

**GENETIC VARIABILITY FOR IRON, ZINC,  
CALCIUM CONTENTS AND SEED YIELD IN  
SELECTED F<sub>4</sub> AND F<sub>5</sub> COWPEA  
[*Vigna unguiculata* (L.) Walp] PROGENIES**

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

**2020**

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*Thesis submitted to the*

**UNIVERSITY OF AGRICULTURAL SCIENCES, BANGALORE**

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*for the award of the degree of*

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in

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**OCTOBER, 2020**



*Affectionately*  
*Dedicated*  
*to*  
**AMUDHA**


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

**CERTIFICATE**

This is to certify that the thesis entitled **GENETIC VARIABILITY FOR IRON, ZINC, CALCIUM CONTENTS AND SEED YIELD IN SELECTED F<sub>4</sub> AND F<sub>5</sub> COWPEA [*Vigna unguiculata* (L.) Walp] PROGENIES** submitted by Ms. MEENAKSHI, J., ID No. PALB 8261 in partial fulfilment of the requirements for the award of 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 her during the period of her study in this University under my guidance and supervision and no part of the thesis has been submitted for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

Bengaluru  
October, 2020

  
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**Meenakshi J**

**GENETIC VARIABILITY FOR IRON, ZINC, CALCIUM  
CONTENTS AND SEED YIELD IN SELECTED F<sub>4</sub> AND F<sub>5</sub>  
COWPEA [*Vigna unguiculata* (L.) Walp] PROGENIES**

**MEENAKSHI. J,**

**ABSTRACT**

Identification of micronutrient dense genotypes is primary goal of crop improvement programmes aimed at developing biofortified cowpea varieties. In this context present study was carried out using two crosses *viz.*, PL-2 × NBC-39 and PL-5 × EC402104. ANOVA indicated significant variance for all traits under study in both F<sub>4</sub> and F<sub>5</sub> generations suggesting existence of adequate amount of variability. The estimates of PCV and GCV were moderate for most of traits studied. Moderate to high narrow sense heritability was observed for seeds pod<sup>-1</sup>, iron, zinc and calcium content indicating that additive gene action was predominant in the expression of these traits. Correlation studies indicated that iron, zinc and calcium content had significant negative correlation with seed yield plant<sup>-1</sup> suggesting selection for high micronutrient content causes reduction in seed yield plant<sup>-1</sup>. Hence selecting lines with optimum amount of iron, zinc, calcium and seed yield plant<sup>-1</sup> will be desirable. Ten such desirable superior lines from F<sub>5</sub> generation were selected from two crosses which had 16, 4, 30 and 90 per cent increase in zinc, iron, calcium content and seed yield plant<sup>-1</sup> respectively as compared to their parents which could be forwarded for further generations. Similarly, ten lines rich in micronutrient content having 60, 233, 40 and 4 per cent increase in zinc, iron, calcium content and seed yield plant<sup>-1</sup> respectively compared to parental lines could be used in hybridization

**October, 2020**

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**N. MARAPPA**  
(Major advisor)

ಅಲಸಂದೆಯ ಎಫ್-೪ ಹಾಗೂ ಎಫ್-೫ ಪೀಳಿಗೆಯಲ್ಲಿ ಆಯ್ದ ಸಾಲುಗಳಲ್ಲಿ ಕಬ್ಬಿಣ, ಸತು,  
ಸುಣ್ಣದ ಅಂಶ ಹಾಗೂ ಬೀಜ ಇಳುವರಿಗೆ ಅನುವಂಶೀಯ ವೈವಿಧ್ಯತೆಯ ಅಧ್ಯಯನ

ಮೀನಾಕ್ಷಿ, ಜಿ.

### ಸಾರಾಂಶ

ಜೈವಿಕ ಸಾರವರ್ಧನೆ ತಳಿ ಅಭಿವೃದ್ಧಿಯ ಕಾರ್ಯದಲ್ಲಿ ಹೆಚ್ಚಿನ ಲಘು ಪೋಷಕಾಂಶ ಹೊಂದಿರುವ ವಂಶವಾಹಿಗಳನ್ನು ಗುರುತಿಸುವುದು ಪ್ರಾಮುಖ್ಯ. ಈ ಹಿನ್ನೆಲೆಯಲ್ಲಿ ಪಿ.ಎಲ್-೨ × ಎನ್.ಬಿ.ಸಿ-೨೯ ಮತ್ತು ಪಿ.ಎಲ್-೫ × ಇ.ಸಿ-೪೦೨೧೦೪ ಸಂಕರಣಗಳಿಂದ ಅಭಿವೃದ್ಧಿ ಪಡಿಸಿದ ಎಫ್-೪ ಹಾಗೂ ಎಫ್-೫ ಪೀಳಿಗೆಗಳಲ್ಲಿ ಅನುವಂಶೀಯ ವೈವಿಧ್ಯತೆಯನ್ನು ಅರಿಯಲು ಅಧ್ಯಯನ ಕೈಗೊಳ್ಳಲಾಯಿತು. ಅಭ್ಯಸಿಸಿದ ಎಲ್ಲಾ ಎಫ್-೪ ಮತ್ತು ಎಫ್-೫ ಸಂತತಿಗಳ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ಗಮನಾರ್ಹ ವೈವಿಧ್ಯತೆಯು ಕಂಡುಬಂದಿತು. ಪ್ರತೀ ಸಸ್ಯದ ಕಾಯಿಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಸಸ್ಯದ ಕಾಯಿ ಗುಚ್ಚಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಕಾಯಿಯಲ್ಲಿನ ಬೀಜಗಳ ಸಂಖ್ಯೆ, ಕಬ್ಬಿಣ, ಸುಣ್ಣದ ಅಂಶ ಮತ್ತು ಪ್ರತಿ ಸಸ್ಯದ ಬೀಜ ಇಳುವರಿಗೆ ಹೆಚ್ಚಿನ ದೃಶ್ಯವಾಹಿ ರೂಪಗುಣಾಂಕ ವಿಭಿನ್ನತೆ ಹಾಗೂ ವಂಶವಾಹಿ ರೂಪಗುಣಾಂಕ ವಿಭಿನ್ನತೆ ಕಂಡುಬಂದಿತು. ಪ್ರತಿ ಕಾಯಿಯಲ್ಲಿನ ಬೀಜಗಳ ಸಂಖ್ಯೆ, ೧೦೦ ಬೀಜಗಳ ತೂಕ, ಕಾಯಿಯ ಉದ್ದ, ಕಬ್ಬಿಣ, ಸತು ಮತ್ತು ಸುಣ್ಣದ ಅಂಶಗಳಿಗೆ ಮಧ್ಯಮದಿಂದ ಹೆಚ್ಚಿನ ಸಂಕುಚಿತ ಅನುವಂಶೀಕತೆಯನ್ನು ಗಮನಿಸಲಾಯಿತು. ಪ್ರತಿ ಸಸ್ಯದ ಬೀಜ ಇಳುವರಿಯೊಂದಿಗೆ ಪ್ರತಿ ಸಸ್ಯದ ಕಾಯಿ ಗುಚ್ಚಗಳ ಸಂಖ್ಯೆ, ಪ್ರತೀ ಸಸ್ಯದ ಕಾಯಿಗಳ ಸಂಖ್ಯೆ, ಕಾಯಿಯ ಉದ್ದ ಮತ್ತು ೧೦೦ ಬೀಜಗಳ ತೂಕವು ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಹಾಗೂ ಕಬ್ಬಿಣ, ಸತು ಮತ್ತು ಸುಣ್ಣದ ಅಂಶಗಳು ಗಮನಾರ್ಹ ನಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಹೊಂದಿವೆ. ಆದ್ದರಿಂದ ಅನುಕೂಲತಮ ಕಬ್ಬಿಣ, ಸತು, ಸುಣ್ಣದ ಅಂಶ ಹಾಗೂ ಬೀಜ ಇಳುವರಿ ಹೊಂದಿರುವ ಸಾಲುಗಳನ್ನು ಆಯ್ಕೆ ಮಾಡುವುದು ಅಪೇಕ್ಷಣೀಯ. ಪೋಷಕ ತಳಿಗಳಿಗಿಂತ ೧೬, ೪, ೩೦ ಹಾಗೂ ೯೦ ಪ್ರತಿಶತ ಕ್ರಮವಾಗಿ ಹೆಚ್ಚಿನ ಸತು, ಕಬ್ಬಿಣ, ಸುಣ್ಣದ ಅಂಶ ಹಾಗೂ ಬೀಜ ಇಳುವರಿ ಹೊಂದಿದ, ಎರಡು ಸಂಕರಣಗಳಿಂದ ಆಯ್ದ ೧೦ ಉತ್ತಮ ಎಫ್-೫ ಪೀಳಿಗೆಯ ಸಾಲುಗಳನ್ನು ಮುಂದಿನ ಪೀಳಿಗೆಗೆ ವರ್ಗಾಯಿಸಬಹುದು. ಹಾಗೆಯೇ ಪೋಷಕ ತಳಿಗಳಿಗಿಂತ ೬೦, ೨೨೩, ೪೦ ಹಾಗೂ ೪ ಪ್ರತಿಶತ ಕ್ರಮವಾಗಿ ಹೆಚ್ಚಿನ ಸತು, ಕಬ್ಬಿಣ, ಸುಣ್ಣದ ಅಂಶ ಹಾಗೂ ಬೀಜ ಇಳುವರಿ ಹೊಂದಿದ ಸಾಲುಗಳನ್ನು ತಳಿ ಅಭಿವೃದ್ಧಿ ಕಾರ್ಯಕ್ರಮದಲ್ಲಿ ಪೋಷಕ ತಳಿಗಳಾಗಿ ಬಳಸಬಹುದು.

ಅಕ್ಟೋಬರ್, ೨೦೨೦

ಅನುವಂಶೀಯ ಮತ್ತು ಸಸ್ಯತಳಿ ಅಭಿವೃದ್ಧಿ ಶಾಸ್ತ್ರ ವಿಭಾಗ  
ಕೃಷಿ ವಿಶ್ವವಿದ್ಯಾನಿಲಯ, ಗಾ.ಕೃ.ವಿ.ಕೇಂ.  
ಬೆಂಗಳೂರು-೫೬೦೦೬೫

ಎನ್. ಮಾರಪ್ಪ  
(ಮುಖ್ಯ ಸಲಹಾಕಾರರು)

# Genetic variability studies for iron, zinc, calcium contents and seed yield in selected F<sub>4</sub> and F<sub>5</sub> cowpea [*Vigna unguiculata* (L.) Walp] progenies



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## Introduction

- Cowpea (*Vigna unguiculata* (L.) Walp.) is an annual self-pollinated legume crop, belongs to genus *Vigna* and family *Fabaceae*. It is an important pulse crop with chromosome number 2n=22.
- Nutrient deficiency attributes to inadequate uptake of various micronutrient viz., iron, zinc and calcium leading to symptoms like short stature, hypogonadism, impaired immune function, skin disorders, cognitive dysfunction, anorexia, anaemia, muscle cramps, depression, hallucination, memory loss in humans.
- Information on genetic variability for iron zinc and calcium in cowpea is very scarce, generating information on genetic variability for these traits is a prerequisite for development of bio-fortified cowpea lines to fight against malnutrition.

Table 1: Genetic variability parameters for iron, zinc, calcium, yield and its attributing traits

Characters	PL-2×NBC-39				PL-5×EC402104			
	F <sub>4</sub>		F <sub>5</sub>		F <sub>4</sub>		F <sub>5</sub>	
	GCV (%)	PCV (%)	GCV (%)	PCV (%)	GCV (%)	PCV (%)	GCV (%)	PCV (%)
Pods per plant	12.72	17.55	12.58	21.68	11.37	15.00	11.11	15.20
Pod length (cm)	4.14	7.76	2.98	7.37	4.45	7.70	3.82	7.75
Seeds per pod	6.23	11.60	4.93	10.34	4.71	8.60	5.26	8.93
Test weight (g)	7.35	11.60	5.75	9.19	5.90	10.48	7.61	11.43
Seed yield per plant (g)	16.32	18.56	13.09	22.16	12.77	15.91	13.32	17.86
Zn (mg kg <sup>-1</sup> )	11.62	18.57	8.04	20.27	10.27	20.47	9.46	20.29
Fe (mg kg <sup>-1</sup> )	13.28	26.70	10.22	30.60	9.70	29.22	14.08	32.14
Ca (mg kg <sup>-1</sup> )	18.73	20.51	17.32	23.02	11.53	24.41	13.83	26.02



Plate 1: General view of cowpea field



Plate 2: Micronutrient analysis

## Objective

- To study genetic variability for iron, zinc, calcium and seed yield

## Material and Methods

Cross	No. of F <sub>4</sub> families	No. of F <sub>5</sub> families
PL-2×NBC-39	12	12
PL-5×EC402104	54	30

- F<sub>4</sub> generation evaluation was carried out in late kharif 2018 and F<sub>5</sub> generation evaluation in kharif 2019.
- Five checks viz., KBC-9, IT-38956-1, KBC-2, C-152, PGCP-6 and the four parents were evaluated along with experimental material.
- Seed iron and zinc contents were analysed using Atomic Absorption Spectrophotometer (Jackson, 1973).
- Estimation of calcium content using EDTA titration method (Jackson, 1973).

## Observations recorded

- Data recorded on all plants in each family in both crosses. Data on five plants in parents and checks was taken.

## Statistical Analysis

- Genetic variability parameters for iron, zinc, calcium, yield and its component traits were estimated (Burton and Devane, 1953).

## Results

- Clusters per plant, pods per plant, seed yield, zinc, iron, calcium in F<sub>4</sub> of cross PL-2×NBC-39 showed moderate GCV and PCV.
- Clusters per plant, seed yield and calcium content in F<sub>4</sub> of cross PL-2×NBC-39 showed high heritability coupled with high GAM.
- Clusters, pods per cluster, pod per plant, pod length, test weight had significant positive correlation on seed yield and negative correlation was observed for zinc, iron and calcium. Zinc and calcium was positively correlated with iron content.
- Pods per cluster, plant height, seeds per pod, test weight in F<sub>4</sub> and F<sub>5</sub> of both crosses had low GCV.

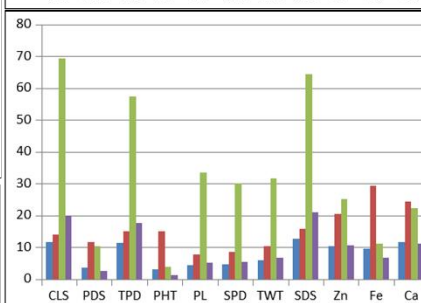
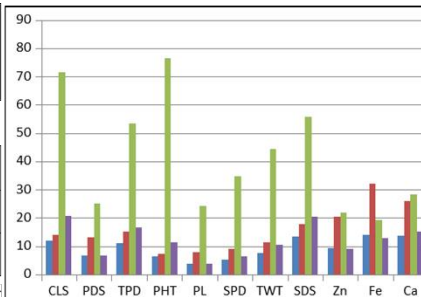


Fig. 1: Graphical representation of genetic variability parameters for 11 traits in F<sub>5</sub> generations of both the crosses

Table 2: Estimates of broad sense heritability (h<sup>2</sup>) and expected genetic advance as per cent mean (GAM) for eleven traits of cowpea

Characters	PL-2×NBC-39				PL-5×EC402104			
	F <sub>4</sub>		F <sub>5</sub>		F <sub>4</sub>		F <sub>5</sub>	
	h <sup>2</sup> (%)	GAM (%)	h <sup>2</sup> (%)	GAM (%)	h <sup>2</sup> (%)	GAM (%)	h <sup>2</sup> (%)	GAM (%)
Pods per plant	52.57	19.00	33.64	15.03	57.47	17.75	53.43	16.73
Pod length (cm)	28.46	4.55	16.38	2.49	33.37	5.29	24.22	3.87
Seeds per pod	28.86	6.90	22.78	4.85	29.99	5.31	34.66	6.38
Test weight (g)	40.11	9.59	39.11	7.41	31.66	6.84	44.35	10.45
Seed yield per plant (g)	77.33	29.57	34.88	15.92	64.41	21.10	55.65	20.47
Zn (mg kg <sup>-1</sup> )	39.15	14.98	15.74	6.57	25.17	10.61	21.76	9.09
Fe (mg kg <sup>-1</sup> )	24.76	13.62	11.16	7.04	11.03	6.64	19.18	12.70
Ca (mg kg <sup>-1</sup> )	83.37	35.22	56.57	26.83	22.32	11.23	28.26	15.15

## Discussion

- The traits reported to have moderate GCV, PCV and high heritability coupled with high GAM indicates that additive gene action is predominant and selection can be practiced.
- Highly significant positive correlation of traits on seed yield suggests that these traits can be used as tool for selection to improve yield.
- Negative correlation of micronutrients with seed yield suggests that selection for high iron, zinc and calcium would decrease yield.

## Summary

- Selection could be done for lines having optimum yield, iron, zinc and calcium.
- Lines having high iron, zinc and calcium could be used as parents in breeding program.



Plate 3: F<sub>5</sub> plants from the cross PL-2×NBC-39

## Reference

SHARMA, A., MISHRA, S. P. AND GOUR, L., 2019, Heritable relationship and variability of yield and yield determinants in cow pea. *Int. J. Chem. Stud.*, 7(3): 3605-3611.

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## LIST OF ABBREVIATIONS

GCV	:	Genotypic Coefficient of Variation
PCV	:	Phenotypic Coefficient of Variation
$h^2$	:	Heritability
cm	:	Centimeters
ns	:	Narrow sense
GA	:	Genetic advance
GAM	:	Genetic advance as per cent mean
g	:	Gram
r	:	Correlation coefficient
%	:	Per cent
$\pm$ SE	:	Standard error of mean
No.	:	Number
mg/kg	:	Milligram per kilogram

## I INTRODUCTION

Pulses engross a prime place in global food and nutrition, since they are important constituent of the diets. Legumes are not only a rich source of proteins but also rich in micronutrients, vitamins and minerals. Most of the nutritional requirements of the rural people met by legumes, which constitute a major source of protein (Mortimore *et al.*, 1997).

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual legume crop, belongs to genus *Vigna*, family *Fabaceae* and tribe *Phaseoleae*. Cowpea is also called by different names viz., Caupea, Black-eyed pea, Catjang, Southern pea, Yardlong bean, Crowder pea, lobia, chowla, Barbati. (Manisha, *et al.* 2018). It is a main pulse crop with chromosome number  $2n=22$ . All cultivated species belongs to *V. unguiculata* ssp. *unguiculata*. *V. unguiculata* ssp. *unguiculata* var. *spontanea* is said to be possible progenitor of cultivated species (Pasquet,1999). The domesticated species are grouped into four viz., *V. unguiculata*, *V. biflora*, *V. sesquipedalis* and *V. textilis* (Verdcourt, 1970).

West Africa is considered as primary center of origin of cowpea (Padulosi and Ng,1997) where first domestication was found and maximum diversity is observed. India is considered as secondary center of origin (Pant,1982) and recognized as one of oldest legume used as protein source for livestock and humans (Steele, 1972).

In India, it is cultivated in Punjab, Haryana, Delhi, West UP and considerable area in Rajasthan, Karnataka, Kerala, Tamil Nadu, Maharashtra and Gujarat. Worldwide it is grown in 14.5 m. ha. with production of 6.5 mm tons out of which, 66 % is from Nigeria and Niger. In India, cowpea is grown in area about 3.1 m. ha. with production of 1.91 mt (Anon, 2016). Karnataka covers 0.80 lakh hectares with production of 0.31 lakh tons (Anon, 2016) and occupies fourth position among the pulses in Karnataka.

Cowpea is a self-pollinated crop and has short bushy or spreading type of growth habit with deep tap root system. Its peduncle can hold four to five pods, flower color varies from shades of purple, pink, yellow, white, blue and the seeds are kidney shaped. Dry seeds are used as food, pods and green seeds are used as vegetable. The whole plant is used to

feed animals and also used as green manure crop. It is early, multi-seasonal, multipurpose crop and versatile food crop. Since it is rich source of protein (23-28 %) and require less inputs, it is popularly called as “poor man’s meat” (Bressani *et al.*, 1985 and Gupta *et al.*, 1988).

Cowpea contains carbohydrate (60.30 %), good amount of quality protein (22-24 %), fat (1.80 %), ash (3.40 mg/100g), calcium (76 mg/100gm), iron (57 mg/100gm), phosphorous (0.14 mg/100g), crude fibre (5.9 mg/100g) and vitamins like thiamine (0.92 mg/100g), nicotinic acid (1.90 mg/100g) and riboflavin (0.18 mg/100g) (Chatterjee and Bhattaacharya, 1986).

Cowpea is a warm season short day crop that adopts to high temperature and drought conditions. It is grown in both *kharif* and spring summer season in most parts of India. It can be grown in both arid and semi-arid region and grows well even if soil contains 85 per cent sand. It has nitrogen fixing ability up to 150 kg per ha. (Summerfield *et al.*, 1977) and can be intercropped with sorghum, millet, maize, cassava and cotton.

Nutrient deficiency attributes to inadequate uptake of various micronutrient *viz.*, iron, zinc and calcium leading to symptoms like short stature, hypogonadism, impaired immune function, skin disorders, cognitive dysfunction, anorexia, anaemia, muscle cramps, depression, hallucination, memory loss in humans (Juliette Steen, 2016). India is home for 46.6 million stunted children due to insufficient nutrient intake for long time span leading to stunting or reduced height (Anon., 2018). As per the United Nations report, 51.4 per cent of women in reproductive ages are anaemic. Maternal Anaemia has a significant effect on the nutritional status of young children leading to stunting and underweight (Mohan and Thakkar, 2019).

