IDENTIFICATION OF CORE SET IN FODDER COWPEA (*Vigna unguiculata* (L.) WALP) GERMPLASM ACCESSIONS

AMRITHA VARANYA

(2019-11-105)

DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM - 695522
KERALA, INDIA
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by
AMRITHA VARANYA
(2019-11-105)

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DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM - 695522
KERALA, INDIA
2021

DECLARATION

I, hereby declare that this thesis entitled **"Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Amritha Varanya

(2019-11-105)

Place : Vellayani

Date : 15/01/2022.

CERTIFICATE

Certified that this thesis, entitled **"Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions"** is a record of research work done independently by **Ms. Amritha Varanya (2019-11-105)** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

Gayathri

Place : Vellayani
Date : 15/1/2022

Dr. Gayathri G
(Chairperson Advisory Committee)
Assistant Professor,
AICRP on Forage Crops & Utilization, RARS(SZ),
College of Agriculture, Vellayani 695522

CERTIFICATE

We, the undersigned members of the advisory committee of **Ms. Amritha Varanya (2019-11-105)**, a candidate for the degree of **Master of Science in Agriculture** with major in Plant Breeding and Genetics, agree that the thesis **"Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions"** may be submitted by **Ms. Amritha Varanya (2019-11-105)**, in partial fulfilment of the requirement for the degree.

Dr. Gayathri G.
Assistant Professor (Plant Breeding and Genetics)
AICRP on Forage Crops & Utilization, RARS(SZ),
College of Agriculture, Vellayani
695522

Dr Arya K.
Professor and Head,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani - 695 522.

Dr. Usha. C. Thomas
Associate Professor (Agronomy),
AICRP on Forage Crops& Utilization,
College of Agriculture, Vellayani
695522

Dr. Ratheesh P Gopinath
Assistant Professor
Dept. of Agricultural Statistics,
College of Agriculture, Vellayani-
695522

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Percent
&	And
ANOVA	Analysis of Variance
CD	Critical difference
Cm	Centimeter
$\chi 2$	Chi-square
CR	Coincidence Rate
d.f.	Degrees of freedom
ERI	Emergence Rate Index
Et al.,	And others or co-workers
FAO	Food and Agricultural Organization
Fig.	Figure
GA	Genetic advance
GAM	Genetic advance as per cent of mean
g	Gram
GCV	Genotypic coefficient of variation
GDP	Gross Domestic Product
GRAPES	General R-shiny based Analysis Platform Empowered by Statistics
GR	Growth Rate
GVA	Gross Value Added
h^2	Heritability
i.e.,	That is
ICAR	Indian Council of Agricultural Research
ICRISAT	International Crop Research Institute for Semi-Arid Tropics

IGFRI	Indian Grassland and Fodder Research Institute
IITA	International Institute for Tropical Agriculture
KAU	Kerala Agricultural University
kg	Kilo gram
kg ha^{-1}	Kilogram per hectare
LAI	Leaf Area Index
MD	Mean Difference
mg	Milli gram
viz.	Namely
NBPGR	National Bureau of Plant Genetic Resources
No.	Number
^{o}C	Degree Celsius
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variation
POP	Package of Practice
$Plant^{-1}$	Per Plant
q/ha/d	Quintal per hectare per day
q/ha	Quintal per hectare
RGR	Relative Growth Rate
cm^2	Square centimeters
SDG	Sustainable Development Goals
Std	Standard Deviation
SE	Standard Error
via	Through
UPGMA	Unweighted Pair-Group Method Arithmetic Average
VD	Variance Difference
VR	Variable Rate

Introduction

1. INTRODUCTION

Agriculture plays a pivotal role in India's economy where it is the primary source of income for around 58 per cent of Indians (Census, 2011). In 2020-21, India has observed a 3.4 per cent increase in GVA (Gross Value Added) of agricultural and allied sectors, despite the overall economy shrinking by 7.2 per cent which is sufficient to display the immense potential and resilience vested in agriculture and the allied sector. According to Economic Survey 2020-21 report, the share of agriculture in GDP (Gross Domestic Product) reached almost 20 per cent after 17 years. India is striving to fulfil its aspiration of two-fold increment in farmer income by 2022. Thus, agriculture and associated sectors own a critical role in any development process, by providing employment opportunities, ensuring food security, thereby leading to the achievement of Sustainable Development Goals (SDG) like zero hunger, no poverty, good health, and well-being.

