IDENTIFICATION OF CROSSES WITH HIGH BREEDING POTENTIAL IN FORAGE COWPEA (*Vigna unguiculata* (L.) Walp.)

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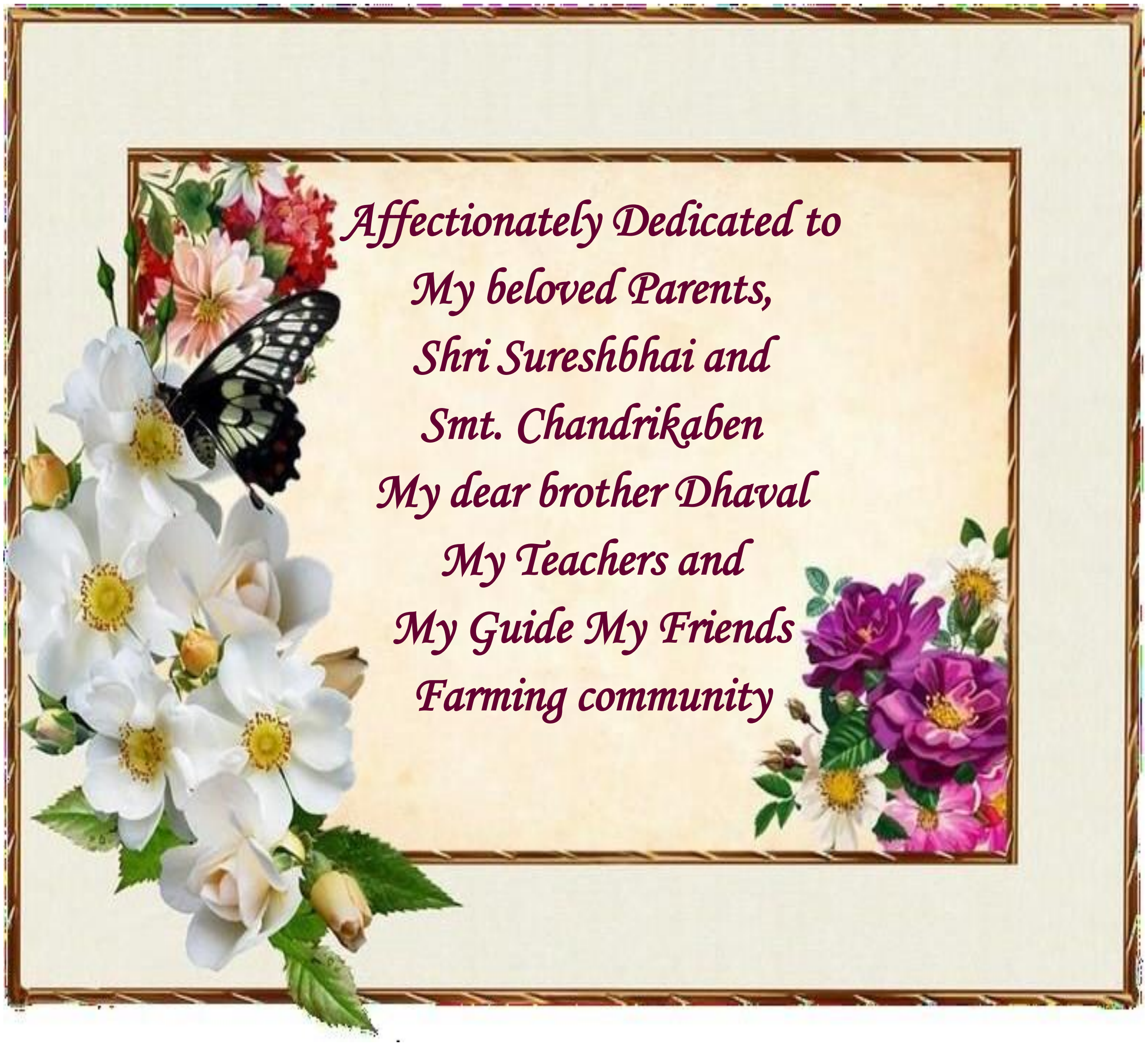

Affectionately Dedicated to
My beloved Parents,
Shri Sureshbhai and
Smt. Chandrikaben
My dear brother Dhaval
My Teachers and
My Guide My Friends
Farming community

DEPARTMENT OF GENETICS AND PLANT BREEDING
UNIVERSITY OF AGRICULTURAL SCIENCES
BANGALORE

CERTIFICATE

This is to certify that the thesis entitled "**IDENTIFICATION OF CROSSES WITH HIGH BREEDING POTENTIAL IN FORAGE COWPEA (*Vigna unguiculata* (L.) Walp.)**" submitted by **Mr. BALAR VIDYUT SURESHBHAI, ID No. PALB 8255** in partial fulfillment of the requirement 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 him during the period of his 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.

M.R. Krishnappa

Bengaluru
October, 2020

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(M. L. REVANNA)

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Bengaluru
October, 2020 ***(Balar Vidyut S.)***

IDENTIFICATION OF CROSSES WITH HIGH BREEDING POTENTIAL IN FORAGE COWPEA (*Vigna unguiculata* (L.) Walp.)

BALAR VIDYUT SURESHBHAI

ABSTRACT

An investigation was carried out to assess the breeding potential of four crosses in F_2 and F_3 generations in forage cowpea. The experimental material consisted of three checks, F_2 and F_3 populations of the four crosses (EC394839 × KBC-5, EC4722 × KBC-5, Pant Lobia × Arka Garima and APC-1218 × RI-60) of *Vigna unguiculata (L.) Walp.* which were evaluated for five quantitative traits at Zonal Agricultural Research Station and K block UAS, GKVK, Bengaluru during late *kharif*-2019 and *rabi*-2019-20 respectively. Variability was higher in F_2 generation for characters like plant height, branches plant^{-1} and leaves plant^{-1} and low variability for days to first flowering in all four crosses. Significant MSS for almost all the traits in F_3 generation, indicated substantial variability. A narrow difference between PCV and GCV was recorded for all the traits studied suggesting less impact of environment on the expression of traits in F_2 and F_3 generation. High heritability coupled with high GAM for plant height, branches plant^{-1}, leaves plant^{-1} and green fodder yield plant^{-1} indicated the larger number of fixable additive factors in the expression of these traits. Among the four crosses, EC394839 × KBC-5 is predicted to have better breeding potential followed by Pant Lobia × Arka Garima. The traits; leaves plant^{-1}, plant height and branches plant^{-1} could be used as surrogates to assist indirect selection for green fodder yield in segregating populations. Top ten high yielding F_3 progenies from all crosses were identified in the study will be further evaluated to derive superior purelines.

October, 2020

Department of Genetics and Plant Breeding	**M. R. KRISHNAPPA**
UAS, GKVK, Bengaluru	(Major Advisor)

ಮೇವಿನ ಅಲಸಂದೆ *(ವಿಗ್ನ ಅಂಗುಕ್ಯುಲಾಟ* (ಎಲ್.) ವಾಲ್ಪ್)ನ ಸಂಕರಣಗಳಲ್ಲಿ ತಳಿವರ್ಧನಾ ಸಾಮಾರ್ಥ್ಯವನ್ನು ಗುರುತಿಸುವುದು.

ಬಲಾರ್ ವಿದ್ಯುತ್ ಸುರೇಶ್‌ಭಾಯ್

ಸಾರಾಂಶ

ಎಫ್ ೨ ಹಾಗೂ ಎಫ್ ೩ ಪೀಳಿಗೆಗಳಲ್ಲಿ ಮೇವಿನ ಅಲಸಂದೆಯ ನಾಲ್ಕು ಸಂಕರಣಗಳಲ್ಲಿ ತಳಿವರ್ಧನಾ ಸಾಮಾರ್ಥ್ಯವನ್ನು ವಿಮರ್ಶಿಸಲು ಈ ಸಂಶೋಧನೆಯನ್ನು ನಡೆಸಲಾಯಿತು. ಈ ಪ್ರಯೋಗದಲ್ಲಿ ನಾಲ್ಕು ಸ್ಥಳಿಯ ತಳಿಗಳು ಮತ್ತು ನಾಲ್ಕು ಸಂಕರಣಗಳಾದ ಇ.ಸಿ.೩೯೪೪೮೩ × ಕೆ.ಬಿ.ಸಿ.–೫, ಇ.ಸಿ.೪೭೨೨ × ಕೆ.ಬಿ.ಸಿ.–೫, ಪಂತ್ ಲೋಬಿಯಾ × ಅರ್ಕಾ ಗರಿಮ ಮತ್ತು ಎ.ಪಿ.ಸಿ.–೧೨೧೮ × ಆರ್.ಐ.–೬೦ ಗಳನ್ನು ವಲಯ ಕೃಷಿ ಸಂಶೋಧನಾ ಕೇಂದ್ರ ಮತ್ತು ಕೆ ಬ್ಲಾಕ್, ಗಾ. ಕೃ. ವಿ. ಕೇಂ., ಬೆಂಗಳೂರಿನಲ್ಲಿ ಐದು ಪರಿಮಾಣಾತ್ಮಕ ಗುಣಗಳನ್ನು ತಿಳಿಯಲು ಬಳಸಲಾಯಿತು. ಎಫ್ ೨ ಪೀಳಿಗೆಯಲ್ಲಿ ಗಿಡದ ಎತ್ತರ, ಗಿಡದ ಕವಲುಗಳು ಮತ್ತು ಒಟ್ಟು ಎಲೆಗಳು ಹೆಚ್ಚು ಭೇದವನ್ನು ಹೊಂದಿದ್ದರೆ, ಮೊದಲ ಹೂ ಬಿಡುವ ದಿನ ಕಡಿಮೆ ಭೇದವನ್ನು ಎಲ್ಲಾ ನಾಲ್ಕು ಸಂಕರಣಗಳಲ್ಲಿ ಹೊಂದಿದ್ದವು. ಎಮ್.ಎಸ್.ಎಸ್ ಎಲ್ಲಾ ಗುಣಗಳಿಗೆ ಗಮನಾರ್ಹ ಭೇದವನ್ನು ತೋರಿಸಿತು. ದೃಶ್ಯರೂಪ ವಂಶವಾಹಕ ಮತ್ತು ವಂಶವಾಹಕ ರೂಪಕ ವಿಶ್ಲೇಷಕಗಳ ನಡುವೆ ಕಡಿಮೆ ಅಂತರದ ವ್ಯತ್ಯಾಸ ಕಂಡುಬಂದಿದ್ದು, ಪರಿಸರದ ಪ್ರಮಾಣ ಕಡಿಮೆ ಇರುವುದಾಗಿ ತಿಳಿಯಿತು. ಗಿಡದ ಎತ್ತರ, ಗಿಡದ ಕವಲುಗಳು ಗಿಡದ ಎಲೆಗಳು ಮತ್ತು ಹಸಿರು ಇಳುವರಿ ಗುಣಗಳು ಅನುವಂಶಿಕತೆಯೊಂದಿಗೆ ಹೆಚ್ಚು ಶೇಕಡಾ ಸರಾಸರಿ ಪ್ರಕಾರ ಅನುವಂಶೀಯ ಮುನ್ನಡೆಯನ್ನು ಹೊಂದಿದ್ದು, ಕೂಡಲ್ಪಡುವ ವಂಶವಾಹಿಗಳ ನಿಯಂತ್ರಣದಲ್ಲಿರುವುದು ಗೊತ್ತಾಯಿತು. ಅಧ್ಯಯನ ಮಾಡಿದ ನಾಲ್ಕು ಸಂಕರಣಗಳಲ್ಲಿ ಇ.ಸಿ.೩೯೪೪೮೩ × ಕೆ.ಬಿ.ಸಿ.–೫ ಹೆಚ್ಚು ತಳಿವರ್ಧನಾ ಸಾಮರ್ಥ್ಯವನ್ನು ಹೊಂದಿತ್ತು. ನಂತರ ಪಂತ್ ಲೋಬಿಯಾ × ಅರ್ಕಾ ಗರಿಮ ಹೆಚ್ಚು ತಳಿವರ್ಧನಾ ಸಾಮರ್ಥ್ಯವನ್ನು ಹೊಂದಿತ್ತು. ಗಿಡದ ಎತ್ತರ, ಗಿಡದ ಕವಲುಗಳು ಮತ್ತು ಗಿಡದ ಎಲೆಗಳನ್ನು ಪರೋಕ್ಷ ಆಯ್ಕೆಯಲ್ಲಿ ಬಳಸಬಹುದಾದ ಗುಣಗಳೆಂದು ತಿಳಿಯಿತು. ಎಫ್ ೩ ಪೀಳಿಗೆಯ ಹತ್ತು ಶ್ರೇಷ್ಠ ಶ್ರೇಣಿಯ ರೂಪಕಗಳನ್ನು ಗುರುತಿಸಿದ್ದು ಇವುಗಳನ್ನು ಮುಂದಿನ ಪೀಳಿಗೆಯಲ್ಲಿ ಪರೀಕ್ಷಿಸಲು ಉಪಯೋಗಿಸಬಹುದು.

ಅಕ್ಟೋಬರ್, ೨೦೨೦

ಅನುವಂಶೀಯ ಮತ್ತು ಸಸ್ಯತಳಿ ಅಭಿವೃದ್ಧಿ ಶಾಸ್ತ್ರ ವಿಭಾಗ	**(ಎಮ್. ಆರ್. ಕೃಷ್ಣಪ್ಪ)**
ಕೃಷಿ ವಿಶ್ವವಿದ್ಯಾನಿಲಯ, ಗಾ.ಕೃ.ವಿ.ಕೇಂ., ಬೆಂಗಳೂರು–೬೫	ಮುಖ್ಯ ಸಲಹೆಗಾರರು

Identification of crosses with high breeding potential in forage cowpea (*Vigna unguiculata. (*L) Walp.)

BALAR VIDYUT S., PALB 8255

Department of Genetics and Plant Breeding, College of Agriculture, UAS, GKVK, Bengaluru

Introduction

❖ Cowpea is cultivated around the world as one of the important food legume but also as a vegetable, cover crop and fodder.

❖ Cowpea forage contains 17-18% crude protein.

❖ The common method to derive improved cultivars is hybridization followed by selection in segregating generations and isolation of pure lines.

Objective

i. To assess the breeding potential of four crosses.

Material and methods

❑ Basic material

❖ The basic experimental material consist of seeds harvested from F_1 generation derived from four crosses (Table 1).

Table 1: Experimental material

Cross codes	Four crosses	No. of F_2 plants	No. of F_3 progenies
C_1	EC394839 × KBC-5	226	150
C_2	EC4722 × KBC-5	208	150
C_3	Pant Lobia × Arka Garima	201	150
C_4	APC-1218 × RI-60	201	150

Fig.1- F_2 population

Fig.2- F_3 progenies

Methods

❖ F_2 seeds of four different crosses were sown along with checks (MFC-08-14, MFC-09-1 and KBC-2) in separate blocks during late *kharif*-2019 and observations were recorded for the characters days to first flowering, plant height (cm), number of branches plant^{-1} and number of leaves plant^{-1} from all the plants.

❖ F_3 generation is sown in progeny rows in *rabi*-2019-20 along with three checks following Augmented design (Federer, 1956) and observation were recorded including characters days to 50% flowering and green fodder yield plant^{-1} from five randomly selected plants from each lines.

❖ The quantitative trait means values, phenotypic coefficient of variation, absolute and standardized range, heritability and genetic advance were used as predictors to compare the four crosses and predict the breeding potential of crosses (Suresh *et al.*, 2017).

Statistical analysis

❖ Statistical parameters like mean, range, GCV, PCV and broad sense heritability were calculated.

❖ ANOVA for Augmented design was performed.

❖ Adjusted trait means of 600 F_3 progenies were used for statistical analysis.

Results

❖ In F_2 generation variability parameters for the yield attributing characters days to first flowering, plant height (cm), number of branches plant^{-1} and number of leaves plant^{-1} in all the four crosses were estimated and found that:

- Low variability, moderate to high heritability and low genetic advance for the trait days to first flowering.
- Moderate to high variability, high heritability and genetic advance for plant height, number of branches and number of leaves.

