00	40.00	60.00
Plant height (cm)	59.87 \pm 1.27	38.32 \pm 3.10	47.44 \pm 1.72	20.00	88.65	22.14	87.85	25.78	85.12
Primary branches plant ⁻¹	1.81 \pm 0.22	1.94 \pm 0.23	1.54 \pm 0.25	1.00	5.00	1.00	2.60	1.00	3.45
Clusters per plant ⁻¹	13.13 \pm 1.00	14.13 \pm 2.91	14.44 \pm 0.95	4.20	53.20	5.00	32.60	4.00	42.15
Pods cluster ⁻¹	2.13 \pm 0.11	1.77 \pm 0.25	1.98 \pm 0.16	1.00	4.00	1.00	4.00	1.00	4.00
Pods plant ⁻¹	19.17 \pm 1.24	25.12 \pm 5.67	23.89 \pm 0.96	6.54	101.20	7.40	86.70	7.25	99.8
Average pod length (cm)	15.77 \pm 1.01	13.60 \pm 1.62	14.73 \pm 0.64	8.52	25.00	6.20	26.40	7.56	24.26
Average seeds per pod	13.43 \pm 0.84	11.95 \pm 1.35	12.41 \pm 0.70	7.41	25.00	4.70	25.50	6.56	23.42
Grain yield plant ⁻¹ (g)	26.75 \pm 1.21	20.02 \pm 4.91	19.43 \pm 1.61	7.69	142.00	6.50	79.30	7.14	150.85
100 seed weight (g)	10.40 \pm 0.45	10.11 \pm 1.29	11.36 \pm 0.55	4.96	16.64	6.56	15.44	5.45	14.26

4.2.10 100 seed weight (g)

For the trait 100 seed weight, range was from 4.96 to 16.64 with mean of 10.40 at Bengaluru location, 6.56 to 15.44 with a mean of 10.11 at Pavagada location and 5.45 to 14.26 with a mean of 11.36 at Mandya location

4.3 Estimation of genetic variability parameters for yield and its components

To understand the extent to which the observed variation is due to genetic factors, the genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability (h^2) and genetic advance as *per cent* of mean (GAM), were computed for all the ten characters under consideration and is presented in the table 7.

4.3.1 Days to fifty *per cent* flowering

Estimates of GCV and PCV were found to be low at all three locations. PCV was 8.47%, 8.38%, and 9.10% at Bengaluru, Pavagada and Mandya locations respectively. GCV was 8.20%, 8.07%, and 7.69% at Bengaluru, Pavagada and Mandya locations respectively. Heritability was high for this trait at all three locations with moderate GAM (Table 7). Least difference between GCV and PCV indicated that there was less environment effect on this trait. Mahmudul *et al.* (2012) found similar result of low GCV, PCV, high heritability and moderate GAM in cowpea.

4.3.2 Plant Height (cm)

PCV was 30.25, 28.35 and 31.08 at Bengaluru, Pavagada and Mandya locations respectively. GCV was 27.21%, 25.20%, and 29.57% at Bengaluru, Pavagada and Mandya locations respectively. GCV and PCV was found to be high. Since environmental effect was low, there was not much difference in GCV and PCV values. Heritability was high with high GAM at all locations (Table 7). Similar results in cowpea were observed by Vishwa Nath *et al.* (2009).

4.3.3. Primary branches per plant

High PCV (53.31% at Bengaluru, 51.32% at Pavagada, 49.12% at Mandya), high GCV (48.16% at Bengaluru, 48.48% at Pavagada, 45.24% at Mandya), heritability and GAM was high at all locations. Environmental effect was low (Table 7). Kharde *et al.* (2014) found high GCV, heritability and GAM.

Characters	Bengaluru				Pavagada				Mandya			
	PCV (%)	GCV (%)	$h^2_{(bs)}$	GAM (%)	PCV (%)	GCV (%)	$h^2_{(bs)}$	GAM (%)	PCV (%)	GCV (%)	$h^2_{(bs)}$	GAM (%)
Days to 50% flowering	8.47	8.20	93.32	16.36	8.38	8.07	90.69	13.29	9.10	7.69	88.45	15.49
Plant height (cm)	30.25	30.10	90.45	61.70	28.35	27.21	83.56	57.60	31.08	24.56	95.11	59.51
Primary branches plant⁻¹	53.31	48.16	81.36	69.65	51.32	48.48	89.55	59.44	49.12	45.24	85.21	64.74
Clusters plant⁻¹	35.99	33.34	21.44	47.51	32.42	28.11	17.36	42.65	44.30	43.32	20.85	46.54
Pods cluster⁻¹	48.61	45.56	45.36	30.56	43.36	41.56	42.56	27.86	41.58	40.31	41.11	41.23
Pods plant⁻¹	52.89	49.09	67.65	60.36	47.49	43.19	61.54	53.70	52.31	50.91	65.36	56.65
Average pod length (cm)	23.05	20.91	62.45	32.95	21.90	18.92	58.36	18.22	19.31	18.31	66.45	35.76
Average seeds pod⁻¹	19.87	18.79	80.35	32.79	28.45	23.56	75.24	40.20	19.17	17.07	78.36	35.11
Average Grain yield plant⁻¹ (g)	60.25	55.12	52.02	70.17	51.18	47.61	54.55	56.95	51.23	46.69	61.24	60.24
100 seed weight (g)	49.87	47.23	43.32	60.21	50.12	47.89	41.22	57.82	52.36	49.23	42.56	61.23

Table 7. Variability statistics of ten traits

PCV (%) – phenotypic coefficient of variance; GCV (%) – genotypic coefficient of variance; $h^2_{(bs)}$ – heritability; GAM (%) – genetic advance *per cent* of mean

4.3.4 Clusters per plant

PCV and GCV was high at three locations. Environmental effect was found low at all location. Since less difference in GCV and PCV was observed at all locations (Table 7). Heritability and GAM was high at all locations. Similar results for GCV and PCV was studied by Thorat and Gadewar (2013).

4.3.5 Pods per cluster

High PCV and GCV was observed at all the locations. Environmental effect was found to be less at all the locations (Table 7). Heritability was high at three locations. GAM was high at observed at all three locations. Pandey *et al.* (2014) found similar results in cowpea. Vir and Singh (2014) reported low heritability similar to the current work.

4.3.6 Pods per plant

Higher PCV and GCV was observed at all three locations (Table 7). Environmental effect was found to be less at all the locations (Table 7). Heritability and GAM was high at observed at all three locations. Pandey *et al.* (2014) found similar results in cowpea.

4.3.7 Average pod length (cm)

PCV was high at Bengaluru (23.05%) and Pavagada (21.90%) and moderate at Mandya (19.31%). GCV was moderate at Pavagada (18.92%) and Mandya (18.22%) locations. Heritability was high at all locations. GAM was high at Bangalore and Mandya location whereas moderate at Pavagada location (Table 7). Pandey *et al.* (2014) found similar results of moderate GCV and high PCV.

4.3.8 Average seeds per pod (g)

PCV was moderate at Bengaluru (19.87%) and Mandya (17.90%) and was high at Pavagada (28.45%) location. Moderate GCV was observed at Bengaluru (18.79%) and Mandya (19.17%) whereas it was high at Pavagada (23.56%). GAM and Heritability was high at all location (Table 7). Vishwa Nath *et al.* (2009) found moderate GCV, PCV, heritability and GAM.

4.3.9 Average Grain yield per plant (g)

High GCV at Bengaluru (55.12%), Mandya (47.61%) and Pavagada (46.69) was observed. PCV was high at all location. Heritability was high at all location indicating environmental effect was absent in all the locations. GAM was high at Bengaluru, Pavagada

and Mandya location (Table 7). High GCV, PCV was observed by Vir and Singh (2014) similar to the present result.

4.3.10 100 seed weight (g)

High GCV and PCV was observed at all the locations. Environmental effect was found to be less at all the locations (Table 7). Heritability was high at Bengaluru, Pavagada and Mandya. GAM was high at observed at all three locations.

In the current study PCV (%) and GCV (%) was high for all traits except days to 50 *per cent* flowering and average seeds per pod at Bengaluru location, while it was high for all traits except days to 50 *per cent* flowering at Pavagada location and high for all traits except days to 50 *per cent* flowering, average pod length and average seeds pod. Heritability was high for all traits except cluster per plant, pods per cluster, average grain yield per plant and 100 seed weight at Bengaluru location, it was high for all traits except cluster per plant, pods per cluster average pod length, average grain yield per plant and 100 seed weight at Pavagada location and it was also high for all traits except cluster per plant, pods per cluster and 100 seed weight. GAM was high for all traits except days to 50 *per cent* flowering at three locations indicating predominance of additive gene action and phenotypic selection for these characters is effective. Days to 50 *per cent* of flowering had moderate GAM indicating moderate possibility for selection for this trait.

4.4 k-means clustering analysis

Millions of data points are put together to form clusters using the clustering technique. The goal of cluster analysis or clustering is to divide a collection of genotypes into several groups so that the items within each cluster are more "similar" to one another and "dissimilar" to those with other clusters. One of the methods to categorize genotypes based on "similarity" and "dissimilarity" is k-means clustering (Kanavi *et al.*, 2020). k-means clustering is a genetic diversity assessment tool that generates genetically varied clusters based on genetic distances between germplasm accessions. Once the various clusters are created, it is simple to identify the genetically distant clusters and the genetically distinct germplasm accessions that belong to same cluster. In turn, this makes it simple for plant breeders to locate genetically varied germplasm accessions that can be used as parental lines in crossing programmes.

Table 8. Grouping of genotypes in 12 clusters obtained using k-means clustering

Clusters	No. of genotypes	Genotypes
1	17	VCP-17-019, EC-458511, IC-402106, IC-402098, 27749(20), 201095(32), NBC-38, NBC-27 SUPER-30, NBC-43, GWHOPECB-10, C-33, NBC-25, CP-98, SKUA-WCP-49 and NBC-24
2	11	NBC-8, IC-202867(99), IC-603187, IC-462099, IC-58905, IC-237422, EC-458470, EC-472257, NBC-40, CPD-340 and NBC-44
3	13	IC-249141, IC-4506, IC-402125, IC-202325, IC-202792(72), IC-402175, EC-271040, EC-458489, EC-402159, V-589, EC-394708, EC-458438 and 202804(83)
4	8	IC-402048, IC-402114, EC-458485, EC-458473, EC-075180, EC-458483, EC-458411 and EC-458425
5	8	IC-402104, VCP-18-032, EC-458490, PMCP-1131, KBC-2, KM-5, GC-1602 and IC-402090
6	13	IC-253251, GC-3, IC-249593, 198355(45), IC-25105, IC-402101, V-604-7-29-3, EC-492292, EC-472250, TPTC-29, GC-1801, IC-2591054 and EC-458418
7	4	V-578, V-585, VC-458492 and NBC-51
8	22	IC-402172, IC-458430, IC-330996, IC-45061, IC-402135, IC-10171, 2574422(7), IC-402161, IC-107120, 202521(93), 202854(97), EC-458469, EC-458505, EC-170574-6, EC-170584-1.1, V-240, V-16, EC-394839, NBC-6, NBC-33, CPD-15 and NBC-7
9	11	IC-422174, IC-198326-38, IC-1070, IC-402164, EC-472252, IC-402166, EC-390287, NBC-23, NBC-36, NBC-4716, and IT-9715499-38
10	15	IC-402159, IC-249588, IC-202781, IC-202777, IC-402162, IC-202711(58), IC-202290, 202329-89, EC-394838, EC-458442, NBC-29, NBC-19, PMCP-1016, GC-1805 and C-24-1
11	7	EC-458440, EC-472271, CB-1024, EC-170604, NBC-30, NBC-18 and EC-458480
12	18	IC-1071, IC-219489, IC-206240, EC-47226, NBC-391, NBC-32, NBC-98, NBC-68, TOME-774, PCP-0306-1, NBC-14, NBC-016, CPD-331, PCD-1124-1, NBC-41, C-457, C-157 and EC-394779

Table 9. Analysis of variance for yield and yield attributing traits between the clusters

Sl. No.	Source of variation	Days to 50% flowering	Plant height (cm)	Primary branches plant ⁻¹	Clusters plant ⁻¹	Pods cluster ⁻¹	Pods plant ⁻¹	Average pod length (cm)	Average seeds pods ⁻¹	Average grain yield plant ⁻¹ (g)	100 seed weight (g)
1	Between clusters	38.29 ***	375.50 1***	0.5 ***	83.12 ***	0.59 ***	499.05 ***	20.49 ***	17.29 ***	619.24 ***	15.12 ***
2	Within clusters	2.97	35.12	0.09	3.14	0.04	12.38	1.24	1.26	22.42	0.96