Development of high yielding variety of crop plants with optimum level of zinc, iron and calcium will help in fighting against malnutrition. Development of micronutrient dense cowpea genotypes with optimum levels of seed yield is main objective of cowpea breeding programs working for nutritional food security.

Information on genetic variability for zinc, iron and calcium in cowpea is very scarce. In this context the present exploration was conducted to help in generating information on genetic variability for iron, zinc and calcium in cowpea which forms a prerequisite for development of bio-fortified cowpea lines.

The correlation coefficient gives a hint about the nature and intensity of association between yield and yield attributing traits Weber and Moorthy (1952). The path analysis gives information about direction and magnitude of direct and indirect effects of the yield attributing traits (Wright, 1921; Dewey and Lu ,1957).

Heritability, genetic advance, genotypic and phenotypic coefficient of variation within a crop will help in selecting superior genotypes which is equivalent to the amount of genetic variability exist and the extent to which the trait is inherited. Hence, having details on all these parameters will aid in the selection process.

To generate information on genetic variability in advanced generations, nature, magnitude, direction of relationship among micronutrient traits with seed yield of cowpea, the present research was conducted with the following objectives;

1. To study genetic variability for iron, zinc, calcium and seed yield
2. To study the narrow sense heritability and intergeneration correlation for iron, zinc, calcium and seed yield

## II REVIEW OF LITERATURE

Genetic improvement of traits requires knowledge about genetic variability, heritability and correlation between yield and its attributing traits. Hence, genetic advancement in any breeding programme requires information about previous work carried out. In this chapter, review of literature related to the objectives of the current investigation is presented under following headings.

### 2.1 Correlation and Path analysis

### 2.2 Genetic variability

### 2.3 Studies on iron, zinc and calcium in cowpea

#### **2.1 Correlation and Path analysis**

Oladejo *et al.* (2011) who carried out cluster analysis and genotype-by-trait analysis observed close associations among the phenological characters. Grain yield had positive correlation with all morphological characters *viz.*, peduncles plant<sup>-1</sup>, number of seeds pod<sup>-1</sup>, pods plant<sup>-1</sup> and hundred seed weight except peduncle and they noticed negative association of grain yield with flowering character.

Muhmudul *et al.* (2012) had conducted path analysis for thirteen stringbean (*Vigna unguiculata* ssp. *sesquipedalis*) genotypes and reported significant positive correlation between number of nodes plant<sup>-1</sup>, number of primary branches plant<sup>-1</sup>, days to first blooming and 50 per cent blooming. They have also noticed that the pod yield plant<sup>-1</sup> had negative correlation with plant height, days to first blooming, days to 50 per cent blooming. They suggested that number of pods plant<sup>-1</sup>, pod length, number of clusters plant<sup>-1</sup> and number of primary branches plant<sup>-1</sup> were contributing to pod yield since they had positive association.

Nwofia *et al.* (2012) investigated twelve cowpea genotypes and reported that number of pods plant<sup>-1</sup> (0.367), number of leaves plant<sup>-1</sup> (0.087) and pod length (0.016) had positive direct effects on seed yield pods plant<sup>-1</sup>. They suggested that selection can be practiced based on these traits to improve yield.

An investigation was carried out by Anamika and Tajane (2014) in forty-four genotypes of cowpea. Through path co-efficient analysis, they have noticed that number of pods plant<sup>-1</sup>, 100 seed weight and number of seeds pod<sup>-1</sup> had high positive direct effect. Number of seeds plant<sup>-1</sup> had highly significant and positive correlation with seed yield plant<sup>-1</sup>.

Om Vir and Singh (2014) evaluated thirty-three accessions of cow pea and reported positive and significant correlation for number of seeds pod<sup>-1</sup>, number of pods clusters<sup>-1</sup>, number of pods plant<sup>-1</sup>, number of pods clusters<sup>-1</sup> on seed yield plant<sup>-1</sup>. They suggested that selection can be practiced based on these traits.

Shanko *et al.* (2014) conducted experiment to know the inter-relationship in forty-nine cowpea genotype and reported that seed yield had positive correlation with number of primary and secondary branches, days to 50 per cent flowering, number of pods plant<sup>-1</sup> and number of seeds plant<sup>-1</sup>. They suggested that number of pods and yield plant<sup>-1</sup> can be used as primary selection index.

Crossing was done involving parents, Dokki331 and IT81D-1137 to study the genetic gain for flowering in F<sub>2</sub> generation of the cross by Raswan and Helaly (2015). They observed positive correlation between days to flowering and dry seed weight. They also noticed moderate to high broad sense heritability for days to fifty per cent flowering, dry seed yield plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, pod length which indicated additive gene effect and suggested that the selection was effective in improving the traits of dry seed yield.

Phenotypic analysis was carried out by Aliyu *et al.* (2016) in twenty-one cowpea breeding lines. They observed positive significant relationships between flowering, pod maturity and seed size, negative correlations between pods plant<sup>-1</sup>, seeds plant<sup>-1</sup> and total seed yield with pod maturity. They suggested that seeds plant<sup>-1</sup> and pods plant<sup>-1</sup> were the main contributory components to seed yield based on correlation coefficients of  $r=0.95$ ,  $0.89$ , respectively.

Khandait *et al.* (2016) investigated fifteen cowpea genotypes and found significant positive phenotypic correlation between pod yield plant<sup>-1</sup> and pods plant<sup>-1</sup> ( $0.589$ ), days to

first flowering (0.415), seeds pod<sup>-1</sup> (0.395), number of flower clusters plant<sup>-1</sup> (0.372) and pod length (0.304). They noted that pods plant<sup>-1</sup> had highest positive direct effect and number of days for first flowering had maximum negative direct effect on pod yield plant<sup>-1</sup>. They concluded that simultaneous selection for both pod yield plant<sup>-1</sup> and pods plant<sup>-1</sup> can help in yield improvement.

An investigation was done by Patel *et al.* (2016) on thirty-two genotypes of cowpea to study path coefficient and correlations. They interpreted that pod length, days to 50 per cent flowering, number of pods plant<sup>-1</sup> and plant height had highest positive direct effect on green pod yield plant<sup>-1</sup> and suggested that these traits can be used for selecting high yielding varieties.

Using F<sub>2</sub>, RC<sub>1</sub> and RC<sub>2</sub> generations derived from crossing cowpea BRS Carijo and BR14 Mulato, Ribeiro *et al.* (2016) noticed significant positive phenotypic correlations between seed weight and number of secondary branches. They suggested that plants with shorter length of primary branches, lower number of nodes, higher and early grain yield were preferable.

Adetiloye *et al.* (2017) studied twenty cowpea genotypes and noticed significant positive genotypic correlations between grain yield and number of pods peduncle<sup>-1</sup> (0.64, 0.72), pods plant<sup>-1</sup> (0.58, 0.57), pod length (0.48, 0.52), seeds pod<sup>-1</sup> (0.55, 0.72) and suggest that these characters can be used as selection criteria for improvement of cowpea yield.

Path co-efficient analysis and correlation studies was carried out in thirty cowpea genotypes by Srinivas *et al.* 2017. They observed positive correlation between pod yield and number of branches plant<sup>-1</sup>, pods plant<sup>-1</sup>, pod length, seeds pod<sup>-1</sup> and negative correlation between pod yield plant<sup>-1</sup>, days to 50 per cent flowering. Branches plant<sup>-1</sup>, nodes plant<sup>-1</sup>, cluster plant<sup>-1</sup>, pods plant<sup>-1</sup>, seeds pod<sup>-1</sup>, pod weight, pod yield plot<sup>-1</sup> and percentage of protein content disclosed positive direct effects on pod yield which could be used as selection index for cowpea improvement.

A study was carried out by Lopes *et al.* (2017) in twenty cowpea lines and found the significant difference between genotypes for almost all the traits under study *viz.*, days

to flowering, number of branches plant<sup>-1</sup>, main stem length, green pod length, grains green pod<sup>-1</sup>, hundred green grains mass, dry grain yield and identified that the number of grains green pod<sup>-1</sup> (0.86) was the main determinant character for dry grain yield since it had high direct effect.

Manisha *et al.* (2018) evaluated twenty F<sub>5</sub> cowpea genotypes and reported comparatively higher degree of genotypic correlation coefficients than the phenotypic correlation coefficients in most of the traits studied like pods plant<sup>-1</sup>, pods cluster<sup>-1</sup>, primary branches plant<sup>-1</sup>, clusters plant<sup>-1</sup>, pod length. They noticed high significant positive correlation at both genotypic and phenotypic levels between pod yield plot<sup>-1</sup> and traits like number of pods plant<sup>-1</sup>, number of pods cluster<sup>-1</sup>, primary branches plant<sup>-1</sup>, number of clusters plant<sup>-1</sup> and pod length. They suggested that cowpea lines can be improved by improving these characters.

Mayuri *et al.* (2018) conducted experiment in seventy-eight germplasm lines along with three checks (TSFC-12-15, UPC-5286 and MFC-8-14) to study genetic architecture through association analysis and variability parameters and reported that pod length (0.87) was positively correlated with seed yield plant<sup>-1</sup> and suggested that this trait can be used for selection.

In study was conducted by Shwetha (2018) to find the breeding potential of four cross of cowpea *viz.*, PL-2 × NBC 39, PL-5 × EC402104, PL-2 × EC402104 and PL-5 × IC-27749 clusters plant<sup>-1</sup> (0.16), pods plant<sup>-1</sup> (0.19), pod yield plant<sup>-1</sup> (0.87) and days to flowering (0.51) had significant positive correlation on seed yield and suggested these traits can be used as surrogates for selection.

Walle *et al.* (2018) analyzed 324 cowpea genotypes for genetic variability and path co-efficient analysis. They deciphered that days to flowering (0.377), harvest index (0.459), hundred seed weight (0.25) had relatively high positive direct effect on seed yield while days to maturity (-0.41) had negative direct effect on seed yield.

Kalambe *et al.* (2019) evaluated twenty-two genotypes and found that the trait like number of primary branches plant<sup>-1</sup>, plant height, number of seeds pod<sup>-1</sup>, number of pods

plant<sup>-1</sup> and hundred seed weight showed the significant positive correlation with pod yield plant<sup>-1</sup>.

Kana and Ndung (2019) from an investigation carried out in nine advanced cowpea genotypes reported that number of seeds pod<sup>-1</sup> (0.443), number of pods plant<sup>-1</sup>(0.618), pod length (0.698), hundred seed weight (0.818) and number of branches had significant correlation with yield plant<sup>-1</sup> (0.403). Hundred seed weight (0.850), seed pod<sup>-1</sup> (0.807) had higher direct effect on yield. They suggested that direct and indirect selection for these traits can help in furtherance of cowpea genotypes.

In correlation and path analysis using sixty cowpea genotypes, high positive association between seed yield and yield contributing traits like number of pods plant<sup>-1</sup>, number of flowers plant<sup>-1</sup>, test weight, number of pods cluster<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, number of clusters plant<sup>-1</sup>, harvest index and plant height was noticed. Also, these traits along with days to 50 per cent flowering, number of flowers cluster<sup>-1</sup>, number of primary branches plant<sup>-1</sup> and plant height directly contributed to the seed yield. Days to maturity had negative and non-significant correlation with seed yield (Sharma *et al.*, 2019).

## 2.2 Reviews on genetic variability parameters

Characters	Material used	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GAM (%)	Reference
Clusters plant <sup>-1</sup>	30 genotypes	25.15	24.73	96.69	64.20	Throat and Gadewar (2013)
	49 germplasm	23.74	21.87	84.85	41.49	Kumar <i>et al.</i> (2015)
	30 genotypes	22.30	18.83	71.29	2.03	Sharma <i>et al.</i> (2017)
	30 genotypes	15.03	11.48	58.00	18.07	Bhagwati <i>et al.</i> (2018)
	16 lines	7.71	6.71	0.76	12.03	Kumar <i>et al.</i> (2018)
	F <sub>2</sub> generation	27.24	26.72	96.22	53.98	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	28.83	26.17	90.00	48.52	Sabale <i>et al.</i> (2018)
	F <sub>2</sub> generation	High	high	-	-	Meenatchi <i>et al.</i> (2019)
22 genotypes	40.57	36.91	81.54	68.65	Sharma <i>et al.</i> (2019)	
Pods cluster <sup>-1</sup>	60 genotypes	22.10	21.76	96.88	44.11	Kanpara <i>et al.</i> (2015)
	49 germplasm	13.39	10.93	66.67	18.38	Kumar <i>et al.</i> (2015)
	16 lines	18.16	17.26	0.90	33.80	Kumar <i>et al.</i> (2018)
	F <sub>2</sub> generation	19.83	18.30	85.23	34.81	Nair <i>et al.</i> (2018)

Characters	Material used	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GAM (%)	Reference
	F <sub>2</sub> generation	9.52	6.30	43.73	8.33	Sabale <i>et al.</i> (2018)
	F <sub>2</sub> generation	low	low	high	High	Meenatchi <i>et al.</i> (2019)
	27 genotypes	25.09	23.09	85.00	43.76	Gupta <i>et al.</i> (2019)
	F <sub>2</sub> generation	20.54	19.67	91.7	38.79	Verma <i>et al.</i> (2019)
<b>Pods plant<sup>-1</sup></b>	11 genotypes	high	Moderate	high	Moderate	Adewale <i>et al.</i> (2010)
	F <sub>3</sub> and F <sub>4</sub> generations	-	-	high	high	Aremu (2011)
	10 cowpea accessions	29.88	28.23	89.23	-	Manggoel <i>et al.</i> (2012)
	30 genotypes	25.13	24.84	97.70	64.82	Throat and Gadewar (2013)
	22 genotypes	28.64	27.59	92.80	54.67	Vavilapalli <i>et al.</i> (2013)
	22 genotypes	41.22	35.51	74.20	-	Gerrano <i>et al.</i> (2015)
	60 genotypes	43.98	41.98	90.99	82.44	Kanpara <i>et al.</i> (2015)
	F <sub>2</sub> and F <sub>3</sub> generations	13.64	7.09	11.27	7.6	Lokesh <i>et al.</i> (2017)
	22 genotypes	69.08	50.96	54.41	77.43	Sarath and Reshma (2017)
	30 genotypes	21.10	19.52	85.90	4.84	Sharma <i>et al.</i> (2017)
	30 genotypes	11.20	9.85	7.3	17.38	Bhagwati <i>et al.</i> (2018)
	16 lines	7.78	7.06	0.78	12.85	Kumar <i>et al.</i> (2018)
	F <sub>2</sub> generation	35.29	34.64	96.38	70.06	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	29.73	28.86	94.23	57.71	Sabale <i>et al.</i> (2018)
	62 genotypes	32.14	31.47	95.89	63.48	Savithri <i>et al.</i> (2018)
	F <sub>2</sub> generation	high	high	-	-	Meenatchi <i>et al.</i> (2019)
	27 genotypes	45.16	43.78	94.00	87.43	Gupta <i>et al.</i> (2019)
	22 genotypes	35.80	31.49	77.36	57.06	Sharma <i>et al.</i> (2019)
F <sub>2</sub> generation	21.86	21.48	96.6	43.52	Verma <i>et al.</i> (2019)	
<b>Plant height</b>	30 genotypes	34.72	34.71	99.95	91.62	Throat and Gadewar (2013)
	22 genotypes	32.05	31.64	97.42	64.32	Vavilapalli <i>et al.</i> (2013)
	25 genotypes	69.70	67.41	93.55	-	Gerrano <i>et al.</i> (2015)
	60 genotypes	23.15	22.37	93.38	44.54	Kanpara <i>et al.</i> (2015)
	49 germplasm	27.31	26.98	97.59	54.90	Kumar <i>et al.</i> (2015)
	200 F <sub>3</sub> progenies	20.40	19.50	90.66	38.25	Dinesh <i>et al.</i> (2017)
	F <sub>2</sub> and F <sub>3</sub> generations	23.13	3.75	36.30	1.25	Lokesh <i>et al.</i> (2017)
	22 genotypes	83.28	75.37	81.89	140.51	Sarath and Reshma (2017)

Characters	Material used	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GAM (%)	Reference
	30 genotypes	52.62	52.62	99.53	65.40	Sharma <i>et al.</i> (2017)
	30 genotypes	37.57	37.14	98.00	75.61	Bhagwati <i>et al.</i> (2018)
	30 genotypes	15.12	13.40	78.53	24.46	Havaraddi and Deshpande (2018)
	16 lines	5.44	3.95	0.53	5.81	Kumar <i>et al.</i> (2018)
	F <sub>2</sub> generation	67.12	65.29	94.62	130.83	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	18.65	17.65	89.61	34.43	Sabale <i>et al.</i> (2018)
	62 genotypes	46.51	46.39	99.51	95.33	Savithri <i>et al.</i> (2018)
	F <sub>2</sub> generation	low	Low	high	high	Meenatchi <i>et al.</i> (2019)
	27 genotypes	51.41	49.71	94.00	99.33	Gupta <i>et al.</i> (2019)
	27 genotypes	29.55	29.03	96.47	58.73	Sharma <i>et al.</i> (2019)
	F <sub>2</sub> generation	15.81	15.61	97.5	31.76	Verma <i>et al.</i> (2019)
Pod length	11 genotypes	low	Low	high	Moderate	Adewale <i>et al.</i> (2010)
	10 cowpea accessions	19.87	15.79	63.16	-	Manggoel <i>et al.</i> (2012)
	30 genotypes	10.76	10.17	89.38	25.39	Throat and Gadewar (2013)
	22 genotypes	24.04	23.85	98.38	48.70	Vavilapalli <i>et al.</i> (2013)
	25 genotypes	21.42	19.97	86.88	-	Gerrano <i>et al.</i> (2015)
	49 germplasm	12.38	10.46	71.35	18.19	Kumar <i>et al.</i> (2015)
	F <sub>2</sub> and F <sub>3</sub> generations	18.44	9.00	23.00	16.69	Lokesh <i>et al.</i> (2017)
	22 genotypes	56.60	46.07	66.123	20.53	Sarath and Reshma (2017)
	30 genotypes	10.78	8.60	64	14.14	Bhagwati <i>et al.</i> (2018)
	30 genotypes	10.86	6.92	40.62	9.09	Havaraddi and Deshpande (2018)
	16 lines	9.39	7.60	0.65	12.65	Kumar <i>et al.</i> (2018)
	F <sub>2</sub> generation	36.41	35.89	97.18	72.89	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	9.29	7.49	65.03	12.44	Sabale <i>et al.</i> (2018)
	62 genotypes	39.65	39.29	98.21	80.12	Savithri <i>et al.</i> (2018)
	F <sub>2</sub> generation	Low	low	high	high	Meenatchi <i>et al.</i> (2019)
	27 genotypes	20.19	19.77	96.00	39.00	Gupta <i>et al.</i> (2019)
	22 genotypes	28.26	21.48	57.78	33.63	Sharma <i>et al.</i> (2019)
F <sub>2</sub> generation	16.57	19.96	92.80	31.68	Verma <i>et al.</i> (2019)	
Seeds pod <sup>-1</sup>	11 genotypes	low	low	high	high	Adewale <i>et al.</i> (2010)
	F <sub>3</sub> and F <sub>4</sub> generations	-	-	high	high	Aremu (2011)

Characters	Material used	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GAM (%)	Reference
	30 genotypes	11.28	10.86	92.63	27.60	Throat and Gadewar (2013)
	25 genotypes	27.01	24.82	84.52	-	Gerrano <i>et al.</i> (2015)
	60 genotypes	11.51	10.44	82.23	19.50	Kanpara <i>et al.</i> (2015)
	49 germplasm	14.95	13.58	82.46	25.40	Kumar <i>et al.</i> (2015)
	200 F <sub>3</sub> progenies	11.63	9.59	68.01	16.29	Dinesh <i>et al.</i> (2017)
	F <sub>2</sub> and F <sub>3</sub> generations	19.78	12.85	42.20	13.3	Lokesh <i>et al.</i> (2017)
	22 genotypes	31.94	26.77	70.22	46.22	Sarath and Reshma (2017)
	30 genotypes	11.85	9.67	67.00	16.24	Bhagwati <i>et al.</i> (2018)
	30 genotypes	11.64	7.72	44.03	10.56	Havaraddi and Deshpande (2018)
	16 lines	9.74	8.17	0.70	14.90	Kumar <i>et al.</i> (2018)
	F <sub>2</sub> generation	13.09	11.40	75.93	20.47	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	11.74	11.27	92.10	22.28	Sabale <i>et al.</i> (2018)
	F <sub>2</sub> generation	low	low	high	High	Meenatchi <i>et al.</i> s(2019)
	27 genotypes	18.7	16.70	85.00	31.80	Gupta <i>et al.</i> (2019)
	22 genotypes	34.88	32.66	87.68	63.00	Sharma <i>et al.</i> (2019)
	F <sub>2</sub> generation	13.04	12.34	89.70	24.09	Verma <i>et al.</i> (2019)
<b>100 seed weight</b>	11 genotypes	Moderate	Moderate	high	High	Adewale <i>et al.</i> (2010)
	F <sub>3</sub> and F <sub>4</sub> generations	-	-	Moderate	moderate	Aremu (2011)
	10 cowpea accessions	41.96	38.47	86.84	-	Manggoel <i>et al.</i> (2012)
	30 genotypes	17.34	17.05	96.71	44.27	Throat and Gadewar (2013)
	25 genotypes	28.01	24.16	74.43	-	Gerrano <i>et al.</i> (2015)
	60 genotypes	25.36	25.25	99.17	51.80	Kanpara <i>et al.</i> (2015)
	49 germplasm	51.18	50.11	70.65	101.05	Kumar <i>et al.</i> (2015)
	200 F <sub>3</sub> progenies	47.80	9.11	3.64	3.58	Dinesh <i>et al.</i> (2017)
	F <sub>2</sub> and F <sub>3</sub> generations	7.24	1.72	6.25	11.10	Lokesh <i>et al.</i> (2017)
	22 genotypes	41.14	24.87	36.53	30.97	Sarath and Reshma (2017)
	30 genotypes	10.86	6.92	40.62	9.09	Sharma <i>et al.</i> (2017)
	30 genotypes	16.92	16.69	97.00	33.92	Bhagwati <i>et al.</i> (2018)
	30 genotypes	21.24	21.24	99.99	4.85	Havaraddi and Deshpande (2018)
	16 lines	6.28	5.01	0.64	8.25	Kumar <i>et al.</i> (2018)