Animal husbandry is one among the highly dynamic sectors of agriculture, where its products have an ever-increasing demand in the global market. India as a country holds the topmost position for livestock rearing and milk production. At the national scale, milk production climbed by 6.5 per cent from 17.63 crore tonnes in 2017-18 to 18.77 crore tonnes in 2018-19, continuing a trend that began three decades ago. Our country has abundant animal resources, which account for 4.11 per cent of GDP and 25.6% of overall agricultural GDP (Economic Review, 2020). The livestock sector is anticipated to become a major driver of agricultural expansion since it possesses a multi-dimensional role in the upliftment of rural households. Livestock production is a leading sector in Kerala which accounts for a population of 38.36 lakh (Livestock Census, 2019). The scarcity of good feed is one of the major obstacles in Kerala for increasing milk production. Only 60% of the roughages required for cattle are produced in Kerala. Due to the scarcity of quality fodder and the high cost of cow feed, these animals are underfed, resulting in unsatisfactory milk output. Livestock requires a balanced diet of three parts green grass and one-part leguminous fodder to balance the carbohydrate-protein proportion in the feed for optimal health and milk supply (Vendramini *et al*., 2012). Legume fodder is considered as 'Natural Protein Banks' as they synthesize and supply the majority of the world's plant protein to

livestock. Feeding fresh green fodder ensures the availability of minerals and micronutrients to the animals. This envisions a deliberate effort to enhance feed supplies by increasing the availability of green fodder.

Fodder cowpea is reported to be a better fodder legume than others in terms of both quantity and quality in semiarid areas. Cowpea has also got a high feeding value. In India, cowpea is predominantly cultivated in Gujarat, Rajasthan, Maharashtra, Kerala, Karnataka, and Tamil Nadu. Around 6.5 lakh hectares of area are considered to be under cowpea cultivation in which 3 lakh hectares are of fodder cowpea (IGFRI, 2013).

Cowpea is a versatile autogamous crop with a wide range of applications. It provides high-quality protein to the human diet in the form of vegetables and pulses, and it can be used as a cover crop, or as green manure. In Indian soils, it has got various agronomic benefits such as shade and drought tolerance, high nutritional value, smothering effect, prevention of soil erosion, and the capacity to provide some yield from less fertile land (Jindal *et al*., 2018). This crop can grow in very poor soil (pH range 4.5-9, organic matter 0.2, and soil sand concentration > 85%) and with a scarce amount of rainfall (Dugje *et al*., 2009). It is the sole major fodder-cum-pulse crop for rainfed and irrigated areas of India.

Cowpea is considered as a precious element in conventional cropping systems because it has the capacity to fix atmospheric nitrogen that can be utilized for future crops (Carsky and Vanlauwe, 2002). Cowpea is believed to fix up to 240 kg of nitrogen per hectare, leaving 60-70 kg for subsequent crops (Aikins and Afuakwa, 2008). The nutritive value of cowpea is very high. It has a protein content of 23-25 per cent in grain (Singh *et al*., 2018), 18-22 per cent in leaf and stem (Nielsen *et al*., 1997), and 22-25 per cent crude fibre, high digestibility (Singh and Tarawali, 1997) and negligible anti-nutritional factor. Cowpea is the only fodder legume which is the richest source of amino acids tryptophan and lysine compared to other fodder crops (Kumar *et al*., 2015). It is utilized as a multicut fodder crop for green feeding, grazing, hay production, ensiling in maize or sorghum, and also as dry fodder. Cowpea haulm has around 70 per cent of dry matter digestibility (Karachi and

Lefofe, 2004). So cowpea is an extraordinary short-duration fodder legume that can even be supplied in lean seasons.

The state's fodder supply is only able to fulfill around a 36per cent of fodder demand. To bridge the gap, new and innovative methods must be implemented. It is the responsibility of plant breeders to develop good quality varieties/hybrids that are economically viable in their yield and productivity. Knowledge of genetic diversity among existing cowpea genotypes will boost the efficacy of cowpea improvement (Gerrano *et al*., 2015). Quantification of genetic variability and identification of the most divergent individuals *via* biometric techniques will help to identify the most promising materials that offer mass production, high nutritional value, adapted to different soil conditions, and show resilience to climate change. Germplasm act as a good measure of a crop's genetic endowment since it contains the majority of the desirable genes. In fact, rather than encouraging broader usage, large germplasm collections are causing more handling issues, and it is extremely difficult for breeders to determine sufficient genetic diversity for their purpose from such a huge collection. Thus, the notion of developing a core collection is a highly successful approach for increasing the value of this conserved germplasm since it captures the whole diversity of the entire collection from which it was identified.