* significance at 5%; ** significance at 1%; *** significance at 0.1%

Table 10. Cluster means of yield and yield-related traits based on k-means clustering

Clust ers	Cluster means									
	Days to 50% flowering	Plant height (cm)	Primary branches plant ⁻¹	Clusters plant ⁻¹	Pods cluster ⁻¹	Pods plant ⁻¹	Average pod length (cm)	Average seeds pods ⁻¹	Average grain yield plant ⁻¹ (g)	100 seed weight (g)
1	53.46	47.67	1.20	13.01	1.88	21.11	15.57	13.80	20.01	11.09
2	53.36	53.01	1.49	14.65	2.26	27.26	14.06	11.87	20.63	8.85
3	51.67	40.55	1.67	14.49	1.86	23.42	14.54	12.49	21.11	10.17
4	51.63	47.98	1.02	14.75	2.31	27.47	15.02	12.72	22.04	13.28
5	50.48	50.65	0.97	18.30	1.89	29.24	13.34	11.94	27.34	10.19
6	50.13	42.27	1.17	11.20	1.84	18.20	16.62	14.25	16.44	9.91
7	48.25	47.91	1.10	23.32	2.00	39.73	13.25	11.98	51.67	8.88
8	49.55	44.66	1.03	12.38	1.98	19.98	13.71	11.89	18.42	9.46
9	51.17	49.75	1.53	14.10	2.23	24.50	16.73	15.27	20.60	10.68
10	53.47	45.92	1.20	11.76	1.61	14.28	13.41	11.77	14.75	9.86
11	53.50	52.77	1.14	18.25	2.34	38.50	16.67	13.88	34.63	9.72
12	49.46	58.94	1.37	12.64	1.81	18.94	13.73	11.82	16.23	11.57

Based on the non-significance of Levene's test that resulted in the homogeneity of variances within the clusters the total genotypes were divided into 12 clusters using non-hierarchical clustering. The mode of distribution of genotypes into 12 clusters was random and it was based on all traits under consideration, not on the geographical distribution as mentioned by Kanavi *et al.* (2020).

Total of 12 clusters were obtained and among them cluster 8 had maximum genotypes of 22 and cluster 7 had 4 genotypes. The distribution of genotypes into 12 clusters is shown in table 8 and fig. 1.

One-way ANOVA was done to know the presence of significant difference between the clusters. It was observed that all the traits considered for this study showed high significant difference indicating each cluster were different from each other (Table 9).

The mean value of twelve cluster is depicted in table 10. Lowest mean for days to fifty *per cent* flowering was observed for Cluster 7 (48.25). Cluster 12 had 58.94 as highest mean for plant height. Primary branch per plant had highest mean of 1.67 for Cluster 3. Highest mean of 23.32 was observed for cluster 7 with respect to cluster per plant. Cluster 11 had highest mean of 2.34 for pods per cluster. Highest mean of 39.73 for pods per plant was observed for cluster 7. Average pod length had highest mean of 16.73 in cluster 9. 15.27 was highest mean in cluster 9 for average seeds per pod. Average grain yield per plant had highest mean of 51.67 in cluster 7. Cluster 4 had 13.28 as highest mean for 100 seed weight.

The highest inter-cluster distance (19.68) was observed between cluster 7 and cluster 6 followed by cluster 7 and cluster 1 (18.95) indicating these clusters were diverse with respect to each other (Table 11). And minimum inter cluster distance (8.71) was observed between cluster 3 and cluster 1 followed by cluster 10 and cluster 8 (8.77). As the thumb rule of hybridization, distant parents are used, similarly genotypes of cluster 7 and cluster 6 can be used for hybridization since genotypes of cluster 7 are high yielders and they have highest inter cluster distance. Similarly, genotypes of cluster 7 can be used for hybridization against genotypes of cluster 1.

Table 11. Intra and inter-cluster distance among the 12 clusters

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12
C1	0	10.80	8.71	10.28	11.28	8.79	18.95	9.64	9.31	9.54	13.15	10.13
C2		0	9.72	11.68	10.77	13.02	16.66	10.57	11.35	11.49	12.49	11.83
C3			0	10.9	10.28	9.984	16.96	9.137	10.15	9.81	14.05	10.24
C4				0	11.12	13.13	18.15	11.52	11.12	13.82	13.25	11.90
C5					0	13.36	12.70	10.09	12.73	12.28	11.96	11.49
C6						0	19.86	9.393	10.0	9.958	15.63	11.14
C7							0	16.15	18.89	19.81	14.76	18.79
C8								0	11.77	8.77	15.73	9.513
C9									0	13.50	12.23	12.19
C10										0	17.30	9.81
C11											0	17.26
C12												0

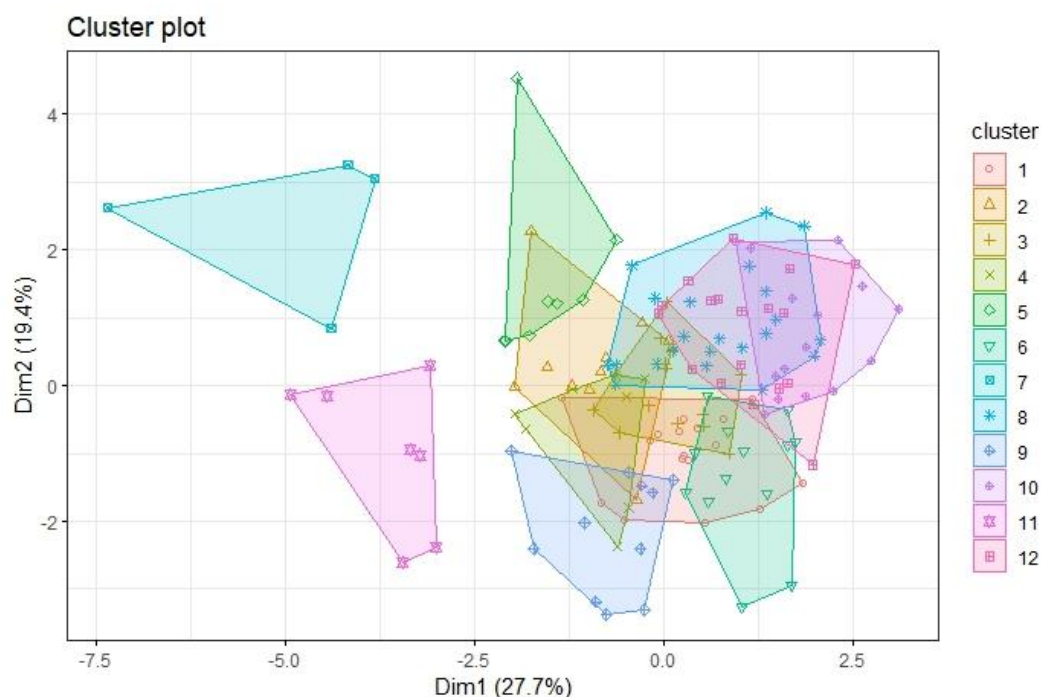


Fig. 1. Cluster plot representing twelve clusters derived using *k means* clustering of cowpea genotypes for yield and yield attributing traits

4.5 Analysis of variance by using AMMI Model

Genotype \times environment interactions are of major consequence to the breeders in the process of evolution of improved varieties. When varieties are grown in different environments for testing their performance, their relative rankings usually do not remain same. Hence, the presence of environmental influence and genotype by location interaction is a pre-requisite for stability analysis.

An analysis of variance based on the AMMI model and *per cent* contribution of each component of variance to the total variation for the studied traits is presented in table 12. The sum of squares due to genotypes, environment and $G \times E$ interaction were significant for days to 50 *per cent* flowering, plant height, primary branches per plant, pods per cluster, pods per plant, average pod length, average seeds per pod and average grain yield per plant. The sum of squares due to genotypes and $G \times E$ interaction were significant for clusters per plant and 100 seed weight.

4.5.1 Biplot analysis

The stability and adaptability of genotypes over spatial environments can be qualitatively assessed using graphical representation of GGE- biplot that scatters genotypes based on their IPCs. Yan *et al.* (2000) proposed, a standard biplot of GGE, genotype (G) + Genotype \times environment (GE) based on site regression model referred to as GGE bi-plot. It is a multivariate analytical tool that graphically displays interaction between each genotype and each location environment. It is a two dimensional bi-plot and allows visualisation of the inter-relationship among three environments, and also the inter-relationship between genotypes and location environments.

Total of four GGE biplot patterns were obtained in the current work which are described as follows

4.5.1.1 Discriminating ability and representativeness

4.5.1.2 Ranking of genotypes relative to ‘ideal genotype’

4.5.1.3 Mean vs. stability

4.5.1.4 ‘Which won where’ pattern

Table 12. AMMI ANOVA for yield and yield related traits in cowpea

Source of variation	Degrees of freedom	Days to 50% flowering		Plant height		Primary branches plant ⁻¹		Clusters per plant ⁻¹		Pods cluster ⁻¹	
		MSS	Proportion	MSS	Proportion	MSS	Proportion	MSS	Proportion	MSS	Proportion
Genotypes	155	34.06***	15.50	346.23***	14.19	0.90***	22.09	52.20***	19.62	0.47***	18.61
Environment	2	397.30***	23.30	37136.54***	19.65	30.89***	9.77	120.81	5.44	10.53**	5.29
Genotype × Environment	310	32.52***	29.60	396.08***	32.48	0.60***	29.86	47.78***	35.91	0.44***	34.04
PC1	156	36.07	55.80	550.70	70.00	0.75	62.00	63.08	66.40	0.48	56.00
PC2	154	28.93	44.20	239.44	30.00	0.46	38.00	32.29	33.60	0.39	44.00
Residuals	465	1.32	1.80	9.46	1.16	0.11	8.18	6.94	7.82	0.07	7.90

Source of variation	Degrees of freedom	Pods plant ⁻¹		Average pod length		Average seeds pod ⁻¹		Grain yield plant ⁻¹		100 seed weight	
		MSS	Proportion	MSS	Proportion	MSS	Proportion	MSS	Proportion	MSS	Proportion
Genotypes	155	278.80***	22.02	15.42***	17.22	14.18***	17.97	383.70****	19.61	11.77***	32.20
Environment	2	2242.00**	2.28	383.91**	5.53	192.06**	3.14	9510.20**	6.20	13.74	0.48
Genotype × Environment	310	222.00***	35.07	15.21***	33.99	14.03***	35.55	384.80***	35.65	5.06***	27.73
PC1	156	74.3	62.20	17.44	57.70	16.59	59.50	548.50	79.20	6.54	65.10
PC2	154	169.00	37.80	12.95	42.30	11.44	40.50	146.30	20.80	3.56	34.90
Residuals	465	23.1	5.46	2.71	9.09	2.02	7.66	17.70	2.71	1.41	11.60

* significance at 5%; ** significance at 1%; *** significance at 0.1%

Out of ten traits five productive traits *viz.*, clusters per plant, pods per plant, average pod length, average seeds per pod and average grain yield per plant were used for biplot analysis.

4.5.1.1 Discriminating ability and representativeness

Assessment of discriminating ability and representativeness of test environment is based on the length of the environment vectors and the angle between the test environment vectors and average environment axis (AEA) in the GGE Biplot graph. more the length of the vector of environment means higher discriminating ability of environment in case of trait variation. The shorter the length of the vector of environment, lesser discriminating ability of environment i.e., less trait variation of genotypes. The average of test environments is denoted by average environment axis (AEA) and the average environment is represented by the small circle at the end of the arrow of AEA. The angle between the AEA and environment vector is less, it denotes more representativeness of the concerned environments over all test environments. If the environment vector has more angle with AEA and it denote less representativeness. Small and large angle between environmental vectors and AEC indicate most and least representative location environments, respectively. Acute and obtuse angle between the location environment vectors indicate similarity and dissimilarity between the test location environments, respectively (Yan and Tinker, 2006). In the present study, E3 (Mandya) environment was more discriminative as its vector is longer compared to other vectors and E2 (Pavagada) environment is more representative for clusters per plant as its angle is smaller with respect to AEC (Fig. 2a). For pods per plant, E3 (Mandya) environment is more discriminative and representative as its vector length is longer and angle with respect to AEC is smaller for the environment E2 (Pavagada) (Fig. 2b). For average pod length E3 (Mandya) environment is more discriminative and environment E2 (Pavagada) is more representative (Fig. 2c). For trait average seeds per pod E2 (Pavagada) environment is more discriminative and E1 (Bengaluru) environment is more discriminative (Fig. 2d). Vector length of E3 is longer and angle between AEC is acute, thus E3 is both discriminative representative for average grain yield per plant (Fig. 2e).