Characters	Material used	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GAM (%)	Reference
	F <sub>2</sub> generation	15.21	14.29	88.39	27.69	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	14.23	13.86	94.85	27.81	Sabale <i>et al.</i> (2018)
	F <sub>2</sub> generation	low	low	high	high	Meenatchi <i>et al.</i> (2019)
	27 genotypes	22.40	22.20	98.00	45.33	Gupta <i>et al.</i> (2019)
	22 genotypes	18.06	15.68	75.33	28.03	Sharma <i>et al.</i> (2019)
	F <sub>2</sub> generation	24.03	21.86	82.70	40.95	Verma <i>et al.</i> (2019)
Seed yield plant <sup>-1</sup>	F <sub>3</sub> and F <sub>4</sub> generations	-	-	Mode-rate	high	Aremu (2011)
	10 cowpea accessions	38.55	36.76	90.91	-	Manggoel <i>et al.</i> (2012)
	30 genotypes	11.25	10.08	80.44	23.88	Throat and Gadewar (2013)
	22 genotypes	20.07	19.03	89.92	37.18	Vavilapalli <i>et al.</i> (2013)
	25 genotypes	50.97	44.10	74.00	-	Gerrano <i>et al.</i> (2015)
	49 germplasm	11.75	11.06	88.65	21.46	Kumar <i>et al.</i> (2015)
	200 F <sub>3</sub> progenies	12.48	8.88	50.60	13.01	Dinesh <i>et al.</i> (2017)
	F <sub>2</sub> and F <sub>3</sub> generations	22.81	7.91	12.05	18.74	Lokesh <i>et al.</i> (2017)
	22 genotypes	96.35	84.06	76.12	151.09	Sarath and Reshma (2017)
	30 genotypes	24.75	24.10	94.60	32.60	Sharma <i>et al.</i> (2017)
	30 genotypes	20.96	20.35	94.00	40.72	Bhagwati <i>et al.</i> (2018)
	30 genotypes	29.00	23.07	63.29	37.81	Havaraddi and Deshpande (2018)
	F <sub>2</sub> generation	36.50	35.97	97.10	73.01	Nair <i>et al.</i> (2018)
	F <sub>2</sub> generation	37.16	36.25	95.15	72.84	Sabale <i>et al.</i> (2018)
	F <sub>2</sub> generation	high	high	high	high	Meenatchi <i>et al.</i> (2019)
22 genotypes	42.49	42.22	98.75	86.43	Sharma <i>et al.</i> (2019)	

### 2.3 Studies on iron, zinc and calcium

Singh (2004) screened cowpea germplasm for micronutrients and reported that iron content ranged from 46 to 79 ppm, calcium 545 to 1330 ppm for calcium and 23 to 48 ppm of Zn. The inbred line IT97K-1042-3 was identified to have high Fe (65 ppm) and Zn (46 ppm).

Mamiro *et al.* (2011) who analysed cowpea varieties for micronutrient composition reported that zinc content ranged from 32.6 to 31.5 mg/kg, iron content from 27.6 to 28.9

mg/kg. They noted cowpea varieties, IT99K-7212-2-1 (23.8 mg/kg) and IT96D-733 (21.2 mg/kg) were recorded to have highest iron content and genotypes IT99K-7-21-2-2-1 (32.2 mg/kg) and IT97K499-38 (28.3 mg/kg) had the highest zinc content.

Moura *et al.* (2012) have estimated the direct and indirect effects of agronomic and culinary traits on iron and zinc content using path analysis. They reported number of grains pod<sup>-1</sup>, grain yield, reduced cooking time, hundred seed weight and number of days to flowering had negative correlation with iron and zinc content whereas grain size and protein content had positive correlation with zinc content while studying eleven cowpea populations derived from three parents BRS xiquexique (iron and zinc rich), IT-98k-205-8 (iron rich), IT-97k-1042-3 (zinc rich).

Santos and Boiteux (2013) screened cowpea lines for seed protein and mineral contents. They observed that seed protein ranged from 22.5 to 34.1 per cent, calcium 410 to 6260 ppm, iron content 36.5 to 137 ppm and zinc content from 36 to 58 ppm.

Manoj (2016) carried out genetic diversity and variability studies in 169 cowpea genotypes for yield and its contributing traits characters. Based on mean performance they identified genotypes rich in iron, zinc and protein contents.

Marappa *et al.* (2016) screened two-hundred cowpea genotypes to study the micronutrient content. They observed high GCV and PCV for pods plant<sup>-1</sup>, pod yield plant<sup>-1</sup>, plant height, clusters plant<sup>-1</sup> and seed yield plant<sup>-1</sup> which had indicated that the additive gene action was predominant and these traits aid in direct selection. They had estimated micronutrient content in cowpea seeds, among them PGCP-6 had high zinc content (48.6 ppm), iron (137.2 ppm) protein (23.85 percent) and KBC-6 had high zinc (41.8 ppm), iron (150.2 ppm), protein (23.11 per cent) and suggested that these lines could be used in future crop improvement program.

Genetic variability studies were conducted by Keethi (2017) for iron, zinc, protein, seed yield and its contributing traits in twenty-two cowpea genotypes. The estimates of heritability and GAM were found to be high for zinc (97.6; 51.17), iron (99.9; 154.62), plant height (98.3; 79.04), secondary branches plant<sup>-1</sup> (78.6; 39.9), clusters plant<sup>-1</sup> (91.5;

67.06), pods plant<sup>-1</sup> (97.5; 81.32), pod yield plant<sup>-1</sup> (92.3; 44.52) and seed yield plant<sup>-1</sup> indicating additive gene action and suggested selection could be practiced.

Evaluation of micronutrient and protein was done by Dakora and Belane (2019) using thirty-two cowpea genotypes in both leaves and seeds. They reported that the average leaf protein content was 23-40 per cent and seed protein content was 28-40 per cent. They even estimated iron and zinc content in seeds with range of 45.1- 67 ppm and 33.9 - 69.2 ppm respectively.

Veeresh (2019) studied genetics of iron, zinc and seed yield in F<sub>2</sub> derived from crosses *viz.*, PL-2 × NBC 39, PL-5 × EC402104, PL-2 × EC402104 and PL-5 × IC-27749 and reported that pod length, iron and zinc content were governed by both additive and dominance effects hence recurrent selection can be practiced for improving the traits.

### **III MATERIAL AND METHODS**

The detailed information about the genetic material used in current investigation, site of experiment, methods followed for recording observation on various characters, statistical tools used for analysis of data are discussed in this chapter.

#### **3.1 Experimental Site**

Approved experiments of the research work were conducted in the experimental blocks of Department of Genetics and Plant Breeding situated at K block, University of Agricultural Sciences, Bangalore. The site is located at an altitude of 930 meters above mean sea level (MSL), 12° 58' North latitude and 77°35' East longitude which belongs to Eastern Dry Zone (Zone V) of Karnataka.

#### **3.2 Nutrient status of soil**

Before starting the experiments, the surface soil sample about 0-15 cm was collected from the experimental site for analysing the fertility status of the plot. Analysis was carried out in the Department of Soil Science and Agricultural Chemistry, College of Sericulture Chintamani, UAS (B). The physico-chemical properties of soil are presented in Table 1.

#### **3.3 Experimental material**

The basic experimental material of the current experiment consists of F<sub>4</sub> and F<sub>5</sub> generations derived from two crosses *viz.*, Pant Lobia-2 (PL-2) × NBC-39 and Pant Lobia-5 (PL-5) × EC402104 along with the five check varieties namely KBC-9, IT-38956-1, KBC-2, C-152, PGCP-6. The salient features of parents and checks along with their nutrient status with respect to zinc, iron and calcium content is presented in Table 2 and 3 respectively.

##### **3.3.1 Development of experimental material**

Selected F<sub>3</sub> family progenies from the previous study conducted by Shwetha (2018) were used to raise F<sub>4</sub> generation.

**Table 1: Soil nutrient status before the conduct of experiment**

Parameters	Values
pH	5.39
EC (dS/m)	0.13
Organic carbon (%)	0.87
Available Nitrogen (kg/ha)	312.23
Available Phosphorous (kg/ha)	10.87
Available Potassium (kg/ha)	434.56
Exchangeable Calcium (c mol/100g of soil)	10.15
Exchangeable Magnesium (c mol/100g of soil)	6.90
Available Sulphur (mg/kg)	6.36
DTPA extractable Zinc (mg/kg)	1.65
DTPA extractable Copper (mg/kg)	1.50
DTPA extractable Iron (mg/kg)	27.37

**Table 2: Salient features of the parents used to generate the material for the experiment**

Parents	NBC - 39	PL -2	PL – 5	EC402104
Clusters plant <sup>-1</sup>	25.43	23.29	22.33	22.50
Pods plant <sup>-1</sup>	39.71	44.43	34.00	37.83
Seed yield plant <sup>-1</sup> (g)	38.14	55.57	48.50	32.42
Zn (mg/Kg)	26.38	32.35	49.61	31.14
Fe (mg/Kg)	168.12	254.49	185.97	216.56
Ca (mg/Kg)	0.98	0.69	0.93	0.68



**Plate 1a: Preparation of experimental plot**



**Plate 1b: Plant protection practices carried out in experimental plot**



**Plate 1c: Crop at the harvesting stage**

**Table 3: Salient features of the checks used in the experiment**

Checks	KBC - 2	KBC - 9	C - 152	IT- 38956 - 1	PGCP - 5
Clusters plant <sup>-1</sup>	18.04	26.45	26.17	24.13	27.34
Pods plant <sup>-1</sup>	35.71	35.27	43.39	36.63	56.98
Seed yield plant <sup>-1</sup> (g)	35.95	45.15	34.66	46.45	65.05
Zn (mg/Kg)	32.90	39.21	34.41	42.42	36.61
Fe (mg/Kg)	133.75	209.75	172.61	195.74	185.01
Ca (mg/Kg)	0.70	0.69	0.81	0.69	0.75

The experimental material included 12 and 54 F<sub>4</sub> families from the cross PL-2 × NBC 39 and PL-5 × EC402104 of cowpea respectively. In the F<sub>5</sub> generation, 12 and 30 families were selected from F<sub>4</sub> generation, which constituted F<sub>5</sub> material (Table 4). The selection in F<sub>4</sub> was based on optimum seed yield per plant and zinc, iron and calcium levels.

**Table 4: Experimental material utilised in the present evaluation**

Crosses	PL-2 × NBC 39	PL-5 × EC402104
No. of F <sub>4</sub> families	12 (110 plants)	54 (330 plants)
No. of F <sub>5</sub> families	12 (100 plants)	30 (209 plants)

### 3.3.2 Evaluation of the experimental material

A total of 110 and 330 F<sub>4</sub> plants derived from two crosses PL-2 × NBC-39 and PL-5 × EC-402104 respectively were evaluated along with five checks (Table 3) in augmented design in contiguous blocks having 0.15 m spacing between plants and 0.45 m between the rows. Sowing was carried out during late *kharif* 2018. A total of 100 and 209 F<sub>5</sub> plants derived from F<sub>4</sub> generation of two crosses PL-2 × NBC-39 and PL-5 × EC-402104 respectively (constituting F<sub>5</sub>) were evaluated in augmented design along with five checks (Table 3). The experiment was conducted during *kharif* 2019 with spacing of 0.15 m between plants and 0.45 m between the rows. Data was recorded for eleven traits on all the

plants in each family and on five randomly selected plants in each of the checks and parents.

### **3.3.3 Recording of observations**

Observations for different yield and its contributing traits were recorded all plants in F<sub>4</sub> and F<sub>5</sub> plants, five plants in each line of the checks excluding the border plants in each row. The procedure carried out for recording observations on these plants is described below.

Observation was recorded on following traits.

1. Clusters plant<sup>-1</sup>
2. Pods cluster<sup>-1</sup>
3. Pods plant<sup>-1</sup>
4. Plant height (cm)
5. Pod length (cm)
6. Seeds pod<sup>-1</sup>
7. Seed yield plant<sup>-1</sup> (g)
8. Test weight (g)
9. Iron (mg kg<sup>-1</sup>)
10. Zinc (mg kg<sup>-1</sup>)
11. Calcium (mg kg<sup>-1</sup>)

#### **3.3.3.1 Clusters plant<sup>-1</sup>**

All the clusters in each plant was counted and expressed as clusters plant<sup>-1</sup>.

#### **3.3.3.2 Pods cluster<sup>-1</sup>**

Total number of pods produced in each cluster were counted and average was considered as pods per plant.



**Plate 1d: General view of experimental plot of F<sub>5</sub> progenies**

#### **3.3.3.3 Pods plant<sup>-1</sup>**

Total number of pods in each plant was counted and recorded as pods plant<sup>-1</sup>.

#### **3.3.3.4 Plant height (cm)**

The height of plant from the ground level of the main axis to the apical leaflet was measured before harvesting and expressed in centimetre.

#### **3.3.3.5 Pod length (cm)**

Mean of five randomly selected mature pods were measured in centimetres and noted as pod length.

#### **3.3.3.6 Seeds pod<sup>-1</sup>**

Seeds present in five randomly selected pod in each plant were counted and the average was noted as seeds per pod.

#### **3.3.3.7 Seed yield plant<sup>-1</sup> (g)**

Seeds from each plant were weighed in grams and recorded as seed yield per plant.

#### **3.3.3.8 Test weight (g)**

Randomly selected 100 seeds were weighed in grams and recorded as test weight

#### **3.3.3.9 Zinc content (mg kg<sup>-1</sup>)**

Seeds were dried after harvest and 0.25 g of fine powdered samples were taken for digestion and is analysed using diacid mixture method using atomic absorption spectrophotometry (Jackson, 1973).

#### **3.3.3.10 Iron content (mg kg<sup>-1</sup>)**

Seeds were dried after harvest and 0.25 g of fine powdered samples were taken for digestion and is analysed using diacid mixture method using atomic absorption spectrophotometry (Jackson, 1973).

### 3.3.3.11 Calcium content (mg kg<sup>-1</sup>)

Calcium content was estimated taking 2 ml of digested aliquot. The aliquot was titrated against EDTA and values were recorded.

### Analysis of iron, zinc and calcium contents (mg kg<sup>-1</sup>)

Estimation of Iron and Zinc in dry seeds in each generation was done using Atomic Absorption Spectrophotometer (AAS) (Jackson, 1973). The protocol is briefly described below.

- Seeds were grinded in the mixer and made into fine powder.
- 0.5g of fine powder, ten ml of 0.1N nitric acid was added to it and kept overnight for pre-digestion.
- Ten ml of diacid (9:4 nitric acid to perchloric acid) was added in the next morning, brown color was noticed.
- The mixture was kept in water bath till the brown color turns to clear white.
- Mixture was diluted by adding 10ml of double distilled water and filtered using Whatman's filter paper.
- The volume of filtered solution was made up to 50ml by adding double distilled water.
- Samples were fed to atomic absorption spectrophotometer (AAS) and values were recorded.
- Concentration in mg Kg<sup>-1</sup> was calculated using formula

$$\text{Zn / Fe (mg kg}^{-1}\text{)} = \frac{\text{Graph ppm} \times \text{volume digested}}{\text{Weight of the sample}}$$

### Protocol for estimation of calcium content using EDTA titration method (Jackson, 1973)

- The same digested sample was subjected for EDTA titration for calcium content estimation.
- 2 mL of aliquot was taken in mortar



**Plate 2a: Estimation of calcium content in cowpea seeds through EDTA titration method**



**Plate 2b: Digestion of cowpea seeds for estimation of iron and zinc using di-acid method**



**Plate 2c: Estimation of iron and zinc content in the cowpea seeds through atomic absorption spectrophotometer**

- 10 mL of NaOH (10%) was added
- Pinch of Patton and Reeder's reagent was added to the mixture
- Titrated against EDTA
- Values were recorded
- Concentration in mg kg<sup>-1</sup> was calculated using formula.

$$\text{Ca (mg kg}^{-1}\text{)} = \frac{\text{titer value} \times \text{N of EDTA} \times \text{volume of extractant added}}{\text{Weight of the sample} \times \text{aliquot taken}}$$

### 3.4 Statistical analysis:

The statistical analysis was done using data recorded on F<sub>4</sub> and F<sub>5</sub> plants derived from two crosses PL-2 × NBC-39 and PL-5 × EC-402104. Mean values of data recorded on five randomly selected plants in each check were used for analysis.

#### 3.4.1 Descriptive statistics

##### 3.4.1.1 Traits mean:

Adjusted trait values of individual plants of F<sub>4</sub> progenies used to compute trait means.

$$\bar{Y} = \frac{1}{n} \sum y_i$$

Where,

$\bar{Y}$  = population means of traits

$y_i$  = adjusted trait value of F<sub>4</sub> progenies

##### 3.4.1.2 Trait Range: Highest and lowest trait means used to estimate range

$$\text{Range} = \frac{\text{highest} - \text{lowest trait mean}}{\bar{Y}}$$

### 3.4.2 Analysis of variance (ANOVA)

ANOVA (Table 3) was performed according to the augmented design given by Federer (1956) using SAS version 9.4 software to examine the statistical significance among the  $F_4$  and  $F_5$  progenies.

**Table 5: Structure of ANOVA for  $F_4$  and  $F_5$  according to augmented design**

Sources of variations	Degrees of freedom (df)	Mean sum of squares (MSS)	'F' ratio
<b>Blocks (b)</b> (eliminating checks + $F_4$ progenies)	$(b - 1)$	MSS(b)	MSS(b)/ EMSS
<b>Entries (e)</b> (checks + $F_4$ progenies) (ignoring blocks)	$(e - 1)$	MSS(e)	MSS(e)/EMSS
<b><math>F_4</math> progenies (v)</b>	$(v - 1)$	MSS(v)	MSS(v)/EMSS
<b>Checks(c)</b>	$(c - 1)$	MSS(c)	MSS(c)/EMSS
<b>Checks vs <math>F_4</math> progenies(vc)</b>	$(c - 1)(v - 1)$	MSS (vc)	MSS (vc)/EMSS
<b>Non-genetic Error</b>	$(b-1)(c-1)$	EMSS	

Where,

b = number of blocks

e = number of entries

c = number of checks

v = number of progenies

### 3.4.3 Genetic parameters

Genetic parameters were estimated for the data recorded on eleven traits

#### 3.4.3.1 Phenotypic variance:

$$\text{Variance} = \frac{1}{n-1} \left( \sum y_i - \bar{Y} \right)^2$$

Where,

$n$  = no. of F<sub>4</sub> progenies.

#### 3.4.3.2 Phenotypic co-efficient of variation (PCV):

PCV and GCV was estimated as suggested by Burton and Devane, 1953

$$\text{PCV (\%)} = \frac{\sigma_p}{\bar{X}} \times 100$$

#### 3.4.3.3 Genotypic co-efficient of variation (GCV):

$$\text{GCV (\%)} = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

$\bar{x}$  = Experimental trait means

$\sigma_p$  = Phenotypic standard deviation

$\sigma_g$  = Genotypic standard deviation

#### 3.4.3.4 Genetic advance (GA)

Improvement in mean genotypic value of selected plants is estimated over the parental population called as genetic advance. It was calculated by using the formula suggested by Johnson *et al.* (1955).

$$\text{GA} = h^2 \times \sigma_p \times K$$

Where,

$h^2$  = heritability estimate

$K$  = selection differential at 5 per cent (*i.e.* 2.06) intensity of selection

$\sigma_p$  = phenotypic standard deviation

### 3.4.3.5 Expected genetic advance GAM:

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

Where,

GA = genetic advance

$\bar{X}$  = general mean of character

The GAM was categorized as suggested by Johnson *et al.* (1995)

0-10% = Low

11 - 20% = Moderate

>20% = High

### 3.4.3.6 Narrow sense heritability ( $h^2_{ns}$ ):

Narrow sense heritability was estimated by using formula suggested by Smith and Kinman (1965).

$$h^2 (F_4.F_5) = 4/5. b (F_4.F_5)$$

Where,

$h^2 (F_4.F_5)$  = heritability in narrow sense using  $F_4.F_5$  regression

$b_{yx}$  = regression of  $F_5$  progeny means on  $F_4$  parental values for respective traits

Here the multiplicative factor 4/5 was used for  $F_5$  on  $F_4$ . The performance of genotypes in future generation can be estimated based on narrow sense heritability estimates of the present generation.