In this context, the present study entitled “Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions” was envisaged with the objectives of the assessment of variability in the fodder cowpea germplasm, constitution of a representative core set from the base collection, and evaluate the representativeness of the core set vis a vis base collection.

Review of Literature

2. REVIEW OF LITERATURE

Cowpea [*Vigna unguiculata* (L.) Walp.], is a autogamous plant species that belongs to the Fabaceae family and has chromosomal number 2n=2x=22 (Steele, 1976; Nwosu *et al*.,2013). It is a versatile short duration leguminous plant, commonly grown as grain pulse, vegetable and fodder in semi-arid and humid tropics (Okigbo and Greenland,1976).

Cowpea is an ancient crop that is said to have originated in Africa, while it has been cultivated in South-Eastern Asia for over 2000 years (Padulosi and Ng,1997). Cowpea has a wide range of genetic diversity which provides a tremendous scope for genetic improvement of economic traits. For the proper understanding and utilization of available variability, conservation of germplasm should be carried out. Germplasm with a larger genetic base acts as a buffer against climatic and other environmental changes, ensures long-term food security. But the most important issue faced by a breeder is the handling of these huge collections. In such a situation, identification of Core Set which is a subset of entire germplasm collection becomes relevant and also enhances the accessibility of these collections to the users.

A brief review of literature pertaining to various parts of the research project has been attempted here. The following themes are addressed in the review:

2.1. Genetic variability studies

2.2. Genetic parameters of fodder cowpea and other legumes

2.3. Correlation studies

2.4. Path Coefficient Analysis

2.5. Principal Component Analysis

2.6. Cluster Analysis

2.7. Core Analysis

2.1. GENETIC VARIABILITY STUDIES

Critical evaluation of available genetic variability in a crop is the primary step for a successful breeding program since it is the hereditary portion of the total variation. Thus, information of genetic variability among different characters in cowpea is needed for a breeder to choose good genotypes for its improvement. Various forms of gene effects impacting the overall variance of a plant character can also be estimated using genetic parameters.

Variability studies of ten Nigerian cowpea seedlings were done by Ajala *et al.* (2003) and reported that all the ten genotypes differ significantly for emergence per cent, emergence rate index (ERI), growth rate (GR) and relative growth rate (RGR).

da Silva Sá *et al*. (2016) evaluated ten cowpea seeds for germination per cent and seed vigour under salt stress condition. Germination per cent under control ranged from 87per cent to 100 per cent while germination per cent under salt stress was lower. Shoot length of accession in control ranged from 7.25 to 13.65 cm and root length ranged from 10.7 to 18.05 cm. All accessions had a lower shoot and radicle length under salt stress. Total dry matter was also estimated and it ranged from 17.9 to 27.9 mg.

Genetic variability studies in 60 fodder cowpea genotypes was carried out by Malarvizhi *et al.* (2005) and found that characters like days to 50 per cent flowering, plant height, number of branches per plant, number of leaves per plant, leaflet length, leaflet width, stem thickness, dry matter yield, green fodder yield, dry weight of leaves, dry weight of stem, leaf: stem ratio and crude protein content differ significantly among the genotypes.

Twenty-five fodder cowpea genotypes were evaluated by Singh *et al*. (2010) for its genetic variability and reported that all the ten characters *viz*., days to flowering, stem weight (g), plant height (cm), biological yield per plant (g), green fodder yield (q/ha), leaves weight (g), leaves/stem ratio, dry matter (per cent), green fodder productivity (q/ha/d), dry matter yield (q/ha) showed significant difference among the genotypes.

Nath and Tajane (2013) studied genetic variability of 44 cowpea genotypes observed significant genotypic difference for all characters *viz.*, green forage yield per plant, days of 50per cent flowering, dry matter yield per plant, leaf stem ratio, number of leaves per plant, plant height, number of branches per plant. Green forage yield per plant had the maximum genotypic variance value (997.37) followed by plant height (329.6).

Nwosu *et al*. (2013) revealed that the six cowpea genotypes under study exhibited significant differences for days of 50per cent flowering, plant height, number of branches, days to maturity, pods / plant, dry pod weight, hundred seed weight, no. of seeds /pod and seed yield/ plant among each other.