4.5.1.2 Ranking of genotypes relative to 'ideal genotype'

An ideal genotype is the one with high mean performance and high stability over the environments. A single arrowed line passing through origin in the biplot and centre of the circle is average environment coordinate (AEC). The average environment is represented by the small



Fig. 2a. Discriminative vs. representativeness view of GGE bi-plot for cluster per plant

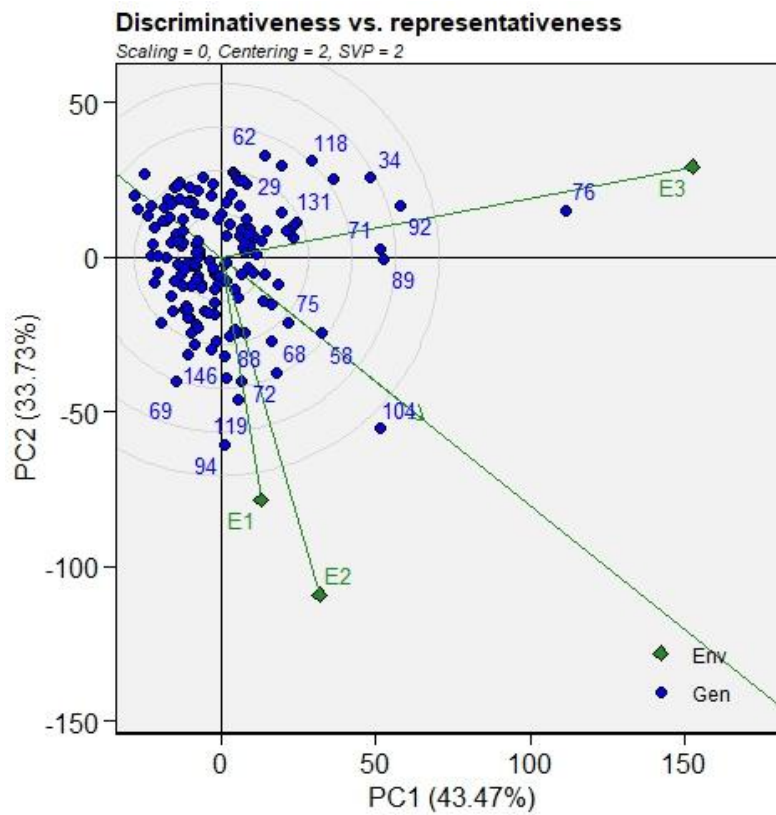


Fig. 2b. Discriminative vs. representativeness view of GGE bi-plot for pods per plant

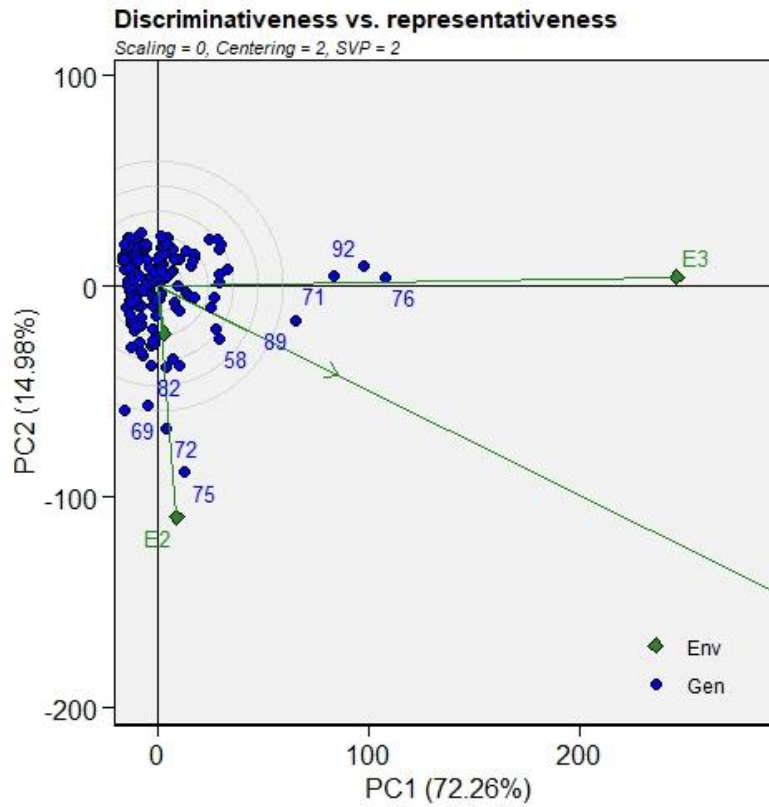


Fig. 2e. Discriminative vs. representativeness view of GGE bi-plot for average yield per plant

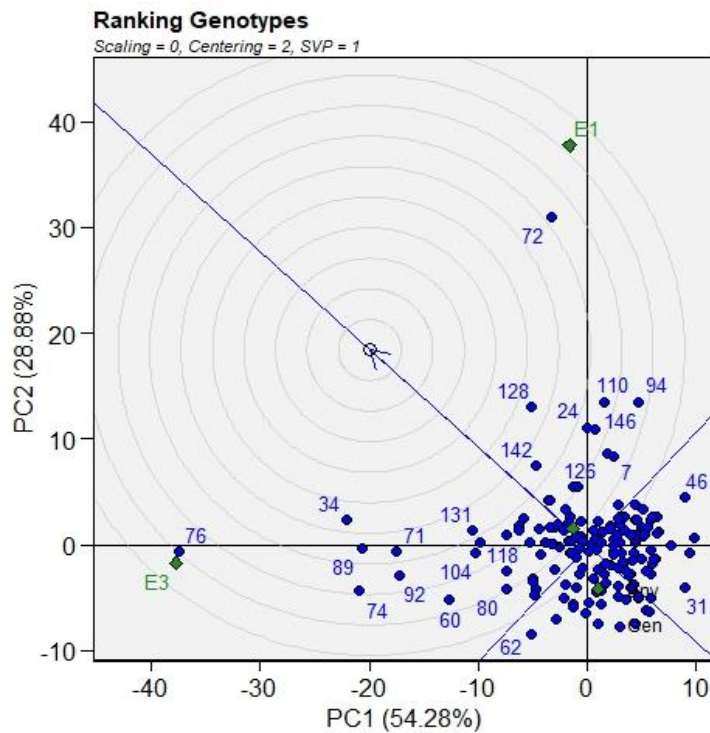


Fig. 3a. Average environment coordination view of GGE-biplot for identification of genotypes ideal for clusters per plant

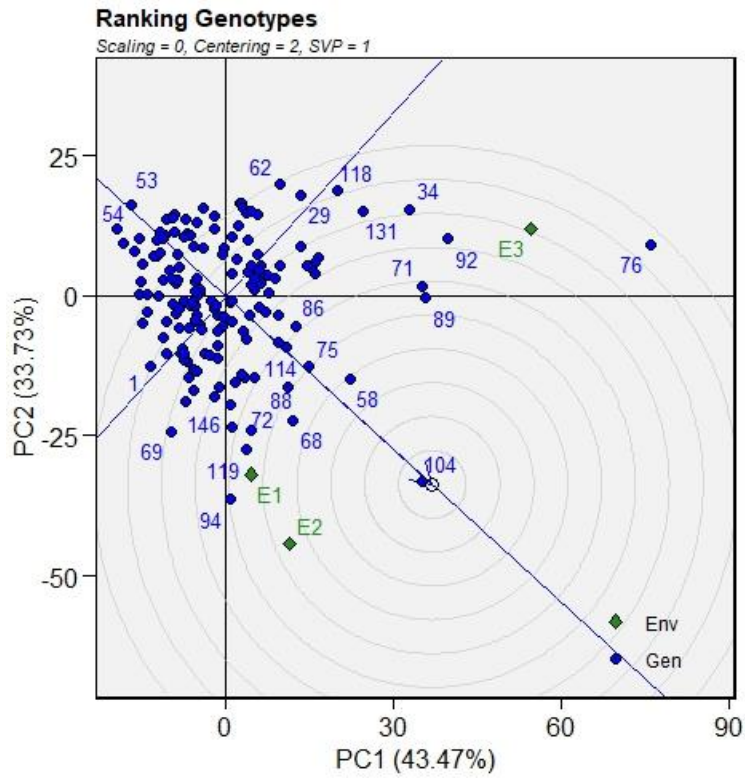


Fig. 3b. Average environment coordination view of GGE-biplot for identification of genotypes ideal for pods per plant

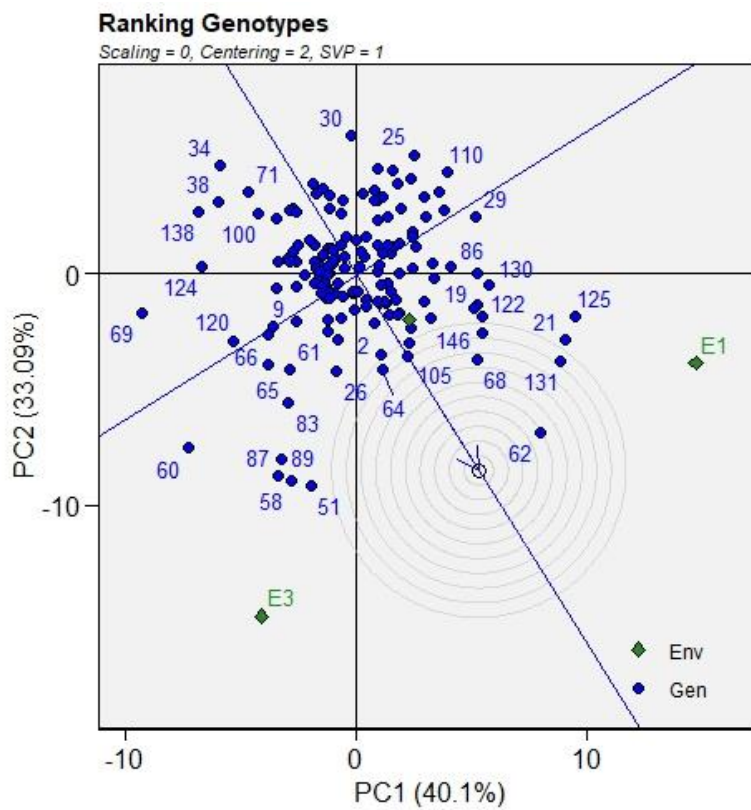


Fig. 3c. Average environment coordination view of GGE-biplot for identification of genotypes ideal for average pod length

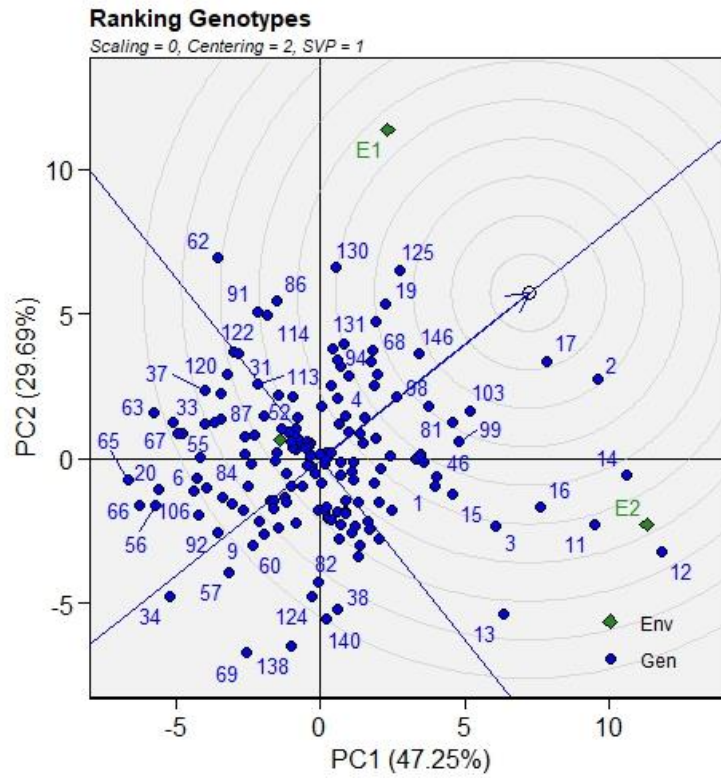


Fig. 3d. Average environment coordination view of GGE-biplot for identification of genotypes ideal for average seeds per pod

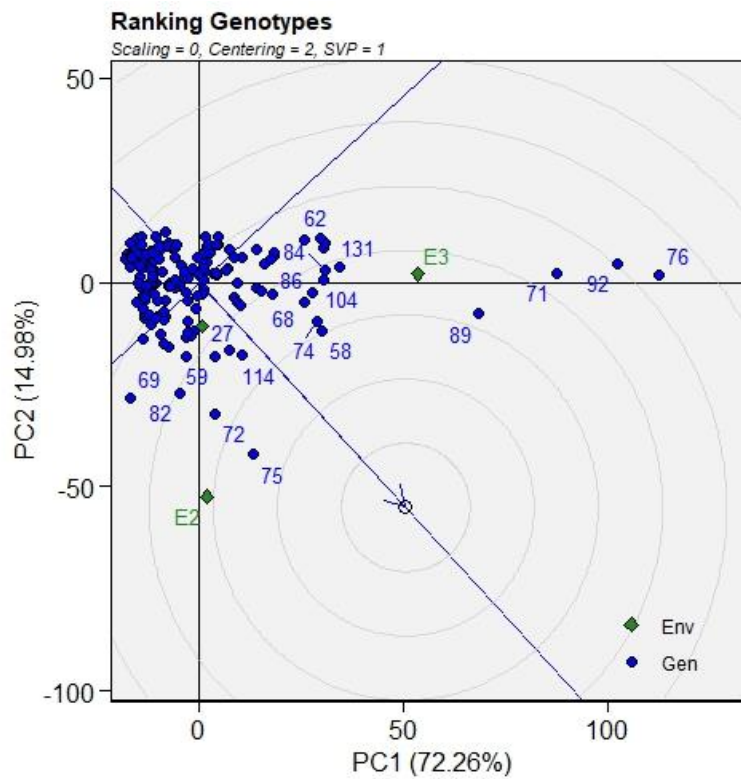


Fig. 3e. Average environment coordination view of GGE-biplot for identification of genotypes ideal for average yield per plant

circle at the end of the arrow (Yan & Tinker, 2006). An ideal genotype is present at the centre of concentric circles with AEC passing through it and stable genotypes are the one that are present in the concentric circle.