$h^2_{ns}$  was categorized as suggested by Robinson *et al.* (1949)

0-10% = Low

10.1 - 30% = Moderate

>30% = High

**3.4.3.7 Phenotypic correlation:**

The relationship of yield with iron, zinc and calcium was studied as suggested by Weber and Moorthy (1952).

$$r = \frac{\sum(x - \bar{x})(y - \bar{y})}{\sqrt{\sum(x - \bar{x})^2 \sum(y - \bar{y})^2}}$$

Where,

$r$  = correlation co-efficient

$\bar{x}$  = mean of dependent variable x

$\bar{y}$  = mean of independent variable y

**3.4.3.8 Path analysis:**

Direct and indirect effects of different traits on yield was estimated as suggested by Wright (1921) and illustrated by Dewey and Lu (1957).

$$r_{1y} = a + r_{12}b + r_{13}c + \dots + r_{1i}i$$

$$r_{2y} = a + r_{21}a + b + r_{23}c + \dots + r_{2i}i$$

$$r_{3y} = r_{31}a + r_{32}b + c + \dots + r_{3i}i$$

$$r_{1y} = r_{11}a + r_{12}b + r_{13}c + \dots + I$$

Where,

$r_{1y}$  to  $r_{11y}$  = Co-efficient of correlation between causal factors 1 to 1 with dependent characters y.

$r_{12}$  to  $r_{1i}$  = Co-efficient of correlation among causal factors

a, b, c...i = Direct effects of characters 'a' to 'i' on the dependent character 'y.'

Lenka and Mishra (1973) have suggested scales for path coefficients analysis.

0.00-0.09	:	Negligible
0.10-0.19	:	Low
0.20-0.29	:	Moderate
0.30-0.99	:	High
>1.00	:	Very high

### **3.5 Criteria for selection of superior genotypes**

The easily observable/assayable traits which had significantly positive correlation with seed yield was considered as tool for selection along with optimum level or more than average level of iron, zinc and calcium content.

## IV RESULTS AND DISSCUSSION

The results procured from the current experiment is presented and discussed in this chapter under following heads.

4.1 Analysis of variance

4.2 Comparison of means of different traits between F<sub>4</sub> and F<sub>5</sub> generation

4.3 Genetic variability studies

4.4 Estimation of narrow sense heritability, intergeneration correlation, using parent offspring regression in F<sub>4</sub>-F<sub>5</sub> generations

4.5 Estimation of correlation and path analysis for the traits studied

4.6 Identification of best plants in F<sub>5</sub> derived from two crosses

### 4.1 Analysis of variance (ANOVA)

Analysis of variance aids in partitioning total variability into components attributable to different sources of variation and it is basic step in detecting the genetic variability in the experimental material.

ANOVA showed statistically significant mean sum of square for all the traits examined and manifests appreciable amount of variability in the selected crosses which justifies the selection of material is suitable for genetical studies. Analysis of variance (Augmented design) for F<sub>4</sub> and F<sub>5</sub> generations obtained from two crosses *viz.*, PL-2 × NBC-39 and PL-5 × EC402104 is estimated and represented in the Tables 6a, 6b, 7a and 7b.

ANOVA of F<sub>4</sub> generation for the cross PL-2 × NBC-39 indicated highly significant mean sum of squares for all the traits under investigation with respect to ‘treatment’ (F<sub>4</sub> progenies + checks), ‘F<sub>4</sub> progenies’, ‘checks’ and ‘check vs F<sub>4</sub> progenies’ except for iron and pods per cluster in ‘checks’ (Table 6a). Block effects were reported to be significant for seeds pod<sup>-1</sup>, pod length, pods cluster<sup>-1</sup>, suggesting the prevalence of variability because of heterogenous area. Aliyu *et al.* (2016), Barroso *et al.* (2017) and Sabale *et al.* (2018) earlier observed similar results.

**Table 6a: Analysis of variance for F<sub>4</sub> generation derived from cross PL-2 × NBC-39 for eleven traits in cowpea**

Source of variation	df	Clusters plant <sup>-1</sup>	Pods cluster <sup>-1</sup>	Pods plant <sup>-1</sup>	Plant height (cm)	Pod length (cm)	Seeds pod <sup>-1</sup>	Test weight (g)	Seed yield plant <sup>-1</sup> (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )
<b>Block</b>	10	2.71	0.16*	8.91	29.95	7.07**	6.14*	0.84	4.00	15.53	1081.65	0.01*
<b>Treatment (F<sub>4</sub> progenies + Checks)</b>	114	62.17**	0.09**	173.75**	126.76**	6.35**	9.01**	9.54**	284.84**	231.67**	5675.18**	0.32**
<b>F<sub>4</sub> progenies</b>	109	35.21**	0.09**	99.43**	100.79**	6.02**	6.90**	5.94**	143.96**	237.92**	5757.07**	0.30**
<b>Checks</b>	4	274.12**	0.08	676.69**	683.09**	6.30**	12.06**	3.14**	728.65**	119.14**	1957.18	0.15**
<b>Checks vs F<sub>4</sub> progenies</b>	1	2153.17**	0.13	6262.18**	731.73**	5.10**	226.97**	428.09**	13865.90**	0.87	11621.85**	3.26**
<b>Error</b>	40	1.63	0.04	13.17	31.51	1.1154	1.65**	1.14	7.39	28.68	1228.51	0.02**

Note: \* and \*\* indicates that particular trait is significant at P=0.05 (5%) and P=0.01 (1%) probability level, respectively.

**Table 6b: Analysis of variance for F<sub>4</sub> generation derived from cross PL-5 × EC402104 for eleven traits in cowpea**

Source of variation	df	Clusters <sup>-1</sup> plant	Pods cluster <sup>-1</sup>	Pods plant <sup>-1</sup>	Plant height (cm)	Pod length (cm)	Seeds pod <sup>-1</sup>	Test weight (g)	Seed yield plant <sup>-1</sup> (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )
<b>Block</b>	10	2.36	0.09*	32.94*	57.97	4.14*	3.39*	0.91	50.65*	20.49	3805.61	0.04
<b>Treatment (F<sub>4</sub> progenies + Checks)</b>	114	50.84**	0.08**	146.24**	94.36**	5.34**	7.97**	10.63**	236.48**	151.83**	7613.01**	0.53**
<b>F<sub>4</sub> progenies</b>	109	26.06**	0.08**	59.69**	84.22**	4.94**	7.23**	5.12**	133.49**	148.73**	7559.47**	0.50**
<b>Checks</b>	4	260.19**	0.05	1034.02**	572.66**	16.60**	9.85**	5.29**	1322.16**	211.05**	4310.10	0.06
<b>Checks vs F<sub>4</sub> progenies</b>	1	7365.44**	0.70*	25069.48**	1517.38**	91.94**	245.06**	1846.20**	29777.97**	935.59**	38435.91**	12.77**
<b>Error</b>	40	3.85	0.03	17.01	43.79	1.35	1.47**	1.00	26.18	39.94	2639.09	0.03

Note: \* and \*\* indicates that particular trait is significant at P=0.05 (5%) and P=0.01 (1%) probability level, respectively.

**Table 7a: Analysis of variance for F<sub>5</sub> generation derived from cross PL-2 × NBC 39 for eleven traits in cowpea**

Source of variation	df	Clusters plant <sup>-1</sup>	Pods cluster <sup>-1</sup>	Pods plant <sup>-1</sup>	Plant height (cm)	Pod length (cm)	Seeds pod <sup>-1</sup>	Test weight (g)	Seed yield plant <sup>-1</sup> (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )
Block	10	1.71	0.09*	44.57*	2.99	2.93*	3.24*	0.69	56.06	24.35	5164.92	0.02
Treatment (F <sub>4</sub> progenies + Checks)	114	96.66**	0.09**	229.07**	104.37**	5.69**	6.90**	8.47**	387.92**	189.93**	11348.94**	0.16**
F <sub>4</sub> progenies	109	93.66**	0.09**	209.19**	78.69**	4.15**	6.99**	5.38**	364.15**	188.44**	10579.66**	0.16**
Checks	4	160.50**	0.04**	757.03**	702.51**	14.48**	5.09**	4.93*	960.88**	173.29**	4177.16	0.04
Checks vs F <sub>4</sub> progenies	1	137.79**	0.21**	85.27*	254.29**	123.93*	6.08*	328.28**	449.77**	403.91**	116194.66**	1.17*
Error	40	3.71	0.03	18.37	3.13	1.36	1.09	0.94	28.64	50.24	3364.15	0.03

Note: \* and \*\* indicates that particular trait is significant at P=0.05 (5%) and P=0.01 (1%) probability level, respectively.

**Table 7b: Analysis of variance for F<sub>5</sub> generation derived from cross PL-5 × EC402104 for eleven traits in cowpea**

Source of variation	df	Clusters plant <sup>-1</sup>	Pods cluster <sup>-1</sup>	Pods plant <sup>-1</sup>	Plant height (cm)	Pod length (cm)	Seeds pod <sup>-1</sup>	Test weight (g)	Seed yield plant <sup>-1</sup> (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )
<b>Block</b>	10	1.99	0.08*	40.12*	71.09	2.64	2.91*	0.99	53.33	23.63	4795.24	0.02
<b>Treatment (F<sub>4</sub> progenies + Checks)</b>	114	104.03**	0.08**	275.19**	75.68	8.52**	6.57**	7.08**	550.41**	227.99**	7480.12**	0.13**
<b>F<sub>4</sub> progenies</b>	109	102.06**	0.07**	264.33**	67.97	6.79**	6.60**	4.06**	528.35**	228.40**	6902.28**	0.13**
<b>Checks</b>	4	192.63**	0.07	812.07**	440.89**	15.41**	6.18**	4.45*	1019.05**	169.16*	5177.55	0.04
<b>Checks vs F<sub>4</sub> progenies</b>	1	159.59**	0.56**	386.63**	217.20*	341.99**	1.17	645.94**	3265.22**	378.81**	136881.52**	0.93**
<b>Error</b>	40	4.029	0.032	17.35	51.96	1.31	1.15	1.16	26.33	48.51	3164.89	0.03

Note: \* and \*\* indicates that particular trait is significant at P=0.05 (5%) and P=0.01 (1%) probability level, respectively.

Table 6b represents ANOVA for the cross PL-5 × EC402104 for the F<sub>4</sub> generation. Highly significant difference among ‘treatment’ (F<sub>4</sub> progenies + checks), ‘F<sub>4</sub> progenies’ were observed. Dinesh *et al.* (2017) reported corroborative findings in previous study.

It also revealed non-significant variation for iron and calcium in ‘checks’ and also significant variation between ‘blocks’ for pods cluster<sup>-1</sup>, pod length, seeds pod<sup>-1</sup>, seed yield and pods plant<sup>-1</sup>. The results are in confirmation with the results obtained by Barroso *et al.* (2017).

Similarly, analysis of variance for F<sub>5</sub> generation derived from the cross PL-2 × NBC-39 revealed significant variance attributable to ‘treatment’ (F<sub>5</sub> progenies + checks) and ‘F<sub>5</sub> progenies’ for all the trait except for iron and calcium in ‘checks’. Significant block effects were noticed for pods plant<sup>-1</sup>, seeds pod<sup>-1</sup>, pod length and pods cluster<sup>-1</sup> (Table 7a). These results are in consonance with the outcomes of Gerrano *et al.* (2015) and Mayuri sahu (2018).

Highly significant variance (Table 7b) was observed in F<sub>5</sub> generation obtained from cross PL-5 × EC402104 pertaining to ‘treatment’ (F<sub>5</sub> progenies + checks), ‘F<sub>5</sub> progenies’, ‘checks’ and ‘check vs F<sub>5</sub> progenies’ for all traits under study. Non-significant mean sum of square was observed for plant height in ‘entries’ (F<sub>5</sub> progenies + checks), pods cluster<sup>-1</sup>, iron and zinc in ‘checks’. Traits like seed pod<sup>-1</sup>, pods cluster<sup>-1</sup> and pods plant<sup>-1</sup> showed significant block effect corroborates with results of Barroso *et al.* (2017) and Sharma *et al.* (2019).

Block effects were statistically significant for pod length, pods cluster<sup>-1</sup> and pods plant<sup>-1</sup> in both the crosses studied indicating the environmental influence like soil heterogeneity on these traits. The non-significant variation attributable to ‘blocks’ for other traits in both the crosses suggested that environmental effect had less influence in expression of traits in F<sub>4</sub> and F<sub>5</sub> generation. It also indicates that variation in these traits is a result of its genotype and less influenced by soil environment.

Significant mean sum of square obtained from analyses of variance for F<sub>4</sub> ‘progenies’ and F<sub>5</sub> ‘progenies’ revealed that there exists appreciable amount of genetic variability between the genotypes and suggested there was scope for selection.

The significant variance with respect to ‘checks’ for all traits excluding iron and calcium in both for F<sub>4</sub> and F<sub>5</sub> generation reveals that diversity exists in each trait between the checks used in the current investigation.

## **4.2 Comparison of means of different traits between F<sub>4</sub> and F<sub>5</sub> generation**

### **4.2.1 Mean**

The mean values of eleven traits of F<sub>4</sub> and F<sub>5</sub> generations derived from two crosses PL 2 × NBC-39 and PL-5 × EC402104 were calculated and presented in the Table 8.

The mean values of pods cluster<sup>-1</sup> (1.56), pod length (16.12cm), seeds pod<sup>-1</sup> (14.49), test weight (12.44 g) were comparable between two crosses in both F<sub>4</sub> and F<sub>5</sub> generations. Clusters plant<sup>-1</sup> (19.26), zinc content (36.97 mg/kg) and pods plant<sup>-1</sup> (30.03) in F<sub>4</sub> generation were higher in the cross PL-2 × NBC 39 when compared to the cross PL-5 × EC402104. Whereas pod length (16.12 cm), test weight (11.89 g), iron (151.36 mg/kg) and calcium (0.90 mg/kg) content in the seed were lower in cross PL 2 × NBC-39 as compared to PL-5 × EC402104. Plant height (46 cm) and pods cluster<sup>-1</sup> (1.50) were almost on par in both the crosses (Table 8).

In F<sub>5</sub> generation, plant height (25.74 cm) was little higher in case of PL-2 × NBC-39 cross. Other yield attributing traits like seed yield (44.99 g), pods plants<sup>-1</sup> (41.31), pod length (17.26 cm) and iron content in seed (200.72 mg/kg) were lower in the cross PL 2 × NBC-39 as compared to PL 5×EC402104. Clusters plant<sup>-1</sup> (25.74), seeds pod<sup>-1</sup> (14.49), pod clusters<sup>-1</sup> (1.60), zinc (39.50 mg/kg), calcium (0.82 mg/kg) content were similar and juxtaposing in both the crosses.

In the cross PL 2 × NBC-39 test weight (11.89 g) and calcium content in seed (0.90 mg/kg) had higher mean values in F<sub>4</sub> compared to F<sub>5</sub> generation. Pods cluster<sup>-1</sup> (1.56), clusters plant<sup>-1</sup> (19.26), plant height (46.4 cm), seeds pod<sup>-1</sup> (13.13), zinc (36.97 mg/ kg)

and iron (151.36 mg/kg) showed lower mean value in F<sub>4</sub> compared to F<sub>5</sub> generation. Similar results were observed in the other cross.

In general, pods cluster<sup>-1</sup>, zinc, seeds pod<sup>-1</sup>, clusters plant<sup>-1</sup>, iron and plant height showed increasing trend in mean values from F<sub>4</sub> to F<sub>5</sub> generation in both the crosses PL 2 × NBC-39 and PL-5 × EC402104. Whereas, calcium content and test weight revealed decreasing trend from F<sub>4</sub> to F<sub>5</sub> generation in both the crosses (Table 8).

**Table 8: Estimates of means of eleven traits in F<sub>4</sub> and F<sub>5</sub> generations derived from the two crosses (mean ± SE)**

Characters	PL-2 × NBC-39		PL-5 × EC402104	
	F <sub>4</sub>	F <sub>5</sub>	F <sub>4</sub>	F <sub>5</sub>
Clusters plant <sup>-1</sup>	19.26 ± 0.55	25.74 ± 0.86	15.41 ± 0.72	25.99 ± 0.85
Pods cluster <sup>-1</sup>	1.56 ± 0.08	1.6 ± 0.08	1.50 ± 0.07	1.64 ± 0.07
Pods plant <sup>-1</sup>	30.03 ± 1.55	41.31 ± 1.92	23.34 ± 1.50	42.59 ± 1.77
Plant height (cm)	46.4 ± 2.39	50.21 ± 0.79	46.38 ± 2.41	49.16 ± 3.07
Pod length (cm)	16.12 ± 0.4	17.26 ± 0.52	17.28 ± 0.42	18.2 ± 0.48
Seeds per pod	13.13 ± 0.54	14.49 ± 0.47	13.35 ± 0.44	14.91 ± 0.46
Test weight (g)	11.89 ± 0.46	11.39 ± 0.43	13.94 ± 0.36	12.44 ± 0.46
Seed yield plant <sup>-1</sup> (g)	30.77 ± 1.15	44.99 ± 2.39	28.61 ± 1.86	54.07 ± 2.19
Zn (mg kg <sup>-1</sup> )	36.97 ± 2.28	39.5 ± 3.17	33.97 ± 2.3	39.34 ± 2.97
Fe (mg kg <sup>-1</sup> )	151.36 ± 14.9	200.72 ± 25.94	178.13 ± 18.75	204.11 ± 23.98
Ca (mg kg <sup>-1</sup> )	0.90 ± 0.03	0.82 ± 0.08	1.06 ± 0.59	0.82 ± 0.08

The mean performance of plant height (50.21cm) and zinc (36.97 mg/kg) content in seed were higher in cross PL 2 × NBC-39. But mean performance of yield and its accrediting traits like seed yield (54.07 g) and pod length (18.2 cm) were higher in cross PL-5 × EC402104.

Overall, the mean performance of F<sub>5</sub> generation was better compared to the F<sub>4</sub> generation. The performance of cross PL-5 × EC402104 was better for most of traits comparing to the cross PL 2 × NBC-39. Ashni (2019) using quantitative trait mean have

discovered better performing lines from a twenty-three advance generation cowpea lines. Selection based on mean value is also supported by Gerrano *et al.* (2015).

#### 4.2.2 Absolute range and standardized range (SR) of two crosses

The standardized range and the absolute range for two crosses for eleven traits were computed and presented in the Table 9a and 9b.

The upper limit of absolute range for zinc content (93.10 mg/kg), pods cluster<sup>-1</sup> (2.33), plant height (66 cm) and pods plant<sup>-1</sup> (62) was higher in F<sub>4</sub> of the cross PL-2 × NBC-39. Whereas, seed yield (74.54 g), pod length (26 cm), clusters plant<sup>-1</sup> (38), test weight (21.20 g), calcium (5.66 mg/kg) and iron content in seed (542.78 mg/kg) were high in the cross PL-5 × EC402104. Seeds pod<sup>-1</sup> was similar for both the crosses. The lower limit for pods cluster<sup>-1</sup> (1.05), plant height (24.5 cm), pod length (11 cm), zinc (15.99 mg/kg), seed yield (8.53 g), seeds pod<sup>-1</sup> (7), calcium content (0.35 mg/kg) and test weight (7.84 g) were high in the cross PL-2 × NBC-39 in F<sub>4</sub>. But clusters plant<sup>-1</sup> (4) and iron content (19 mg/kg) was high in the cross PL-5 × EC402104. The lower limit of absolute range for pods cluster<sup>-1</sup> was same in both the crosses.

The absolute maximum value in F<sub>5</sub> for pods cluster<sup>-1</sup> (2.89), calcium content (2.88 mg/kg), seed yield plant<sup>-1</sup> (159 g), plant height (85 cm) and cluster plant<sup>-1</sup> (69) were higher in the cross PL-2 × NBC-39. While, the upper limit was higher in the cross PL-5 × EC402104 for traits like pods plant<sup>-1</sup> (99), pod length (26 cm), test weight (20 g), zinc (98.52 mg/kg) and iron content (538.7 mg/kg). The absolute minimum for pod length (10 cm), pods plant<sup>-1</sup> (11), iron content (31.46), clusters plant<sup>-1</sup> (7), seeds pod<sup>-1</sup> (8) and plant height (20 cm) in F<sub>5</sub> generation were lower in the cross PL-5 × EC402104. Whereas, pods cluster<sup>-1</sup> (9), test weight (6 g), seed yield plant<sup>-1</sup> (10 g) and zinc content (4.68 mg/kg) the lower limit of absolute range was lower in the cross PL-2 × NBC-39 and calcium content (0.28 mg/kg) was juxtaposing in both the crosses (Table 9a and 9b).

Wider range values imply that there is scope for selection and material consists of high and low yielding genotypes. Similar studies were made by Shwetha, (2018), Havaraddi and Deshpande (2018).