❖ In F_3 analysis of variance revealed significant mean sum of squares for all the five traits (Table 2).

❖ High broad sense heritability were reported for all the traits under study in F_3 generation (Table 3).

❖ The 42 F_3 progenies in C_1, 38 F_3 progenies in C_2, 51 F_3 progenies in C_3 and 39 F_3 progenies in C_4 found superior to all three checks in terms of earliness and green fodder yield.

❖ Increasing trend in quantitative trait mean and decreasing in values of variability were observed from F_2 to F_3 generation

Table 2: ANOVA for quantitative traits

Source of variation	Degrees of freedom	Days to 50% flowering	Plant height (cm)	No. of Branches plant^{-1}	No. of leaves plant^{-1}	Green fodder yield (g)
Block	42	5.592**	49.959**	1.383**	81.705**	20205.100**
Entries (F_3 progenies + checks)	602	5.824**	47.754**	0.709**	39.744**	6322.960**
F_3 progenies	599	6.191**	50.542**	0.790**	44.434**	7608.901**
Checks	2	6.519**	23.879**	0.003	26.984*	2416.705*
Checks vs F_3 progenies	1	0.001	399.888**	0.763*	94.127**	53009.490**
Error	84	0.537	2.912	0.144	6.558	560.307

*Significant @ P=0.05 **Significant @ P=0.01

Table 3: Estimates of descriptive statistics and genetic variability parameters of five traits.

Characters	Mean± SE	Min.	Max.	Std. Range	PCV	GCV	h^2	GAM
Days to 50% flowering	74.58 ± 0.10	69.41	81.58	0.16	3.14	2.98	90.18	5.83
Plant height (cm)	43.74 ± 0.29	21.00	59.13	0.87	15.25	14.74	93.46	29.36
No. of Branches plant^{-1}	6.98 ± 0.04	4.03	9.10	0.73	12.05	10.76	79.70	19.78
No. of leaves plant^{-1}	29.51 ± 0.27	13.44	46.64	1.13	21.33	19.49	83.45	36.67
Green fodder yield plant^{-1} (g)	229.84 ± 3.56	27.73	536.16	2.21	35.65	34.13	91.66	67.32

Discussion

❖ MSS attributed to F_3 progenies and checks were significant, indicating existence of variability

❖ The phenotype of the individuals is predominantly due to the genotypic constitution of the individual itself indicated by narrow difference between PCV and GCV for most of the traits.

❖ The crosses C_1 and C_3 is predicted to have better breeding potential which indicates high recovery of desirable RILs in advanced generations.

Summary

❖ All the crosses in F_2 and F_3 generation has shown greater variability for yield and yield attributing characters.

❖ The crosses C_1 and C_3 have performed better in terms of earliness and high biomass yield as well as higher variability for most of traits.

Advisory committee

Chairperson

Dr. M. R. Krishnappa

Members

Dr. S. Ramesh

Dr. N. Marappa

Dr. M. L. Revanna

Reference

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I INRODUCTION

Vigna unguiculata (L.) Walp. is commonly referred as cowpea with a chromosome number of 2n=22 belongs to the tribe Phaseolae of the family Fabaceae, is an important *kharif* food legume and forms an integral part of traditional crop systems in tropical semi-arid regions where other food legumes may not perform well. It is commonly referred as lobia, china pea, black eye pea, roungi, kaffir pea and southern pea. This is known for its broad geographical distribution and adaption across the types of soil, soil inputs and agro-climatic zones. Cowpea is mostly cultivated in arid and semi arid area of Rajasthan, Karnataka, Gujarat, Tamilnadu, Kerala and Maharashtra. It is one of the most ancient sources of human food, and has probably been used since Neolithic times as a crop plant (Chevalier, 1964).

Cowpea is a major dietary protein source in traditional diets (rich in lysine) that supplements staple low-protein cereals and tuber crops nutritionally (Singh *et al.,* 2002; Langyintuo *et al.*, 2003). Cowpea is a major source of protein, minerals and vitamins in daily diets and is equally important as nutritious fodder for livestock (Table 1). Cowpea contains highest iron (8.6 mg/100g.) after mothbean (9.5 mg/100g.) and soybean (10.4 mg/100g.) among pulses and legumes. It also plays a crucial role as a cover crop and a green manure crop (Quin, 1997), as well as being a major staple food of man. Cowpea in the form of forage, hay and silage can be used as a good fodder source of the livestock. It is regarded as an essential component of farming systems, as it has the ability to restore soil fertility for successive crops grown with it in rotation (Carsky *et al*., 2002; Tarawali *et al.*, 2002; Sanginga *et al.*, 2003).

Table 1: Nutritional value of cowpea per 100 gms. of edible portion

Particulars	Protein g.	Fat g.	Minerals g.	Crude Fibre g.	Carbo hydrates g.	Energy Kcal.	Calcium mg.	Phosphorus mg.	Iron mg.
Grain	24.1	1.0	3.2	3.8	54.5	323	77	414	8.6
Leaves	3.4	0.7	1.6	1.2	4.1	38	290	58	20.1

Gopalan *et al.,* 1989

In India, pulses are cultivated on an area of 28.83 million hectares with a production of 23.94 million tons (*Anon*, 2018) and cowpea is sixth among grain legumes in India with a production share of 6.8 *per cent* (*Anon*, 2014). In India, cowpea is cultivated across an area of 3.9 m ha with 2.21 m tonnes output (FAO, 2016). India represents one third of the world's area under pulses and one fourth of the world's production. Most specifically in central and peninsular regions, it is widely grown throughout India. It is the only important crop for rainfed *kharif* fodder cum pulse as well as irrigated areas. The productivity of green forage is around 25-45 t / ha with a seed production capacity of 3 q / ha. The national crop production is 0.9 million tons of seed and 5.00 million tonnes of forage (*Anon* (b), 2015).The region and crop production aren't recorded separately in the country's crop census. Cowpea ranks fourth among all pulses in Karnataka with an area of 0.08 million hectares, producing 0.031 million tonnes (*Anon* (a), 2015).

Urbanization has brought about a marked change in people's feeding habits towards milk, meat and eggs, with the consequent rise in livestock products demand. There is no solution to support livestock husbandry without dwelling on the country's fodder and feed development issues. The country currently faces a net deficit of 35.6% green fodder, 10.95% dry crop residues and 44% concentrate feed ingredients. Green and dry fodder demand is expected to reach 1012 and 631 million tonnes by 2050. At the current level of growth in forage supplies, green fodder will have a deficit of 18.4 *per cent* and dry fodder will have a deficit of 13.2 *per cent* in 2050. To meet the shortfall, green forage supply will have to rise at 1.69 *per cent* per annum (*Anon* (b), 2015).

Farmers are also cultivating a short-duration spreading grain variety and a long-duration spreading variety for fodder, but the grain yield and fodder are poor due to the low yield ability of the spreading varieties and also due to early cessation of rainfall. The majority of cultivars derived from and erect growth habit their high productivity (Singh and Sharma, 1996). Using cowpea as a fodder crop is attractive in mixed crop / livestock systems where soil and feed are becoming increasingly scarce, particularly in the dry season (Tarawali *et al.*, 1997). Though the high yields of grain and fodder, the varieties of green fodder have crude protein content (15-20%) and digestibility over the whole plant base (50-56%).

There is an urgent need to satisfy the fodder demand for growing number of livestock and also to increase their productivity, for which the availability of feed supplies must be increased. For many decades the enhancement of genetic resource in forage crops remained limited to cultivated crops. Improvement programs on range grasses and legumes, which is important restriction in the growth of grasslands and pastures, have not been given proper attention. Therefore nutrient rich and high yielding cultivars of forage crops must be generated.

Only the way to bridge the gap between green fodder demand and supply is to maximize the production of fodder over time and space by identifying new forage resources and increasing the forage production within the current farming system. This demands need to rejuvenate fodder crops and also to increase their productivity by developing new varieties. (*Anon,* 2011).

Cowpea being a predominantly self-pollinated crop, pure-lines is the best commercial production choice for the cultivar. For the isolation of superior recombinant inbred lines in advanced segregating generations, plant breeder carry out large number of crosses to combine desirable traits distributed over a wide number of parents. Therefore, plant breeders are often faced with a problem of handling large segregating populations resulting from such a large number of crosses that have the lacunae of time, space, and human resources. So it is important to predict any cross's performance in terms of recovering desirable purelines in advanced generation. On this basis, the early removal of weak crosses and the identification of only a few successful crosses aid in the effective use of land, time and human resources and also help in the improvement of the breeding performance.

Furthermore, direct selection for economically important traits such as green fodder yield was less successful, as they are traits that are difficult to breed. Indirect selection for such traits based on easily observable traits are likely to be more successful, requiring prior determination of significantly associated traits with green fodder yield. The present investigation was conducted with this assumption, with the following objectives.

i. To asses genetic variability for traits related to fodder yield in F_2 population.

ii. To assess the breeding potential of four crosses.

iii. To identify traits associated with fodder yield in F_3 generation.

II REVIEW OF LITERATURE

Reviews related to the present study are given under following sub-heads,

2.1 Genetic Variability

2.2 Breeding potential

2.3 Heritability and Genetic advance

2.4 Correlation studies

2.1 Genetic variability

Information on genetic variability in a population and heritability estimation are prerequisites for preparing a successful breeding program to improve any crop. The genetic variability is measured using certain genetic parameters such as genotypic variation coefficient, heritability and genetic advance.

Borah and Fazlullahkhan (2000) evaluated 60 cowpea accessions and reported high estimates of phenotypic and genotypic coefficient of variation for number of branches and leaves, dry weight of leaves and stem, dry matter and green fodder yield implying possible variation present in fodder cowpea for these traits. They also observed low estimates for traits like days to 50% flowering, stem thickness and leaflet length that implies low variability.

Manonmani *et al.* (2000) reported high estimates of genotypic and phenotypic coefficient of variation for green fodder yield in fodder cowpea.

Verma and Mishra (2005) evaluated 35 cowpea exotic genotypes and reported of genotypic and phenotypic coefficient of variation for dry matter per plant and seed yield per plant.

Malarvizhi *et al.* (2005) evaluated 60 genotypes of forage cowpea and revealed high value of phenotypic and genotypic coefficient of variation for no. of branches, no. of leaves, dry weight of leaves, dry weight of stem, green fodder yield and dry matter yield.

Low genotypic coefficient of variation observed for traits including crude protein content, stem thickness, days to 50 *per cent* flowering and leaflet length.

Genetic variability in 25 cowpea genotypes were studied by Singh *et al.* (2010) and recorded the highly significant mean square for all traits suggesting adequate genotypic variability. High phenotypic and genotypic variation coefficient coupled with high heritability and genetic advance as a percentage of mean for plant height, stem weight, leaves weight, biological yield, dry matter yield and green fodder productivity were recorded suggesting predominance of additive gene effects in controlling these characters.

Kohli (2012) shown that the extent of phenotypic variability and estimates of phenotypic and genotypic variances and coefficient of variation were high for green forage yield, plant height and days to 50 *per cent* flowering.

Sivakumar *et al.* (2013) examined 22 diffrent genotypes of bush cowpea and revealed that the high phenotypic and genotypic coefficient of variation for pod weight, plant height and pod length.

Ajayi et al. (2014) studied 10 genotypes and reported wide range of significant variation were observed in plant height, no. of leaves, no. of nodes on main stem, no. of peduncle per plant, peduncle length, no. of days to flowering, no. of pods per peduncle, no. of pods per plant, pod length, no. of seeds per pod, no. of seeds per plant, seed length, seed width and 100 seed weight for all the characters, The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV).

Olayiwola *et al.* (2014) evaluated 11 cowpea accessions and reported high phenotypic and genotypic coefficient of variation for the traits like no. of pods/plants, pod, seed and dry fodder yields.

Anamika and Tajane (2014) analyzed 44 genotypes of cowpea and high estimates of genotypic coefficient of variation were recorded for green forage yield per plant, dry matter yield per plant, branches per plant in cowpea forage. For all characters, the magnitude of phenotypic coefficient of variation was greater than the genotypic coefficient of variation.

Shanko *et al.* (2014) studied 49 cowpea accessions and reported significant differences for all the characters studied. High phenotypic and genotypic coefficient of variations for the characters like yield per plant, number of pods per plant and 100 seed weight was recorded. The contrast among phenotypic and genotypic coefficient of variation values was high for plant height, number of secondary branches per plant, number of pods per plant and seed yield per plant.

Khan *et al.* (2015) studied 196 different cowpea accessions and revealed that phenotypic coefficient of variation values were of higher magnitude than genotypic coefficient of variation for all the traits studied by them. The estimates of phenotypic and genotypic coefficient of variation were also high for plant height, pod length, no. of pods per plant, pod length, no. of branches per plant, seed yield per plant and test weight.

Sanjeev *et al.* (2016) investigated 96 accessions and recorded high estimates of phenotypic coefficient of variation for green fodder yield, leaf area, dry weight of stem, dry matter yield and dry weight of leaf. They were accounted for moderate phenotypic coefficient of variation for plant height, leaf/stem ratio, no. of branches per plant and no. of leaves per plant. The comparison between assessments of phenotypic and genotypic coefficient of variation was least for all the characteristics.

Sarath and Reshma (2017) studied 12 characters of 22 genotypes and recorded the large degree of variability were observed for all the traits. High magnitude of the phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance for traits like plant height, grain yield per plant and length of the pods were recorded.

Dinesh *et al.* (2017) evaluated set of 194 F_3 progenies and reported moderate phenotypic coefficient of variation and genotypic coefficient of variation and estimates were recorded for number of pods per plant and plant height.

Jogdhande *et al*. (2017) examined 30 genotypes and stated that the estimate of genotypic and phenotypic coefficient of variation were high for no. of branches per plant, pod yield per plot, total number of pods per plant, no. of seeds per pod and high heritability along with high genotypic co-efficient of variation observed for number of branches per plant, pod yield per plot, total number of pods per plant and number of seeds per pod indicating scope for improvement by selection and breeding programme.

Sahu (2019) studied 78 germplasm lines for green fodder yield and its 15 characters viz.,plant height, number of primary branches, days to 50% flowering, pod length, number of locules per pod, days to maturity, 100 Seed weight, seed yield per plant, leaf length, leaf width, leaf stem ratio, green fodder yield per day, dry matter yield and dry matter yield per day. All the fifteen characters exhibited significant variability.

Meenatchi *et al.* (2019) studied nine F_2 populations and stated that high level of phenotypic coefficient of variation and genotypic coefficient of variation were observed for no. of branches per plant, no. of clusters per plant, no. of pods per plant and single plant yield. Low level of phenotypic and genotypic coefficient of variation were obtained for all the crosses except for cross IV (CO4 × VCP-09-024).

2.2 Breeding potential

Breeding potential is the genetic worth of a cross in terms of recovery in the advanced generations of superior recombinant inbred lines (RILs). Predicting a cross's breeding potential using different predictors overcomes the land, time and human resource constraints expended on handling large segregating populations. The reported results and literature relating to the cowpea breeding potential assessment of crosses are minimal. Therefore related literature reviewed and discussed here in other crops.

Krishnappa *et al.* (2009) conducted a study in finger millet evaluating the utility of the general combining ability (gca) of selected parents to make crosses that are likely to result in advanced generations of superior recombinant inbred lines (RILs). They found that the crosses involving at least one of their parents with high gca effects were successful in deriving desired traits from recombinant inbred lines and desired mean voice.

Suresh *et al.* (2017) conducted a study to assess the breeding potential of three crosses derived from parents contrasting for fresh pod yield per plant on the contribution of 10 quantitative trait mean and phenotypic variation coefficient in F_2 and F_3 generations in Dolichos bean. They reported an increasing trend in quantitative trait means and phenotypic coefficient of variation (PCV) from F_2 to F_3 generations of HA-10-8 × RIL 180 and FPB 21 × RIL 180, thus concluded that these two crosses had greater breeding potential. In addition, the discovery of recombinant inbred lines superior to HA 4 in F_5 generation derived from HA-10-8 × RIL 180 suggested the usefulness of quantitative trait means and variances in early segregating generations to assess the breeding potential of crosses in order to maximize the frequency of desirable recombinant inbred lines in advanced generations.