Genotypes IC-402104 (34) and GC-1602 (128) were found near ideal as they were nearer to origin for clusters per plant (Fig. 3a). For pods per plant genotype NBC-18 (104) was identified as near ideal on account of being closer to origin (Fig. 3b). For average pod length genotype EC-472252 (62) was found to be ideal (Fig. 3c). Genotype IC-402164 (17) was ideal for the trait average seeds per pod (Fig. 3d). Genotype CB-1024 (75) was near ideal for average grain yield per plant (Fig. 3e).

4.5.1.3 Mean vs. stability

The mean performance and stability could be visualized based on the location of genotypes in relation to AEC using AEC view of GGE bi-plot. The single arrowed AEC points to higher mean performance of the genotypes across locations (Yan & Tinker, 2006). The genotypes with their points located towards arrow of AEC are considered to exhibit high mean performance. On the contrary, the genotypes with their points located opposite to AEC arrow are considered to exhibit lower performance. Further, the relative lengths of projections of the genotypes from AEC are indicative of their relative stability, shorter the length of the projections of genotypes from AEC, greater is the adaptability of the genotypes. The greater the absolute length of the projections of genotypes, greater would be their poor adaptability (Yan *et al.*, 2007).

In the present study, genotypes EC-458411 (86), PCD-1124-1 (117) and EC-472271 (68) being closer to AEC line, were identified as highly stable with higher mean performance for clusters per plant (Fig. 4a). The genotypes CB-1024 (75), KBC-9 (114) and EC-472257 (65) were identified as stable with higher mean for pods per plant because of their shorter projection from AEC and also towards the arrow of AEC (Fig. 4b). For average pod length genotypes NBC-27 (105), IC-2591054 (141) and IC-402166 (78) were found to be stable with high mean performance (Fig. 4c). Genotypes KBC-9 (check), NBC-25 (132) and IC-402114 (47) were stable with high mean performance for average seeds per pod (Fig. 4d). As far as average grain yield per plant was concerned, genotypes KBC-2 (114), IC-237422 (27) and EC-170574-6 (59) were found to be highly stable with higher mean performance combined on account of them being on AEC and towards the arrow of AEC (Fig. 4e).

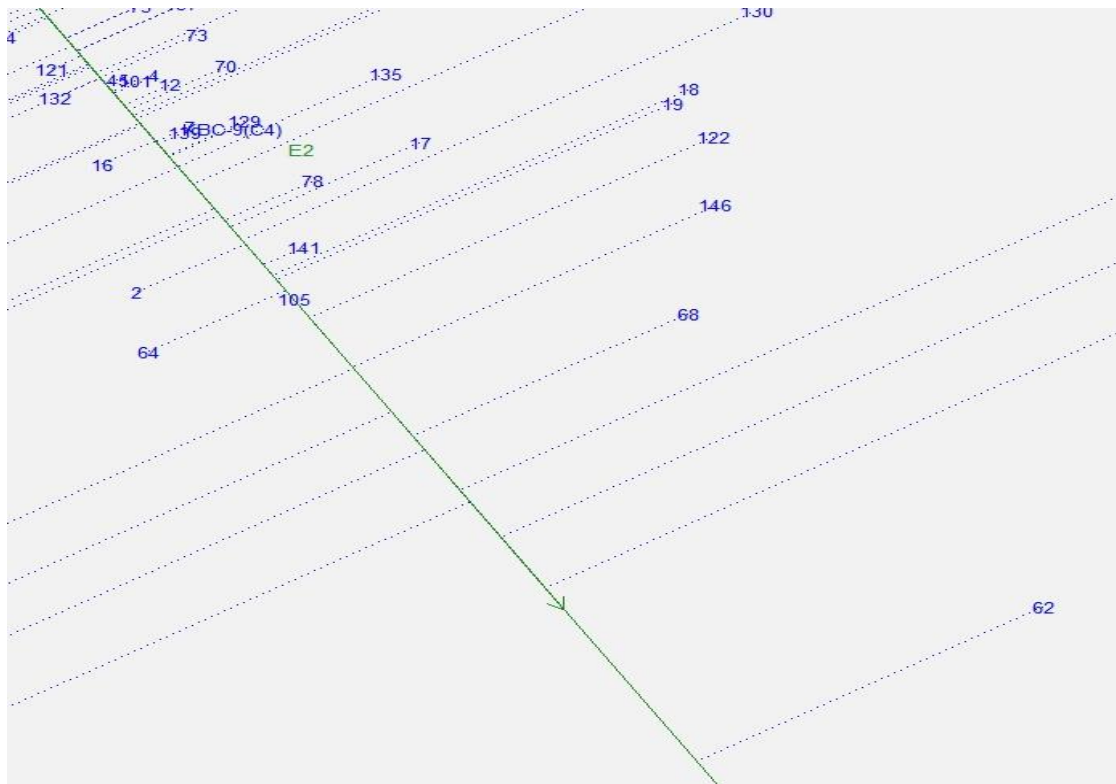


Fig. 4c. Average environment coordination view of GGE-based on location environment focused scaling for the mean performance vs. stability for average pod length

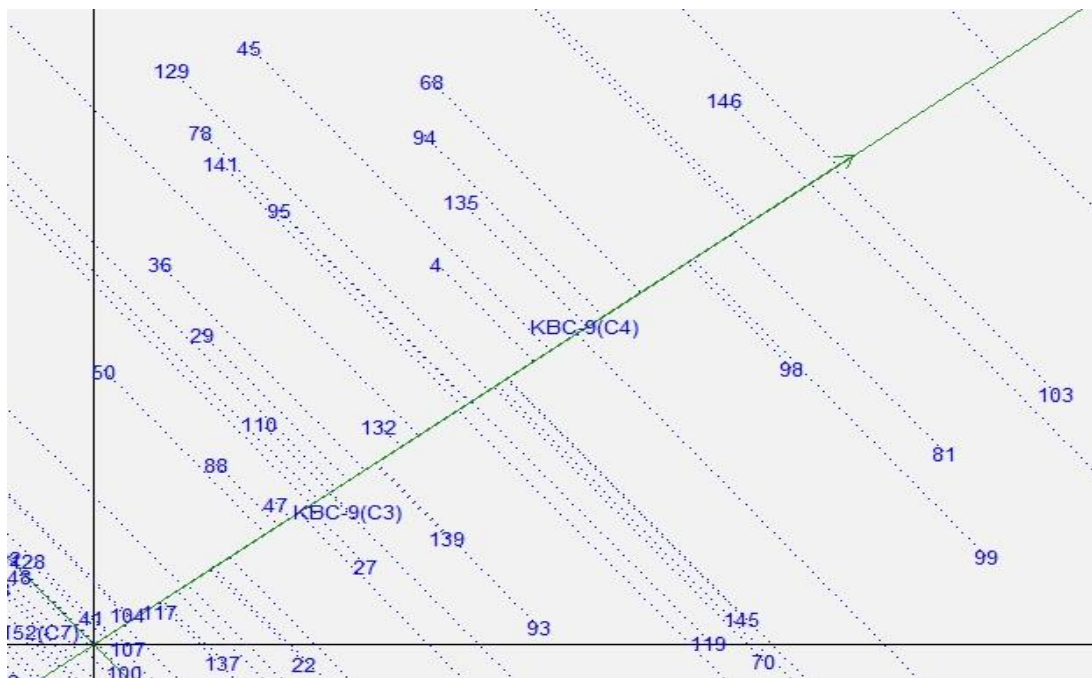


Fig. 4d. Average environment coordination view of GGE-based on location environment focused scaling for the mean performance vs. stability for average seeds pod⁻¹

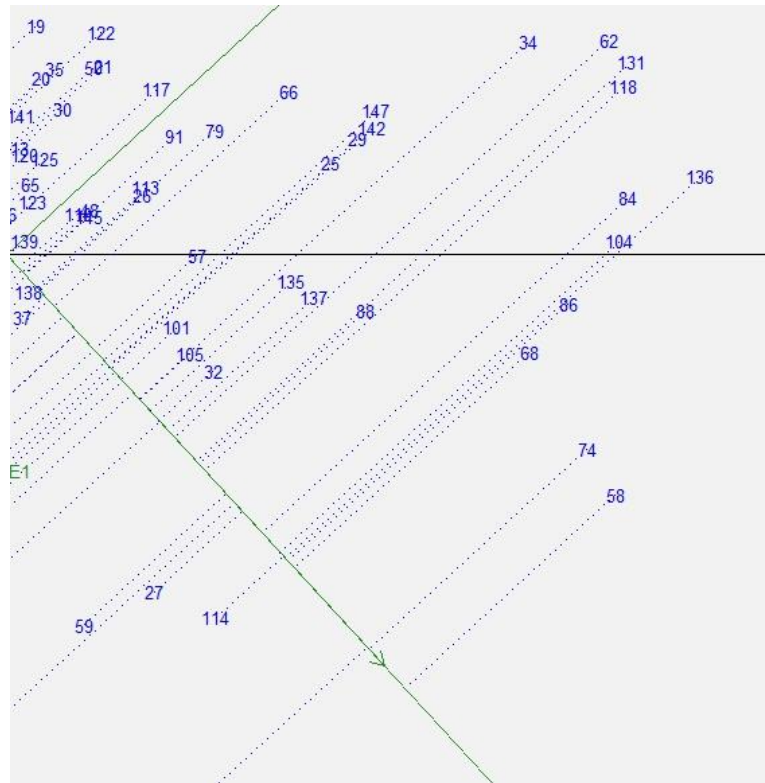


Fig. 4e. Average environment coordination view of GGE-based on location environment focused scaling for the mean performance *vs.* stability for average yield plant⁻¹

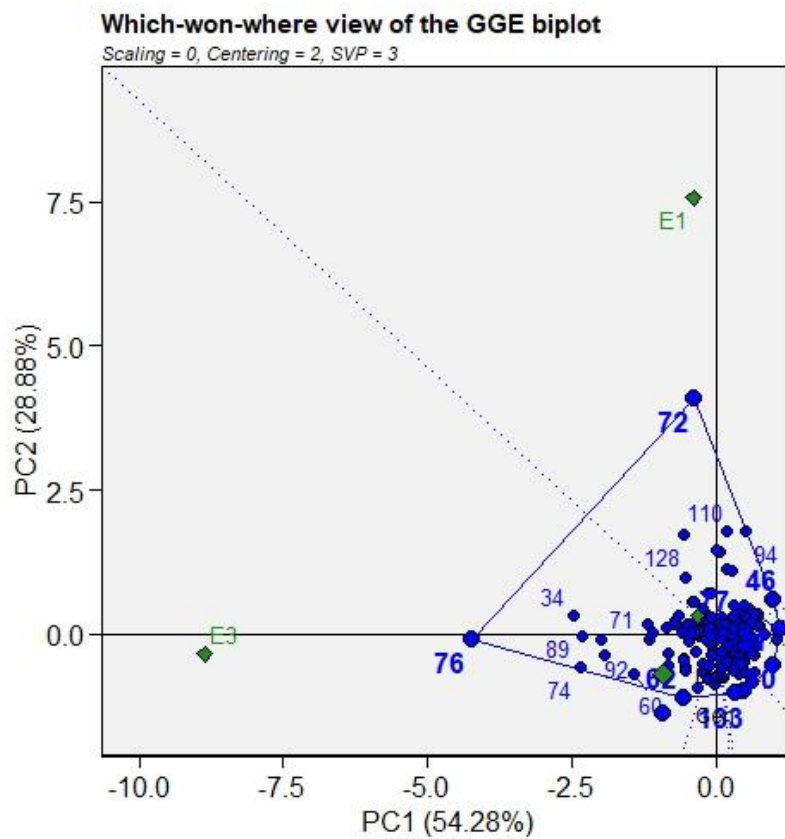


Fig. 5a. Polygon view of GGE-biplot based on the symmetrical scaling for “which won-where” pattern of genotypes and location environments for cluster plant⁻¹