In the cross PL-2 × NBC-39, the absolute minimum for test weight (7.84 g), pods cluster<sup>-1</sup> (1.05), zinc (15.99 mg/kg) and calcium content (0.35 mg/kg) were high in F<sub>4</sub> and rest of the traits *viz.*, pod length (12 cm), pods plant<sup>-1</sup> (13), plant height (28 cm), clusters plant<sup>-1</sup> (9) were high in F<sub>5</sub> generation. Similarly, the upper limit of absolute range was high for test weight (19 g), pods cluster<sup>-1</sup> (2.89), pods plant<sup>-1</sup> (87), plant height (85 cm), pod length (23 cm), seeds pod<sup>-1</sup> (26), seed yield plant<sup>-1</sup> (159 g) and clusters plant<sup>-1</sup> (69) in F<sub>5</sub> but for zinc content (85.3 mg/kg) it was high in F<sub>4</sub> and for calcium (2.8 mg/kg) and iron content (447 mg/kg) the absolute maximum was almost same and comparable.

The maximum limit of absolute range for F<sub>5</sub> in the cross PL-5 × EC402104 was higher for plant height (72 cm), zinc content (98.52 mg/kg), clusters plant<sup>-1</sup> (67), pods clusters<sup>-1</sup> (2.73), seeds pod<sup>-1</sup> (23) and seed yield plant<sup>-1</sup> (135 g). While, low for pod length (25 cm), test weight (20 g) and calcium content (2.8 mg/kg). Iron content (538.7 mg/kg) had comparable upper limits in F<sub>4</sub> and F<sub>5</sub> generations. Similarly, the minimum limit of absolute range for F<sub>4</sub> generation in the cross PL-5 × EC402104 was high only for plant height (23 cm). Whereas, for other traits *i.e.*, pods plant<sup>-1</sup> (11), pod length (10 cm), seeds pod<sup>-1</sup> (8), clusters plant<sup>-1</sup> (7), seed yield plant<sup>-1</sup> (10.5 g), zinc (8.42 mg/kg), iron (31.46 mg/kg) and calcium content (0.28 mg/kg) it was high in F<sub>5</sub> generation. Pods cluster<sup>-1</sup> (0.96) and test weight (7 g) had juxtaposing values in F<sub>4</sub> and F<sub>5</sub> generations (Table 9a and 9b).

Standardized range was comparable between F<sub>4</sub> and F<sub>5</sub> for clusters plant<sup>-1</sup>, calcium content, zinc, pod length and seeds pod<sup>-1</sup>. But standardized range in F<sub>5</sub> in the cross PL-2 × NBC-39 was higher for pods cluster<sup>-1</sup>, test weight, seed yield plant<sup>-1</sup>, plant height and lower for iron content and pods cluster<sup>-1</sup>.

In the cross PL-5 × EC402104, seeds pod<sup>-1</sup>, iron content, pods clusters<sup>-1</sup>, pods plant<sup>-1</sup>, seed yield and clusters plant<sup>-1</sup> showed comparable standardized range in both F<sub>4</sub> and F<sub>5</sub> generation. While, calcium, zinc content and test weight had higher standardized range and plant height had lower standardized range in F<sub>4</sub>.

**Table 9a: Estimates of absolute and standardized range of eleven traits in F<sub>4</sub> and F<sub>5</sub> generations derived from two crosses**

Characters	Progeny	PL-2 × NBC-39			PL-5 × EC402104		
		Absolute range		SR	Absolute range		SR
		Min.	Max.		Min.	Max.	
Clusters plant <sup>-1</sup>	F <sub>4</sub>	3.92	32.00	1.56	4.00	38.00	1.62
	F <sub>5</sub>	9.00	69.00	1.54	7	67	1.62
Pods cluster <sup>-1</sup>	F <sub>4</sub>	1.05	2.33	0.76	0.96	2.67	0.94
	F <sub>5</sub>	0.59	2.89	1.33	0.76	2.73	1.12
Pods plant <sup>-1</sup>	F <sub>4</sub>	6.00	62.00	1.60	6.00	55.00	1.61
	F <sub>5</sub>	13.00	87.00	1.48	11.00	99.00	1.60
Plant height (cm)	F <sub>4</sub>	24.50	66.00	0.92	23.00	65.00	0.95
	F <sub>5</sub>	28.00	85.00	1.01	20.00	72.00	1.13
Pod length (cm)	F <sub>4</sub>	11.00	21.00	0.63	6.00	26.00	1.25
	F <sub>5</sub>	12.00	23.00	0.63	10.00	25.00	0.86

**Table 9b: Estimates of absolute and standardized range of eleven traits in F<sub>4</sub> and F<sub>5</sub> generations derived from two crosses**

Characters	Progeny	PL-2 × NBC-39			PL-5 × EC402104		
		Absolute range		SR	Absolute range		SR
		Min.	Max.		Min.	Max.	
Seeds pod <sup>-1</sup>	F <sub>4</sub>	7.00	18.00	0.90	6.00	18.00	1.00
	F <sub>5</sub>	9.00	26.00	0.97	8.00	23.00	0.97
Test weight (g)	F <sub>4</sub>	7.84	18.40	0.80	6.50	21.20	1.06
	F <sub>5</sub>	6.00	19.00	1.04	7.00	20.00	0.96
Seed yield per plant (g)	F <sub>4</sub>	8.53	67.50	1.55	6.00	74.54	1.70
	F <sub>5</sub>	10.00	159.00	1.76	10.50	135.00	1.71
Zn (mg kg <sup>-1</sup> )	F <sub>4</sub>	15.99	93.10	1.41	5.74	84.06	1.74
	F <sub>5</sub>	4.68	85.30	1.79	8.42	98.52	1.68
Fe (mg kg <sup>-1</sup> )	F <sub>4</sub>	14.50	447.60	1.87	19.64	542.78	1.86
	F <sub>5</sub>	38.26	447.14	1.68	31.46	538.70	1.78
Ca (mg kg <sup>-1</sup> )	F <sub>4</sub>	0.35	2.82	1.56	0.05	5.66	1.96
	F <sub>5</sub>	0.28	2.88	1.65	0.28	2.80	1.64

Note: Min. - Minimum

Max.- Maximum

SR - Standard range

The standardized range for pods plant<sup>-1</sup>, seeds pod<sup>-1</sup>, plant height, pod length, clusters plant<sup>-1</sup> were higher in the cross PL-5 × EC402104 for both F<sub>4</sub> and F<sub>5</sub> generation compared to PL-2 × NBC-39 and for pods cluster<sup>-1</sup>, calcium, test weight, zinc, seeds pod<sup>-1</sup> were higher in F<sub>5</sub> and lower in F<sub>4</sub> in the cross PL-2 × NBC-39 compared to cross PL-5 × EC402104. Iron content had comparable standardized range between two crosses in their respective generation.

Upon comparing standardized range between two generations, the cross PL-5 × EC402104 showed increasing trend for pods cluster<sup>-1</sup>, seed yield and plant height. While pods plant<sup>-1</sup>, seeds pod<sup>-1</sup>, calcium, iron, pod length, zinc and test weight showed decreasing trend. Pods cluster<sup>-1</sup>, test weight, seeds pod<sup>-1</sup>, seed yield plant<sup>-1</sup>, zinc, plant height and calcium content revealed increasing trend in standardized range in the cross PL-2 × NBC-39 from F<sub>4</sub> to F<sub>5</sub> generation but clusters plant<sup>-1</sup>, iron and pods plant<sup>-1</sup> indicated decreasing trend from F<sub>4</sub> to F<sub>5</sub> generation.

In general, the cross PL-5 × EC402104 had higher number of maximum absolute range. Similar results were obtained by Shwetha, 2018. Higher estimates of both upper and lower limits of absolute range for majority of traits were noted in the cross PL-2 × NBC-39 suggesting that extremes phenotypes were available in this cross. Absolute maximum was recorded in F<sub>5</sub> in both crosses for more than half of the traits compared to F<sub>4</sub> generation.

Higher magnitude of standardized range was recorded in the cross PL-5 × EC402104 for most of the traits in F<sub>4</sub> and F<sub>5</sub> generations. Both crosses exhibited transgressive segregants which may provide ample scope for selection of better phenotypes in future generations. Similar studies were reported by Ashni (2019) utilizing absolute and standardized range in cowpea.

### **4.3 Genetic variability studies**

The parameters like mean and range helps in recognizing the existence of variance but not the extent of variation hence there is necessity to estimate genetic parameters *viz.*, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). But these estimates do not provide any information about heritable portion of variability.

Hence, estimation of heritability becomes essential along with genetic advance, which reveals extent of improvement in base population for every selection cycle (Johnson *et al.*, 1995).

The genetic variability parameters *viz.*, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent mean for iron, zinc, calcium, yield and its attributing traits in F<sub>4</sub> and F<sub>5</sub> generation derived from two crosses of cowpea were estimated and represented in the Table 10 and 11.

#### **i. Clusters plant<sup>-1</sup>**

Moderate GCV and PCV were estimated for clusters plant<sup>-1</sup> in F<sub>4</sub> and F<sub>5</sub> in both crosses. High estimates of heritability combined with GAM were noticed in F<sub>4</sub> and F<sub>5</sub> of cross PL-2 × NBC-39. While, moderate heritability and GAM were noticed for the cross PL-5 × EC402104 in both F<sub>4</sub> and F<sub>5</sub> generations. Narrow difference between GCV and PCV indicates less effect of environment on the trait and selection will be favorable. The outcomes were in agreement with the previous studies of Bhagawati *et al.* (2018) and Meenatchi *et al.* (2019).

#### **ii. Pods cluster<sup>-1</sup>**

Low GCV and moderate PCV in both the crosses was discovered. Low heritability accompanied with low GAM estimates were noticed in F<sub>4</sub> and F<sub>5</sub> generations in two crosses. The results suggest that environmental and environment × genotype interaction exist and selection cannot be practiced for this trait. Dinesh *et al.* (2017) reported similar results and suggested less scope for selection for this trait.

#### **iii. Pods plant<sup>-1</sup>**

The cross PL-2 × NBC-39 had moderate GCV, PCV along with moderate heritability and GAM in F<sub>4</sub> and F<sub>5</sub> generations. Similar results reported by Bhagawati *et al.* (2018). While in the cross PL-5 × EC402104, GCV was recorded moderate with high PCV in F<sub>4</sub>, the results were corroborating with Havaraddi and Deshpande (2018), Dinesh *et al.* (2018) and Sabale *et al.* (2018) indicating that considerable amount of environment effect

other than non-additive gene action was present. Moderate PCV and GCV in F<sub>5</sub> accompanied with moderate heritability and moderate GAM in both F<sub>4</sub> and F<sub>5</sub> generations was noticed, findings are on par with Kumar *et al.* (2015). Therefore, selection based on two or more traits is more reliable.

#### **iv. Plant height**

The trait showed low estimate of GCV in both crosses which is in agreement with the observation made by Thorat and Gadewar (2013) and Aliyu *et al.* (2016). Moderate PCV with low heritability and GAM in F<sub>4</sub>, high heritability along with moderate GAM in F<sub>5</sub> was noticed in the cross PL-2 × NBC-39. But lower estimates of heritability and GAM was reported in cross PL-5 × EC402104. Low estimates of GCV than PCV indicates that the environmental effect influences the expression of trait where the heritability is also low contradicting to the results by Dinesh *et al.* (2017) and Bhagwati *et al.* (2018).

#### **v. Pod length**

Low estimates of PCV, GCV, heritability along with GAM was noticed for pod length in both F<sub>4</sub> and F<sub>5</sub> generations in the two crosses. Which indicates that the trait is influenced by environmental effects and non-additive gene action. Similar kind of findings were reported by Havaraddi and Deshpande (2018) and contrary to Patel *et al.* (2016) and Verma *et al.* (2019).

#### **vi. Seed pod<sup>-1</sup>**

The trait showed low GCV in F<sub>4</sub> and F<sub>5</sub> and moderate PCV in F<sub>4</sub> of both the cross, while low PCV was observed in F<sub>5</sub> of both crosses. Heritability and GAM was also low in both the crosses which reveals that the trait is under governance of non-additive gene action and selection is not favoured. The observations were contrasting to results observed by Havaraddi and Deshpande (2018) and Aliyu *et al.* (2016).

#### **vii. Test weight**

Moderate PCV and low GCV, moderate heritability along with low GAM observed in the cross PL-2 × NBC-39 except in F<sub>5</sub> where GAM was moderate. On the other hand,

the cross PL-5 × EC402104 had low PCV and GCV in F<sub>4</sub>, suggesting selection based on this trait would not be helpful as the trait is influenced by non-additive gene action and environmental interactions and these observations were in accordance with Havaraddi and Deshpande (2018). While moderate PCV and low GCV was reported in F<sub>5</sub>. The heritability and GAM estimates were low in both F<sub>4</sub> and F<sub>5</sub>. These results were corroborating to Dinesh *et al.* (2017) but contrasting to the results obtained by Bhagawati *et al.* (2018).

#### **viii. Seed yield plant<sup>-1</sup>**

Moderate PCV and GCV, high heritability and with high GAM was discovered in cross PL-2 × NBC-39 in F<sub>4</sub> and similar out comes were reported by Sharma *et al.* (2019) and Bhagawati *et al.* (2018). Similarly, moderate PCV and GCV was spotted together with moderate heritability and moderate GAM in the cross PL-5×EC402104. The reports are in accordance with Dinesh *et al.* (2017) and suggests that selection based on two or more traits is effective. Selection based on this trait could be effective because the trait is governed by additive gene action.

#### **ix. Zinc content**

PCV and GCV estimates were noted as moderate in F<sub>4</sub> of cross PL-2 × NBC-39 and F<sub>5</sub> of cross PL-5×EC402104. Low GCV with moderate PCV was observed in F<sub>5</sub> of cross PL-2 × NBC-39 and F<sub>4</sub> of cross PL-5×EC402104. Moderate heritability, GAM was reported in F<sub>4</sub> and moderate heritability along with low GAM noticed in F<sub>5</sub> of cross PL-2 × NBC-39, while low heritability, GAM in F<sub>4</sub> and low heritability with moderate GAM in F<sub>5</sub> of PL-5 × EC402104 was discovered. Moderate to low GCV implies that the trait is likely to be influenced by environment and selection may not be very much effective.

#### **x. Iron content**

The estimates disclosed moderate GCV in both crosses except in F<sub>4</sub> of cross PL-5×EC402104, while PCV was high in F<sub>4</sub> and F<sub>5</sub> of both the crosses. The higher estimate of PCV suggests that iron content is influenced by environment. Moderate heritability and GAM were noted in the cross PL-2 × NBC-39.

## xi. Calcium content

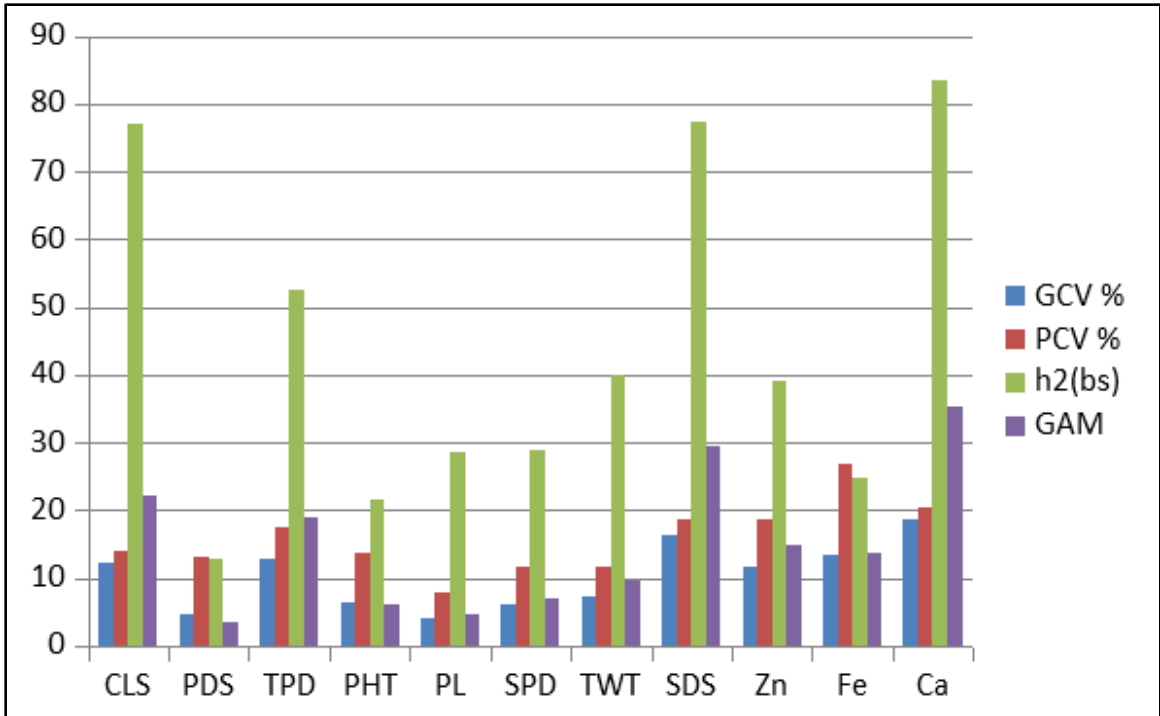
It was observed that GCV was moderate while PCV was high in both the crosses in F<sub>4</sub> and F<sub>5</sub>, while the cross PL-2 × NBC-39 had high heritability with high GAM in F<sub>4</sub>. This implies phenotype is due to genotypes and selection based on phenotypic value could be authentic. Similar results were noted by Kanpara *et al.* (2015) for seeds pod<sup>-1</sup>. Moderate heritability combined with high GAM in F<sub>4</sub> but low heritability and moderate GAM in F<sub>5</sub> of cross PL-5 × EC402104 was recorded.

PCV was high for iron, calcium in F<sub>4</sub> and F<sub>5</sub> of cross PL-2 × NBC-39 and PL-5 × EC402104. These traits had PCV greater than GCV suggesting that there exists environment influence in the expression such of traits. Most of the traits indicated moderate PCV and GCV, suggests the trait expression is controlled by additive gene action due to its dominance and could be helpful in selection in future generations (Table 10 and Fig. 1a, 1b, 2a, 2b).

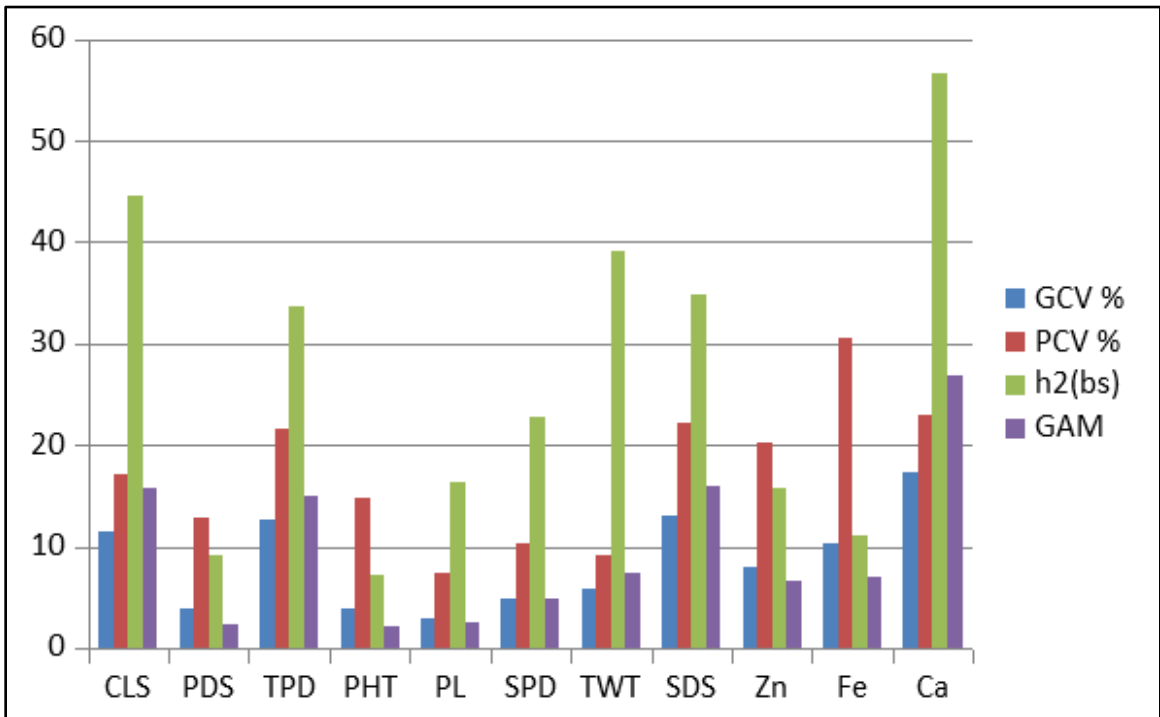
There is decreasing trend in GCV from F<sub>4</sub> and F<sub>5</sub> for the following traits *viz.*, clusters plant<sup>-1</sup>, pods cluster<sup>-1</sup>, zinc, seeds pod<sup>-1</sup>, calcium content, pod length and seed yield plant<sup>-1</sup> while increasing trend for test weight, pods cluster<sup>-1</sup> and iron in cross PL-2 × NBC-39 (Table 10 and Fig. 1a, 1b). Similarly, in the cross PL-5 × EC402104 calcium, plant height, iron, seed yield and pods cluster<sup>-1</sup> showed decreasing trend, whereas pod length, zinc content and clusters plant<sup>-1</sup> depicted increasing trend from F<sub>4</sub> to F<sub>5</sub>. It was observed that PCV was decreasing for majority of traits. (Table 10 and Fig. 2a, 2b).