Shweta (2018) examined four crosses of cowpea in F_2 and F_3 generation and assessed breeding potential of four crosses for seed yield and demonstated that four crosses differed in the estimates of quantitative trait means, absolute and standardized range, PCV and frequency of transgressive segregants in F_2 and F_3 generations and among the four crosses PL-2 × NBC-39 followed by PL-5 × EC-402104 found to have better breeding potential in terms of recovery of superior recombinant inbred lines in advanced generations.

2.3 Heritability and Genetic advance

Heritability is the heritable part of phenotypic variation and is a strong measure of a character transmission from parents to offspring. (Falconer and Mackay, 1981) Heritability in a broad sense is the ratio of genotypic variance to phenotypic variance. Its determination is important because it determines the gene expressivity that a genotype bears. When a character's heritability is high, the phenotypic value gives a relatively similar estimate of the genotypic value and thus breeder may focus his selection on phenotypic efficiency, while awareness of heritability allows the plant breeder to pre-assess the selection outcomes for a specific character.

However, for predicting the effect of selection, heritability estimates along with genetic advance are more useful than the heritability estimates alone (Johnson et al., 1955).

Borah and Fazlullahkhan (2000) studied 60 cowpea genotypes and revealed high heritability associated with high genetic advance as percentage of mean for characters like plant height, number of branches, leaves, stem and leaf dry weight, dry matter and green fodder yield. Low heritability reported for crude protein content, days to 50% flowering, stem thickness and leaf length and width with low genetic advance.

Kumar and Sangwan (2000) analysed 72 cowpea genotypes and reported moderate to high heritability and high genetic advance for number of branches and plant height).

Malarvizhi *et al.* (2005) studied 60 accessions of fodder cowpea and concluded high heritability accompanied with genetic advance for the traits like plant height, number of branches per plant, number of leaves per plant, dry weight of stem, dry weight of leaves, dry matter yield and green fodder yield. High heritability with low genetic advance is reported for characters like days to 50 *per cent* flowering, leaflet length, leaflet width, stem thickness and crude protein content.

Bhandari and Verma (2008) evaluated 20 advanced generation cowpea lines and reported high heritability with high to moderate genetic advance for plant height, days to 50 *per cent* flowering, number of leaves per plant and green forage yield.

Kohli (2012) revealed that for days to 50% of flowering, green forage yield per plant and length of the main branch were recorded high estimates of expected genetic advance for *per cent* of mean went with high or moderately high heritability in cowpea.

Sivakumar *et al.* (2013) examined 22 diffrent lines of bush cowpea and observed high heritability associated with high genetic advance observed for all characters studied, aside from days to first flowering and days to first harvest indicating these characters suggesting additive gene action for the character under study.

Ajayi *et al.* (2014) examined 10 genotypes of cowpea and revealed high heritability for all the traits except moderate heritability for plant height. High genetic advance as *per cent* of mean observed for all the traits except terminal leaflet length which is accounted for low genetic advance as per cent of mean.

Anamika *et al.* (2014) examined 44 genotypes of cowpea and reported high heritability accompanied with high genetic advance showed for green forage yield, dry matter yield, plant height at 50 per cent flowering and branches per plant.

Olayiwola *et al.* (2014) examined 11 cowpea lines and observed high heritability for number of pods/plant, 100 seed weight and dry fodder yield. Genetic advance was high for seed, pod and dry fodder yield. All characters had high genetic advance as *per cent* of mean except days to 50% flowering and number of seeds/pods. Dry fodder yield alone had combined high genetic advance and heritability values.

Shanko *et al.* (2014) studied 49 cowpea accession and observed high heritability in broad sense and genetic advance estimated for the characters like yield, no. of pods, and 100-seed weight. The contrast among phenotypic and genotypic coefficient of variance was high for plant height, no. of secondary branches, number of pods and seed yield.

Khan *et al.* (2015) studied 196 different cowpea genotypes and reported high heritability and high genetic advance as *per cent* (GAM) of mean for plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, pod length, seed yield per plant and test weight.

Sanjeev *et al.* (2016) studied 96 accessions and observed high heritability and genetic advance for no. of branches per plant, no. of leaves per plant, total leaf area, green fodder yield, dry weight of stem, dry weight of leaf, dry matter yield and leaf/stem ratio.

Dinesh *et al.* (2017) evaluated a set of 194 F_3 progenies. High heritability coupled with high genetic advance as *per cent* of mean was observed for plant height and moderate heritability and genetic advance as *per cent* of mean was observed for number pods per plant.

Meenatchi *et al.* (2019) studied nine F_2 populations and stated that high heritabilty and high genetic advance as *per cent* of mean were recorded for plant height, pod length, seeds per pod, hundred seeds weight and single plant yield.

2.4 Correlation studies

The correlation studies are helpful in formulating effective multi-trait selection breeding programmes. Coefficient of correlation tests the mutual relationship between different plant characters and gives fair indication that plant breeders should face their selection of characters in order to improve economic yield and also to prepare more productive breeding programmes. In crops such as cowpea, where hybrid development is out of question and hybridization accompanied by selection is the key improvement method. Hence, information about correlation is an essential requirement to achieve genetic improvement. In the selection method, the value of correlation analysis is appreciable when highly heritable characters are paired with important characters such as yield that have low heritability. It is important to stress that inferenced type will only be relevant if this analysis is based on individual plant observations in generations such as F_2, F_3 and F_4, which are segregating. Additionally, variation should reflect a wide range of gene segregation and recombination affecting various quantitative traits to provide an accurate and reliable measure of character association. The magnitude of the observed two-character interaction is defined as a single overall phenotypic association. Investigations into the correlation of cowpea characters are briefly reviewed as below.

Manonmani *et al.* (2000) demonstrated positive correlation of green fodder yield with number of branches per plant, leaf length and leaf weight in forage cowpea.

Tyagi *et al* . (2000) analyzed 24 genotypes of cowpea and recorded the highest (0.550) and lowest (0.003) direct positive effects on seed yield per pod and plant height, respectively. Days to 50 percent flowering observed a direct impact (-0.129) on seed yield per plant.

Mittal *et al.* (2006) reported that the forage yield in cowpea can be increased by choosing plants with higher stem diameter and length in the segregating populations.

Sheela Maryand and Gopalan (2006) revealed that number of branches, number of leaves, leaf weight, stem weight, green fodder yield and crude protein content had positive and significant phenotypic and genotypic correlation with dry matter yield. The phenotypic and genotypic inter-correlations among the characters with dry matter yield revealed that the seven character namely plant height, number of branches, number of leaves, leaf length, leaf breadth, stem weight and green fodder yield exhibited positive significant inter-correlation. The maximum positive direct effect contributing to dry matter yield was exhibited by green fodder yield followed by days to 50% flowering, crude protein content, stem thickness, number of branches and number of leaves.

Bhandari and Verma (2007) performed correlation analysis in 22 genotypes of cowpea and reported that plant height, number of leaves per plant, leaf: stem ratio, crude protein content and dry matter digestibility had large contribution in determining quantity and quality of green and dry forage yield.

Mittal *et al.* (2009) carried out correlation and path coefficient analysis in forage cowpea indicated that dry matter yield as well as green fodder yield had significant positive association with stem length, primary branches per plant, leaflet length, and leaflet breadth. Significant positive association to the extent of 0.99 was observed between dry matter yield and green fodder yield indicting that moisture content did not differently influence different genotypes. High positive genotypic correlation of dry matter as well as green fodder yield was reported with primary branches per plant, leaflet length and leaflet breadth.

Imran *et al*. (2010) studied 14 local lines of cowpea germplasm recommended that number of branches per plant showed a significant correlation (r =0.585) with leaf area and non-significant association with number of leaves per main branch and green fodder yield. Leaf area showed a negative and significant correlation (r =0.583) with pod length which is indicative of the fact that a plant having more vegetative growth (i.e., leaf area) produces small pods.

Sahai *et al.* (2013) examined 168 genotypes of cowpea and recorded large impact of direct effects of correlation (0.9714) and recommended that going for plant types with higher biomass per plant (0.8856), dry weight per plant (0.4598), stem girth (0.2336) number of secondary branches (0.2788), leaves per plant (0.3251), pods per plant (0.9059) and pod clusters per plant (0.7718) It will be successful in boosting both fodder yield and cowpea seed yield.

Gitanjali *et al.* (2013) carried out correlation and path analysis and stated that going for plant types with higher biomass per plant, dry weight per plant, stem girth, number of secondary branches, leaves per plant, pods per plant and pod clusters per plant would be effective for improvement of fodder and seed yield in cowpea.

Anamika *et al.* (2014) carried out correlation studies in 44 genotypes of cowpea for the traits dry matter yield per plant, days to 50% flowering, plant height, leaf: stem ratio and no. of leaves per plant for green forage yield. Correlation findings stressed the role of characters viz., dry matter yield per plant, days to 50% flowering, plant height at 50% flowering, leaf: stem ratio and number of leaves per plant for green forage yield purpose.

Meena *et al.* (2015) studied 72 genotypes of cowpea to estimate the correlations and path coefficients for 10 quantitative traits and reported seed yield per plant had positive significant correlation with days to 50% flowering, plant height, primary branches per plant, pods per plant, pod length, seeds per pod and 100-seed weight at both genotypic and phenotypic levels.

Navaselvakkumaran *et al.* (2019) studied 136 fodder cowpea germplasm accessions to determine the correlation among 11 quantitative traits and stated that it is evident that the traits viz., number of primary branches per plant, number of leaves per plant and leaf area exhibited significant positive correlation towards green fodder yield per plant as well as dry matter yield per plant. The highest positive direct effect of leaf area and the highest positive indirect effects of number of leaves per plant and dry matter yield per plant via leaf area would contribute more towards increasing green fodder yield per plant.

Kalambe *et al.* (2019) studied 22 accessions for character association of yield and its components for 12 traits and reported that the magnitude of association varied among the genotypes. The traits like plant height, no. of primary branches per plant, no. of pods per plant, no. of seeds per pod, mean pod weight and 100 seed weight showed the positive and significant correlation with pod yield per plant.

III MATERIAL AND METHODS

This chapter describes the descriptions of the experimental site, the basic experimental material, the generation of experimental material, its assessment procedure and data collection on various quantitative traits and the statistical methods used for genetic analysis.

3.1 The Experimental Site

The present investigation carried out during late *kharif* 2019 and *rabi* 2019-2020 at the experimental plots of Zonal Agricultural Research Station and K block respectively, University of Agricultural Sciences, Gandhi Krishi Vignana Kendra, Bengaluru. The campus is geographically located at an altitude of 930 m above mean sea level 12˚ 58' North and 77˚35' East latitude and longitude, respectively**.**

3.2 Experimental Material

The basic experimental material for the study consisted of F_2 and F_3 generations derived from the following four crosses along with three check entries of fodder cowpea *viz.*,

Crosses

1. EC394839 × KBC-5
2. EC4722 × KBC-5
3. Pant Lobia × Arka Garima
4. APC-1218 × RI-60

Checks

1. MFC-08-14
2. MFC-09-1
3. KBC-2

3.3 Experimental design and layout

The experimental material consists of three checks, F_2 and F_3 populations of the four crosses. Approximately ~200 F_2 plants derived from each of the four crosses will be evaluated in a in contiguous block with the spacing of 0.3m × 0.1m. The experimental design followed for F_3 was augmented design (Federer, 1956).

3.4 Development and evaluation of experimental material

The F_1 seeds were collected from four crosses (EC394839 × KBC-5, Pant Lobia × Arka Garima, EC4722 × KBC-5 and APC-1218 × RI-60), developed and evaluated by Khandu in *kharif* 2018. In late *kharif* 2019 at ZARS, UAS, GKVK (Table 2), the seeds thus collected from F_1 plants of four crosses were sown in contiguous blocks to raise F_2 populations (~200). Seeds from 150 F_2 plants randomly selected from each F_2 population derived from the four crosses EC394839 × KBC-5, EC4722 × KBC-5, Pant Lobia × Arka Garima and APC-1218 × RI-60 were collected to raise F_3 generations, respectively. The seeds from the four crosses derived from F_2 plants were planted in plant to row progenies at ' K ' block, Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bengaluru during *rabi*, 2019 (constituted the F_3 material) (Table 2).

Table 2: Experimental material used in the current study

Cross codes	Four crosses	No. of F_2 plants	No. of F_3 families
C_1	EC394839 × KBC-5	226	150
C_2	EC4722 × KBC-5	208	150
C_3	Pant Lobia × Arka Garima	201	150
C_4	APC-1218 × RI-60	201	150

3.5 OBSERVATIONS RECORDED

Observations for different traits related to yield were recorded on all the F_2 plants and five plants in each line of checks. Observations for different yield and its attributes were recorded for five randomly selected plants in each of the F_3 progenies and checks. The procedure followed in recording observations on these plants is described below.

Plate 1: Field view of crop in F_2 generation

Plate 2: Field view of crop in F_3 generation

3.5.1 Days to first flowering: The number of days taken from sowing to the first emergence of flowers was recorded.

3.5.2 Days to 50 *per cent* flowering: The number of days taken for the emergence of flowers in 50 *per cent* of plants from the date of sowing was recorded.

3.5.3 Plant height (cm): The height of plant from the ground level of the main axis to the apical leaflet was measured at 50 *per cent* flowering stage and expressed in centimetres.

3.5.4 Branches plant^{-1} : The number of branches on the main axis was counted at 50 *per cent* flowering stage.

3.5.5 Leaves plant^{-1} : Total number of trifoliate leaves from each sample plant was counted and data was recorded.

3.5.6 Green fodder yield plant^{-1} (g): The green fodder yield on five plants was recorded at harvest and expressed in grams.

3.6 Statistical analysis

The statistical analysis was carried out using the adjusted trait means of 600 F_3 progenies. Mean values of the five randomly selected plants in F_3 progenies and checks were used for statistical analysis.

Analysis of variance (ANOVA)

ANOVA (Table 3) was performed following Augmented design (Federer, 1956) using WINDOWSTAT software to examine statistical significance or otherwise of the differences among F_3 progenies.

Adjusted quantitative trait value of each of the individuals in F_3 progenies were estimated by subtracting observed quantitative trait value of the individuals of F_3 progenies from the block effect, 'aj' of jth block; 'aj' was estimated as 'aj' = (xj – x…), xj = trait mean of checks in the jth block and x…= the experimental quantitative trait mean of parents as checks in the experiment (Federer,1956).

Table 3: Structure of ANOVA (Augmented Design; Federer, 1956) of F_3 progenies

Source of variation	Degrees of freedom	Mean Sum of squares	"F" Ratio
Blocks (b) (Eliminating F_3 progenies + check entries)	(b-1)	MSS(B)	MSS(B) / EMSS
Entries (g) (F_3 progenies + check entries) (ignoring blocks)	(g-1)	MSS(G)	MSS(G) / EMSS
F_3 progenies (f)	(f-1)	MSS(F)	MSS(F) / EMSS
Check entries (c)	(c-1)	MSS(C)	MSS(C) / EMSS
F_3 progenies *vs.* Check varieties	(f-1) (c-1)	MSS(FC)	MSS (FC) / EMSS
Non genetic (Error)	(c-1) (b-1)	EMSS	

Where,

b = number of blocks
g =number of entries
f = number of F_3 progenies
c = number of check entries

Adjusted quantitative trait means of 600 F_3 progenies were used for estimating five quantitative traits mean, absolute range (highest - lowest trait mean), standardized range, PCV, GCV, heritability (broad sense), expected genetic advance as *per cent* of mean (GAM) and correlation coefficient of days to 50% flowering, plant height, branches plant^{-1}, leaves plant^{-1} and green fodder yield plant^{-1}.

Descriptive statistics to assess genetic variability

Genetic variability among the genotypes was assessed using first-degree and second-degree statistics.