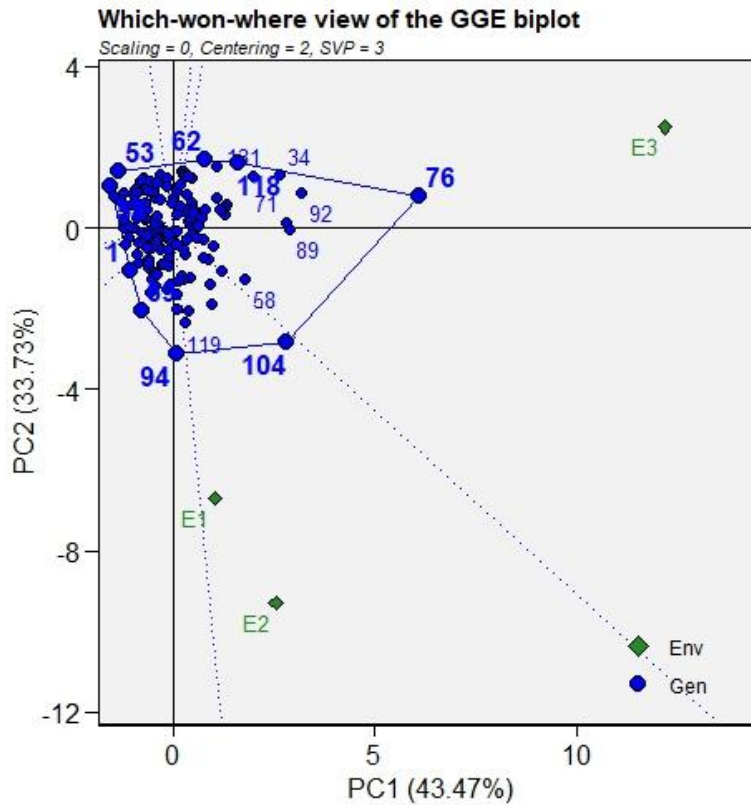


Fig. 5b. Polygon view of GGE-biplot based on the symmetrical scaling for “which won-where” pattern of genotypes and location environments for pods plant⁻¹

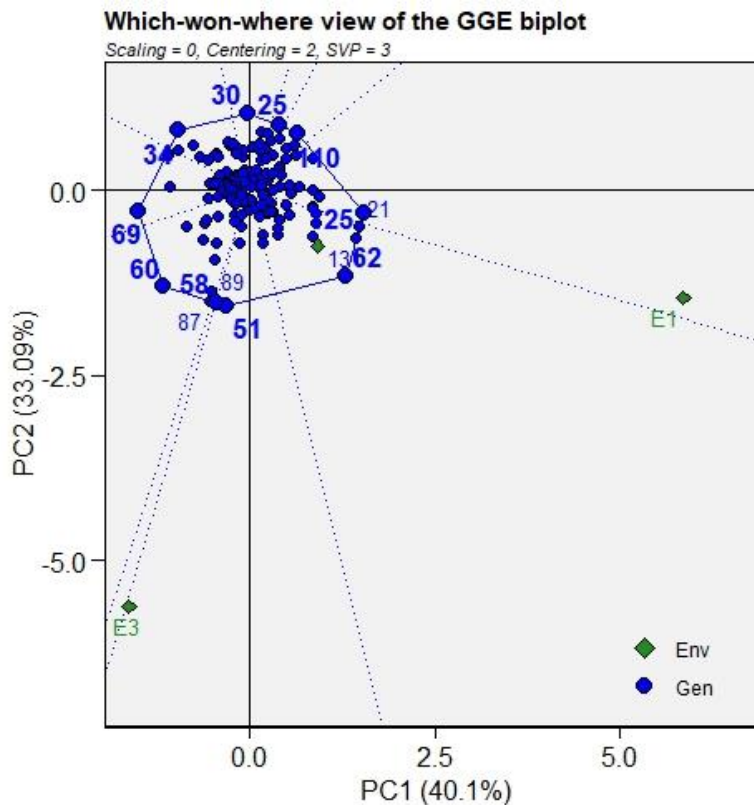


Fig. 5c. Polygon view of GGE-biplot based on the symmetrical scaling for “which won-where” pattern of genotypes and location environments for average pod length

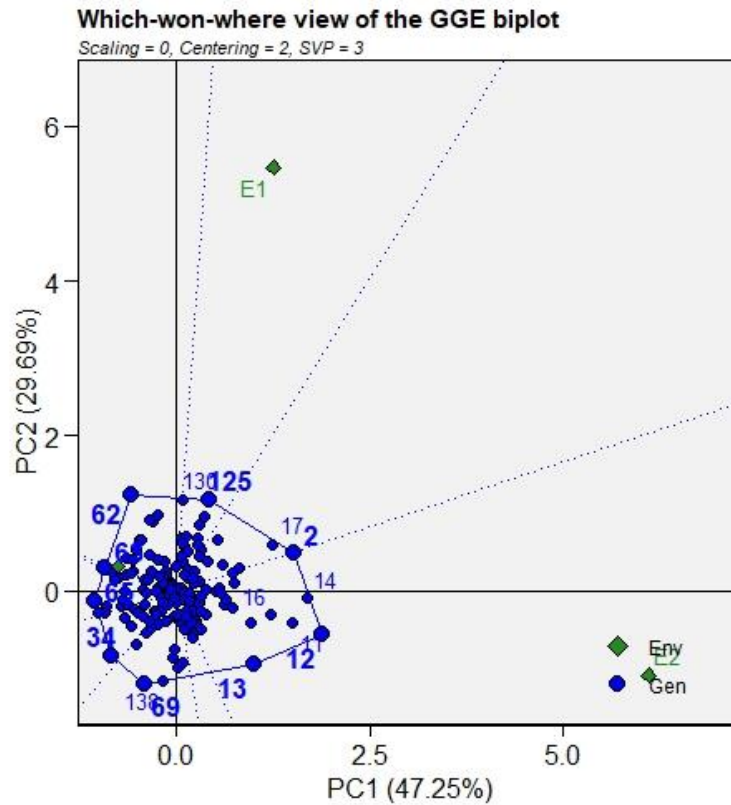


Fig. 5d. Polygon view of GGE-biplot based on the symmetrical scaling for “which won-where” pattern of genotypes and location environments for average seeds pod⁻¹

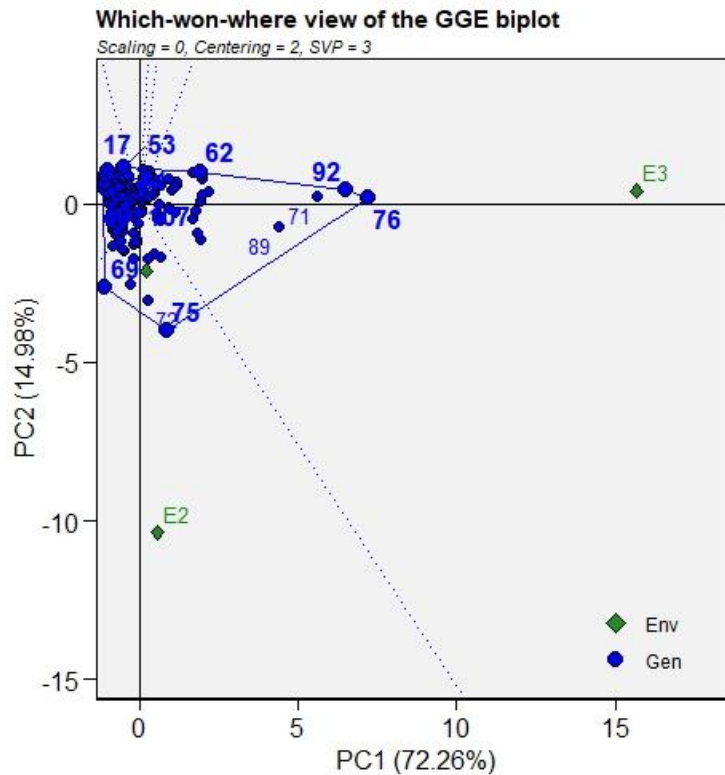


Fig. 5e. Polygon view of GGE-biplot based on the symmetrical scaling for “which won-where” pattern of genotypes and location environments for average grain yield plant⁻¹

4.5.1.4 'Which won where' pattern

Polygon view of GGE biplot helps in identifying which won where pattern of genotypes. A polygon is formed by joining all the genotypes farther from the biplot origin in such a way that all the other genotypes fall within the polygon. Dotted perpendicular lines called equality lines, originating from biplot origin are drawn to each side of the polygon. The equality lines divide the bi-plot into sectors. The vertex genotype in each sector is the winning genotype at environments whose point fall into the respective sector (Yan *et al.*, 2000). Thus, location environments whose point fall in the sector will have the same winning genotype, while location environments of different sectors have different winning genotypes. Thus, polygon view of GGE biplot indicates the presence or absence of crossover genotype \times location interaction.

In present study, genotypes V-585 (72) and IC-402098 (46) were the winning genotypes for E1 (Bengaluru) environment, genotypes VC-458492 (76), EC-472252 (62) and TPTC-29 (103) were winning genotypes in E2 (Pavagada) and E3 (Mandya) environment on account of them occupying the vertices of the polygon for clusters per plant (Fig. 5a). Further genotypes NBC-30 (94), NBC-18 (104), EC-402159 (69) and VCP-17-019 (1) were winning in E1 (Bengaluru) and E2 (Pavagada) environment and genotype VC-458492 (76), KM-5 (118) and EC-472252 (62) were winning in E3 (Mandya) environment for pods per plant (Fig. 5b). For average pod length EC-472252 (62) and 201095(32) (51) were the winning genotypes for E2 (Pavagada) and E3 (Mandya) environments and IC-330996 (25) and PMCP-1131 (110) were winning genotypes for E1 (Bengaluru) environment (Fig. 5c). Genotype NBC-4716(125) was winner in E1 (Bengaluru) environment, genotypes IC-249593 (12) and IC-4506 (13) were the winners in E2 (Pavagada) environment and genotype EC-472252 (62) was winner in E3 (Mandya) environment for average seeds per pod (Fig. 5d). For grain yield per plant, genotypes EC-402159 (69) and CB-1024 (75) were the winners in E1 (Bengaluru) and E2 (Pavagada) environments and genotype VC-458492 (76), NBC-51 (92) and EC-472252 (62) were the winners in E3 (Mandya) environment (Fig. 5e).

4.6 AMMI based stability parameters

4.6.1 AMMI Stability value (ASV)

ASV provides objective assessment of stability and hence help to identify genotypes stable over the three spatial environments. ASV is the distance from zero in a two-

dimensional scatter-gram of IPCA 1 (Interaction Principal Component Analysis Axis 1) scores against IPCA 2 (Interaction Principal Component Analysis Axis 2) scores. In the present study, ASV were estimated using both IPCA1 and IPCA2, as they significantly contributed towards total genotype \times location interaction variance of all the traits.

In the present study, the estimates of ASV were lower in magnitude with respect to the top three genotypes, EC-458483 (85), EC-394708 (79), NBC-18 (104) with ASV of 0.22, 0.29 and 0.33, respectively for average grain yield per plant (Table 13). And these genotypes were considered stable across three locations.

4.6.2 Stability Index

Stability index (SI) which incorporates both quantitative traits mean and stability in a single criterion helps in simultaneous selection of genotypes with desired performance for different quantitative traits coupled with stability. The genotypes with low SI are regarded as those with high trait expression and high stability.