Eleven cowpea genotypes were evaluated by Olayiwola and Soremi (2014) and reported significant variability for days to 50per cent flowering, number of pods/plant, 100 seed weight, seed yield and dry fodder yield.

In 7 x 7 triple lattice design, Shanko *et al.* (2014) studied the variability of 49 cowpea accessions for number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, pod length, days to 50 per cent flowering, days to 95per cent maturity, plant height, 100 seed weight and grain yield in kg/ha. Analysis of variance revealed significant differences among the accessions for all the traits.

Khanpara *et al*. (2016) estimated the genetic variability of sixty vegetable cowpea genotypes in which all the accessions showed significant difference among each other for all the 12 characters studied. Green pod yield per plant had the greatest range of variance, followed by ten pod weight, number of pods per plant, and plant height.

One hundred and sixty-nine cowpea germplasm lines were evaluated by Lesly (2005) and it was reported that quantitative characters like germination percentage, plant height, number of branches per plant, days to flower initiation, seed yield per plant, 100 seed weight, seeds per pod showed significant difference among the genotypes. The mean germination percentage was noted as 76.35 with a range of 15 and 99 for minimum and

maximum respectively. Qualitative traits were observed and classified the accessions into various groups. Sixty-one germplasm lines showed determinate growth, seventy-four were bushy and thirty-four lines were intermediate spreading types. Majority of the genotypes *ie.,*145 out of 160 had mauve pink flowers followed by white flowers.

Kumar *et al*. (2015) classified 20 cowpea forage genotypes into different groups based on plant growth habit, flower colour, seed eye colour, plant pigmentation, determinacy etc. Out of 20 genotypes, nine genotypes had erect growth habit, four were semi-erect, five were semi-prostrate and two were acute type. All genotypes showed indeterminate growth. 12 genotypes had brown eyed seed followed by four black-blue eyed seed, two red eyed seed, one tan brown and speckling eyed seed.

In a study conducted by Shaibu and Ibrahim (2016) significant differences were observed for emergence per cent emergence rate index (ERI), growth rate (GR) and relative growth rate (RGR) among the accessions of common bean (*Phaseolus vulgaris* L.). They reported high heritability for emergence per cent, EI and RGR.

Sharma *et al*. (2017) studied thirty cowpea genotypes and analysis of variance revealed significant variation among genotypes for all the characters and it indicated the presence of sufficient variability for these 10 characters *viz.*, days to 50 per cent flowering, number of flowers per plant, days to maturity, plant height (cm), primary branches per plant, pods per plant, number of clusters per plant, test weight (g), seed yield/ plant (g.) and harvest index (per cent).

Thirty two cowpea genotypes were evaluated for eleven quantitative characters viz. days to flower initiation, days to maturity, plant height (cm), number of branches per plant, leaf length (cm), leaf width (cm), leaf:stem ratio, Stover of yield per plant (gm.) and seed yield per plant (gm.).All genotypes significantly differ from each other and showed considerable amount of variability (Singh *et al*., 2018)

Devi and Jayamani (2018) conducted variability study in 180 cowpea genotypes for 13 biometric characters viz., plant height (cm), number of primary branches per plant, days to

50 per cent flowering, number of clusters per plant, number of pods per cluster, days to maturity, pod length (cm), number of seeds per pod, hundred seed weight (g) and single plant yield (g), number of racemes per plant, peduncle length (cm), number of pods per plant. All the traits showed significant difference among genotypes.

Seedling variability studies of 16 vegetable pea genotypes were carried out in CRD with 3 replications by Panwar *et al.* (2020). Characters like standard germination (per cent), root length (cm), shoot length (cm), seedling length (cm), seedling fresh weight (g), seedling dry weight (g), vigour Index-I were observed and found out that all the genotypes significantly differ from each other for the characters studied. The population mean values observed for different seedling characters are germination per cent -87.5per cent, root length- 10.9 cm, shoot length- 5cm, seedling length-15.5 cm, seedling fresh weight- 3.21 g, seedling dry weight – 0.73 g and seed vigour index - 1358

Significant genetic variability among all the 42 cowpea accessions for the eight characters viz., days to flowering, grain filling period, days to maturity, plant height, pod length, number of seeds per pod, seed yield and thousand seed weight was reported by Belay and Fisseha (2020)

2.2. GENETIC PARAMETERS OF FODDER COWPEA AND OTHER LEGUMES

Genotypic and phenotypic coefficients of variation, as well as heritability and genetic advance, are the key factors for enhancing different traits in a crop (Denton and Nwangburuka, 2011). According to Johnson *et al*. (1955), strong heritability paired with high genetic advance is an indication of additive gene action, and selection based on these factors would be more reliable. Thus, heritability and genetic variance are significant genetic parameters needed for the selection of best parents from the population for our traits of interest (Ubi *et al.*, 2001). Various studies on genetic parameters are given in table 1 and 2.