Mean

Mean for each trait was computed on the basis of observations recorded on ten randomly selected plants.

$$\text{General mean} = \frac{\text{Sum of observations of all the selected plants for each progeny row}}{\text{Number of plants}}$$

Range

Range was calculated by the difference between minimum and maximum value recorded for each character on individual plants. Absolute range and standardized range were calculated by using the following formula.

Absolute range (R) = (Max-Min).

$$\text{Standardized range (SR)} = \frac{\text{Max} - \text{Min}}{\text{Mean}}$$

Estimation of genetic parameters

The genetic parameters such as genotypic variance and phenotypic variance were estimated to assess and quantify the genetic variability for the traits among the F_3 progenies.

$$\text{Genotypic variance } \left(\sigma^2{}_g\right) = \frac{\text{MSS due to Progenies } - \text{ MSS due to error}}{\text{Number of blocks}}$$

$$\text{Phenotypic variance } \left(\sigma^2{}_p\right) = \sigma^2{}_g + \text{ MSS due to error}$$

Coefficient of variation

$$\text{Coefficient of variation (CV \%)} = \frac{\sigma_p}{\overline{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviation

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

Burton and De Vane (1953) suggested the formula for estimation of both Phenotypic and Genotypic coefficient of variation for all the characters using the components namely, phenotypic, genotypic and environmental variances.

Phenotypic coefficient of variation (PCV)

$$\mathrm{PCV}\ (\%) = \frac{\sigma_P}{\overline{\overline{X}}} \times 100$$

Genotypic coefficient of variation (GCV)

$$\mathrm{GCV}\ (\%) = \frac{\sigma_g}{\overline{\overline{X}}} \times 100$$

Where,

$\overline{\overline{X}}$ = General mean of the trait

σ_p = Phenotypic standard deviation

σ_g = Genotypic standard deviation

As proposed by Sivasubramanian and Menon (1973), the PCV and GCV were classified as;

Low	:	0 – 10%
Moderate	:	10.1 – 20%
High	:	>20%

Heritability (broad sense)

Heritability in broad sense for all the characters was taken as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Lush, 1945).

$$\mathrm{h}^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

h^2 = Heritability (broad sense)

σ^2_g= Genotypic variance

σ^2_p= Phenotypic variance

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

Low : 0-30%
Moderate : 30-60%
High : 60% and above

Expected Genetic Advance (eGA)

Expected genetic advance was estimated as suggested by Johnson *et. al.* (1955).

$$GA = h^2 \times K \times \sigma_P$$

Where,

h^2 = Heritability
σ_P = Phenotypic standard deviation
K = Standardized selection differential at given intensity and it is 2.06 at 5 *per cent* intensity of selection.

Expected Genetic advance as *per cent* of mean (eGAM)

Expected Genetic advance as *per cent* of mean was estimated using the following formula;

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

Where,

GA = Genetic advance
$\overline{X}$ = General mean

Genetic advance as *per cent* of mean is classified as; (Johnson *et al*. 1955)

Low : 0 - 10%
Moderate : 10.1 – 20%
High : >20%

Criteria to assess breeding potential of crosses

The quantitative trait means values, phenotypic coefficient of variation, absolute and standardized range (SR) were used as predictors to compare the four crosses and predict the breeding potential of crosses. The crosses with high quantitative trait mean, range and PCV were considered to have better breeding potential to result in high frequency of desirable recombinant inbred lines (RIL) in advanced generations.

Estimation of correlation coefficient

In F_3 progenies, simple correlation coefficients were calculated to determine the direction and magnitude of associations among different characters and tested against table 'r' values (Fisher and Yates, 1963) for (n-2) degrees of freedom both at 0.05 and 0.01 probability levels for their significance. Simple correlations were calculated by using the formula as given by Weber and Murthy (1952).

$$r = Cov_{xy} / \sigma_x . \sigma_y$$

where,

Cov_{xy} = Covariance between the quantitative traits 'x' and 'y'

σ_x= Standard deviation of the trait 'x';

σ_y= Standard deviation of the trait 'y'

Phenotypic correlation coefficient was estimated in F_3 generation by following the formula given by Sundararaj *et al.* (1972).

$$\text{rp (x, y)} = \frac{Px.Py}{\sqrt{\text{Vpx . Vpy}}} \text{Where,}$$

P_xP_y = Phenotypic covariance of x and y

Vp_x = Phenotypic variance of x

Vp_y = Phenotypic variance of y

r_p (x,y) = Phenotypic correlation of x and y

Significance of correlation coefficients was tested at (n-2) degrees of freedom using 't' table from Fisher and Yates (1963) at 5 *per cent* and 1 *per cent* probability level.

IV RESULTS AND DISCUSSION

The results pertaining to assessment of breeding potential, analysis of variances (ANOVA) and genetic parameters are presented under the following headings;

4.1 Analysis of variance

4.2 Genetic variability in F_2 population

4.3 Breeding potential of the four crosses

4.4 Correlation analysis in F_3 generation

4.5 Identification of best plants in F_3 population derived from four different crosses

4.1 Analysis of variance

The analysis of variance of F_3 progenies of four crosses is presented in table 4. The analysis of variance revealed significant mean sum of squares attributable to blocks, ‘entries (F_3 progenies + checks), ‘F_3 progenies’ for all the traits studied, ‘checks’ were significant to all trait studied except number of branches plant^{-1} and ‘checks vs F_3’ indicated significant mean sum of squares for all traits except days to 50% flowering (Table 4).

Table 4: Analysis of variance of F_3 progenies derived from four crosses for quantitative traits in cowpea

Source of variation	Degrees of freedom	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Leaves plant^{-1}	Green fodder yield plant^{-1} (g)
Block	42	5.592**	49.959**	1.383**	81.705**	20205.100**
Entries (F_3 progenies + checks)	602	5.824**	47.754**	0.709**	39.744**	6322.960**
F_3 progenies	599	6.191**	50.542**	0.790**	44.434**	7608.901**
Checks	2	6.519**	23.879**	0.003	26.984*	2416.705*
Checks vs F_3 progenies	1	0.001	399.888**	0.763*	94.127**	53009.490**
Error	84	0.537	2.912	0.144	6.558	560.307
Total	1330	24.664	574.934	3.792	293.552	90123.463

* Significant @P=0.05 ** Significant @P=0.01

4.2 Genetic variability in F_2 population

4.2.1 Mean performance and range of variability

The mean performance with standard error of four F_2 populations for four characters studied is presented in table 5 and range of variability is presented in table 6a and 6b.

The quantitative trait mean for days to first flowering was ranged from 50.21 days to 53.21 days and variation for days to first flowering observed was ranged from 49 days to 59 days after sowing. The range mean value of the plant height was observed from 36.41cm to 38.07cm. The range for plant height was noticed from 14cm to 56cm. The phenotypic range of the trait branches plant^{-1} was recorded from 4 to 9 and the mean value across the crosses was observed from 6.34 lowest to 6.53 highest value. The wide phenotypic range for leaves plant-^{1} was observed from 12 to 44. The mean value of leaves plant^{-1} recorded was ranged from 24.42 to 27.79 (Table 5, 6a and 6b).

The similar results were obtained by Malarvizhi *et al.* (2005), Sivakumar *et al.* (2013), Shanko *et al.* (2014), Khan *et al.* (2015), Sanjeev *et al.* (2016) and Jogdhande *et al.* (2017).

Table 5: Estimates of means of four quantitative traits in F_2 generation of the four crosses of cowpea

Characters	EC394839 × KBC-5	EC4722 × KBC-5	Pant Lobia × Arka Garima	APC-1218 × RI-60
Days to first flowering	52.62 ± 0.16	51.33 ± 0.12	50.21 ± 0.06	53.21 ± 0.19
Plant height (cm)	37.96 ± 0.62	36.41 ± 0.62	38.07 ± 0.65	37.80 ± 0.56
Branches plant^{-1}	6.53 ± 0.07	6.42 ± 0.07	6.34 ± 0.08	6.40 ± 0.06
Leaves plant^{-1}	27.79 ± 0.46	24.42 ± 0.48	25.87 ± 0.47	24.62 ± 0.46

Table 6a: Estimates of absolute and standardized range (SR) of quantitative traits in F_2 generations derived from crosses of forage cowpea

Characters	EC394839 × KBC-5				EC4722 × KBC-5			
	Lowest	Highest	Range	SR	Lowest	Highest	Range	SR
Days to first flowering	50	58	8.00	0.15	49	58	9.00	0.18
Plant height (cm)	17	56	39.00	1.03	16	54	38.00	1.04
Branches plant^{-1}	4	8	4.00	0.61	4	8	4.00	0.62
Leaves plant^{-1}	14	42	28.00	1.01	12	44	32.00	1.31

Table 6b: Estimates of absolute and standardized range (SR) of quantitative traits in F_2 generations derived from crosses of forage cowpea

Characters	Pant Lobia ×Arka Garima				APC-1218 × RI-60			
	Lowest	Highest	Range	SR	Lowest	Highest	Range	SR
Days to first flowering	49	54	5.00	0.10	49	59	10.00	0.19
Plant height (cm)	14	53	39.00	1.02	19	53	34.00	0.90
Branches plant^{-1}	4	9	5.00	0.79	4	8	4.00	0.63
Leaves plant^{-1}	14	44	30.00	1.16	13	44	31.00	1.26

4.2.2 Genotypic and phenotypic coefficient of variation

The estimates of the genotypic and phenotypic coefficient of variation are given as under:

In actual, the phenotypic coefficient of variation was observed higher in magnitude than genotypic coefficient of variation as most of the quantitative traits are polygenic in nature and environment plays important role in expression of phenotype.

Phenotypic and genotypic coefficient of variation for the trait days to first flowering was observed lowest across all the four crosses in F_2 population. For the trait branches plant^{-1} moderate phenotypic and genotypic coefficient of variation was observed among all the four crosses. Plant height and leaves plant^{-1} exhibited high estimates of phenotypic and genotypic coefficient of variation in all the crosses of F_2 population. The results revealed that high magnitude of phenotypic and genotypic coefficient of variation for most of the traits indicates there is great potential for selection in further segregating generations. These results are in confirmation with Borah and Fazlullahkhan (2000), Manonmani *et al.* (2000), Verma and Mishra (2005), Malarvizhi *et al.* (2005), Singh *et al.* (2010), Kohli (2012), Sivakumar *et al.* (2013), Ajayi *et al.* (2014), Anamika *et al.* (2014), Shanko *et al.* (2014), Khan *et al.* (2015), Sanjeev *et al.* (2016), Sarath and Reshma (2017), Dinesh *et al.* (2017), Jogdhande *et al.* (2017), Sahu (2019) and Meenatchi *et al.* (2019) (Table 7a and 7b).

4.2.3 Heritability and genetic advance as *per cent* of mean

The character days to first flowering exhibited high heritability in all the crosses except the cross Pant Lobia × Arka Garima as in this cross the less variability observed for days to first flowering than other crosses. The genetic advance as *per cent* of mean was lower in all the crosses for days to first flowering as it exhibited low genetic variability. All the other traits such as plant height, branches plant^{-1} and leaves plant^{-1} exhibited high heritability coupled with high genetic advance as *per cent* of mean across the all four crosses in F_2 population. The result indicates effectiveness of selection for any character will be high from one generation to next generation (Table 7a and 7b).

Table 7a: Estimates of genetic variability parameters of quantitative traits in F_2 generation derived from crosses of cowpea

Characters	EC394839 × KBC-5				EC4722 × KBC-5			
	PCV	GCV	Heritability (BS)	GAM	PCV	GCV	Heritability (BS)	GAM
Days to first flowering	4.60	4.49	95.71	9.07	3.52	3.36	92.25	6.68
Plant height (cm)	24.68	24.12	95.94	48.77	24.68	24.45	98.19	49.93
Branches plant^{-1}	17.22	16.84	96.03	34.07	14.69	13.89	89.48	27.33
Leaves plant^{-1}	25.13	24.68	96.89	50.15	28.16	28.02	98.99	57.42

Table 7b: Estimates of genetic variability parameters of quantitative traits in F_2 generation derived from crosses of cowpea

Characters	Pant Lobia ×Arka Garima				APC-1218 × RI-60			
	PCV	GCV	Heritability (BS)	GAM	PCV	GCV	Heritability (BS)	GAM
Days to first flowering	1.69	1.23	53.41	1.86	5.00	4.87	95.27	9.82
Plant height (cm)	24.09	23.62	96.65	47.96	21.12	21.03	99.62	43.35
Branches plant^{-1}	17.39	16.96	95.59	34.24	13.27	13.05	97.21	26.57
Leaves plant^{-1}	25.52	24.94	95.98	50.47	26.36	26.21	99.40	53.97

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

GAM = Genetic advance as *per cent* of mean

These results are in agreement with Borah and Fazlullahkhan (2000), Kumar and Sangwan (2000), Malarvizhi *et al.* (2005), Bhandari and Verma (2008), Kohli (2012), Sivakumar *et al.* (2013), Ajayi *et al.* (2014), Anamika *et al.* (2014), Olayiwola *et al.* (2014), Shanko *et al.* (2014), Khan *et al.* (2015), Sanjeev *et al.* (2016), Dinesh *et al.* (2017) and Meenatchi *et al.* (2019).

4.3 Breeding potential of the four crosses

The quantitative trait mean values, phenotypic coefficient of variation, absolute and standardized range (SR) were used as predictors to compare the four crosses and predict the breeding potential of crosses.

4.3.1 Comparison of quantitative trait mean of the four crosses

In F_2 generation the highest value of mean for days to first flowering was observed in the cross APC-1218 × RI-60. The cross Pant Lobia × Arka Garima recorded lowest value of mean among the crosses for days to first flowering and branches plant^{-1} whereas highest mean value for plant height. The highest value of mean for number of branches plant^{-1} and leaves plant^{-1} was observed in the cross EC394839 × KBC-5. The cross EC4722 × KBC-5 exhibited lowest value of mean for the quantitative trait for plant height and number of leaves plant^{-1} (Table 5).

In general, the highest mean performance for all quantitative traits was observed in the cross EC394839 × KBC-5 and Pant Lobia × Arka Garima indicating these crosses have better breeding potential. In F_3 generation the quantitative trait mean value for all the traits was higher than F_2 generation (Table 5 and 8).

Krishnappa *et al.* (2009) in finger millet, Suresh *et al.* (2017) in dolichos bean and Shweta (2018) have also identified promising crosses among a large number of crosses utilizing quantitative trait mean values, which are expected to recover superior pure-lines in advanced generations.

4.3.2 The comparison of phenotypic coefficient of variation (PCV) of all the four crosses

The estimates of phenotypic coefficient of variation was maximum for the trait days to first flowering in the cross APC-1218 × RI-60. Maximum phenotypic coefficient of variation for the plant height was observed in EC394839 × KBC-5 and EC4722 × KBC-5. The highest phenotypic coefficient of variation for the branches plant^{-1} was found in the cross Pant Lobia × Arka Garima. The EC4722 × KBC-5 showed greater phenotypic coefficient of variation for leaves plant^{-1} (Table 7a and 7b).

High magnitude of phenotypic coefficient of variation for all the traits was recorded in the cross EC394839 × KBC-5 followed by EC4722 × KBC-5 in F_2 generation. These results depicted that there is scope for selection in the segregating generations of these crosses and the same can be inferred as these two crosses have better breeding potential. The phenotypic coefficient of variation in F_3 generation has shown decreasing trend than F_2 generation for all the traits (Table 7a,7b and 8).

The similar results for breeding potential of crosses were also predicted based on phenotypic coefficient of variation by Krishnappa *et al.* (2009) in finger millet and Suresh *et al.* (2017) in dolichos bean and Shweta (2018) in cowpea.