In the present study, genotypes IC-198355(45) (18), EC-472271 (68), EC-394708 (79) were found with lower SI estimates of 35, 47, 51, respectively for average grain yield per plant (Table 13). These genotypes were regarded as the best ones with high trait mean and stability.

Based on ASV and SI top five stable cowpea genotypes across three different locations for different traits is listed in table 14.

Based on SI, the stable genotypes which were stable for multiple traits are listed in table 15. The genotype IC-402161 found stable for plant height (cm) and average pod length (cm), IC-25105 for plant height (cm) and clusters per plant, IC- 198355(45) for traits clusters per plant, pods per plant and average grain yield per plant and IC-402159 for clusters per plant and pods per plant.

Table 13. Estimates of AMMI model-based parameters to assess stability of cowpea genotypes across three locations for grain yield plant⁻¹

Sl. No	Genotype	Means (Y)	RY	ASV	RASV	SI
1	VCP-17-019	27.08	24	4.78	135	159
2	IC-253251	20.94	55	1.18	28	83
3	GC-3	23.64	37	2.86	101	138
4	EC-458511	22.73	42	2.21	75	117
5	NBC-8	22.60	43	3.75	124	167
6	IC-202867(99)	15.13	120	0.51	7	127
7	IC-603187	30.82	13	6.51	145	158
8	IC-462099	25.16	34	1.48	42	76
9	IC-402048	18.83	74	0.90	19	93
10	IC-249141	10.35	155	2.31	78	233
11	IC-422174	20.58	58	2.86	100	158
12	IC-249593	15.48	117	3.48	116	233
13	IC-4506	17.69	92	3.58	118	210
14	IC-198326-38	21.25	54	0.97	22	76
15	IC-402125	14.45	133	1.96	64	197
16	IC-1070	18.68	77	0.93	21	98
17	IC-402164	21.83	50	1.88	60	110
18	198355(45)	30.93	12	1.03	23	35
19	IC-402106	15.07	122	2.95	105	227
20	IC-1071	13.18	139	1.94	63	202
21	IC-25105	20.74	57	2.52	88	145
22	IC-402172	28.00	21	7.59	150	171
23	IC-458430	21.48	52	1.33	36	88
24	IC-58905	11.18	152	1.70	46	198
25	IC-330996	19.22	70	0.87	18	88
26	IC-202325	18.76	75	2.95	106	181
27	IC-237422	16.90	101	2.87	102	203
28	IC-45061	19.84	64	0.71	13	77
29	IC-219489	14.53	129	0.63	11	140
30	IC-402159	18.99	72	1.20	29	101
31	IC-206240	12.38	143	1.77	54	197
32	IC-202792(72)	16.77	104	2.17	70	174
33	IC-402135	25.30	33	2.82	97	130
34	IC-402104	20.53	61	2.99	108	169
35	IC-249588	19.02	71	0.85	17	88
36	IC-202781	12.59	142	2.44	83	225
37	IC-202777	28.72	17	7.52	149	166
38	IC-402162	18.18	85	0.80	16	101
39	IC-402175	15.22	119	2.00	66	185
40	IC-202711(58)	14.34	135	1.45	40	175
41	IC-10171	25.84	32	2.85	99	131

Sl. No	Genotype	Means (Y)	RY	ASV	RASV	SI
42	IC-202290	30.19	14	8.07	152	166
43	2574422(7)	27.01	26	2.83	98	124
44	IC-402161	19.77	67	0.93	20	87
45	IC-402101	18.65	78	1.12	26	104
46	IC-402098	17.90	88	1.44	38	126
47	IC-402114	11.29	151	0.38	5	156
48	IC-107120	16.55	108	1.65	45	153
49	202521(93)	26.68	27	4.07	128	155
50	27749(20)	26.54	28	4.57	130	158
51	201095(32)	22.17	46	1.73	50	96
52	202854(97)	19.53	69	1.76	52	121
53	202329-89	27.84	22	5.36	137	159
54	EC-394838	22.48	44	5.40	138	182
55	EC-458469	18.41	83	1.20	30	113
56	EC-458505	17.78	89.5	1.11	25	114.5
57	EC-458470	10.83	154	1.77	53	207
58	EC-458440	14.50	130	1.13	27	157
59	EC-170574-6	17.38	97	1.82	56	153
60	EC-458485	14.11	137	1.73	51	188
61	EC-271040	16.55	107	1.97	65	172
62	EC-472252	17.05	99	2.81	95	194
63	EC-458442	13.16	140	2.36	79	219
64	V-604-7-29-3	14.35	134	2.50	85	219
65	EC-472257	15.53	115	3.91	126	241
66	EC-458489	26.31	30	3.46	115	145
67	EC-170584-1.1	21.65	51	1.88	59	110
68	EC-472271	28.77	16	1.22	31	47
69	EC-402159	14.91	124	1.61	44	168
70	EC-492292	23.44	38	4.78	134	172
71	V-578	11.70	149	2.21	74	223
72	V-585	17.39	95	2.04	68	163
73	V-589	14.11	136	2.64	91	227
74	VCP-18-032	24.22	36	2.31	77	113
75	CB-1024	17.38	96	0.52	8	104
76	VC-458492	26.17	31	6.70	146	177
77	V-240	16.30	111	2.27	76	187
78	IC-402166	15.11	121	0.60	10	131
79	EC-394708	21.97	49	0.30	2	51
80	EC-458473	14.48	132	1.44	39	171
81	EC-075180	18.43	82	2.38	81	163
82	V-16	18.04	86	2.98	107	193
83	EC-472250	14.60	127	3.60	120	247
84	EC-458490	16.61	106	2.52	87	193

Sl. No	Genotype	Means (Y)	RY	ASV	RASV	SI
85	EC-458483	14.66	125	0.22	1	126
86	EC-458411	12.04	146	1.29	35	181
87	EC-390287	11.75	148	1.70	47	195
88	EC-458425	17.78	89.5	2.51	86	175.5
89	EC-170604	19.95	63	4.83	136	199
90	EC-472267	22.04	48	0.73	14	62
91	EC-394839	24.76	35	1.23	32	67
92	NBC-51	10.99	153	2.61	90	243
93	NBC-391	14.66	126	2.81	96	222
94	NBC-30	17.43	94	2.53	89	183
95	NBC-23	9.74	156	1.80	55	211
96	NBC-32	16.80	103	0.36	4	107
97	NBC-98	12.15	145	0.45	6	151
98	NBC-68	11.53	150	2.43	82	232
99	NBC-36	16.67	105	1.27	33	138
100	NBC-6	14.48	131	1.73	49	180
101	NBC-38	28.26	19	1.46	41	60
102	NBC-33	32.96	9	5.84	142	151
103	TPTC-29	28.17	20	1.87	58	78
104	NBC-18	12.21	144	0.33	3	147
105	NBC-27	16.97	100	0.79	15	115
106	NBC-29	18.27	84	1.70	48	132
107	NBC-19	27.30	23	7.62	151	174
108	TOME-774	11.82	147	2.47	84	231
109	PCP-0306-1	23.03	41	1.92	61	102
110	PMCP-1131	19.82	66	0.71	12	78
111	NBC-14	20.55	60	4.65	132	192
112	NBC-016	15.88	114	1.28	34	148
113	SUPER-30	34.07	7	3.97	127	134
114	KBC-2	22.11	47	6.75	147	194
115	CPD-331	18.50	81	3.85	125	206
116	PMCP-1016	20.88	56	3.41	114	170
117	PCD-1124-1	48.39	3	19.36	154	157
118	KM-5	41.76	5	6.08	143	148
119	NBC-40	23.15	39	2.03	67	106
120	NBC-43	32.11	10	5.63	141	151
121	GWHOPE	40.17	6	3.65	121	127
122	GC-1801	61.98	1	23.04	156	157
123	NBC-41	14.54	128	1.86	57	185
124	GC-1805	20.41	62	4.64	131	193
125	NBC-4716	23.09	40	2.69	92	132
126	C-457	17.70	91	1.52	43	134
127	CPD-15	22.38	45	1.09	24	69

Sl. No	Genotype	Means (Y)	RY	ASV	RASV	SI
128	GC-1602	18.71	76	2.17	71	147
129	CB-10	26.45	29	4.42	129	158
130	C-33	15.41	118	2.11	69	187
131	IT-9715499-38	28.26	18	7.52	148	166
132	NBC-25	16.36	110	2.36	80	190
133	C-157	31.46	11	5.44	139	150
134	C-24-1	17.48	93	1.94	62	155
135	CP-98	27.07	25	3.66	122	147
136	CPD-340	47.45	4	13.38	153	157
137	SKUA-WCP-49	21.36	53	4.69	133	186
138	NBC-44	13.08	141	2.18	72	213
139	NBC-24	20.55	59	2.78	94	153
140	EC-394779	54.53	2	22.12	155	157
141	IC-2591054	13.50	138	0.56	9	147
142	IC-402090	29.10	15	6.17	144	159
143	NBC-7	16.47	109	2.91	103	212
144	EC-458438	14.99	123	1.35	37	160
145	EC-458418	17.24	98	3.37	112	210
146	EC-458480	15.51	116	2.18	73	189
147	202804(83)	33.01	8	5.52	140	148

Where, Y – mean value of grain yield per plant; RY – rank of mean; ASV – AMMI stability value; RASV – rank of AMMI stability value; SI – stability index

Table 14. Top five stable cowpea genotypes across three locations identified based on ASV and SI for different traits.

Characters	Based on SI	Based on ASV
Days to 50% flowering	NBC-29, V-16, EC-458473, IC-58905, IC-202781	NBC-29, NBC-27, TOME-774, NBC-4716, NBC-44
Plant height (cm)	CP-98, IC-45061, IC-402161, IC-25105, IC-402098	IC-402161, 202804(83), CP-98, IC-402098, IC-458430
Primary branches plant⁻¹	EC-458480, 202804(83), KBC-2(c), EC-458485, IC-402048	EC-458485, EC-472250, PCD-1124-1, IC-402048, NBC-25
Clusters plant⁻¹	198355(45), IC-402159, V-589, NBC-14, IC-25105	IT-9715499-38, V-240, IC-202711(58), EC-394708, IC-402159
Pods cluster⁻¹	IC-10171, IC-4506, V-604-7-29-3, C-24-1, IT-9715499-38	IC-58905, IC-202781, IC-402106, EC-458483, IC-4506

Characters	Based on SI	Based on ASV
Pods plant ⁻¹	198355(45), C-33, IC-202290, GC-1805, IC-402159	IC-202792(72), NBC-23, IC-402090, EC-458490, EC-472271
Average pod length (cm)	IC-402162, KBC-2(C), NBC-25, IC-402175, IC-603187	EC-472250, IC-402162, C-152 (c), IC-249593, NBC-25
Average seeds pod ⁻¹	GC-1801, IC-402161, EC-170574-6, IC-462099, C-152(C)	NBC-23, EC-472250, KBC-9 (c), SKUA-WCP-49, IC-422174
Average Grain yield plant ⁻¹ (g)	198355(45), EC-170584-1.1, IC-402166, NBC-36, EC-458425	EC-458490, IC-402166, NBC-33, NBC-30, IC-402098
100 seed weight (g)	NBC-4716, TPTC-29, NBC-7, CB-10, IC-402106	IC-198326-38, Genotype-36, GC-1801, NBC-27, 202521(93)

Table 15. Stable cowpea genotypes across three different locations identified based on SI for multiple traits.

Stable genotypes based on SI	Multiple traits for which genotypes found stable
IC-402161	Plant height (cm) and average pod length (cm)
IC-25105	Plant height (cm) and clusters plant ⁻¹
IC- 198355(45)	Clusters plant ⁻¹ , pods plant ⁻¹ and average grain yield plant ⁻¹ (g)
IC-402159	clusters plant ⁻¹ and pods plant ⁻¹

SUMMARY

V. SUMMARY

Preamble: Cowpea is predominantly a self-pollinated crop with good source of protein (popularly known as poor man's meat) and a multi utility crop, cultivated in semi-arid and arid regions of the world. Variability, clustering and stability studies are essential to exercise selection in any crop. Variability and cluster studies are helpful in selection of parents. The performance of different varieties varies significantly. Some genotypes perform well in certain environments but not so well in others. Plant breeders should focus on developing cowpea genotypes with consistent high yielding capacity in a range of environments. Keeping all these aspects, the current research was carried out at Zonal Agricultural research Station (ZARS), GKVK, Bengaluru, ZARS, VC Farm, Mandya and Agricultural Research Station (ARS), Pavagada to generate information for variability, diversity and stability parameters.