Heritability was high in F<sub>5</sub> generation as compared to F<sub>4</sub> generation in most of the yield attributing traits in both the crosses. Seeds pod<sup>-1</sup>, pods cluster<sup>-1</sup>, seed yield and clusters plant<sup>-1</sup> showed increasing trend in GAM while other traits had decreasing trend.

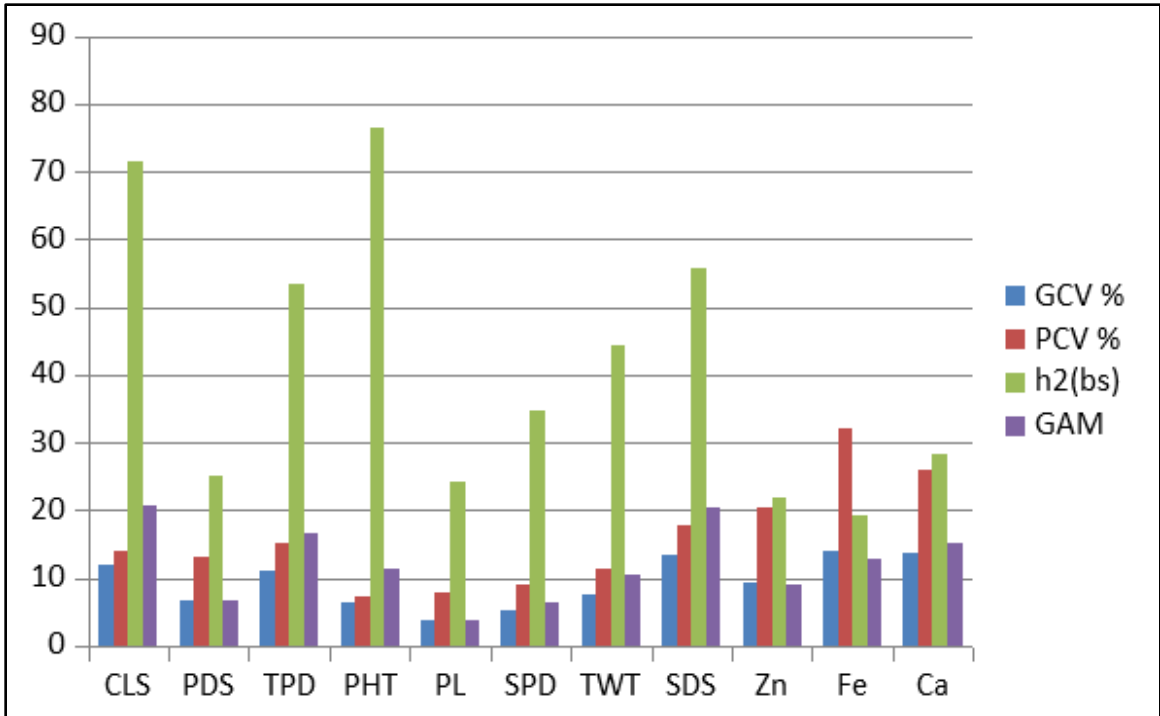
Generally genotypic variation determines heritable and non-heritable portion of variability. All the traits under examination showed high PCV than GCV indicating environmental effect had influence on expression of the traits.



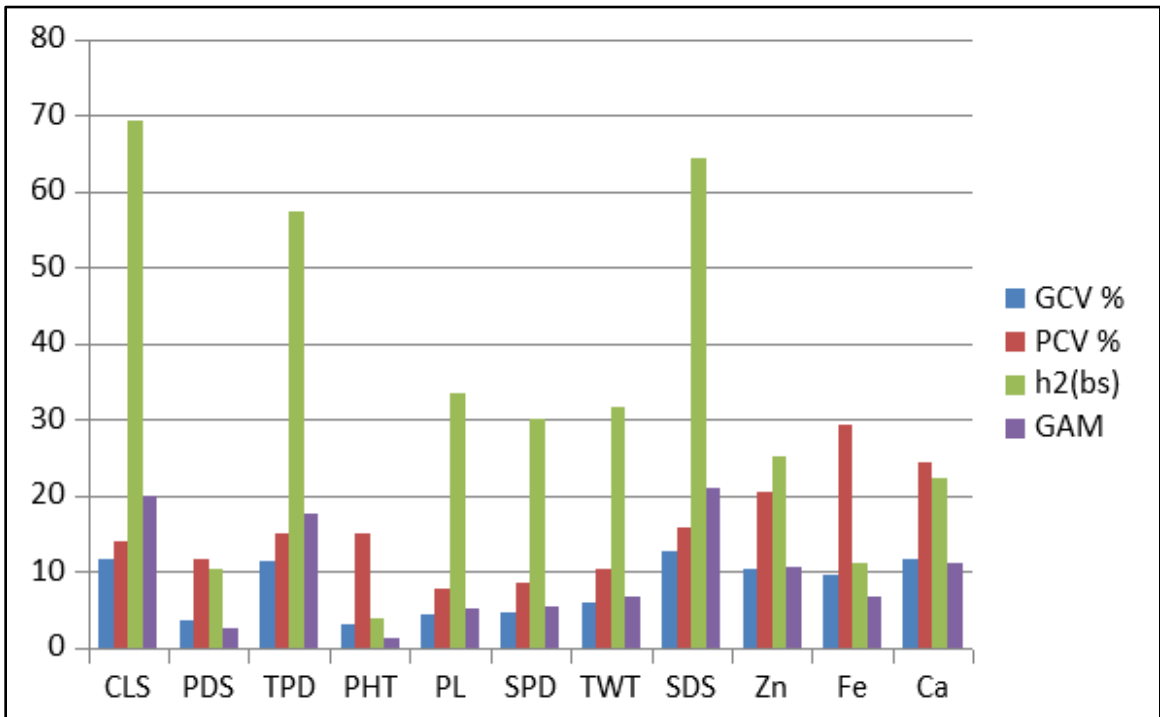
**Fig. 1a:** Graphical representation of genetic variability parameters for 11 traits in F<sub>4</sub> cross PL-2 × NBC-39



**Fig. 1b:** Graphical representation of genetic variability parameters for 11 traits in F<sub>5</sub> cross PL-2 × NBC-39



**Fig. 2b: Graphical representation of genetic variability parameters for 11 traits F<sub>4</sub> in cross PL-5 × EC402104**



**Fig. 2b: Graphical representation of genetic variability parameters for 11 traits F<sub>5</sub> in cross PL-5 × EC402104**

**Table 10: Estimates of genetic variability parameters for iron, zinc, calcium, yield and its attributing traits in F<sub>4</sub> and F<sub>5</sub> generations derived from two crosses**

Characters	PL-2 × NBC-39				PL-5 × EC402104			
	F <sub>4</sub>		F <sub>5</sub>		F <sub>4</sub>		F <sub>5</sub>	
	GCV (%)	PCV (%)	GCV (%)	PCV (%)	GCV (%)	PCV (%)	GCV (%)	PCV (%)
Clusters plant <sup>-1</sup>	12.18	13.87	11.48	17.19	11.60	13.94	11.84	14.01
Pods cluster <sup>-1</sup>	4.74	13.18	3.87	12.83	3.72	11.53	6.60	13.15
Pods plant <sup>-1</sup>	12.72	17.55	12.58	21.68	11.37	15.00	11.11	15.20
Plant height (cm)	6.35	13.68	3.96	14.81	2.99	14.96	6.34	7.25
Pod length (cm)	4.14	7.76	2.98	7.37	4.45	7.70	3.82	7.75
Seeds pod <sup>-1</sup>	6.23	11.60	4.93	10.34	4.71	8.60	5.26	8.93
Test weight (g)	7.35	11.60	5.75	9.19	5.90	10.48	7.61	11.43
Seed yield plant <sup>-1</sup> (g)	16.32	18.56	13.09	22.16	12.77	15.91	13.32	17.86
Zn (mg kg <sup>-1</sup> )	11.62	18.57	8.04	20.27	10.27	20.47	9.46	20.29
Fe (mg kg <sup>-1</sup> )	13.28	26.70	10.22	30.60	9.70	29.22	14.08	32.14
Ca (mg kg <sup>-1</sup> )	18.73	20.51	17.32	23.02	11.53	24.41	13.83	26.02

**Note:** GCV- Genotypic coefficient of variation;

PCV- Phenotypic coefficient of variation;

**Table 11: Estimates of broad sense heritability ( $h^2$ ) and expected genetic advance as per cent mean (GAM) in two crosses of cowpea**

Characters	PL-2 × NBC-39				PL-5 × EC402104			
	F <sub>4</sub>		F <sub>5</sub>		F <sub>4</sub>		F <sub>5</sub>	
	$h^2$ (%)	GAM	$h^2$ (%)	GAM	$h^2$ (%)	GAM	$h^2$ (%)	GAM
Clusters plant <sup>-1</sup>	77.15	22.04	44.62	15.80	69.29	19.89	71.47	20.63
Pods cluster <sup>-1</sup>	12.95	3.51	9.09	2.40	10.43	2.48	25.17	6.82
Pods plant <sup>-1</sup>	52.57	19.00	33.64	15.03	57.47	17.75	53.43	16.73
Plant height (cm)	21.56	6.08	7.15	2.18	3.98	1.23	76.38	11.41
Pod length (cm)	28.46	4.55	16.38	2.49	33.37	5.29	24.22	3.87
Seeds pod <sup>-1</sup>	28.86	6.90	22.78	4.85	29.99	5.31	34.66	6.38
Test weight (g)	40.11	9.59	39.11	7.41	31.66	6.84	44.35	10.45
Seed yield plant <sup>-1</sup> (g)	77.33	29.57	34.88	15.92	64.41	21.10	55.65	20.47
Zn (mg kg <sup>-1</sup> )	39.15	14.98	15.74	6.57	25.17	10.61	21.76	9.09
Fe (mg kg <sup>-1</sup> )	24.76	13.62	11.16	7.04	11.03	6.64	19.18	12.70
Ca (mg kg <sup>-1</sup> )	83.37	35.22	56.57	26.83	22.32	11.23	28.26	15.15

Similar observations were earlier recorded by Manggoel *et al.* (2012), Mahmudul *et al.* (2012), Thorat and Gadewar (2013), Lokesh and Niranjana (2017), Sarath and Reshma (2017), Sharma *et al.* (2017), Savithiri *et al.* (2018) and Nair *et al.* (2018).

Traits like clusters plant<sup>-1</sup>, test weight, pod length, seed pod<sup>-1</sup>, pods plant<sup>-1</sup> and seed yield had narrow difference between PCV and GCV giving hint that environment has less influence on these traits. Sarath and Reshma (2017) and Savithiri *et al.* (2018) found similar results. Pods plant<sup>-1</sup>, plant height, calcium, iron and zinc content had wider difference indicating that traits were influenced by environment effect and also environment genotype interaction. These results were in consonance with the findings of Kanpara *et al.* (2015) and Gupta *et al.* (2019).

Overall, the cross PL-2 × NBC-39 had moderate PCV, GCV estimates, with moderate heritability and GAM estimates for most of the traits revealing that additive gene action is predominant and simple selection could be practiced in future generations (Table 10 and Fig 1a, 1b).

#### **4.4 Estimation of narrow sense heritability and intergeneration correlation using parent offspring regression in F<sub>4</sub>-F<sub>5</sub> generations**

The information on intergeneration correlation using parent offspring regression helps in knowing the extent of transfer of genetic potential from one generation to the next generation. It also helps determining the relationship and dependency of the F<sub>5</sub> families on F<sub>4</sub> plant. Narrow sense heritability was estimated using formula suggested by Lush (1940).

The parent offspring regression was estimated by taking mean data of traits as dependent trait in F<sub>5</sub> families regressed on F<sub>4</sub> plant. These estimates of regression were used to determine the narrow sense heritability and also to predict the response to selection. The estimates of parent offspring correlation, regression and narrow sense heritability is presented in the Table 12.

Positive significant parent offspring correlation was noted for pods cluster<sup>-1</sup>, test weight and calcium content in the cross PL-2 × NBC-39. While, significant positive parent

offspring correlation was noticed for calcium content, test weight and seeds pod<sup>-1</sup> in the cross PL-5 × EC402104. Millawithanachchi *et al.* (2015) also observed similar results for pod length and pods plant<sup>-1</sup>. Non-significant correlation was observed for clusters plant<sup>-1</sup>, zinc content, pod length and pods plant<sup>-1</sup> in cross PL-2 × NBC-39 and for clusters plant<sup>-1</sup>, seed yield, pods clusters<sup>-1</sup>, pods plant<sup>-1</sup>, pod length and zinc content in cross PL-5 × EC402104.

**Table 12: Estimates of regression, parent offspring correlation and narrow sense heritability for eleven traits in two crosses of cowpea**

Characters	PL-2 × NBC-39			PL-5 × EC402104		
	b <sub>yx</sub>	r	h <sup>2</sup> (ns)	b <sub>yx</sub>	r	h <sup>2</sup> (ns)
Clusters plant <sup>-1</sup>	0.12	0.15	9.26	0.08	0.08	6.26
Pods cluster <sup>-1</sup>	0.11	0.42*	8.94	0.03	0.05	2.47
Pods plant <sup>-1</sup>	0.08	0.14	6.32	0.11	0.10	8.80
Plant height (cm)	-0.28	-0.31*	22.18	-0.09	-0.15	7.55
Pod length (cm)	0.08	0.10	6.50	0.14	0.17	11.55
Seeds pod <sup>-1</sup>	-0.13	-0.23*	10.63	0.13	0.29*	10.22
Test weight (g)	0.53	0.57**	42.64	0.50	0.77**	40.01
Seed yield plant <sup>-1</sup> (g)	-0.06	-0.09	4.46	0.10	0.12	7.97
Zn (mg kg <sup>-1</sup> )	0.13	0.17	10.08	0.12	0.10	9.78
Fe (mg kg <sup>-1</sup> )	-0.22	-0.40*	17.90	-0.04	-0.10	3.25
Ca (mg kg <sup>-1</sup> )	0.31	0.48*	25.17	0.10	0.25*	8.02

**Note:** b<sub>yx</sub> – Regression; r – Parent offspring correlation; h<sup>2</sup>(ns) – Narrow sense heritability; \*Significant @ P=0.05; \*\*Significant @ P=0.01;

Moderate narrow sense heritability was recorded for plant height, seeds pod<sup>-1</sup>, calcium content in cross PL-2 × NBC-39 and for seeds pod<sup>-1</sup> and pod length in cross PL-5 × EC402104. High narrow sense heritability was observed for test weight in both the

crosses. The findings were in harmony with the results obtained by Gupta and Patel (2017). Moderate and high narrow sense heritability indicates that the traits are under control of additive gene action. Selection for these traits may be rewarding in future generations.

Low narrow sense heritability was noticed for clusters  $\text{plant}^{-1}$ , seed yield and pods  $\text{cluster}^{-1}$  in PL-2  $\times$  NBC-39, while for clusters  $\text{plant}^{-1}$ , pods  $\text{plant}^{-1}$ , pods  $\text{clusters}^{-1}$ , plant height, seed yield, zinc, iron, and calcium content in the cross PL-5  $\times$  EC402104 indicates that selection was not fruitful for these traits and may not be rewarding in future generations.

#### **4.5 Estimation of phenotypic correlation and path analysis for the traits under examination**

The phenotypic correlation is estimated using formula proposed by Weber and Moorthy (1952). It reveals us about the kind of association between the traits *i.e.*, mutual or reciprocal association. The economic trait is considered as dependent trait and indirect selection can be practiced on the basis of component trait. Correlation analysis provides understanding about yield components and thus guides in the selection of high-ranking genotypes from diverse population. The idea was supported by Manggoel *et al.* (2012), Patel *et al.* (2016) and Kalambe *et al.* (2019). The correlation coefficient estimates are represented in the Table 13a and 13b.

Significant positive correlation estimates were noticed for pods  $\text{plant}^{-1}$ , pod length, clusters  $\text{plant}^{-1}$ , test weight and pods  $\text{cluster}^{-1}$  on seed yield  $\text{plant}^{-1}$  in both F<sub>4</sub> and F<sub>5</sub> generations in the cross PL-2  $\times$  NBC-39 (Fig. 3a and 3b). Bhagawati *et al.* (2018) Kana and Kwon (2019) observed similar kind of relationship. Clusters  $\text{plant}^{-1}$ , pods  $\text{plant}^{-1}$ , seeds  $\text{pod}^{-1}$ , plant height, pod length, test weight in F<sub>4</sub> (Fig. 4a) and clusters  $\text{plant}^{-1}$ , seeds  $\text{pod}^{-1}$ , pods  $\text{plant}^{-1}$  had significant and positive correlation on seed yield  $\text{plant}^{-1}$  in F<sub>5</sub> of the cross PL-5  $\times$  EC402104 (Fig. 4b). Similar results were reported by Thorat and Gadewar (2013), Shanko *et al.* (2014) Aliyu *et al.* (2016), Adetiloye *et al.* (2017), Dinesh *et al.* (2017) Walle *et al.* (2018) and Sharma *et al.* (2019). Positive association indicates that any improvement in these traits will have direct impact on yield.

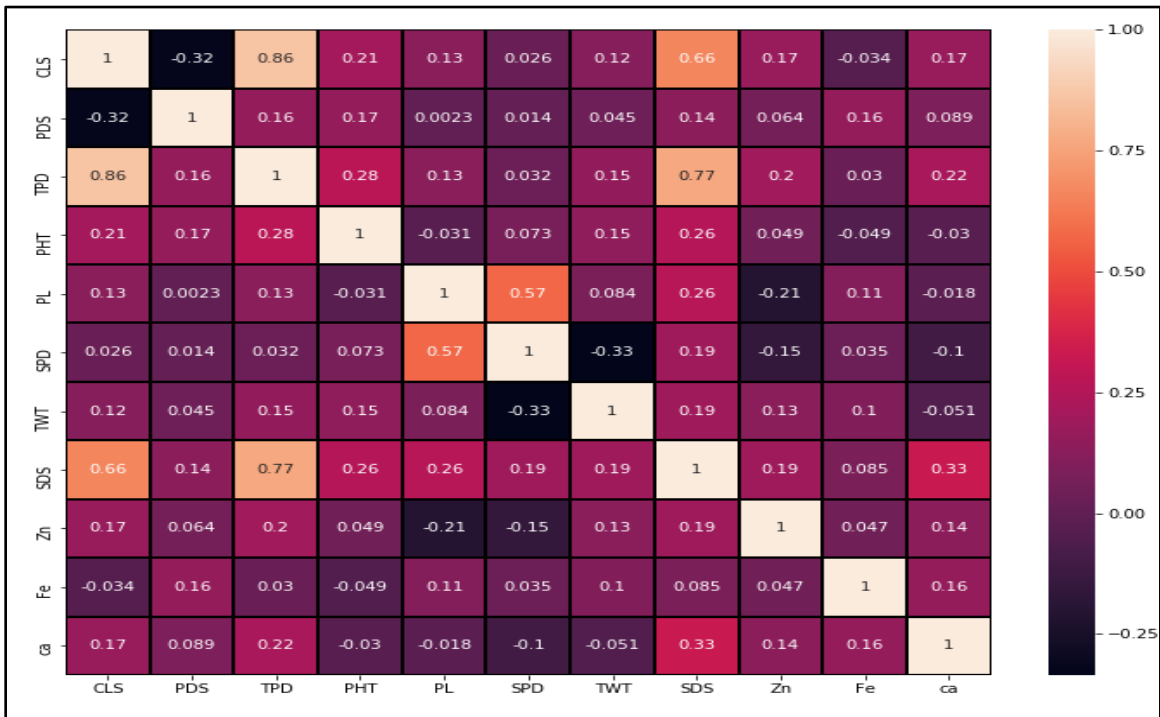
**Table 13a: Estimates of correlation coefficient of different traits on zinc, iron, calcium and seed yield plant<sup>-1</sup> of the cross PL 2×NBC-39**

Characters	F <sub>4</sub>				F <sub>5</sub>			
	Seed yield per plant (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )	Seed yield per plant (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )
Clusters plant <sup>-1</sup>	0.76**	-0.3*	0.07	-0.16	0.66*	0.17	-0.07	0.17
Pods cluster <sup>-1</sup>	0.22*	0.10	-0.04	0.05	0.14	0.07	0.11	0.09
Pods plant <sup>-1</sup>	0.85**	-0.21*	0.05	-0.13	0.77**	0.20	-0.03	0.22
Plant height (cm)	0.04	0.07	0.10	0.08	0.26**	0.05	-0.02	-0.04
Pod length (cm)	0.32**	0.08	-0.04	0.01	0.26*	-0.21	0.02	-0.2
Seeds pod <sup>-1</sup>	0.13	0.07	-0.17	-0.1	0.19	-0.15	0.17	-0.10
Test weight (g)	0.32**	-0.09	0.04	-0.13	0.19	0.13	-0.10	-0.05
Seed yield plant <sup>-1</sup> (g)	1	-0.26*	0.12	-0.22*	1	0.19	0.03	-0.32*
Zn (mg kg <sup>-1</sup> )	-0.26*	1	0.20*	0.29*	0.19	1	-0.13	0.14
Fe (mg kg <sup>-1</sup> )	0.12	0.20*	1	-0.16	0.03	-0.13	1	0.08
Ca (mg kg <sup>-1</sup> )	-0.22*	0.29*	-0.16	1	-0.32*	0.14	0.08	1

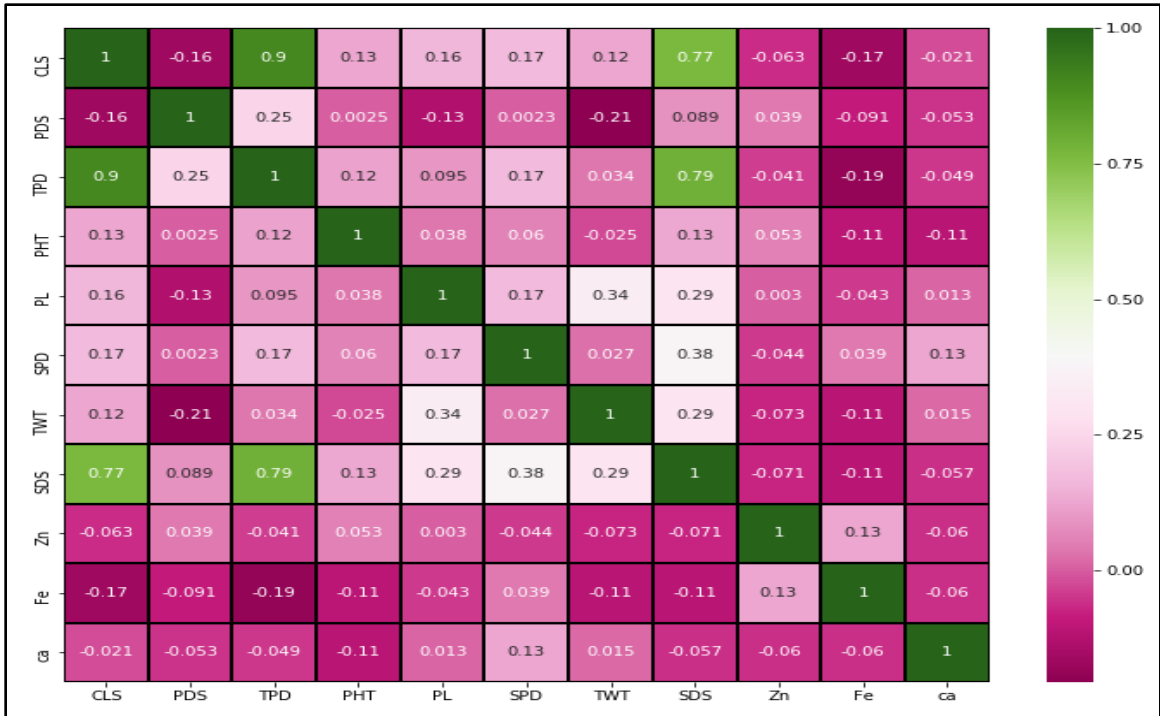
Note: \* and \*\* indicates that particular trait is significant at P=0.05 (5%) and P=0.01 (1%) probability level, respectively.