Table 8: Estimates of descriptive statistics and genetic variability parameters of quantitative traits of four crosses in F_3 generation

Characters	Mean± SE	Lowest	Highest	Range	Std. Range	PCV	GCV	$h^2_{(BS)}$	GAM
Days to 50% flowering	74.58 ± 0.10	69.41	81.58	12.17	0.16	3.14	2.98	90.18	5.83
Plant height (cm)	43.74 ± 0.29	21.00	59.13	38.13	0.87	15.25	14.74	93.46	29.36
Branches plant^{-1}	6.98 ± 0.04	4.03	9.10	5.07	0.73	12.05	10.76	79.70	19.78
Leaves plant^{-1}	29.51 ± 0.27	13.44	46.64	33.20	1.13	21.33	19.49	83.45	36.67
Green fodder yield plant^{-1} (g)	229.84 ± 3.56	27.73	536.16	508.43	2.21	35.65	34.13	91.66	67.32

4.3.3 The comparison of absolute and standardized range

The absolute and standardized ranges for four quantitative traits in F_2 generation of four crosses were computed and indicated in table 6a and 6b. The absolute and standardized range as well as upper limit for the days to first flowering was higher in the cross APC-1218 × RI-60 while for branches plant^{-1} it was higher in Pant Lobia × Arka Garima. For plant height highest standardized range reported in EC4722 × KBC-5 population while the absolute range and highest value for the plant height was reported in EC394839 × KBC-5 population. The absolute and standardized range was observed highest in EC4722 × KBC-5 cross for leaves plant^{-1}. The absolute range for leaves plant^{-1} was observed higher in all the crosses except EC394839 × KBC-5. The higher estimates of upper limits of absolute range for most of the yield attributing traits in F_2 generation was found in all the crosses except Pant Lobia × Arka Garima, suggested the presence of desirable extreme phenotypes in three crosses. The higher *per se* estimates of standardised range and absolute range in F_2 generation of Pant Lobia × Arka Garima followed by EC4722 × KBC-5, suggested better breeding potential in terms of recovery of desirable extreme genotypes (RILs) in advanced generations for crosses Pant Lobia × Arka Garima and EC4722 × KBC-5. There is a general decrease in value of absolute and standardized range in F_3 generation for most of the traits (Table 6a, 6b and 8).

Krishnappa *et al.* (2009), Suresh *et al.* (2017) and Shweta (2018) also predicted the breeding potential of crosses based on absolute and standardized range in finger millet, dolichos bean and cowpea respectively.

4.3.4 Comparison of broad sense heritability and expected genetic advance as *per cent* mean (GAM) in four crosses

Altogether, all traits in F_2 generation of EC394839 × KBC-5 followed by cross APC-1218 × RI-60 showed moderate to high broad sense heritability and moderate to high genetic advance as *per cent* of mean. It can be inferred as the phenotypic performance of these crosses in F_2 generation was basically due to higher contribution of its genotype and is less influenced by environment and genotype by environment interaction effects. In other words, the phenotype of the individuals is predominantly due to the genotypic constitution of the individual itself. Hence selection would be effective in this population as the variability is predominantly governed by the genetic constitution of the genotypes. Similarly in F_3 high heritability and moderate to high genetic advance as *per cent* of mean reported for all the character studied except days to 50% flowering which have shown low genetic advance as *per cent* of mean (Table 7a, 7b and 8).

Thus by comparing all three predictors such as, quantitative trait means, absolute and standardised range, phenotypic coefficient of variation in terms of their magnitude, it can be suggested that cross EC394839 × KBC-5 is predicted to have better breeding potential in terms of recovery of desirable RILs in advanced generations followed by Pant Lobia × Arka Garima, from among the four crosses studied. High broad sense heritability, coupled with moderate to high genetic advance as *per cent* of mean for these crosses, supports the above statement.

4.4 Correlation analysis in F_3 generation

Correlation studies were conducted at the phenotypic level to establish the degree and significance of the relationship between yield and its attributes. The correlation coefficients were worked out among five quantitative traits under study in F_3 generation at phenotypic levels. The result of correlation coefficient between different pairs of characters is presented as under:

Green fodder yield plant^{-1} indicated significant positive relationship with leaves plant (0.869), plant height (0.798), branches plant^{-1} (0.659) and days to 50% flowering (0.102) indicating importance of these traits in enhancing fodder yield and indirect selection of these traits will help in improving the green fodder yield of plants in further segregating generation (Table 9). This result is in confirmation with findings of Manonmani *et al.* (2000), Sheela Maryand and Gopalan (2006), Bhandari and Verma (2007), Mittal *et al.* (2009), Sahai *et al.* (2013), Gitanjali *et al.* (2013), Anamika and Tajane (2014) and Navaselvakkumaran *et al.* (2019).

Table 9: Estimates of phenotypic correlation coefficients for green fodder yield and its component traits in F_3 generation

Characters	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Leaves plant^{-1}	Green fodder yield plant^{-1} (g)
Days to 50% flowering	1.00				
Plant height (cm)	0.129**	1.00			
Branches plant^{-1}	0.028	0.449**	1.00		
Leaves plant^{-1}	0.050	0.701**	0.754**	1.00	
Green fodder yield plant^{-1} (g)	0.102*	0.798**	0.659**	0.869**	1.00

* Significant @P=0.05 ** Significant @P=0.01

4.5 Identification of best plants in F_3 population derived from four different crosses

Forty two F_3 lines in the cross of EC394839 × KBC-5, 38 lines in EC4722 × KBC-5, 51 lines in Pant Lobia × Arka Garima and 39 lines in APC-1218 × RI-60 were identified to be surpassing the checks with respect to earliness and green fodder yield plant^{-1} and most other yield attributing traits out of which top ten F_3 lines which were identified to be superior to all the checks are depicted in tables 10, 11, 12 and 13. The results suggests that these F_3 plants could be selected and forwarded to next generations. Their performance can be evaluated and confirmed in the further generations.

Table 10: Top ten F_3 progenies assessed by their adjusted means for green fodder yield plant^{-1} (g) along with its component traits in cross EC394839 × KBC-5

F_3 progenies	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Leaves plant^{-1}	Green fodder yield plant^{-1} (g)
EC3K5-216-146	72.41	54.27	7.90	46.64	477.73
EC3K5-56-34	73.08	52.87	7.63	38.67	407.86
EC3K5-188-136	71.58	51.20	8.93	41.90	384.66
EC3K5-149-100	74.08	50.90	8.60	42.17	368.59
EC3K5-206-143	72.41	53.67	8.30	37.64	364.93
EC3K5-66-38	74.08	48.27	8.03	41.67	341.46
EC3K5-5-5	71.24	44.60	7.27	35.64	341.38
EC3K5-220-150	73.41	54.07	7.90	37.24	333.53
EC3K5-38-23	70.91	49.43	6.77	34.60	318.79
EC3K5-217-147	73.41	51.87	7.50	32.04	316.33
Checks					
MFC-08-14	74.13	41.10	6.91	27.66	199.21
MFC-09-1	74.80	41.70	6.90	28.96	209.44
KBC-2	74.80	42.59	6.89	29.09	213.82
SE ±	0.16	0.37	0.08	0.55	5.11
CD @ 5%	0.31	0.73	0.16	1.10	10.15

Table 11: Top ten F_3 progenies assessed by their adjusted means for green fodder yield plant^{-1} (g) with its component traits in cross EC4722 × KBC-5

F_3 progenies	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Leaves plant^{-1}	Green fodder yield plant^{-1} (g)
EC4K5-7-153	69.41	45.07	8.90	46.64	479.33
EC4K5-121-239	71.41	55.47	9.10	44.04	421.53
EC4K5-24-157	70.58	54.00	8.50	40.94	411.96
EC4K5-25-158	74.08	50.60	8.33	39.07	384.26
EC4K5-26-159	72.08	50.80	8.33	35.47	363.26
EC4K5-71-192	72.58	51.33	7.80	34.70	336.49
EC4K5-31-160	74.08	49.80	8.33	36.07	330.26
EC4K5-40-166	71.08	44.13	8.43	43.87	328.56
EC4K5-53-176	72.41	46.37	7.87	37.20	325.99
EC4K5-54-177	71.41	54.97	7.07	29.20	298.79
Checks					
MFC-08-14	74.13	41.10	6.91	27.66	199.21
MFC-09-1	74.80	41.70	6.90	28.96	209.44
KBC-2	74.80	42.59	6.89	29.09	213.82
SE ±	0.16	0.37	0.08	0.55	5.11
CD @ 5%	0.31	0.73	0.16	1.10	10.15

Table 12: Top ten F_3 progenies assessed by their adjusted means for green fodder yield plant^{-1} (g) with its component traits in cross Pant Lobia ×Arka Garima

F_3 progenies	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Leaves plant^{-1}	Green fodder yield plant^{-1} (g)
PLAG-7-301	74.08	55.60	8.80	42.27	490.59
PLAG-9-303	70.74	51.87	7.70	37.30	414.16
PLAG-13-306	73.74	52.67	7.90	35.50	413.16
PLAG-177-449	72.08	47.00	8.90	41.84	407.23
PLAG-167-443	71.08	50.00	7.00	34.07	395.79
PLAG-28-313	73.74	53.07	8.03	40.04	378.89
PLAG-31-316	71.24	48.87	8.23	36.84	372.53
PLAG-34-319	71.24	54.87	8.43	33.04	365.13
PLAG-36-321	73.91	51.50	6.90	33.20	358.83
PLAG-37-322	73.91	46.90	8.43	36.57	346.16
Checks					
MFC-08-14	74.13	41.10	6.91	27.66	199.21
MFC-09-1	74.80	41.70	6.90	28.96	209.44
KBC-2	74.80	42.59	6.89	29.09	213.82
SE ±	0.16	0.37	0.08	0.55	5.11
CD @ 5%	0.31	0.73	0.16	1.10	10.15

Table 13: Top ten F_3 progenies assessed by their adjusted means for green fodder yield plant^{-1} (g) along with its component traits in cross APC-1218 × RI-60

F_3 progenies	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Leaves plant^{-1}	Green fodder yield plant^{-1} (g)
APCRI-88-517	72.74	52.43	7.73	38.64	466.86
APCRI-79-508	72.74	49.63	8.33	35.84	432.66
APCRI-106-535	70.58	52.37	8.13	34.30	369.76
APCRI-100-529	71.41	47.17	7.20	34.50	366.59
APCRI-55-490	71.24	46.57	7.13	37.64	317.93
APCRI-165-577	72.24	51.40	8.37	38.80	310.76
APCRI-129-557	70.91	49.97	8.60	14.57	299.99
APCRI-38-477	71.24	53.97	7.13	38.64	299.73
APCRI-18-461	73.74	47.57	7.77	32.94	286.53
APCRI-21-463	73.24	45.17	8.07	36.97	283.46
Checks					
MFC-08-14	74.13	41.10	6.91	27.66	199.21
MFC-09-1	74.80	41.70	6.90	28.96	209.44
KBC-2	74.80	42.59	6.89	29.09	213.82
SE ±	0.16	0.37	0.08	0.55	5.11
CD @ 5%	0.31	0.73	0.16	1.10	10.15

V SUMMARY

Preamble: Cowpea is predominantly a self-pollinated crop, the best option for varietal improvement is hybridization followed by selection in segregating generations. Plant Breeder carries out a large number of crosses to combine useful traits distributed in a large number of parents and therefore has to deal with the problem of handling large segregating populations with the lacunae of time, land and human resources. Therefore, evaluating the breeding potential of crosses in the early segregating generations along with the use of easily assayable morphometric traits that are substantially correlated with yield to indirectly select for yield can solve such lacunae.

Objectives: (1) To asses genetic variability for traits related to fodder yield in F_2 population; (2) To assess the breeding potential of four crosses and (3) To identify traits associated with fodder yield in F_3 generation.

Material and methods: The material used in the experiment were F_2 and F_3 generations derived from the four crosses viz., EC394839 × KBC-5, Pant Lobia × Arka Garima, EC4722 × KBC-5 and APC-1218 × RI-60. The experimental material was evaluated with checks MFC-08-14, MFC-09-1 and KBC-2 for yield and yield attributing quantitative traits at Main Zonal Agricultural Research Station (ZARS) and at K block, Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bengaluru during late *kharif*-2019 and *rabi*, 2019-20 respectively.

Sampling and data collection: Data was recorded on all the F_2 plants for four quantitative traits and on five randomly selected plants from each F_3 progenies of each cross and checks for five quantitative traits.

Statistical Analysis: The adjusted quantitative trait values of F_3 progeny plants and individual F_2 plants were used for computing descriptive statistics such as mean, absolute and standardized range. Phenotypic coefficient of variation, genotypic coefficient of variation, heritability (broad sense) and expected genetic advance as *per cent* of mean (GAM) for days to first flowering in F_2 generation, days to 50% flowering and green fodder yield (g) in F_3 generation, plant height, primary branches plant^{-1}, and leaves plant^{-1} in both the generations were estimated. Correlation coefficient was estimated in F_3 generation.

Criteria to assess breeding potential of the crosses: The quantitative trait means, standardized range, phenotypic coefficient of variation and supplemented with broad sense heritability and genetic advance as *per cent* of mean were used as criteria to assess the breeding potential of the crosses. The crosses with high quantitative trait mean, absolute and standardized range and phenotypic coefficient of variation were considered to have better breeding potential.

The salient features of experimental findings summarized as follows

- The extent of variability was substantially higher in F_2 generation for the characters for plant height, branches plant^{-1} and leaves plant^{-1} and low variability for days to first flowering in all the four crosses.

- All the crosses in F_2 generation reported higher estimates of phenotypic and genotypic coefficient of variation for characters plant height and leaves plant^{-1} while it was moderate for branches plant^{-1} and low for days to first flowering. Higher broad sense heritability with high genetic advance as *per cent* of mean reported for characters plant height, branches plant^{-1} and leaves plant^{-1}. Moderate to high broad sense heritability with low genetic advance observed for days to first flowering in all the crosses.

- Highly significant mean sum of squares indicated substantial variability not only among the F_3 progenies but also their significant differences with check varieties for most of the quantitative traits as indicated by ANOVA which is a diagnostic tool for detection of variability.

- There is an increasing trend in quantitative trait mean value and reduction in the variability parameters for most of the traits in F_3 generation as compared to F_2 generation.

- The estimates for genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance as *per cent* of mean were higher for green fodder yield plant^{-1}. Moderate to high genotypic and phenotypic coefficient of variation and moderate to high genetic advance as *per cent* of mean with high broad sense heritability reported for plant height, branches plant^{-1} and leaves plant^{-1} whereas it was low for days to 50% flowering with high broad sense heritability in F_3 generation.

- Narrow difference between phenotypic coefficient of variation and genotypic coefficient of variation observed for most of the traits in both F_2 and F_3 generation. Hence, there is an ample scope for improvement of these traits.

- Top ten F_3 progenies were identified from each of the four crosses that were superior to all three checks in terms of earliness and green fodder yield plant^{-1}.

- The comparison of quantitative trait mean, phenotypic coefficient of variation, absolute and standardized range revealed that the cross EC394839 × KBC-5 is predicted to have better breeding potential in terms of recovery of desirable RILs in advanced generations followed by Pant Lobia × Arka Garima, from among the four crosses studied.

- The highly significant and positive phenotypic correlation for green fodder yield plant^{-1} was observed with leaves plant^{-1} followed by plant height, branches plant^{-1} and days to 50% flowering. Hence selection for these traits helps for indirect selection of green fodder yield plant^{-1}.

Future line of work:

- Top ten F_3 progenies such as EC3K5-216-146, EC3K5-56-34, EC3K5-188-136, EC3K5-149-100, EC3K5-206-143, EC3K5-66-38, EC3K5-5-5, EC3K5-220-150, EC3K5-38-23, EC3K5-217-147 from EC394839 × KBC-5 cross, EC4K5-7-153, EC4K5-121-239, EC4K5-24-157, EC4K5-25-158, EC4K5-26-159, EC4K5-71-192, EC4K5-31-160, EC4K5-40-166, EC4K5-53-176, EC4K5-54-177 from EC4722 × KBC-5 cross, PLAG-7-301, PLAG-9-303, PLAG-13-306, PLAG-177-449, PLAG-167-443, PLAG-28-313, PLAG-31-316, PLAG-34-319, PLAG-36-321, PLAG-37-322 from Pant Lobia ×Arka Garima cross, APCRI-88-517, APCRI-79-508, APCRI-106-535, APCRI-100-529, APCRI-55-490, APCRI-165-577, APCRI-129-557, APCRI-38-477, APCRI-18-461, APCRI-21-463 from APC-1218 × RI-60 are suggested to be forwarded to future generations, either to obtain superior purelines for release as a variety if considered better than tests or to recover superior recombinant inbred lines for use as parents in more breeding programmes.