Objectives: (i) To study the genetic variability for yield and its associated traits. (ii) To work out the G x E interaction for yield and yield attributes. (iii) Identification of high yielding cowpea lines

Material and methods: For the present study 147 cowpea germplasm accessions were used along with two checks KBC-9 and C-152 for evaluation in alpha lattice design with two replications in summer season of 2022. Data was recorded on days to 50 *per cent* flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, average pod length, average seeds per pod, average grain yield per plant and 100 seed weight from five randomly selected plants, avoiding border plants and averaged.

Data obtained for above traits were subjected to alpha lattice ANOVA, descriptive statistics, variability studies, clustering studies, Additive Main Effects and Multiplicative Interaction (AMMI) model Analysis to detect Genotype × Environment interaction, four types of Genotype + Genotype × Environment (GGE) bi-plots, AMMI Stability Value (ASV), Stability Index (SI) to interpret the results.

Salient features of experimental findings are summarized below.

- Alpha lattice ANOVA showed significant differences among genotypes for all traits under study indicating that all genotypes performed differently with respect to each other in three environments

- Pooled alpha lattice ANOVA showed significant genotype \times environment interaction for all traits under study
- High heritability with high genetic advance as *per cent* of mean was observed for plant height, primary branches per plant, pods per plant, average pod length, average seeds per pod and average grain yield per plant at all three locations
- K- means clustering method was used to classify the 147 genotypes, as a result 12 clusters were identified
- The cluster 8 was the largest with 22 genotypes and cluster 4 was smallest with four genotypes.
- Genotypes with highest average grain yield per plant were observed in cluster 7 which can be used for selection of parent with grain yield as target trait
- Cluster 7 and cluster 6 had highest inter cluster distance as evident by inter cluster distance and genotypes belonging to these clusters can be used as parents for further crop improvement programme
- Based on mean vs. stability pattern, the genotypes KBC-2, IC-237422 and EC-170574- 6 were found to be highly stable with high mean average grain yield per plant
- Based on ‘which won- where’ pattern for average grain yield per plant, genotypes IC-402159 and CB-1024 were better in Bengaluru, and Pavagada location and genotypes IC-458492, NBC-51 and EC-472252 were better in Mandya location
- Based on ASV, the genotypes EC-458483, EC-394708, NBC-18 were found to be stable across all three locations
- Based on SI, the genotypes IC-198355(45), EC-472271, EC-394708 were found stable with high mean average grain yield per plant
- The genotype IC-198355(45) was found stable for clusters per plant, pods per plant and average grain yield per plant

Future line of work

- Based on clustering results, genotypes from cluster 7 and cluster 6 can be used as parents for crossing for crop improvement
- Genotypes IC-198355(45), EC-472271, EC-394708 which were found to have high SI are suggested for large scale evaluation to confirm their stability

REFERENCES

VI. REFERENCES

- ADEIGBE, O. O., ADEWALE, B. D. AND FAWOLE, I. O., 2011, Genetic variability, stability and relationship among some cowpea, [*Vigna unguiculata* (L.) Walp] breeding lines. *J. Plant Breed. Crop Sci.*, **3**(9): 203-208.
- ADEWALE, B. D., OKONJI, C., OYEKANMI, A. A., AKINTOBI D. A. C. AND AREMU, C. O., 2010, Genotypic variability and stability of some grain yield components of cowpea. *Afr. J. Agric. Res.*, **5**(9): 874-880.
- AGBAHOUNGBA, S., KARUNGI, J., ODONG, T. L., BADJI, A., SADIK, K. AND RUBAIHAYO, P. R., 2017. Stability and extent of resistance of cowpea lines to flower bud thrips in Uganda. *Afr. Crop Sci. J.* **25**(1): 1-24.
- AHAMED, K. U., AKHTER, B., ISLAM, M. R., ALAM, M. A. AND HUMAUAN, M. R., 2014, Assessment of genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm. *Bull. Inst. Trop. Agr.*, **37**: 57-63.
- AJAYI, A. T., ADEKOLA, M. O., TAIWO, B. H. AND AZUH, V. O., 2014, Character expression and differences in yield potential of ten genotypes of cowpea [*Vigna unguiculata* (L.) Walp]. *Int. J. Plant Res.*, **4**(3): 63-71.
- AKANDE, S. R., 2007, Genotype \times environment interaction for cowpea seed yield and disease reaction in the forest and derived savanna agro-ecologies of south-west Nigeria. *American-Eurasian J. Agric. Environ. Sci.*, **2**(2): 163-168.
- ALI, Y., ASLAM, Z., HUSSAIN, F. AND SHAKUR, A., 2004, Genotype and environmental interaction in cowpea (*Vigna Unguiculata*. (L) Walp) for yield and disease resistance. *Int. J. Environ. Sci. Technol.*, **1**: 119-123.
- ALLARD, R. W. AND BRADSHAW, A. D., 1964, Implication of genotype \times environmental interactions in plant breeding. *Crop Sci.*, **4**: 503-8.
- ALLARD, R. W., 1960, Selection under self-fertilization. Principles of Plant Breeding. John Wiley & Sons, Inc. New York, USA.
- ANIMASAUN, D. A., OYEDEJI, S., MUSTAPHA, O. T. AND AZEEZ, M. A., 2015, Genetic variability study among ten cultivars of cowpea [*Vigna unguiculata* (L.)

Walp] using morpho-agronomic traits and nutritional composition. *J. Agric. Sci.*, **10**(2): 119-130.

AREMU, C. O., ARIYO, O. J. AND ADEWALE, B. D., 2007, Assessment of selection techniques and genotype × environment interaction in cowpea. *Afr. J. Agric. Res.*, **2**(8): 352-355.

BHANDARI, M. S. AND VERMA, J. S., 2007. Genetic divergence and correlation studies in forage cowpea [*Vigna unguiculata* (L.) Walp]. *Forage Res.*, **33**(33): 133-138.

BORAH, H. K. AND KHAN, A. K. E., 2001, Genetic divergence in fodder cowpea [*Vigna unguiculata* (L.) Walp] *Madras Agric. J.*, **88**(10-12): 625-628.

CHANDRAKAR, R., VERMA, A., SINGH, J. AND MEHTA, N., 2016, Studies on genetic divergence in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. *Int. J. Agric. Sci.* **63**(8): 3545-3547.

CHATTERJEE, B. N. AND BHATTACHARYA, K. K., 1986, Principle and practices of grain legume production. Oxford and IBH publishing Co. Ltd., New Delhi.

CHATTOPADHYAY, A., RANA, N. P., SETH, T., DAS, S., CHATTERJEE, S. AND DUTTA, S., 2014, Identification of selection indices and choosing of parents for vegetable cowpea [*Vigna unguiculata* ssp. *sesquipedalis*] breeding programme. *Legume Res.*, **37**(1): 19-25.

DALSANIYA, S. B., POSHIYA, V. K., SAVALIYA, J. J. AND DAVADA, B. K., 2009. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp]. *Legume Res.*, **32**(4): 250-254.

DEVI, S. M. AND JAYAMANI, P., 2018, Genetic variability, heritability, genetic advance studies in cowpea germplasm [*Vigna unguiculata* (L.) Walp.]. *Electron. J. Plant Breed.*, **9**(2): 476-481.

DINESH, H. B., VISWANATHA, K. P., LOHITHASWA, H. C., PAVAN, R. AND POONAM, S., 2017, Variability, correlation and path analysis studies in F₃ generation of cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Curr. Microbiol. Appl. Sci.*, **9**(9): 1420-1428.

- EBERHART, S. T. AND RUSSELL, W. A., 1966, Stability parameters for comparing varieties 1. *Crop Sci.*, **6**(1): 36-40.
- EHLERS, J. D. AND HALL, A. E., 1997, Cowpea [*Vigna unguiculata* (L.) Walp.] *Field Crops Res.*, **53**:187-204.
- EL-SHAIENY, A. H., ABDEL, Y. Y., EL-DAMARANY, A. M. AND RASHWAN, A. M., 2015, Stability analysis of components characters in cowpea (*Vigna unguiculata* (L.) Walp.). *J. Hort. Forest.*, **7** (2): 24-35.
- FARSHADFAR, E., MAHMODI, N., AND YAGHOTIPOOR, A., 2011, AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum*). *Aust. J. Crop sci.*, **5**(13): 1837-1844.
- GABRIEL, D., CARLOS, A. S., PETER, O., MILDRED, A. AND CHARLES, K. L., 2015, Grain yield and protein content of Brazilian cowpea genotypes under diverse Ugandan environments. *American J. Plant Sci.*, **6**: 2074-2084.
- GARDENER, F. P., PEARCE, R. B. AND MICHELL, R. L., 1985, *Physiology of Crop Plants*. United Press Iowa State.
- GAUCH, H. G. AND ZOBEL, R.W., 1988, Predictive and postdictive success of statistical analyses of yield trials. *Theor. Appl. Genet.*, **76**(1): 1-10.
- GERRANO, A. S., JANSEN VAN RENSBURG, W. S., MATHEW, I., SHAYANOWAKO, A. I., BAIRU, M.W., VENTER, S. L., SWART, W., MOFOKENG, A., MELLEM, J. AND LABUSCHAGNE, M., 2020, Genotype and genotype × environment interaction effects on the grain yield performance of cowpea genotypes in dryland farming system in South Africa. *Euphytica*, **216**(5): 1-11.
- HANUMANTHRAYA, B. H, 2003, Genetic evaluation and stability analysis for yield and its components in cowpea (*Vigna unguiculata* (L) Walp.). *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).
- HORN, L., NGHITUWAMATA, S. N. AND UEITELE, I., 2022, Cowpea production challenges and contribution to livelihood in Sub-Sahara region. *J. Agric. Sci.*, **13**: 25-32.

- HUQUE, A. K. M., HOSSAIN, M. K., ALAM, N., HASANUZZAMAN, M. AND BISWAS, B. K., 2012, Genetic divergence in yardlong bean [*Vigna unguiculata* (L.) Walp. ssp. *sesquipedalis* verdc.]. *Bangladesh J. Bot.*, **41**(1): 61-69.
- IDAHOUSA, D. O., ALIKA, J. E. AND OMOREGIE, A. U., 2010, Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in cowpea [*Vigna unguiculata* (L.) Walp]. *Acad. Arena*, **2**(5): 22-26.
- IMRAN, M., HUSSAIN, A., HUSSAIN, S., KHAN, S., BAKHSH, A., ZAHID, M. AND BAIG, D., 2010, Character association and evaluation of cowpea germplasm for green fodder and grain yield under rainfed conditions of Islamabad. *Sarhad J. Agric.*, **26**(3): 319-323.
- INUWA, A. H., AJEIGBE, H. A., MUHAMMAD, M. I. AND MUSTAPHA, Y., 2012, Genetic variability and heritability of some selected cowpea [*Vigna unguiculata* (L.) Walp] lines. *Int. Proc. 46th Ann. Conf. Agric. Soc. Niger.*, 5th – 9th Nov. Kano, Nigeria.
- JOHNSON, R. W., ROBINSON, H. F. AND COMSTOCK, R. E., 1955, Estimates of genetic and environment variability in soybean. *Agron. J.*, **47**: 314-318.
- KANAVI, P. M. S., KOLER, P., SOMU, G. AND MARAPPA, N., 2020, Genetic diversity study through k-means clustering in germplasm accessions of green gram [*Vigna radiata* (L.)] under drought condition. *Int. J. Bio-resour. Stress Manag.*, **11**(2):138-147.
- KHAN, H., VISWANATHA, K. P. AND SOWMYA, H. C., 2015, Study of genetic variability parameters in cowpea [*Vigna unguiculata* (L.) Walp] germplasm lines. *Bioscan*, **10**(2): 747-750.
- KHANPARA, S. V., JIVANI, L. L., VACHHANI, J. H. AND KACHHADIA, V. H., 2016, Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. *Electron. J. Plant Breed.*, **7**(2):408-413.
- KHARDE, R. P., KALE, V. S. AND BHOGAVE, A. F., 2014, Genetic variability studies in cowpea. *Bioinfolet.*, **11**(1): 113-118.