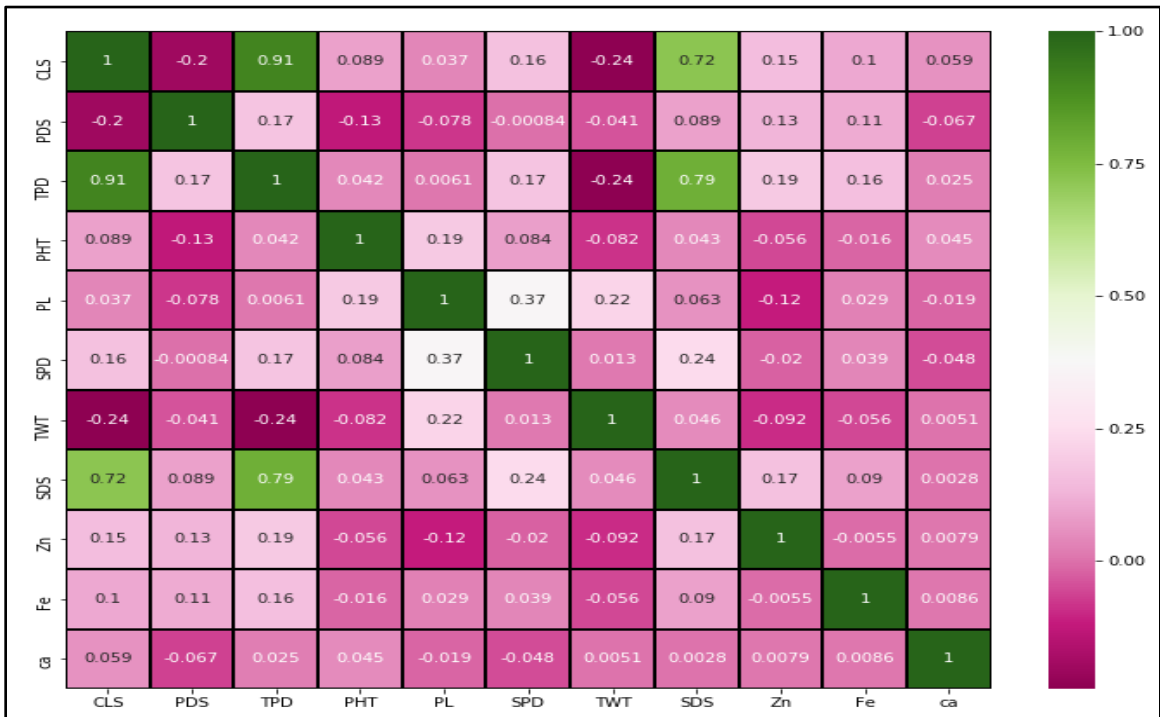
**Fig. 3a:** Graph depicting phenotypic correlation coefficient for seed yield per plant and its component traits in F<sub>4</sub> generation of cross PL-2 × NBC-39



**Fig. 3b:** Graph depicting phenotypic correlation coefficient for seed yield per plant and its component traits in F<sub>5</sub> generation of cross PL-2 × NBC-39



**Fig. 4a:** Graph depicting phenotypic correlation coefficient for seed yield per plant and its component traits in F<sub>4</sub> generation of cross PL-5 × EC-402104



**Fig. 4b:** Graph depicting phenotypic correlation coefficient for seed yield per plant and its component traits in F<sub>5</sub> generation of cross PL-5 × EC-402104

**Table 13b: Estimates of correlation coefficient of different traits on zinc, iron, calcium and seed yield plant<sup>-1</sup> of the cross PL-5×EC402104**

Characters	F <sub>4</sub>				F <sub>5</sub>			
	Seed yield per plant (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )	Seed yield per plant (g)	Zn (mg kg <sup>-1</sup> )	Fe (mg kg <sup>-1</sup> )	Ca (mg kg <sup>-1</sup> )
Clusters plant <sup>-1</sup>	0.77*	-0.06	-0.17	-0.02	0.72**	0.09	0.10	0.06
Pods cluster <sup>-1</sup>	0.09	0.04	-0.09	-0.05	0.09	0.08	0.11	-0.07
Pods plant <sup>-1</sup>	0.79**	-0.04	-0.19	-0.05	0.79**	0.12	0.16*	0.02
Plant height (cm)	0.13*	0.05	-0.11	-0.11	0.04	-0.02	-0.02	0.05
Pod length (cm)	0.29**	0.03	-0.04	0.01	0.06	-0.20*	0.03	-0.2
Seeds pod <sup>-1</sup>	0.38**	-0.04	0.04	0.13*	0.24*	0.01	0.04	-0.05
Test weight (g)	0.29**	-0.07	-0.11	0.01	0.05	-0.06	-0.06	0.01
Seed yield plant <sup>-1</sup> (g)	1	-0.07	-0.11	-0.06	1	0.11	0.09	-0.01
Zn (mg kg <sup>-1</sup> )	-0.07	1	0.13*	-0.06	0.11	1	-0.05	-0.01
Fe (mg kg <sup>-1</sup> )	-0.11	0.13*	1	-0.06	0.09	-0.05	1	0.01
Ca (mg kg <sup>-1</sup> )	-0.06	-0.06	-0.06	1	-0.01	-0.01	0.01	1

Note: \* and \*\* indicates that particular trait is significant at P=0.05 (5%) and P=0.01 (1%) probability level, respectively.

On the contrary, negative and non-significant estimation of correlation for iron, zinc, calcium on seeds pod<sup>-1</sup> and seed yield was noticed. Selection on the basis of these traits may reduce yield. Hence selection should be focused on genotypes having optimum level of all traits. But iron content had positive and significant correlation with zinc content. These reports were similar to results observed by Moura *et al.* (2012) and Dakora *et al.* (2019).

Pods plant<sup>-1</sup> (1.06) showed high direct effect on seed yield plant<sup>-1</sup> and these reports are in accordance with the results obtained by Mahmudul *et al.* (2012), Anamika and Tajane (2014), Manisha *et al.* (2018) and Sharma *et al.* (2019). Clusters plant<sup>-1</sup> (-0.23), test weight (0.34) showed high direct effect, pods cluster<sup>-1</sup> (-0.24) and seeds pod<sup>-1</sup> (0.21) had moderate direct effect which is in accordance with observation made by Mahmudul *et al.* (2012), Dinesh *et al.* (2018) and Kana and Kwon (2019). Whereas, pod length (0.07) and plant height (0.08) had negligible direct effect on seed yield plant<sup>-1</sup> but pod length had high direct effect on seed yield in F<sub>5</sub> generation in the cross PL-2 × NBC-39 (Table 14). The outcomes were in conformity with Srinivas *et al.* (2017). Hence, path analysis revealed that improvement of seed yield could be obtained by focusing on pods plant<sup>-1</sup>, test weight and seeds pod<sup>-1</sup>.

**Table 14: Estimates of direct effects of traits on seed yield plant<sup>-1</sup> in F<sub>4</sub> and F<sub>5</sub> generations derived from the two crosses**

Characters	PL 2 × NBC 39		PL 5 × EC402104	
	F <sub>4</sub>	F <sub>5</sub>	F <sub>4</sub>	F <sub>5</sub>
Clusters plant <sup>-1</sup>	-0.229	0.15	0.28	-0.392
Pods cluster <sup>-1</sup>	-0.242	0.077	0.081	-0.191
Pods plant <sup>-1</sup>	1.061	0.590	0.457	1.223
Plant height (cm)	0.084	0.023	0.024	0.021
Pod length (cm)	0.07	0.61	0.102	-0.041
Seed pod <sup>-1</sup>	0.211	0.176	0.232	0.101
Test weight (g)	0.335	0.128	0.220	0.249
R <sup>2</sup>	0.839	0.645	0.768	0.703

#### 4.6 Identification of best plants in F<sub>5</sub> derived from two crosses

As observed in both correlation and path analysis studies, zinc, iron and calcium had negative relationship with seed yield. Hence, while selecting lines to forward for next generation, optimum levels of micronutrients with optimum yield were selected and presented in Table 15a and 15b.

**Table 15a: Superior lines selected from the cross PL-2 × NBC-39 (F<sub>5</sub>)**

Genotypes	Seed yield plant <sup>-1</sup> (g)	Zinc (mg/kg)	Iron (mg/kg)	Calcium (mg/kg)
7.189.22.2.8	98.00	34.90	120.78	1.40
7.161.1.6.9	92.65	30.66	175.22	0.68
7.161.1.6.4	63.50	48.06	171.36	0.70
7.331.18.1.4	62.00	70.58	114.84	0.40
7.189.22.2.5	61.05	42.42	71.42	0.66
7.40.12.5.1	60.00	45.26	156.06	0.86
7.150.12.4.1	55.00	70.84	172.84	1.28
7.161.1.7.2	54.50	52.72	162.80	1.16
7.161.1.6.8	53.50	54.96	183.64	1.26
7.331.18.4.5	49.00	33.20	140.76	0.70
KBC - 2	35.95	32.90	133.75	0.70
KBC - 9	45.15	39.21	209.75	0.69
C -152	34.66	34.41	172.61	0.81
IT - 38956 -1	46.45	42.42	195.74	0.69
PGCP - 6	65.05	36.61	185.01	0.75

**Table 15b: Superior lines selected from the cross PL-5 × EC402104 (F<sub>5</sub>)**

<b>Genotypes</b>	<b>Seed yield plant<sup>-1</sup> (g)</b>	<b>Zinc (mg/kg)</b>	<b>Iron (mg/kg)</b>	<b>Calcium (mg/kg)</b>
8.12.25.4.1	99.00	20.76	113.28	0.68
8.145.1.1.7	91.50	51.36	181.70	0.84
8.19.24.7.4	90.00	43.48	110.96	0.40
8.19.12.6.3	83.00	43.16	182.08	1.12
8.12.11.2.7	82.50	47.60	164.28	0.62
8.19.28.4.1	80.00	43.08	156.10	1.24
8.250.2.2.4	77.00	48.94	142.46	0.58
8.19.28.4.2	77.00	30.60	130.82	0.80
8.250.2.2.1	76.50	35.92	161.42	0.70
8.12.11.2.4	72.50	21.88	163.54	0.86
KBC - 2	35.95	32.90	133.75	0.70
KBC - 9	45.15	39.21	209.75	0.69
C -152	34.66	34.41	172.61	0.81
IT - 38956 -1	46.45	42.42	195.74	0.69
PGCP - 6	65.05	36.61	185.01	0.75



**Plate 3a: Selected F<sub>5</sub> plant from the cross PL-5 × EC402104**



**Plate 3b: Selected F<sub>5</sub> plant from the cross PL-2 × NBC 39**

**Table 16a: Lines selected from cross PL-2 × NBC-39 with high micronutrient content and low yield**

<b>Genotypes</b>	<b>Seed yield plant<sup>-1</sup> (g)</b>	<b>Zinc (mg/kg)</b>	<b>Iron (mg/kg)</b>	<b>Calcium (mg/kg)</b>
7.150.10.4.10	36.00	46.08	392.20	1.38
7.189.22.2.4	25.50	40.28	447.14	0.68
7.161.1.7.6	24.00	44.96	193.48	1.58
7.161.1.6.3	34.00	44.68	330.50	1.34
7.331.2.1.6	20.00	46.00	329.74	1.54
7.161.1.6.1	25.00	50.82	171.72	0.84
7.331.18.1.9	13.00	45.82	153.42	0.96
7.150.20.5.7	24.50	64.62	284.00	1.28
7.161.1.7.7	24.50	54.14	204.72	0.86
7.150.20.5.6	47.00	51.80	282.00	1.32
KBC - 2	35.95	32.90	133.75	0.70
KBC - 9	45.15	39.21	209.75	0.69
C -152	34.66	34.41	172.61	0.81
IT - 38956 -1	46.45	42.42	195.74	0.69
PGCP - 6	65.05	36.61	185.01	0.75

**Table 16b: Lines selected from cross PL-5 × EC402104 having high micronutrient content with low yield**

<b>Genotypes</b>	<b>Seed yield plant<sup>-1</sup> (g)</b>	<b>Zinc (mg/kg)</b>	<b>Iron (mg/kg)</b>	<b>Calcium (mg/kg)</b>
8.145.2.2.7	39.50	46.44	508.66	0.84
8.121.8.4.4	31.00	45.68	373.96	0.68
8.250.30.2.5	55.00	37.70	316.94	1.16
8.19.43.3.5	52.00	40.48	301.58	0.88
8.12.11.2.3	42.00	50.44	264.96	0.80
8.250.2.2.2	52.00	49.20	159.02	1.78
8.250.31.5.2	10.50	49.04	123.44	1.26
8.250.30.2	24.00	43.18	244.68	0.60
8.121.8.4.9	24.50	40.56	137.90	1.80
8.19.12.3.5	26.00	33.08	254.66	0.84
KBC – 2	35.95	32.90	133.75	0.70
KBC – 9	45.15	39.21	209.75	0.69
C -152	34.66	34.41	172.61	0.81
IT - 38956 -1	46.45	42.42	195.74	0.69
PGCP - 6	65.05	36.61	185.01	0.75

## V SUMMARY

Cowpea is predominantly a self-pollinated crop with good source of protein (poor man's meat) and a multi utility crop, cultivated in semi-arid and arid regions of the world. Variability is essential to exercise selection in any crop. Though sustainable seed yield levels were achieved through conventional and biotechnological interventions, breeding crop for nutritional security has become an important breeding goal in crops like cowpea. Development of micronutrient dense genotypes through breeding approaches is very much necessary and need of hour. Information on variability for iron, zinc and calcium in cowpea is very scarce. In this context, the current exploration was carried out at Experimental Block of Genetics and Plant Breeding, 'K' Block, College of Agriculture, GKVK, Bengaluru to generate information on genetic variability parameters. The experimental material consisted of F<sub>4</sub> and F<sub>5</sub> generations derived from two crosses *viz.*, PL-2 × NBC-39 and PL-5 × EC402104 sown using augmented design. The germplasm was evaluated by Manoj in 2016. The F<sub>1</sub>'s were evaluated by Keerthi in *kharif* 2016, F<sub>2</sub> and F<sub>3</sub> material was evaluated by Shwetha in summer 2017 and *rabi* 2017, at Main research station, Hebbal.

- Statistical analysis was done on data collected for different traits *viz.*, pods cluster<sup>-1</sup>, hundred seed weight, plant height, clusters plant<sup>-1</sup>, seeds pod<sup>-1</sup>, pods plant<sup>-1</sup>, zinc, iron, seed yield, calcium and pod length. Descriptive statistics *viz.*, trait mean, range and variance were estimated. Genetic variability parameters *viz.*, GCV, PCV, broad sense heritability, GAM, inter-generation correlation using parent offspring regression, narrow sense heritability, path analysis and correlation for iron, zinc, calcium and seed yield were assessed for both F<sub>4</sub> and F<sub>5</sub> generations of crosses PL-2 × NBC-39 and PL-5×EC402104.
- **The experimental outcomes are summarised below**
- The ANOVA disclosed remarkable difference for all traits under research in both F<sub>4</sub> and F<sub>5</sub> suggesting that material has sufficient variability and suitable for genetical studies.
- The mean of pods cluster<sup>-1</sup>, seeds pod<sup>-1</sup>, test weight, pod length was comparable between two crosses in both F<sub>4</sub> and F<sub>5</sub> generations. The performance of F<sub>5</sub> generation

was better compared to the F<sub>4</sub> generation. The mean performance of plant height and zinc concentration in seed were higher in cross PL-2 × NBC-39. But mean performance of yield and its accrediting traits like seed yield, pod length were higher in the cross PL-5 × EC402104. The cross PL-5 × EC402104 was better performing for most of the traits as compared to the cross PL-2 × NBC-39.

- Higher estimates of lower and upper limits of absolute range for majority of the characters were observed in the cross PL-2 × NBC-39 suggesting that transgressive phenotypes were accessible in this cross. Higher magnitude of standardized range was detected in the cross PL-5 × EC402104 for more than half of traits in F<sub>4</sub> and F<sub>5</sub> generations. Both crosses had extreme phenotypes in the F<sub>4</sub> and F<sub>5</sub> which helps in selecting better plants in future generations.
- GCV was low for pods cluster<sup>-1</sup>, plant height, seeds pod<sup>-1</sup> and test weight in F<sub>4</sub> and F<sub>5</sub> generations of both the crosses. Moderate PCV and GCV reported for clusters plant<sup>-1</sup>, zinc, seed yield, iron, pods plant<sup>-1</sup>, calcium in F<sub>4</sub> of cross PL-2 × NBC-39, whereas pods cluster<sup>-1</sup>, test weight along with above mentioned traits had moderate GCV in F<sub>5</sub>.
- In the cross PL-5 × EC402104, moderate GCV was noted for clusters plant<sup>-1</sup>, seeds pod<sup>-1</sup>, pods plant<sup>-1</sup>, iron, calcium in F<sub>4</sub>, in case of F<sub>5</sub> clusters plant<sup>-1</sup>, seed yield, zinc, pods plant<sup>-1</sup> and calcium had moderate GCV. Clusters plant<sup>-1</sup>, pod length, pods plant<sup>-1</sup>, plant height was reported to have moderate PCV in F<sub>4</sub> and F<sub>5</sub> generations.
- Pods per plant, zinc in F<sub>4</sub> and F<sub>5</sub> of cross PL-2 × NBC-39 showed moderate heritability and seed yield, calcium content, pods plant<sup>-1</sup> in F<sub>4</sub> and F<sub>5</sub> of cross PL-5 × EC402104. Whereas, high heritability was detected for clusters plant<sup>-1</sup>, seed yield and calcium content in F<sub>4</sub> of cross PL-2 × NBC-39.
- Moderate to high heritability coupled with GAM was spotted because additive gene action was commanding the traits. Hence, simple selection can be practiced. The traits which were reported to have moderate to high heritability are yield accrediting traits so selection can be practiced on basis of these characters in order to develop superior genotypes having good yield. Overall, the cross PL-2 × NBC-39 had moderate PCV, GCV, heritability and GAM for majority of the characters since additive gene action was commanding the traits and simple selection can be practiced.