- The traits such as leaves plant^{-1}, plant height and branches plant^{-1} could be used as surrogates to assist in indirect selection for green fodder yield plant^{-1} in segregating populations.
- Quality test to be performed in advance generations for better nutritional composition and bioavailability of fodder to be examined for animal nutrition.

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Appendix 1: Estimates of five quantitative trait means of 150 F_3 progenies derived from EC394839 × KBC-5 of forage cowpea

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
1	EC3K5-1-1	73.24	42.40	5.67	27.24	176.18
2	EC3K5-2-2	75.24	46.60	5.87	30.64	224.78
3	EC3K5-3-3	72.24	49.00	5.87	30.84	265.58
4	EC3K5-4-4	74.24	52.20	7.67	35.64	357.38
5	EC3K5-5-5	71.24	44.60	7.27	35.64	341.38
6	EC3K5-6-6	71.24	43.40	8.47	27.64	221.38
7	EC3K5-10-7	73.24	40.80	5.27	22.64	145.18
8	EC3K5-12-8	73.24	35.60	4.67	14.44	82.98
9	EC3K5-13-9	74.24	37.40	7.07	24.04	165.98
10	EC3K5-14-10	75.24	54.20	7.27	26.24	254.78
11	EC3K5-15-11	73.24	43.00	7.27	25.44	214.58
12	EC3K5-16-12	73.24	29.80	6.27	22.44	91.18
13	EC3K5-17-13	75.24	54.40	6.67	27.24	267.98
14	EC3K5-18-14	81.24	44.40	7.47	28.04	230.58
15	EC3K5-21-15	73.91	50.63	4.77	30.20	230.19
16	EC3K5-22-16	72.91	21.83	5.17	18.80	79.79
17	EC3K5-27-17	72.91	23.83	5.77	17.40	68.79
18	EC3K5-28-18	72.91	24.03	5.37	18.20	71.79
19	EC3K5-34-19	73.91	42.43	5.97	23.60	182.99
20	EC3K5-35-20	71.91	47.83	7.37	30.00	218.79
21	EC3K5-36-21	74.91	40.83	6.77	24.60	173.79
22	EC3K5-37-22	74.91	51.83	5.37	21.20	220.19
23	EC3K5-38-23	70.91	49.43	6.77	34.60	318.79
24	EC3K5-42-24	76.91	42.43	5.97	25.40	177.19
25	EC3K5-44-25	76.91	51.43	7.57	39.80	392.59
26	EC3K5-45-26	70.91	46.43	6.77	26.60	200.59
27	EC3K5-46-27	74.91	33.63	5.57	20.40	119.59
28	EC3K5-47-28	73.91	56.63	6.77	27.00	259.39
29	EC3K5-48-29	77.08	53.27	7.43	34.07	280.06
30	EC3K5-49-30	80.08	43.27	9.03	36.07	253.46
31	EC3K5-53-31	74.08	51.67	7.63	36.67	267.86
32	EC3K5-54-32	71.08	27.07	6.63	18.87	76.06
33	EC3K5-55-33	74.08	43.27	7.43	33.87	217.26
34	EC3K5-56-34	73.08	52.87	7.63	38.67	407.86
35	EC3K5-57-35	78.08	37.67	7.63	33.07	174.46
36	EC3K5-58-36	71.08	43.67	8.23	36.67	262.06

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
37	EC3K5-65-37	72.08	42.67	8.03	36.47	261.86
38	EC3K5-66-38	74.08	48.27	8.03	41.67	341.46
39	EC3K5-67-39	77.08	43.47	7.63	29.87	216.26
40	EC3K5-68-40	78.08	43.87	7.23	33.47	234.26
41	EC3K5-69-41	72.08	38.27	6.63	25.67	197.06
42	EC3K5-73-42	76.08	31.47	6.83	25.07	129.46
43	EC3K5-74-43	72.08	26.93	5.87	16.37	78.09
44	EC3K5-75-44	72.08	36.33	6.47	23.97	139.49
45	EC3K5-76-45	71.08	46.33	7.47	29.17	211.09
46	EC3K5-77-46	80.08	47.33	6.47	27.17	264.69
47	EC3K5-78-47	72.08	35.53	6.47	21.17	113.29
48	EC3K5-79-48	71.08	43.73	6.67	28.37	222.29
49	EC3K5-80-49	74.08	35.93	7.67	29.57	196.29
50	EC3K5-81-50	72.08	36.13	5.47	15.37	82.09
51	EC3K5-82-51	77.08	27.53	7.07	17.57	77.09
52	EC3K5-83-52	71.08	53.13	6.67	28.77	248.89
53	EC3K5-84-53	72.08	46.73	7.67	35.77	264.09
54	EC3K5-85-54	77.08	50.33	7.47	31.77	257.29
55	EC3K5-86-55	81.08	59.13	7.47	37.57	290.89
56	EC3K5-87-56	72.08	24.53	6.27	21.57	118.29
57	EC3K5-91-57	77.91	46.27	6.50	28.84	224.99
58	EC3K5-92-58	70.91	41.07	7.10	27.84	176.59
59	EC3K5-93-59	73.91	39.27	6.70	26.44	165.99
60	EC3K5-94-60	80.91	44.67	7.50	30.84	244.59
61	EC3K5-97-61	73.91	47.67	6.50	33.44	242.99
62	EC3K5-98-62	70.91	47.27	7.50	33.64	243.39
63	EC3K5-99-63	72.91	48.67	7.10	32.44	174.79
64	EC3K5-101-64	74.91	46.27	6.70	33.04	243.79
65	EC3K5-104-65	72.91	39.67	7.50	28.84	232.79
66	EC3K5-105-66	78.91	41.27	8.90	34.44	232.99
67	EC3K5-106-67	72.91	42.47	7.30	28.04	229.59
68	EC3K5-107-68	75.91	55.27	8.50	46.24	401.59
69	EC3K5-108-69	70.91	50.47	6.70	31.84	219.39
70	EC3K5-112-70	71.91	44.67	8.10	38.24	248.19
71	EC3K5-113-71	75.24	52.53	6.97	34.17	280.59
72	EC3K5-114-72	75.24	55.93	8.77	43.77	305.99
73	EC3K5-115-73	74.24	36.53	7.17	31.57	213.79
74	EC3K5-116-74	73.24	42.13	6.97	30.17	208.59

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
75	EC3K5-117-75	76.24	44.13	5.77	26.97	216.79
76	EC3K5-118-76	76.24	27.53	8.17	27.37	138.79
77	EC3K5-119-77	72.24	47.13	8.77	43.17	311.79
78	EC3K5-120-78	71.24	34.33	7.17	25.57	164.19
79	EC3K5-121-79	75.24	41.53	5.97	26.37	165.99
80	EC3K5-122-80	73.24	52.33	6.17	30.37	215.59
81	EC3K5-123-81	73.24	44.53	6.77	30.37	210.79
82	EC3K5-126-82	77.24	47.93	6.17	27.57	220.79
83	EC3K5-127-83	81.24	53.93	7.37	36.17	342.39
84	EC3K5-128-84	76.24	48.53	7.97	38.57	278.59
85	EC3K5-129-85	74.41	38.83	6.70	29.44	176.43
86	EC3K5-130-86	76.41	29.63	6.30	18.44	55.03
87	EC3K5-131-87	78.41	45.03	6.70	32.64	232.23
88	EC3K5-132-88	73.41	42.83	6.70	26.44	180.23
89	EC3K5-133-89	76.41	43.83	7.10	27.64	209.03
90	EC3K5-134-90	75.41	35.63	6.10	31.24	149.83
91	EC3K5-137-91	77.41	42.03	7.50	25.84	218.63
92	EC3K5-138-92	80.41	40.83	6.70	23.44	183.23
93	EC3K5-139-93	75.41	41.83	7.70	28.24	207.03
94	EC3K5-140-94	79.41	44.23	6.10	16.04	73.83
95	EC3K5-141-95	77.41	42.03	4.10	21.24	103.83
96	EC3K5-142-96	74.41	41.23	5.90	23.84	154.83
97	EC3K5-143-97	74.41	30.63	6.10	21.44	86.23
98	EC3K5-147-98	75.41	44.63	6.30	28.64	185.03
99	EC3K5-148-99	74.08	37.70	5.60	19.77	118.99
100	EC3K5-149-100	74.08	50.90	8.60	42.17	368.59
101	EC3K5-150-101	77.08	51.70	7.20	33.97	299.99
102	EC3K5-151-102	75.08	47.50	6.00	25.77	217.59
103	EC3K5-152-103	78.08	41.70	6.20	24.37	182.39
104	EC3K5-153-104	79.08	46.10	7.60	33.57	261.79
105	EC3K5-154-105	71.08	43.30	7.40	34.17	223.19
106	EC3K5-155-106	74.08	29.30	5.60	19.97	314.19
107	EC3K5-156-107	72.08	42.30	6.80	25.17	211.79
108	EC3K5-157-108	73.08	41.30	8.00	37.97	244.99
109	EC3K5-158-109	77.08	38.90	7.20	34.77	200.59
110	EC3K5-159-110	73.08	41.70	7.40	27.37	182.39
111	EC3K5-160-111	75.08	53.30	7.20	37.77	316.79
112	EC3K5-161-112	73.08	41.70	5.60	22.77	153.79

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
113	EC3K5-162-113	76.24	50.43	5.30	23.17	193.76
114	EC3K5-163-114	75.24	38.23	6.70	24.57	164.56
115	EC3K5-167-115	80.24	51.83	7.70	34.97	281.76
116	EC3K5-168-116	72.24	41.03	5.90	23.37	174.96
117	EC3K5-169-117	74.24	46.03	7.50	32.17	219.56
118	EC3K5-170-118	75.24	42.03	6.90	24.77	195.96
119	EC3K5-171-119	75.24	37.63	7.30	30.97	169.56
120	EC3K5-172-120	71.24	40.03	7.30	28.57	184.36
121	EC3K5-173-121	74.24	45.43	7.70	35.97	267.36
122	EC3K5-174-122	72.24	42.63	6.70	29.57	193.96
123	EC3K5-175-123	75.24	34.03	5.50	21.37	109.76
124	EC3K5-176-124	73.24	52.83	7.70	35.37	283.36
125	EC3K5-177-125	74.24	51.83	6.50	31.17	271.96
126	EC3K5-178-126	78.24	50.43	6.70	35.37	225.16
127	EC3K5-179-127	76.58	36.40	6.13	22.90	131.06
128	EC3K5-180-128	74.58	45.60	6.33	27.90	209.26
129	EC3K5-181-129	70.58	23.80	6.13	19.90	72.06
130	EC3K5-182-130	70.58	49.60	7.33	31.50	260.46
131	EC3K5-183-131	77.58	38.00	5.73	25.30	170.46
132	EC3K5-184-132	73.58	32.40	7.53	18.90	79.86
133	EC3K5-185-133	75.58	36.60	5.53	20.10	98.46
134	EC3K5-186-134	74.58	43.00	6.93	26.70	182.06
135	EC3K5-187-135	70.58	52.80	7.73	37.70	299.66
136	EC3K5-188-136	71.58	51.20	8.93	41.90	384.66
137	EC3K5-189-137	74.58	44.40	8.53	40.50	276.66
138	EC3K5-190-138	72.58	49.60	8.73	41.30	310.66
139	EC3K5-191-139	73.58	50.60	6.73	36.90	278.66
140	EC3K5-203-140	71.58	41.40	6.13	31.50	215.66
141	EC3K5-204-141	69.41	50.67	8.10	38.84	298.73
142	EC3K5-205-142	77.41	45.27	7.50	37.24	249.73
143	EC3K5-206-143	72.41	53.67	8.30	37.64	364.93
144	EC3K5-207-144	78.41	28.07	5.90	24.24	133.93
145	EC3K5-208-145	70.41	42.87	6.70	29.04	196.53
146	EC3K5-216-146	72.41	54.27	7.90	46.64	477.73
147	EC3K5-217-147	73.41	51.87	7.50	32.04	316.33
148	EC3K5-218-148	69.41	46.07	6.70	29.24	278.53
149	EC3K5-219-149	71.41	40.07	6.50	24.24	168.93
150	EC3K5-220-150	73.41	54.07	7.90	37.24	333.53

Appendix 2: Estimates of five quantitative trait means of 150 F_3 progenies derived from EC4722 × KBC-5 of forage cowpea

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
1	EC4K5-1-151	80.41	52.87	7.50	39.84	344.33
2	EC4K5-2-152	69.41	22.47	4.70	13.44	27.73
3	EC4K5-7-153	71.41	55.47	9.10	44.04	421.53
4	EC4K5-16-154	69.41	45.07	8.90	46.64	479.33
5	EC4K5-17-155	80.58	44.20	7.70	33.14	244.96
6	EC4K5-23-156	75.58	34.80	7.50	24.74	164.96
7	EC4K5-24-157	70.58	45.80	7.90	38.14	289.16
8	EC4K5-25-158	70.58	54.00	8.50	40.94	411.96
9	EC4K5-26-159	70.58	55.20	7.70	39.34	259.16
10	EC4K5-31-160	70.58	50.20	7.30	39.94	279.96
11	EC4K5-32-161	71.58	48.20	7.10	32.94	250.36
12	EC4K5-33-162	75.58	42.80	7.30	31.34	211.16
13	EC4K5-34-163	77.58	30.60	6.70	20.14	112.56
14	EC4K5-37-164	77.58	55.60	7.90	41.14	536.16
15	EC4K5-39-165	78.58	55.40	7.10	24.54	278.16
16	EC4K5-40-166	73.58	50.20	5.30	22.14	182.36
17	EC4K5-41-167	70.58	21.80	5.70	14.54	40.56
18	EC4K5-42-168	81.58	49.80	7.90	32.94	270.36
19	EC4K5-43-169	74.08	35.90	6.43	25.30	170.36
20	EC4K5-44-170	74.08	41.10	7.43	30.90	213.56
21	EC4K5-45-171	76.08	45.90	5.03	23.10	187.36
22	EC4K5-46-172	78.08	44.30	6.63	30.70	221.56
23	EC4K5-50-173	74.08	37.50	7.03	27.70	191.76
24	EC4K5-51-174	72.08	45.10	7.83	34.50	254.16
25	EC4K5-52-175	78.08	45.70	7.63	36.50	260.56
26	EC4K5-53-176	71.08	48.50	6.83	33.30	272.36
27	EC4K5-54-177	73.08	50.10	7.43	34.70	287.16
28	EC4K5-55-178	74.08	38.90	7.03	24.90	212.76
29	EC4K5-56-179	74.08	45.10	6.63	28.70	234.96
30	EC4K5-57-180	77.08	47.50	7.03	30.30	269.76
31	EC4K5-58-181	76.08	38.70	7.03	26.10	205.76
32	EC4K5-59-182	78.08	44.90	6.63	27.30	195.16
33	EC4K5-60-183	78.74	47.63	7.23	33.34	280.26
34	EC4K5-61-184	77.74	43.83	6.63	26.14	232.86
35	EC4K5-62-185	70.74	32.63	5.63	14.94	55.06
36	EC4K5-63-186	77.74	43.23	7.23	31.94	234.46