- KINDIE, Y., TESSO, B. AND AMSALU, B., 2021. Genotype \times Environment interaction and yield stability in early-maturing cowpea (*Vigna unguiculata* (L.) Walp.) landraces in Ethiopia. *Adv. Agric.*, **2021**: 1-10
- KUMAR, N. M., GANGAPRASAD, S. AND SUNIL, M. G., 2015, Genetic variability and heritability studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *Res. J. Agric. Sci.*, **6**(4): 763-766.
- KURUMA, R.W., SHEUNDA, P. AND KAHWAGA, C. M., 2019, Yield stability and farmer preference of cowpea (*Vigna unguiculata*) lines in semi-arid eastern Kenya. *Afr. Focus*, **32**(2): 65-82.
- LOVELY, B. AND RADHADEVI, D. S., 2017, Estimates of genetic variability, heritability and genetic advance for yield and yield component traits in vegetable cowpea [*Vigna unguiculata* ssp. *sesquipedalis* (L.) Verdc.] genotypes. *J. Pharmacogn. Phytochem.*, **6**(5): 1165-1169.
- LUSH, J. L., 1945, Heritability of quantitative characters in farm animals. *Proc. 8th Cong. Hereditas, (Suppl)* **35**: 356-375.
- MACQUEEN, J., 1967, Classification and analysis of multivariate observation. *5th Berkeley Symp. Math. Statist. Probability*: 281-297.
- MAHMUDUL HUQUE, A. K. M., HOSSAIN, M. K., ALAM, N., HASANUZZAMAN, M., BISWAS, B. K. AND ARIFUZZAMAN, M., 2012, Genetic variability, correlation and path analysis for yield and its component characters in string bean (*Vigna unguiculata* ssp. *sesquipedalis* L.), *J. Biol. Sci.*, **1**(1): 1-10.
- 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 cowpea [*Vigna unguiculata* (L.) Walp] accessions. *J. Plant Breed. Crop Sci.*, **4**(5): 80-86.
- MEENA, H. K., KRISHNA, K. R. AND SINGH, B., 2015, Genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata* (L.) Walp.]. *J. Plant Sci. Res.*, **31**(1): 13-16.

- MEENA, H. K., KRISHNA, K. R., SINGH, B. AND KARELA, T., 2015, Assessment of genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp] germplasm. *Bioscan.*, **10**(4): 1921-1924.
- MOFOKENG, M. A., MASHILO, J., RANTSO, P. AND SHIMELIS, H., 2020, Genetic variation and genetic advance in cowpea based on yield and yield-related traits. *Acta. Agr. Scand. B-S P.* **1**(1):1-11.
- NAGALAKSHMI, R. M., KUMARI, R. U. AND BORANAYAKA, M. B., 2010, Assessment of genetic diversity in cowpea (*Vigna unguiculata*). *Electron. J. Plant Breed.*, **1**(4): 453-461.
- NELIA, N., 2013, Stability of yield and antioxidant content of selected advanced cowpea (*Vigna unguiculata* [L] Walp.) mutation derived lines. *M. Sc Thesis*. University of Zambia, Lusaka.
- NKOANA, D. K., GERRANO, A. S. AND GWATA, E. T., 2019, Agronomic performance and genetic variability of cowpea (*Vigna unguiculata*) accessions. *Legume Res.*, **42**(6): 757-762.
- NWOSU, D. J., OLATUNBOSUN, B. D. AND ADETILOYE, I. S., 2013, Genetic variability, heritability and genetic advance in cowpea genotypes in two agro-ecological environments. *Greener J. Biol. Sci.*, **3**: 202–207.
- OLAWALE, M. A. AND BUKOLA, O. M., 2016, Phenotypic analysis of seed yield and yield components in cowpea (*Vigna unguiculata* (L) Walp.). *Plant Breed. Biotechnol.*, **4**(2): 252-261.
- OLAYIWOLA, M. O. AND SOREMI, P. A. S., 2014, Variability for dry fodder yield and component traits in cowpea [*Vigna unguiculata* (L.) Walp]. *Electron. J. Plant Breed.*, **5**(1): 58-62.
- OLAYIWOLA, M. O., SOREMI, P. A. AND OKELEYE, K. A., 2015, Evaluation of some cowpea (*Vigna unguiculata* (L) Walp.) genotypes for stability of performance over 4 years. *Curr. Res. Agric. Sci.*, **2**(1): 22-30.
- OWUSU, E. Y., KARIKARI, B., KUSI, F., HARUNA, M., AMOAH, R. A., ATTAMAH, P., ADAZEBRA, G., SIE, E. K. AND ISSAHAKU, M., 2021, Genetic variability, Characterization of germplasm for yield and it's associated traits in cowpea [*Vigna unguiculata* (L.) Walp] 70

- heritability and correlation analysis among maturity and yield traits in cowpea (*Vigna unguiculata* (L.) Walp) in Northern Ghana. *Heliyon*, **7**(9): e07890.
- PANDEY, P. K., LAL, H. AND VISHWA NATH, 2014, Hierarchical clustering, genetic variability, correlation and path analysis studies in cowpea (*Vigna unguiculata* L. Walp.). *J. Food Legumes*, **27**(2): 158-160.
- PASQUET, R. S., 1999, Genetic relationships among subspecies of *Vigna unguiculata* (L.) Walp. based on allozyme variation. *Theor. Appl. Genet.*, **98**(6-7): 1104-1119.
- 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. *Electron. J. of Plant Breed.*, **8**(1): 331-335.
- PATTERSON, H. D. AND WILLIAMS, E., 1976, A new class of resolvable incomplete block designs. *Biometrika.*, **63**(1): 83-92.
- PHOGAT, D. S., PANCHTA, R., KUMARI, P., NIWAS, R. AND ARYA, S., 2017, Variability, correlation and path analysis studies in fodder cowpea [*Vigna unguiculata* (L.) Walp]. *Trends Biosci.*, **10**(3): 1130-1132.
- PURCHASE, H. C., 2000, Effective information visualisation: a study of graph drawing aesthetics and algorithms. *Interact. Comput.*, **13**(2): 147-162.
- PUROHIT, P., NAUTIYAL, M. K., BHATT, L., MASSEY, P. AND PAL, K., 2020, Estimation of genetic advance, heritability, genetic gain and genetic diversity of elite genotypes of grain cowpea [*Vigna unguiculata* (L.) Walp]. *Int. J. Chem. Stud.*, **8**(2): 631-637.
- ROBINSON, H. F., COMSTOCK, R. E. AND HARVEY, P. H., 1949, Estimates of heritability and degree of dominance in corn. *Agron. J.*, **41**: 353-359.
- SABALE, G. R., BHAVE, S. G., DESAI, S. S., DALVI, M. B. AND PAWAR, P. R., 2018, Variability, heritability and genetic advance studies in F₂ generation of cowpea (*Vigna unguiculata* ssp. *unguiculata*). *Int. J. Curr. Microbiol. App. Sci.*, **7**(9): 3314-3320.
- SAPARA, G. K., JAVIA, R. M. AND POKAR, M. V., 2014, Genetic variability, heritability and genetic advance in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. *Int. J. Plant Sci.*, **9**(2): 326-329.

- SEGHERLOO, A. E., SABAGHPOUR, S. H., DEGHANI, H. AND KAMRANI, M., 2010, Screening of superior chickpea genotypes for various environments of Iran using genotype plus genotype \times environment (GGE) biplot analysis. *J. Plant Breed. Crop Sci.*, **2**(9): 286-292.
- SHANKO, D., ANDARGIE, M. AND ZELLEKE, H., 2014, Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.). *Res. Plant Biol.*, **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. *J. Pharmacogn. Phytochem.*, **6**(4): 1384-1387.
- SHINDE, V. N., SARGAR, P. R., TOPROPE, R. J., GAVALI, R. G. AND SAMINDRE, S., 2021, Heritability and genetic advance as indices for yield and yield components selection in cowpea (*Vigna unguiculata* L. Walp.). *Int. J. Plant Animal Env. Sci.*, **7**(04): 297-299.
- SINGH A., DEEPANSHU, BAHADUR V., 2022, Genetic variability, heritability, correlation studies and path coefficient in cowpea [*Vigna unguiculata* (L.) Walp.]. *Pharma Innov.*, **11**(5): 1318-1324.
- SINGH, O. V., SHEKHAWAT, N., SINGH, K. AND GOWTHAMI, R. 2018, Genetic divergence studies in cowpea [*Vigna unguiculata* (L.) Walp] germplasm using Mahalanobis D^2 analysis. *Int. J. Curr. Microbiol. App. Sci.*, **7**(3): 2616-2624.
- SINGH, O. V., SHEKHAWAT, N., SINGH, K. AND GOWTHAMI, R., 2020, Assessment of genetic variability and inter-character association in the germplasm of cowpea (*Vigna unguiculata* (L.) Walp) in hot arid climate. *Legume Res.*, **43**(3): 332-336.
- SULNATHI, G., PRASANTHI, L. AND SEKHAR, M. R., 2007. Character contribution to diversity in cowpea. *Legume Res.*, **30**(1): 70 - 72.
- SURPURA, M. H. AND SHARMA, S. C., 2017, Association studies for morphological and physiological traits in cowpea (*Vigna unguiculata* (L.) Walp.). *Allahabad Farmer.*, **73**(2): 52-56.

- TARIKU, S., WASSU, M., AND BERHANU, A., 2018. Genotype by environment interaction and stability analysis of cowpea [*Vigna unguiculata* (L.) Walp] genotypes for yield in Ethiopia. *J. Plant Breed. Crop Sci.*, **10**(9): 249-257.
- THORAT, A. AND GADEWAR, R. D., 2013, Variability and correlation studies in cowpea (*Vigna unguiculata*). *Int. J. Environ. Rehab. Conserv.*, **4**(1): 44-49.
- TIGGA, K. AND TANDEKAR, K., 2013, Genetic Divergence for yeild and quality components in cowpea [*Vigna unguiculata* (L.) Walp]. *Biosci. Trends*, **6**(5): 555-557.
- TIMKO, M. P., EHLERS, J. D., AND ROBERTS, P. A., 2007, Cowpea. In Pulses, sugar and tuber crops. *Springer Sci. Rev.*, **3**: 49-67.
- TORRES, F. E., TEODORO, P. E., RODRIGUES, E. V., SANTOS, A., CORREA, A. M. AND CECCON, G., 2016, Simultaneous selection for cowpea (*Vigna unguiculata* L.) genotypes with adaptability and yield stability using mixed models. *Genet. Mol. Res.*, **15** (2): 1-11.
- UDENSI, O. U. AND EDU, N. E., 2015, Evaluation and identification of genetic variation pattern in cowpea [*Vigna unguiculata* (L.) Walp] accessions using multivariate analyses. *J. Basic App. Sci.*, **11**: 149-158.
- USHAKUMARI, R., BACKIYARANI S. AND DHANAKODI, C. V., 2000. Character contribution to diversity in cowpea. *Legume Res.*, **23**(2): 122-125.
- VAVILAPALLI, S. K., CELINE, V. A., DUGGI, S., PADAKIPATIL, S. AND MAGADUM, S., 2013, Genetic variability and heritability studies in bush cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Genomics Genet.*, **4**(4): 27-31.
- VAVILOV, N. I. 1951, The origin, variation, immunity and plant breeding of cultivated plants. *Cron. Bot.*, **13**: 364.
- VENKATESAN A., VEERAMANI, N., THANGAVEL, P. AND GANESAN, J., 2004, Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp]. *Legume Res.*, **27**(3): 223-225.
- VERMA, A. K., MEHTA, A. K., GONTIA, A. S., SHARMA, D., SINGH, R. P. AND SINGH, P., 2019, Genetic variability, heritability and genetic advance studies for yield

components in F₂ generation of cowpea (*Vigna unguiculata* (L.) Walp). *Int. J. Chem.*, **7**(6): 3084-3088.

VINAY, K., RAO, P. J. M., KISHORE, N. S. AND HARI, Y., 2022, Genetic variability studies for seed yield and yield component traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *Electron. J. Plant Breed.*, **13**(2): 544-548.

VIR, O. AND SINGH, A. K., 2014, Genetic variability and inter-characters associations studies in the germplasm of cowpea [*Vigna unguiculata* (L.) Walp.] in fragile climate of western Rajasthan, India. *Legume Res.*, **37**(2): 126-132.

VISHWA NATH, LAL, H., RAI, M., RAI, N. AND RAM, D., 2009, Hierarchical clustering and character association studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *Indian J. Plant Genet. Resour.*, **22**(1): 22-25.

VISHWANATHAN, P. L., RAMAMOORTHY, N., BADARAJAN, N., MANIVANNAN, N. AND MURUGAN, E., 1998. D² statistics on cowpea genotypes. *Madras Agric. J.*, **85**(2): 132-133.

YAN, W. AND TINKER., N. A., 2006, Biplot analysis of multi-environment trial data. Principles and applications. *J. Plant Sci.*, **86**: 623–645.

YAN, W., HUNT, L. A., SHENG, Q. AND SZLAVNICS, Z., 2000, Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.*, **40**(3): 597-605

YAN, W., KANG, M. S., MA, B., WOODS, S. AND CORNELIUS, P. L., 2007, GGE Biplot vs. AMMI Analysis of genotype-by-environment data. *Crop Sci.*, **47**:643-655.