Table 1. Genetic variability in fodder cowpea and other legume crops

Sl.No.	Characters	PCV Per cent	GCV Per cent	Reference
	Number of branches per plant	High	High	Anbuselvam *et al.*, 2000; Malarvizhi *et al*., 2005; Marappa, 2007; Nath and Tajane, 2013; Thorat and Gadewar, 2013; Khan *et al*., 2015; Sharma *et al*., 2017
		High	Moderate	Devi and Jayamani, 2018
		Moderate	Moderate	Shanko *et al*., 2014; Phogat *et al.*, 2017;Singh *et al*., 2018
	Number of leaves per plant	High	High	Gupta and Lodhi, 1979; Malarvizhi *et al*., 2005; Nath and Tajane, 2013; Gerrano *et al*.,2015
	Leaflet length (cm)	Moderate	Moderate	Malarvizhi *et al*., 2005
		Moderate	Low	Gerrano *et al*.,2015
		Low	Low	Singh *et al*., 2018
	Leaflet width (cm)	Moderate	Moderate	Malarvizhi *et al*., 2005; Singh *et al*., 2018
		Moderate	Low	Gerrano *et al*.,2015
	Stem girth(cm)	Low	Low	Malarvizhi *et al*., 2005
	Days to 50per cent flowering	High	High	Vineeta *et al*., 2003; Manggoel *et al*., 2012; Thorat and Gadewar, 2013
		Moderate	Moderate	Nath and Tajane, 2013; Shanko *et al*., 2014; Gerrano *et al*.,2015; Phogat *et al.*, 2017; Belay and Fisseha, 2020

		Low	Low	Malarvizhi *et al*., 2005; Singh *et al*., 2010; Nwosu *et al*., 2013; Olayiwola and Soremi, 2014; Khanpara *et al*., 2016; Sharma *et al*., 2017; Devi and Jayamani, 2018
	Leaf Area Index	High	High	Thorat and Gadewar, 2013; Gerrano *et al*.,2015
	Green fodder yield per plant (g)	High	High	Gupta and Lodhi, 1979; Malarvizhi *et al*., 2005; Singh *et al*., 2010; Nath and Tajane, 2013; Gerrano *et al*.,2015; Phogat *et al.*, 2017
	Dry matter yield per plant(g)	High	High	Gupta and Lodhi, 1979; Malarvizhi *et al*., 2005; Singh *et al*., 2010; Nath and Tajane, 2013;Olayiwola and Soremi, 2014; Gerrano *et al*.,2015; Phogat *et al.*, 2017; Singh *et al*., 2018
	Leaf Stem Ratio (LSR)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2018
		Moderate	Moderate	Singh *et al*., 2010; Nath and Tajane, 2013; Phogat *et al.*, 2017
	Leaf dry weight per plant(g)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2010
	Stem dry weight per plant(g)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2010

	Number of seeds per pod	High	High	Sreekumar *et al*., 1996; Manggoel *et al*., 2012;Nwosu *et al*., 2013
		High	Moderate	Shanko *et al*., 2014; Gerrano *et al*.,2015
		Moderate	Moderate	Thorat and Gadewar, 2013;Khanpara *et al*., 2016; Belay and Fisseha, 2020
		Moderate	Low	Olayiwola and Soremi, 2014; Devi and Jayamani, 2018
	100 seed weight (g)	High	High	Vineeta *et al*., 2003; Manggoel *et al*., 2012; Nwosu *et al*., 2013; Shanko *et al*., 2014; Gerrano *et al*.,2015; Khanpara *et al*., 2016; Sharma *et al*., 2017; Devi and Jayamani, 2018; Belay and Fisseha, 2020
		Moderate	Moderate	Thorat and Gadewar, 2013; Olayiwola and Soremi, 2014
	Seed yield per plant(g)	High	High	Vineeta *et al*., 2003; Manggoel *et al*., 2012; Meshram *et al*., 2013; Nwosu *et al*., 2013; Olayiwola and Soremi, 2014; Gerrano *et al*.,2015; Sharma *et al*., 2017; Singh *et al*., 2018; Devi and Jayamani, 2018; Belay and Fisseha, 2020
		High	Moderate	Shanko *et al*., 2014
	Plant height (cm)	High	High	Gupta and Lodhi, 1979; Vardhan and Savithramma,1998; Anbuselvam *et al.*, 2000;