Sl. No.	**F_3 progenies**	**D50%F**	**PHT**	**NB**	**NLVS**	**GFY**
37	EC4K5-64-187	74.74	33.03	5.23	19.34	131.26
38	EC4K5-65-188	73.74	40.43	7.23	32.34	220.86
39	EC4K5-68-189	74.74	56.63	4.03	16.34	151.66
40	EC4K5-69-190	72.74	43.43	7.83	30.54	233.86
41	EC4K5-70-191	71.74	36.63	5.83	23.74	153.46
42	EC4K5-71-192	71.74	38.43	6.83	27.94	186.46
43	EC4K5-72-193	71.74	46.03	6.43	30.34	248.86
44	EC4K5-74-194	73.74	47.43	7.63	32.74	267.86
45	EC4K5-75-195	74.74	42.83	6.23	24.74	204.46
46	EC4K5-76-196	74.74	42.83	6.83	29.94	245.66
47	EC4K5-77-197	77.08	39.80	7.13	26.07	170.46
48	EC4K5-78-198	78.08	35.60	7.13	26.27	156.86
49	EC4K5-79-199	76.08	49.80	6.13	27.47	249.46
50	EC4K5-80-200	74.08	50.60	8.33	39.07	384.26
51	EC4K5-81-201	74.08	42.00	6.53	23.87	198.06
52	EC4K5-82-202	78.08	44.80	6.73	26.07	208.46
53	EC4K5-83-203	77.08	41.80	7.33	31.67	210.46
54	EC4K5-84-204	73.08	47.00	6.53	26.67	234.66
55	EC4K5-85-205	72.08	50.80	8.33	35.47	363.26
56	EC4K5-86-206	75.08	40.40	6.93	26.27	191.26
57	EC4K5-87-207	75.08	44.80	7.33	32.07	225.46
58	EC4K5-88-208	71.08	42.60	6.33	25.67	195.66
59	EC4K5-89-209	75.08	41.20	7.13	29.07	206.86
60	EC4K5-90-210	74.08	46.20	6.73	28.87	240.86
61	EC4K5-91-211	75.74	50.77	7.43	32.60	274.79
62	EC4K5-92-212	71.74	30.77	4.43	14.20	57.59
63	EC4K5-93-213	72.74	29.57	5.63	16.80	94.59
64	EC4K5-94-214	72.74	48.97	5.83	34.60	229.79
65	EC4K5-95-215	75.74	39.57	9.03	41.80	224.59
66	EC4K5-96-216	72.74	38.97	8.23	32.20	210.19
67	EC4K5-97-217	75.74	45.97	9.03	35.40	254.99
68	EC4K5-98-218	76.74	48.57	8.03	25.80	245.79
69	EC4K5-99-219	77.74	50.97	7.83	38.80	309.99
70	EC4K5-100-220	74.74	53.97	9.03	45.60	456.19
71	EC4K5-101-221	73.74	42.17	8.63	38.40	235.99
72	EC4K5-102-222	76.74	46.17	6.83	30.20	236.19
73	EC4K5-103-223	74.74	43.17	5.23	22.00	154.39
74	EC4K5-104-224	73.74	39.17	5.63	26.60	161.99

Sl. No.	**F$_3$ progenies**	**D50%F**	**PHT**	**NB**	**NLVS**	**GFY**
75	EC4K5-105-225	72.41	36.77	6.87	19.60	125.99
76	EC4K5-106-226	74.41	52.77	7.47	33.80	361.99
77	EC4K5-107-227	71.41	54.97	7.07	29.20	298.79
78	EC4K5-108-228	80.41	44.57	5.47	25.80	208.39
79	EC4K5-109-229	74.41	33.77	7.27	27.40	163.39
80	EC4K5-110-230	75.41	41.37	5.07	19.60	154.19
81	EC4K5-111-231	76.41	29.37	5.27	17.60	77.39
82	EC4K5-112-232	76.41	51.37	5.47	26.20	335.39
83	EC4K5-113-233	73.41	52.37	6.27	35.40	284.39
84	EC4K5-114-234	78.41	46.57	7.87	37.00	321.99
85	EC4K5-115-235	77.41	49.57	7.07	32.00	288.79
86	EC4K5-116-236	78.41	49.97	8.07	35.40	334.79
87	EC4K5-119-237	72.41	46.37	7.87	37.20	325.99
88	EC4K5-120-238	74.41	28.57	6.27	19.00	54.19
89	EC4K5-121-239	78.58	51.23	7.57	31.74	315.43
90	EC4K5-122-240	79.58	53.23	7.77	37.54	438.63
91	EC4K5-123-241	76.58	42.63	6.97	32.14	255.43
92	EC4K5-124-242	74.58	51.43	5.97	30.14	270.63
93	EC4K5-125-243	73.58	35.23	4.97	21.54	157.03
94	EC4K5-126-244	74.58	43.03	4.97	23.54	209.43
95	EC4K5-127-245	75.58	43.03	6.97	33.34	301.23
96	EC4K5-128-246	71.58	37.43	5.17	24.14	186.03
97	EC4K5-129-247	79.58	42.83	7.77	34.54	296.43
98	EC4K5-130-248	74.58	40.63	7.17	25.14	198.83
99	EC4K5-131-249	71.58	27.43	5.97	16.94	48.43
100	EC4K5-132-250	74.58	46.03	8.37	35.74	269.63
101	EC4K5-133-251	75.58	48.83	5.97	22.14	231.43
102	EC4K5-134-252	78.58	45.73	5.97	27.74	231.03
103	EC4K5-135-253	76.08	31.53	5.83	27.07	216.56
104	EC4K5-137-254	74.08	36.33	7.03	31.47	214.36
105	EC4K5-138-255	71.08	28.73	5.83	13.47	89.76
106	EC4K5-139-256	72.08	43.33	7.03	31.87	213.36
107	EC4K5-140-257	74.08	38.53	7.23	30.47	208.36
108	EC4K5-141-258	75.08	52.73	7.83	43.67	489.76
109	EC4K5-142-259	73.08	46.93	6.23	33.47	222.76
110	EC4K5-143-260	71.08	44.13	8.43	43.87	328.56
111	EC4K5-144-261	75.08	35.33	7.43	29.67	201.96
112	EC4K5-147-262	72.08	49.13	6.63	31.47	241.96

Sl. No.	**F_3 progenies**	**D50%F**	**PHT**	**NB**	**NLVS**	**GFY**
113	EC4K5-150-263	77.08	37.33	7.63	30.07	199.36
114	EC4K5-151-264	75.08	38.73	7.23	29.67	203.76
115	EC4K5-152-265	71.08	41.93	7.03	28.07	221.76
116	EC4K5-153-266	71.08	50.33	6.83	34.67	292.16
117	EC4K5-154-267	72.41	41.83	7.20	30.24	244.16
118	EC4K5-161-268	74.41	40.63	6.00	20.44	146.76
119	EC4K5-162-269	73.41	45.43	7.60	33.84	229.56
120	EC4K5-163-270	75.41	34.43	6.40	21.44	135.56
121	EC4K5-164-271	75.41	30.43	6.00	16.04	55.36
122	EC4K5-167-272	78.41	48.03	7.40	33.64	291.76
123	EC4K5-168-273	75.41	43.23	7.00	32.04	224.36
124	EC4K5-169-274	74.41	45.03	8.00	35.84	302.56
125	EC4K5-170-275	76.41	44.23	7.40	31.84	236.36
126	EC4K5-171-276	74.41	44.43	7.80	32.84	255.96
127	EC4K5-174-277	74.41	41.43	6.00	23.64	176.96
128	EC4K5-178-278	76.41	53.03	7.80	28.04	266.56
129	EC4K5-179-279	73.41	45.63	8.20	36.04	284.76
130	EC4K5-180-280	76.41	24.63	5.20	16.84	47.96
131	EC4K5-182-281	75.08	43.40	7.13	25.67	193.06
132	EC4K5-184-282	74.08	41.60	6.53	24.27	177.26
133	EC4K5-185-283	75.08	40.60	6.33	26.47	164.06
134	EC4K5-186-284	74.08	42.80	6.33	25.07	165.06
135	EC4K5-187-285	75.08	42.80	6.53	29.07	210.86
136	EC4K5-188-286	72.08	47.80	7.73	30.67	294.06
137	EC4K5-189-287	75.08	39.20	6.53	28.27	182.86
138	EC4K5-190-288	74.08	45.60	8.13	37.47	275.06
139	EC4K5-191-289	76.08	42.00	6.93	25.27	204.66
140	EC4K5-193-290	78.08	49.20	8.33	39.47	465.86
141	EC4K5-194-291	75.08	42.00	6.93	23.07	208.86
142	EC4K5-195-292	76.08	43.40	7.13	25.07	202.26
143	EC4K5-196-293	74.08	49.80	8.33	36.07	330.26
144	EC4K5-197-294	74.08	52.80	6.93	31.47	287.06
145	EC4K5-198-295	74.58	36.73	7.20	25.90	177.69
146	EC4K5-199-296	74.58	25.13	4.80	17.30	139.29
147	EC4K5-200-297	74.58	35.93	7.60	31.90	205.89
148	EC4K5-205-298	77.58	47.93	6.60	27.30	217.49
149	EC4K5-207-299	72.58	51.33	7.80	34.70	336.49
150	EC4K5-208-300	78.58	42.53	8.20	39.50	289.29

Appendix 3: Estimates of five quantitative trait means of 150 F_3 progenies derived from Pant Lobia × Arka Garima of forage cowpea

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
1	PLAG-7-301	73.58	55.73	6.00	24.90	227.89
2	PLAG-8-302	76.58	50.73	7.00	39.50	358.49
3	PLAG-9-303	73.58	34.33	5.40	18.50	112.89
4	PLAG-10-304	73.58	45.13	5.80	29.70	224.69
5	PLAG-11-305	72.58	38.53	7.20	26.10	167.29
6	PLAG-13-306	71.58	47.93	8.20	36.70	262.69
7	PLAG-21-307	71.58	35.53	6.00	23.10	135.29
8	PLAG-22-308	71.58	36.13	6.00	23.30	156.69
9	PLAG-24-309	72.08	42.80	6.20	26.27	208.79
10	PLAG-25-310	71.08	50.00	7.00	34.07	395.79
11	PLAG-26-311	73.08	44.20	7.00	31.47	228.39
12	PLAG-27-312	78.08	47.60	7.40	33.67	310.99
13	PLAG-28-313	71.08	51.00	7.20	35.67	320.99
14	PLAG-29-314	76.08	44.60	6.20	30.07	248.99
15	PLAG-30-315	72.08	35.80	5.80	24.07	147.99
16	PLAG-31-316	74.08	48.20	7.40	39.67	345.99
17	PLAG-32-317	76.08	34.80	7.20	26.47	139.59
18	PLAG-33-318	75.08	43.20	7.20	33.87	248.39
19	PLAG-34-319	73.08	43.20	8.60	34.27	238.79
20	PLAG-35-320	76.08	53.60	6.20	31.07	289.79
21	PLAG-36-321	74.08	55.60	8.80	42.27	490.59
22	PLAG-37-322	72.08	47.00	7.20	32.07	294.39
23	PLAG-38-323	77.74	54.67	6.23	25.64	247.89
24	PLAG-39-324	72.74	51.67	7.83	35.24	281.49
25	PLAG-41-325	75.74	43.07	7.23	27.04	213.49
26	PLAG-43-326	71.74	32.47	5.63	20.44	92.89
27	PLAG-44-327	71.74	37.07	5.03	26.44	145.49
28	PLAG-45-328	71.74	47.27	7.23	31.64	237.69
29	PLAG-46-329	70.74	41.27	8.63	38.44	286.29
30	PLAG-47-330	71.74	51.27	7.83	39.04	310.09
31	PLAG-48-331	73.74	53.07	8.03	40.04	378.89
32	PLAG-51-332	75.74	49.07	7.43	21.04	205.09
33	PLAG-52-333	78.74	46.67	7.03	27.24	234.89
34	PLAG-53-334	73.74	50.27	7.03	35.64	273.09
35	PLAG-54-335	75.74	42.47	6.43	28.24	206.89
36	PLAG-55-336	74.74	44.87	7.23	32.24	268.49

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
37	PLAG-56-337	71.08	34.60	5.10	21.04	100.43
38	PLAG-57-338	73.08	48.20	8.50	37.84	307.43
39	PLAG-58-339	73.08	51.20	7.90	35.04	337.83
40	PLAG-59-340	74.08	36.60	7.50	29.04	200.83
41	PLAG-60-341	79.08	41.80	6.70	24.84	170.83
42	PLAG-61-342	72.08	47.00	8.90	41.84	407.23
43	PLAG-63-343	80.08	51.00	7.90	30.84	270.23
44	PLAG-64-344	72.08	44.80	6.90	31.04	268.03
45	PLAG-65-345	74.08	50.40	7.70	37.84	321.23
46	PLAG-66-346	75.08	28.00	5.90	21.24	147.03
47	PLAG-67-347	77.08	50.80	6.50	30.64	256.83
48	PLAG-68-348	81.08	50.40	7.70	36.64	316.63
49	PLAG-69-349	71.08	40.40	6.30	21.24	145.63
50	PLAG-70-350	74.08	41.60	8.70	31.44	232.43
51	PLAG-71-351	74.24	38.27	6.63	26.64	174.13
52	PLAG-72-352	75.24	42.67	7.03	26.04	196.53
53	PLAG-74-353	78.24	52.67	7.03	31.04	343.33
54	PLAG-75-354	72.24	46.27	6.43	26.84	215.13
55	PLAG-77-355	74.24	46.27	7.83	32.84	248.13
56	PLAG-78-356	71.24	48.87	8.23	36.84	372.53
57	PLAG-79-357	75.24	43.67	6.23	30.84	230.13
58	PLAG-80-358	74.24	51.27	6.63	25.24	245.33
59	PLAG-81-359	76.24	52.27	6.63	29.44	253.13
60	PLAG-82-360	74.24	31.07	5.43	21.04	131.73
61	PLAG-83-361	76.24	56.47	6.63	38.84	474.93
62	PLAG-84-362	74.24	36.47	7.43	27.44	164.73
63	PLAG-85-363	73.24	46.67	8.23	32.64	292.13
64	PLAG-86-364	71.24	54.87	8.43	33.04	365.13
65	PLAG-87-365	76.91	49.90	6.43	24.17	259.76
66	PLAG-88-366	72.91	47.50	7.23	33.57	305.96
67	PLAG-89-367	72.91	45.50	7.83	35.17	309.16
68	PLAG-90-368	77.91	41.70	7.43	32.37	216.16
69	PLAG-91-369	73.91	37.70	6.43	23.77	181.76
70	PLAG-92-370	73.91	46.90	8.43	36.57	346.16
71	PLAG-93-371	71.91	45.50	7.03	33.97	267.36
72	PLAG-94-372	76.91	46.10	6.83	35.57	274.76
73	PLAG-95-373	78.91	46.10	7.63	31.97	307.16
74	PLAG-96-374	74.91	34.10	6.43	17.17	117.56

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
75	PLAG-97-375	77.91	40.50	6.83	24.37	205.16
76	PLAG-98-376	74.91	46.50	7.83	32.57	312.56
77	PLAG-99-377	74.91	43.90	6.23	25.37	219.36
78	PLAG-100-378	76.91	40.50	7.43	23.77	200.36
79	PLAG-101-379	74.74	47.67	7.50	32.70	263.96
80	PLAG-102-380	76.74	46.87	7.90	34.50	329.96
81	PLAG-103-381	71.74	42.47	6.70	32.70	232.16
82	PLAG-105-382	73.74	47.47	8.30	36.10	327.36
83	PLAG-106-383	75.74	45.07	6.70	23.50	224.56
84	PLAG-107-384	75.74	41.07	5.70	25.10	159.16
85	PLAG-108-385	73.74	52.67	7.90	35.50	413.16
86	PLAG-110-386	70.74	39.47	6.90	23.30	168.36
87	PLAG-111-387	72.74	46.87	7.30	26.90	224.96
88	PLAG-112-388	76.74	53.27	6.90	33.30	418.16
89	PLAG-113-389	70.74	51.87	7.70	37.30	414.16
90	PLAG-114-390	71.74	47.47	6.70	27.70	257.96
91	PLAG-115-391	77.74	52.07	7.10	32.70	296.56
92	PLAG-116-392	76.74	44.67	6.90	28.10	200.36
93	PLAG-117-393	73.91	55.20	7.20	37.20	337.96
94	PLAG-118-394	73.91	46.80	6.60	32.00	243.96
95	PLAG-119-395	74.91	43.80	7.20	32.60	250.16
96	PLAG-120-396	76.91	53.00	6.80	33.00	316.76
97	PLAG-121-397	74.91	43.80	7.00	30.20	248.16
98	PLAG-122-398	77.91	45.60	8.20	30.40	257.76
99	PLAG-123-399	74.91	46.40	7.20	34.20	309.56
100	PLAG-124-400	78.91	47.00	6.80	25.60	226.76
101	PLAG-125-401	76.91	37.20	6.40	21.80	131.96
102	PLAG-126-402	73.91	41.20	6.80	27.40	199.36
103	PLAG-127-403	70.91	46.60	7.00	29.00	265.76
104	PLAG-128-404	74.91	47.00	7.40	34.80	272.36
105	PLAG-129-405	74.91	51.00	8.00	39.20	407.36
106	PLAG-130-406	75.91	52.40	7.20	38.60	407.16
107	PLAG-131-407	74.91	38.50	5.70	20.80	147.83
108	PLAG-132-408	75.91	43.70	5.50	25.40	196.23
109	PLAG-133-409	74.91	45.70	8.10	33.00	241.63
110	PLAG-134-410	77.91	43.30	6.10	25.60	212.43
111	PLAG-135-411	73.91	51.30	6.90	34.00	317.43
112	PLAG-136-412	73.91	51.50	6.90	33.20	358.83