- Moderate narrow sense heritability for iron, seeds pod<sup>-1</sup>, plant height, zinc, calcium content in cross PL-2 × NBC-39 and for seeds pod<sup>-1</sup>, pod length in the cross PL-5 × EC402104 was noticed. High narrow sense heritability noted for test weight in both the crosses. It is also suggested that selection was fruitful and effective for these traits.
- Narrow sense heritability was noticed low for clusters plant<sup>-1</sup>, pods cluster<sup>-1</sup>, seed yield in PL-2 × NBC-39, while for clusters plant<sup>-1</sup>, pods plant<sup>-1</sup>, iron, plant height, zinc, pods clusters<sup>-1</sup>, seed yield and calcium in the cross PL-5 × EC402104. Selection was not efficacious for these traits in F<sub>5</sub> generation.
- Clusters plant<sup>-1</sup>, pod plant<sup>-1</sup>, pod length, test weight, pods cluster<sup>-1</sup> had significant and positive correlation on seed yield in both F<sub>4</sub> and F<sub>5</sub> generations in the cross PL-2 × NBC-39. Clusters plant<sup>-1</sup>, pods plant<sup>-1</sup>, plant height, pod length, seed pod<sup>-1</sup>, test weight in F<sub>4</sub> and clusters plant<sup>-1</sup>, seeds pod<sup>-1</sup>, pods plant<sup>-1</sup> had positive and remarkable correlation on seed yield in F<sub>5</sub> of the cross PL-5 × EC402104. Hence selection on basis of these traits will be fruitful.
- On contrary seed yield and seeds pod<sup>-1</sup> had negative and non-significant coalition with iron, zinc, calcium gives hint that these traits are not associated with yield. Selection on basis of these traits may cause reduction in yield. Hence selection should be focused on genotypes having optimum expression of all traits. But iron content had significant positive correlation with zinc content.
- Pods plant<sup>-1</sup> had very high direct effect on seed yield plant<sup>-1</sup> and moderate direct effect by test weight, clusters plant<sup>-1</sup>, pods cluster<sup>-1</sup> and seeds pod<sup>-1</sup> in both the crosses.
- Ten superior lines with optimum yield, iron, zinc and calcium were identified in both the crosses. 7.189.22.2.8, 7.161.1.6.9, 7.161.1.6.4, 7.331.18.1.4, 7.189.22.2.5, 7.40.12.5.1, 7.150.12.4.1, 7.161.1.7.2, 7.161.1.6.8, 7.331.18.4.5 from cross PL-2 × NBC-39. 8.12.25.4.1, 8.145.1.1.7, 8.19.24.7.4, 8.19.12.6.3, 8.12.11.2.7, 8.19.28.4.1, 8.250.2.2.4, 8.19.28.4.2, 8.250.2.2.1, 8.12.11.2.4 were opted from cross PL-5×EC402104.

**Future line of work:**

The superior lines identified can be forwarded and evaluated in further generation to obtain a superior pure line for releasing as a variety if its performance is better than check.

Progenies identified as rich in iron, zinc and calcium along with yield could be used as parents in cowpea crop improvement program.

Selection for high iron, zinc and calcium content may reduce yield, hence selection should be aimed on all traits to get better line. Traits like pods plant<sup>-1</sup>, pod length, clusters plant<sup>-1</sup> can be used as agent for indirect selection for yield improvement.

Selection of lines for high iron, zinc and calcium may also be carried out based on high correlation of micronutrient content with yield attributing traits which have showed positive correlation with seed yield.

## VI REFERENCES

- ADETILOYE, I. S., ARIYO, O. J. AND AWOYOMI, O. L., 2017, Study of genotypic and phenotypic correlation among 20 accessions of Nigerian cowpea. *J. Agri. Vet. Sci.*, **10**: 36-39.
- 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.
- ALIYU, O. M. AND MAKINDE, B. O., 2016, Phenotypic analysis of seed yield and yield components in cowpea [*Vigna unguiculata* (L.) Walp]. *Plant Breed. and Biotechnol.*, **4**(2): 252-261.
- ANAMIKA, N. AND TAJANE, P. A., 2014, Path analysis for seed yield in cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Plant Sci.*, **9**(1): 291-292.
- ANONYMOUS, 2016, Agriculture production year book. Food and Agriculture Organization of United Nations, Rome.
- ANONYMOUS, 2016, Directorate of economics and statistics, GOK.
- ANONYMOUS, 2018, Global nutrition report. <https://globalnutritionreport.org/reports/global-nutrition-report-2018/>
- AREMU, C. O., 2011, Trait response to early-generation selection using a common parent in two crosses of cowpea [*Vigna unguiculata* (L.) Walp.] for humid environment performance. *Pelagia Res. Lib.*, **2**(6): 155-160.
- ASHNI, V., 2019, Development of stabilised population of cowpea segregants [*Vigna unguiculata* (L.) Walp.] with high protein content and grain yield. *Doctoral dissertation*, Dept. Plant Breed. Genet., COH, Vellanikkara.

- BARROSO NETO, A. M., MATOS, R. F. D., PINHEIRO, M. D. S., BERTINI, C. H. C. D., AND DOVALE, J. C., 2017, Genetic variability and selection of extra-early cowpea progenies. *Revista Caatinga*, **30**(3): 698-707.
- BHAGWATI, B., MEGHAWAL, D. R., SHARMA, P. P. AND SHARMA, H., 2018, To estimate genetic variability parameters, correlation and path coefficient in cowpea [*Vigna unguiculata* (L.) Walp]. *Int. J. Curr. Microbiol. App. Sci.*, **7**: 3013-3023.
- BRESSANI, R., SINGH, S. R., RACHIE, K. O., 1985. Nutritive value of cowpea, Cowpea research production and utilisation. John Wiley and Sons, Chichester. New York. 353–359.
- BURTON, G. W. AND DEVANE, E. M., 1953, Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron.J.*, **45**: 478- 481.
- CHATTERJEE, B. N., AND BHATTACHARYYA, K. K., 1986, Principles and practices of grain legume production. *Principles pract. grain leg. prod.*
- DAKORA, F. D. AND BELANE, A. K., 2019, Evaluation of Protein and micronutrient levels in edible cowpea [*Vigna unguiculata* (L.) Walp.] leaves and seeds. *Front. in Sustainable Food Systems*, **3**(70): 1-10.
- DEWEY, D. R. AND LU, K. K., 1957, A correlation and path analysis of components of crested grass seed production. *Agron. J.*, **51**: 515-520.
- DINESH, H. B., VISWANATHA, K. P., LOHITHASWA, H. C., PAVAN, R. AND POONAM, S., 2017. Genetic variability, correlation and path analysis studies in early segregating generation of cowpea [*Vigna unguiculata* (L.) Walp]. *Int. J. Pure App. Biosci*, **5**(5): 1389-1395.
- FEDERER, W.T., 1956. Augmented designs. *Hawain planters*, **55**: 191-208

- GERRANO, A. S., ADEBOLA, P. O., JANSEN VAN RENSBURG, W. S. AND LAURIE, S. M., 2015, Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. *S. Afr. J. Plant Soil*, **32**(3): 165-174.
- GUPTA, Y.P., BALDEV, B., RAMANUJAM, S., JAIN, H.K., 1988, Nutritive value of pulses, Pulse crops, New Delhi: Oxford and IBH Publishing Company. 561–601.
- GUPTA, R., AND PATEL, S., 2017, Heritability studies in Cowpea [*Vigna unguiculata* (L.) Walp.]. *Trends Biosci.*, **10**(23): 4751-4755.
- GUPTA, R. K., ARYA, M., KUMAR, A., AND KUMARI, P., 2019, Study on Genetic Variability in Cowpea [*Vigna unguiculata* (L.) Walp]. *Curr. J. Appl. Sci. Tech.* 1-8.
- HAVARADDI, U. AND DESHPANDE, S. K., 2018, Genetic Variability Studies in Advanced Stabilized Lines of Cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Pure App. Biosci.*, **6**(6): 221-226.
- JACKSON, M, L., 1973, *Soil chemical analysis*. Prentice Hall (India) Pvt. Ltd., New Delhi.
- JOHNSON, H. W., ROBINSON, H. F., COMSTOCK, R. E., 1955, Estimates of genetic and environmental variability in soybeans. *Agron. J.*, **47**(7): 314-318.
- JULIETTE STEEN., 2016, Common signs of vitamins and mineral deficiency, HuffPost, Australia.
- KALAMBE, A. S., WANKHADE, M. P., DESHMUKH, J. D., CHAVAN, B. R. AND SHINDE, A. V., 2019, Correlation studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *J. Pharmacognosy Phytochem.*, **8**(3): 321-323.
- KANA, H.A AND KWON-NDUNG E.H., 2019, Correlation and path coefficient analysis of some growth and yield contributing traits in cowpea [*Vigna unguiculata* (L.) Walp.] exposed to alpha-spin nano particles. *J. Sci. Technol.*, **5**(2): 18-23.

- KEERTHI, A. P., 2017, Combining ability for grain zinc, iron and protein contents and pod yield and its component traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bangalore.
- KHANDAIT, R., JAIN, P. K., PRAJAPATI, S. AND DANGI, A. S., 2016, Correlation and path coefficient analysis for yield and its attributing traits in diverse genotypes of cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Bio-resource Stress Management*, **7**(1): 8-17.
- KHANPARA, S. V., JIVANI, L. L., VACHHANI, J. H. AND KACHHADIA, V. H., 2015, Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. *Electronic J. Plant Breed.*, **7**(2): 408-413.
- 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.
- KUMAR, S., PATEL, P. S. AND KUMAR, P., 2018, Genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata* (L.) Walp.]. *Plant Archives*, **18**(2): 1268-1270.
- LENKA, D. AND MISHRA, B., 1973, Path coefficient analysis in rice varieties. *Indian J. of Agric. Sci.*, **43**: 376-379.
- LOKESH, G.V., AND NIRANJANA MURTHY., 2017, Genetic variability for yield and yield component traits in advanced F<sub>2</sub> and F<sub>3</sub> generations of cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Pure App. Biosci.*, **5**(5): 1156-1160.
- LOPES, K. V., TEODORO, P. E., SILVA, F. A., SILVA, M. T., FERNANDES, R. L., RODRIGUES, T. C., FARIA T.C. AND CORREA, A. M., 2017, Genetic parameters and path analysis in cowpea genotypes grown in the Cerrado/Pantanal ecotone. *Genet. Mol. Res.*, **16**(2): 1-10.

- LUSH, J. L., 1940, Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *J. Animal Sci.*, **1**: 293-301.
- MAHESH SHARMA, SHARMA, P.P., UPADHYAY, B. AND BAIRWA, H.L., 2016, Study of correlation coefficient and path analysis in cowpea (*Vigna unguiculata* L. Walp) germplasm line. *Int. J. Dev. Res.*, **06**(08): 9011-9016.
- 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.) Verdc.]. *J. Biol. Sci.* **1**(1): 1-10.
- MAMIRO, P. S., MBWAGA, A. M., MAMIRO, D. P., MWANRI, A. W. AND KINABO J. L., 2011, Nutritional quality and utilization of local and improved cowpea varieties in some regions in tanzania, *Afri. J. Food Agric. Nutr. Develop.* **11**(1): 4490-4506.
- 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.
- MANISHA, R. P., VIJAY, S. K., MADHAVI, B. B. AND JADHAV, R. D., 2018, Correlation and path analysis study in F<sub>5</sub> generation of cowpea. *Int. J. Curr. Microbiol. App. Sci.*, **6**:1529-1537.
- MANOJ, C. A., 2016, Identification of cowpea germplasm for iron, zinc, protein, seed yield and its attributing traits. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bangalore.
- MARAPPA, N., MANOJ, C, A., SAVITHRAMMA, D. L., VENKATARAVANA, P., RUDRASWAMY., GANGADHAR E. R. G., PAPIREDDY, M., KEERTHI A. P., MADHU, S. V. AND MAHANTESH., 2016 Screening of elite cowpea genotypes for zinc, iron, protein and yield attributes. *J. Proteom. Bioinform.*, **9**:12.

- MAYURI SAHU, 2018, Path analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Chem. Studies*, **7**(1): 912-914.
- MEENATCHI, T., THANGARAJ, K., GNANAMALAR, R. P. AND PUSHPAM, K., 2019, Genetic variability and heritability study on yield and its component traits in segregating population of cowpea [*Vigna unguiculata* (L.) Walp.]. *Electronic J. Plant Breed.*, **10**(2): 736-741.
- MILLAWITHANACHCHI, M. C., SUMANASINGHE, V. A., BENTOTA, A. P., AND ABEYSIRIWARDENA, S. D. Z., 2015, Performance of different breeding methods in cowpea [*Vigna unguiculata* (L.) Walp] improvement programmes. *Trop. Agric. Res.*, **26**(2).
- MOHAN, S., AND THAKKAR, H., 2019., Food for Thought: Fighting malnutrition in rural India one meal at a time. *AMSA J. Global Health*. **13**(1):85-93.
- MORTIMORE, M. J., SINGH, B. B., HARRIS, F., AND BLADE, S. F., 1997, Cowpea in traditional cropping systems. *Adv. cowpea res.*, 99.
- MOURA, J. D. O., ROCHA M. D. M., GOMES, R. L. F., FILHO, F. R. F., SILVA, K. J. E. E. AND RIBEIRO, V. Q., 2012, Path analysis of iron and zinc contents and others traits in cowpea. *Braz. Soc. Plant Breed.*, **12**: 245-252.
- OLADEJO, A. S., AKINWALE, R. O. AND OBISESAN, I. O., 2011, Interrelationships between grain yield and other physiological traits of cowpea cultivars. *Afri. Crop Sci. J.*, **19**(3): 189-200.
- OM VIR 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.
- NAIR, K. R., DESAI, S. S., SAWARDEKAR, S. V. AND BURONDKAR, M. M., 2018, Study of genetic variability parameters in F<sub>2</sub> Generation of interspecific hybrids in cowpea. *Int. J. Pure App. Biosci.*, **6**(1): 954-958.

- NWOFIA, G. E., NWANEBU, M. AND AGBO, C. U., 2012, Variability and inter-relationships between yield and associated traits in cowpea [*Vigna unguiculata* (L.) Walp.] as influenced by plant populations. *World J. Agric. Sci.*, **8**(4): 396-402.
- PADULOSI, S., AND NG, N. Q., 1997, Origin, taxonomy and morphology of *Vigna unguiculata*.
- PANT, P. C., 1982, Prehistoric Uttar Pradesh: A Study of Old Stone Age. *Agam*
- PASQUET, R. S., 1999, Genetic relationships among subspecies of [*Vigna unguiculata* (L.) Walp.] based on allozyme variation. *Theor. Appl. Genet.*, **98**(6): 1104-1119.
- PATEL, P. S., KUMAR, S., MEENA, R. K., KUMAR, P. AND RAI, T., 2017, Correlation and path analysis in Cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Pure App. Biosci.* **6**(5): 142-146.
- PATEL, U. V., PARMAR, V. K., PATEL, P. B. AND MALVIYA, A. V., 2016, Correlation and path analysis study in cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Sci., Environ. Technol.*, **5**(6): 3897 – 3904.
- RASHWAN, A. M. A. AND HELALY, A. A., 2015, Genetic improvement for yield and its components in cowpea [*Vigna unguiculata* (L.) Walp.] via., cycles of selection program. *J. Am. Sci.*, **11**(1): 52-58.
- RIBEIRO, H. L. C., SANTOS, C. A. F., DINIZ, L. D. S., NASCIMENTO, L. A. D. AND NUNES, E. D., 2016, Phenotypic correlations and path analysis for plant architecture traits and grain production in three generations of cowpea. *Revista Ceres*, **63**(1): 33-38.
- ROBINSON, H. F., COMSTOCK, R. E. AND HARNEY, P. H., 1949, Estimates of heritability and degree in corn. *Agron. J.*, **41**: 353-359.

- SABALE, G. R., BHAVE, S.G., DESAI, S. S., DALVI, M, B. AND PAWAR, R. R., 2018, Variability, heritability and genetic advance studies in F<sub>2</sub> generation of cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Curr. Microbiol. App. Sci.*,**7**(09): 3314-3320.
- SANTOS, C. A. F. AND BOITEUX, L. S., 2013, Breeding biofortified cowpea lines for semi-arid tropical areas by combining higher seed protein and mineral levels. *Genet. Mol. Res.*,**12**(4): 6782-6789.
- SARATH P. S. AND RESHMA. T.,2017, Genetic variability studies in cowpea [*Vigna unguiculata* L. Walp]. *Int. J. Agric. Sci. Res.*,**7**(3):129-132.
- SAVITHIRI, N., BEAULAH, A., SHOBA T. K., RAJESWARI, S. AND RAKESH KUMAR, 2018, Study on genetic variability for yield and quality of different genotypes of yard longbean [*Vigna unguiculata* ssp. *sesquipedalis* (L.) Verd.]. *Int. J. Curr. Microbiol. App. Sci* **7**(9): 3613-3617.
- SHANKO, D., ANDARGIE, M. AND ZELLEKE, H., 2014, Interrelationship and path coefficient analysis of some growth and yield characteristics in cowpea [*Vigna unguiculata* L. Walp.] genotypes. *J. Plant Sci.*, **2**(2): 97-101.
- SHARMA, A., MISHRA, S. P. AND GOUR, L., 2019, Heritable relationship and variability of yield and yield determinants in cow pea. *Int. J. Chem. Stud.*, **7**(3): 3605-3611.
- SHARMA, M., SHARMA, P. P., SHARMA, H. AND MEGHAWAL, D. R., 2017, Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm lines. *J. Pharm. Phytochem.*, **6**(4): 1384-1387.
- SINGH, S. P., KUMAR, R, JOSHI, A. K. AND SINGH, B., 2004, Genetic architecture of yield traits in cowpea [*Vigna unguiculata* (L) Walp.], *Adv. Plant sci.*, **17**(2): 495-502.
- SHWETHA, H. R., 2018, Breeding potential of four crosses for quantitative traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bangalore.

- SMITH, J. D. AND KINMAN, M. L., 1965, The use of parent-offspring regression as an estimator of heritability. *Crop Sci.*, **5**: 595-596.
- SRINIVAS, J., KALE, V. S., NAGRE, P. K. AND MESHAM, S., 2017, Correlation and path analysis study in cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. *Int. J. Curr. Microbiol. App. Sci.*, **6**(6): 3305-13.
- STEELE, W. M., 1972, Cowpea in Africa. *Ph. D. thesis of the University of Reading, UK*.
- SUMMERFIELD, R. J., DART, P. J., HUXLEY, P. A., EAGLESHAM, A. R. J., MINCHIN, F. R. AND DAY, J. M., 1977, Nitrogen nutrition of cowpea [*Vigna unguiculata* (L.) Walp.]. I. Effects of applied nitrogen and symbiotic nitrogen fixation on growth and seed yield. *Exp. Agri.*, **13**(2): 129-142.
- THORAT, A. AND GADEWAR, R. D., 2013, Variability and correlation studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *Int. J. Environ. Rehabilitation and Conservation*, **4**(1): 44-49.
- VAVILAPALLI, S., CELINE, V. A., DUGGI, S., PADAKIPATIL, S., AND MAGADUM, S., 2013, Genetic variability and heritability studies in bush cowpea [*Vigna unguiculata* (L.) Walp.]. *Leg. Genom. and Genet.*, **4**(4): 27-31.
- VERDCOURT, B., 1970, Studies in the Leguminosae - *Papilionoideae* for the flora of tropical East Africa. *Kew, Bulletin.*; **24**:507.
- 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 F<sub>2</sub> generation of cowpea [*Vigna unguiculata* L. Walp.]. *Int. J. Chem. Studies.*, 2019, **7**(6): 3084-3088.
- VEERESH ANGADI, 2019, Genetics of iron, zinc and seed yield in cow pea [*Vigna unguiculata* (L.) Walp.]. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bengaluru.

- WALLE, T., MEKBIB, F., AMSALU, B. AND GEDIL, M., 2018, Correlation and path coefficient analyses of cowpea [*Vigna unguiculata* (L.) Walp.] landraces in Ethiopia. *Am. J. Plant Sci.*, **9**: 2794-2812.
- WEBER, C. R. AND MOORTHY, B. R., 1952, Heritability and non-heritability relationship and variability of oil content and agronomic characters in F<sub>2</sub> generations of soya bean crosses. *Agron. J.*, **44**:202-209.
- WRIGHT, S., 1921, Correlation and causation. *J. Agril. Res.*, **20**: 557-585.

## APPENDIX

**Monthly Meteorological data of College of Agriculture, GKVK, Bengaluru (January to December 2019)**

Sl. No.	Month	Rain fall (mm)			Temperature (°C)		Relative humidity (%)		Sun shine Hrs.
		Normal	Actual	No. of rainy days	Maximum	Minimum	7.00 Hrs.	14.00 Hrs.	
1	January	14.00	0.0	0	27.9	13.1	88.7	53.7	8.5
2	February	9.70	0.0	0	30.6	17.2	87.1	47.1	9.4
3	March	17.00	0.0	0	33.7	20.1	81.1	36.9	9.1
4	April	42.80	54.00	2	34.7	20.7	77.0	35.2	8.6
5	May	97.00	131.20	7	33.7	20.3	80.5	37.2	7.9
6	June	82.30	40.40	3	30.6	19.5	85.7	49.1	7.1
7	July	102.30	107.40	8	29.5	18.8	90.0	52.6	4.9
8	August	127.90	186.40	12	27.5	18.1	92.9	62.0	4.1
9	September	203.70	145.60	10	27.9	18.5	91.9	57.4	3.5
10	October	176.70	329.20	14	27.7	18.3	92.5	58.2	4.9
11	November	52.7	15.40	2	27.6	16.9	89.8	57.7	6.5
12	December	11.3	2.40	0	26.0	16.4	91.4	62.1	5.0
	Total	937.4	1012.00	58					

**Note:** Normal rainfall is average of 10 years from 2009 to 2018.