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
113	PLAG-137-413	78.91	51.90	7.70	33.80	334.23
114	PLAG-138-414	74.91	51.30	7.10	30.40	307.63
115	PLAG-139-415	79.91	45.70	6.50	27.40	268.63
116	PLAG-140-416	80.91	49.10	6.70	33.20	277.23
117	PLAG-141-417	76.91	46.50	7.10	29.20	262.03
118	PLAG-142-418	76.91	43.10	6.30	25.60	222.23
119	PLAG-143-419	75.91	49.90	7.10	30.60	271.43
120	PLAG-144-420	74.91	51.50	7.70	34.00	327.23
121	PLAG-145-421	73.74	42.07	6.47	23.94	195.79
122	PLAG-146-422	73.74	51.27	7.07	35.34	315.39
123	PLAG-147-423	74.74	44.07	6.87	28.14	198.79
124	PLAG-148-424	73.74	50.07	7.67	31.54	290.99
125	PLAG-149-425	76.74	45.07	7.07	29.54	230.79
126	PLAG-150-426	73.74	46.67	7.07	31.34	242.79
127	PLAG-151-427	74.74	44.87	6.67	26.94	222.59
128	PLAG-152-428	75.74	47.87	6.67	32.14	270.79
129	PLAG-153-429	72.74	51.07	7.67	34.34	301.19
130	PLAG-154-430	72.74	46.47	6.87	33.14	243.19
131	PLAG-155-431	74.74	44.67	6.67	27.14	211.79
132	PLAG-156-432	73.74	43.87	7.27	30.74	228.39
133	PLAG-157-433	71.74	42.27	6.47	23.74	160.99
134	PLAG-158-434	74.74	51.07	7.27	32.74	252.19
135	PLAG-159-435	77.08	41.53	7.40	23.87	200.76
136	PLAG-160-436	76.08	50.53	7.00	32.87	310.36
137	PLAG-161-437	74.08	49.93	7.40	31.07	293.56
138	PLAG-162-438	77.08	49.53	8.20	33.47	328.96
139	PLAG-163-439	74.08	41.53	6.60	23.67	197.36
140	PLAG-164-440	72.08	37.93	7.20	29.87	181.36
141	PLAG-165-441	74.08	41.33	8.20	25.67	198.36
142	PLAG-166-442	75.08	48.53	7.40	28.87	269.36
143	PLAG-167-443	75.08	40.93	7.00	23.07	147.56
144	PLAG-168-444	76.08	42.13	6.80	29.27	207.36
145	PLAG-169-445	73.08	43.93	7.00	31.87	252.56
146	PLAG-172-446	74.08	41.13	7.20	24.27	190.76
147	PLAG-173-447	73.08	45.53	7.00	33.07	295.56
148	PLAG-174-448	74.08	45.13	7.60	32.07	267.76
149	PLAG-177-449	76.74	40.37	6.37	22.94	170.93
150	PLAG-200-450	73.74	35.57	6.77	25.74	160.33

Appendix 4: Estimates of five quantitative trait means of 150 F_3 progenies derived from APC-1218 × RI-60 of forage cowpea

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
1	APCRI-1-451	75.74	47.77	7.57	31.54	283.33
2	APCRI-2-452	73.74	45.77	7.37	31.14	281.73
3	APCRI-9-453	79.74	36.97	6.17	23.14	158.33
4	APCRI-10-454	75.74	42.17	6.77	29.54	213.73
5	APCRI-11-455	76.74	49.97	8.37	35.94	384.53
6	APCRI-12-456	74.74	51.57	5.37	22.14	214.53
7	APCRI-13-457	75.74	50.57	7.37	33.94	289.33
8	APCRI-14-458	73.74	46.57	7.37	31.14	268.53
9	APCRI-16-459	77.74	42.57	7.17	29.14	226.13
10	APCRI-17-460	72.74	47.37	7.37	30.94	275.73
11	APCRI-18-461	73.74	47.57	7.77	32.94	286.53
12	APCRI-20-462	70.74	47.57	7.57	33.54	277.93
13	APCRI-21-463	73.24	45.17	8.07	36.97	283.46
14	APCRI-25-464	76.24	44.57	7.87	34.37	253.46
15	APCRI-26-465	72.24	43.97	7.67	30.37	234.86
16	APCRI-27-466	74.24	40.37	7.27	25.17	212.86
17	APCRI-28-467	72.24	34.97	6.07	19.57	121.46
18	APCRI-29-468	79.24	38.97	5.67	19.37	158.66
19	APCRI-30-469	73.24	47.57	8.27	32.57	250.86
20	APCRI-31-470	75.24	43.77	7.67	39.37	257.26
21	APCRI-32-471	74.24	41.77	8.27	39.97	265.06
22	APCRI-33-472	75.24	33.57	7.87	25.97	144.66
23	APCRI-34-473	72.24	23.77	7.07	19.77	90.46
24	APCRI-35-474	75.24	53.17	5.67	26.97	209.06
25	APCRI-36-475	71.24	55.97	6.67	25.97	195.26
26	APCRI-37-476	73.24	54.77	8.67	37.57	268.66
27	APCRI-38-477	71.24	53.97	7.13	38.64	299.73
28	APCRI-39-478	77.24	34.77	7.13	25.64	141.53
29	APCRI-40-479	73.24	27.17	6.13	19.44	107.53
30	APCRI-41-480	70.24	46.77	7.73	31.64	241.13
31	APCRI-42-481	72.24	36.97	6.53	29.24	179.53
32	APCRI-43-482	76.24	58.77	6.33	42.04	310.13
33	APCRI-44-483	75.24	37.37	6.73	26.84	142.93
34	APCRI-45-484	72.24	44.57	6.93	33.44	236.93
35	APCRI-46-485	79.24	42.77	6.53	28.04	204.53
36	APCRI-48-486	73.24	53.57	6.13	32.24	237.33
37	APCRI-49-487	81.24	35.57	6.53	21.84	143.93
38	APCRI-50-488	75.24	26.17	6.13	21.64	73.33

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
39	APCRI-54-489	74.24	32.37	6.53	22.84	130.93
40	APCRI-55-490	71.24	46.57	7.13	37.64	317.93
41	APCRI-56-491	71.74	51.10	7.33	40.30	278.83
42	APCRI-57-492	70.74	46.70	7.53	32.10	236.83
43	APCRI-60-493	76.74	27.90	6.33	17.30	61.83
44	APCRI-62-494	70.74	42.30	6.53	23.50	173.63
45	APCRI-65-495	73.74	43.90	7.13	32.30	233.03
46	APCRI-66-496	72.74	41.50	7.53	40.70	216.03
47	APCRI-67-497	76.74	42.90	7.13	32.50	216.03
48	APCRI-68-498	70.74	36.70	6.73	24.70	159.23
49	APCRI-69-499	71.74	45.50	6.33	26.50	230.43
50	APCRI-70-500	71.74	47.50	7.73	38.70	248.03
51	APCRI-71-501	72.74	33.30	6.13	23.30	137.03
52	APCRI-72-502	74.74	48.50	7.53	36.10	234.83
53	APCRI-73-503	78.74	43.50	6.73	27.30	203.03
54	APCRI-75-504	79.74	54.90	6.53	25.10	217.63
55	APCRI-76-505	73.74	35.23	7.53	24.84	140.06
56	APCRI-77-506	73.74	41.23	5.93	21.04	161.46
57	APCRI-78-507	76.74	37.83	6.93	22.44	139.26
58	APCRI-79-508	72.74	49.63	8.33	35.84	432.66
59	APCRI-80-509	75.74	51.43	8.53	38.84	440.06
60	APCRI-81-510	72.74	41.03	6.13	26.44	184.66
61	APCRI-82-511	72.74	43.83	7.93	32.24	239.06
62	APCRI-83-512	70.74	48.03	7.13	30.04	268.66
63	APCRI-84-513	76.74	52.23	7.53	22.04	254.26
64	APCRI-85-514	73.74	50.83	6.33	23.64	231.86
65	APCRI-86-515	78.74	46.43	5.93	21.24	130.06
66	APCRI-87-516	78.74	46.23	7.33	31.44	229.86
67	APCRI-88-517	72.74	52.43	7.73	38.64	466.86
68	APCRI-89-518	75.74	37.43	5.33	20.04	126.06
69	APCRI-90-519	74.41	51.77	6.80	32.90	389.39
70	APCRI-91-520	77.41	51.77	6.20	22.70	221.19
71	APCRI-92-521	71.41	40.17	6.80	22.50	142.79
72	APCRI-93-522	76.41	43.17	7.00	25.70	223.59
73	APCRI-94-523	76.41	45.37	7.00	23.90	215.99
74	APCRI-95-524	77.41	43.97	7.20	32.70	222.79
75	APCRI-96-525	80.41	50.77	7.00	33.90	352.39
76	APCRI-97-526	74.41	47.17	7.20	33.50	246.59
77	APCRI-98-527	77.41	41.77	6.60	24.90	206.19
78	APCRI-99-528	77.41	48.37	6.80	26.90	241.59
79	APCRI-100-529	71.41	47.17	7.20	34.50	366.59

Sl. No.	F_3 progenies	D50%F	PHT	NB	NLVS	GFY
80	APCRI-101-530	76.41	41.17	6.00	25.30	172.19
81	APCRI-102-531	75.41	30.77	5.00	15.90	85.19
82	APCRI-103-532	75.41	50.97	7.00	26.70	271.59
83	APCRI-104-533	74.58	36.17	5.93	23.10	147.96
84	APCRI-105-534	76.58	44.57	7.13	30.10	216.36
85	APCRI-106-535	70.58	52.37	8.13	34.30	369.76
86	APCRI-107-536	75.58	46.17	7.33	32.70	264.16
87	APCRI-109-537	73.58	41.37	7.33	31.30	167.76
88	APCRI-110-538	75.58	43.37	6.73	31.70	185.96
89	APCRI-111-539	73.58	52.17	7.73	24.50	273.36
90	APCRI-112-540	77.58	41.37	6.13	23.50	170.36
91	APCRI-113-541	75.58	33.77	5.93	19.30	133.56
92	APCRI-114-542	72.58	47.17	7.13	31.10	276.56
93	APCRI-115-543	76.58	46.17	7.13	31.10	241.56
94	APCRI-116-544	74.58	32.17	6.33	17.50	83.56
95	APCRI-117-545	75.58	42.77	7.13	30.50	239.76
96	APCRI-118-546	79.58	52.17	7.93	33.90	303.76
97	APCRI-119-547	73.91	33.77	6.00	20.87	56.79
98	APCRI-120-548	75.91	35.17	7.00	23.47	94.59
99	APCRI-121-549	72.91	39.97	7.60	36.47	123.99
100	APCRI-122-550	78.91	44.97	8.00	36.47	324.79
101	APCRI-123-551	73.91	41.17	6.20	22.67	105.79
102	APCRI-124-552	72.91	43.57	6.80	23.07	157.39
103	APCRI-125-553	75.91	38.77	8.20	34.87	208.59
104	APCRI-126-554	71.91	30.97	6.80	24.47	115.79
105	APCRI-127-555	75.91	27.37	6.80	17.67	88.19
106	APCRI-128-556	72.91	43.17	8.00	26.87	214.79
107	APCRI-129-557	70.91	49.97	8.60	44.070	299.99
108	APCRI-131-558	71.91	45.97	6.60	27.27	218.79
109	APCRI-132-559	77.91	45.97	6.80	27.27	216.79
110	APCRI-133-559	71.91	40.97	8.20	34.47	190.39
111	APCRI-134-560	72.24	29.50	5.13	21.90	142.16
112	APCRI-135-561	73.24	43.10	7.53	30.50	221.56
113	APCRI-137-562	77.24	51.90	7.93	44.90	451.36
114	APCRI-141-563	71.24	42.70	7.53	29.50	189.36
115	APCRI-142-564	72.24	26.30	6.73	18.90	74.56
116	APCRI-143-565	74.24	55.10	7.53	33.10	267.96
117	APCRI-144-566	80.24	35.50	5.13	19.30	93.56
118	APCRI-145-567	75.24	44.90	6.33	26.70	200.96
119	APCRI-150-568	81.24	54.50	7.13	44.30	404.16
120	APCRI-151-569	76.24	48.70	8.53	41.70	305.16

Sl. No.	**F_3 progenies**	**D50%F**	**PHT**	**NB**	**NLVS**	**GFY**
121	APCRI-153-570	72.24	47.70	7.93	32.10	262.76
122	APCRI-154-571	74.24	43.70	6.73	28.10	229.56
123	APCRI-156-572	72.24	26.70	6.13	18.10	73.16
124	APCRI-157-573	71.24	46.90	7.53	37.90	276.16
125	APCRI-158-574	76.24	48.80	8.37	40.60	320.96
126	APCRI-163-575	74.24	42.20	7.37	33.80	235.76
127	APCRI-164-576	73.24	21.00	6.17	17.00	66.16
128	APCRI-165-577	72.24	51.40	8.37	38.80	310.76
129	APCRI-167-578	71.24	40.40	6.17	21.40	184.76
130	APCRI-168-579	72.24	38.20	6.37	21.60	142.96
131	APCRI-169-580	71.24	23.80	6.17	18.00	66.56
132	APCRI-170-581	71.24	37.00	7.57	28.00	169.16
133	APCRI-171-582	74.24	37.80	6.57	24.60	158.16
134	APCRI-172-583	73.24	40.20	7.37	23.60	179.96
135	APCRI-173-584	72.24	49.00	7.17	32.20	269.16
136	APCRI-174-585	77.24	44.00	7.37	37.60	281.76
137	APCRI-175-586	78.24	32.60	6.37	20.20	132.36
138	APCRI-176-587	78.24	40.40	7.37	27.00	200.76
139	APCRI-177-588	74.91	40.57	6.73	21.60	150.89
140	APCRI-180-589	70.91	32.37	5.93	20.00	78.49
141	APCRI-182-590	72.91	37.37	6.33	17.80	96.49
142	APCRI-184-591	71.91	44.17	6.93	39.80	219.69
143	APCRI-185-592	72.91	34.97	6.33	20.00	118.09
144	APCRI-186-593	72.91	38.57	7.13	23.60	157.29
145	APCRI-187-594	78.91	47.37	6.93	39.60	275.49
146	APCRI-188-595	76.91	50.97	6.53	39.60	273.69
147	APCRI-189-596	76.91	45.57	7.53	31.20	242.69
148	APCRI-190-597	70.91	45.37	8.13	34.20	228.89
149	APCRI-191-598	71.91	34.57	7.13	28.40	181.49
150	APCRI-193-600	74.91	46.37	8.33	42.60	290.29

Where,

D50%F	Days to 50% flowering	NB	Branches plant^{-1}
PHT	Plant height (cm)	NLVS	Leaves plant^{-1}
GFY	Green fodder yield plant^{-1}		