				Malarvizhi *et al*., 2005; Marappa *et al.*, 2007; Singh *et al*., 2010; Nath and Tajane, 2013; Thorat and Gadewar, 2013; Gerrano *et al*.,2015; Khanpara *et al*., 2016; Khan *et al*., 2015; Sharma *et al*., 2017; Singh *et al*., 2018
		High	Moderate	Shanko *et al*., 2014
		Moderate	Moderate	Nwosu *et al*., 2013; Phogat *et al.*, 2017; Devi and Jayamani, 2018; Belay and Fisseha, 2020;
	Days to maturity	Moderate	Moderate	Thorat and Gadewar, 2013; Singh *et al*., 2018
		Moderate	Low	Shanko *et al*., 2014; Phogat *et al.*, 2017
		Low	Low	Nwosu *et al*., 2013; Khan *et al*., 2015; Sharma *et al*., 2017; Devi and Jayamani, 2018; Belay and Fisseha, 2020
	Crude protein	Low	Low	Malarvizhi *et al*., 2005; Nath and Tajane, 2013

Table 2. Heritability and Genetic Advance of fodder cowpea and other legume crops

Sl.No.	Characters	Heritability h^2	Genetic Advance	Reference
	Number of branches per plant	High	High	Malarvizhi *et al*., 2005; Thorat and Gadewar, 2013; Nath and Tajane, 2013; Khanpara *et al*., 2016; Khan *et al*., 2015; Sharma *et al*., 2017; Phogat *et al.*, 2017; Singh *et al*., 2018
		Moderate	Moderate	Shanko *et al*., 2014
	Number of leaves per plant	High	-	Gerrano *et al*.,2015
		High	High	Malarvizhi *et al*., 2005
	Leaflet length (cm)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2018
		Moderate	-	Gerrano *et al*.,2015
	Leaflet width (cm)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2018
		Moderate	-	Gerrano *et al*.,2015
	Stem girth(cm)	High	Moderate	Malarvizhi *et al*., 2005
	Days to 50 per cent flowering	High	High	Idahosa *et al*., 2010; Thorat and Gadewar, 2013; Nath and Tajane, 2013; Shanko *et al*., 2014; Phogat *et al.*, 2017; Belay and Fisseha, 2020
		High	-	Gerrano *et al*.,2015
		High	Moderate	Malarvizhi *et al*., 2005; Nwosu *et al*., 2013

		High	Low	Singh *et al*., 2010; Khanpara *et al*., 2016;Devi and Jayamani, 2018
		Moderate	Low	Olayiwola and Soremi, 2014; Sharma *et al*., 2017
	Leaf Area Index	High	High	Thorat and Gadewar, 2013;Gerrano *et al*.,2015
		High	Moderate	Idahosa *et al*., 2010
	Green fodder yield per plant (g)	High	High	Gupta and Lodhi, 1979; Malarvizhi *et al*., 2005; Singh *et al*., 2010; Nath and Tajane, 2013; Phogat *et al.*, 2017
		High	-	Gerrano *et al*.,2015
	Dry matter yield per plant(g)	High	High	Gupta and Lodhi, 1979; Malarvizhi *et al*., 2005; Singh *et al*., 2010;Nath and Tajane, 2013; Olayiwola and Soremi, 2014; Phogat *et al.*, 2017; Singh *et al*., 2018
		High	-	Gerrano *et al*.,2015
	Leaf Stem Ratio (LSR)	High	High	Malarvizhi *et al*., 2005;Nath and Tajane, 2013; Singh *et al*., 2018;
		Moderate	Moderate	Singh *et al*., 2010
	Leaf dry weight per plant(g)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2010
	Stem dry weight per plant(g)	High	High	Malarvizhi *et al*., 2005; Singh *et al*., 2010
		High	-	Gerrano *et al*.,2015

	Number of seeds per pod	High	High	Roquib and Patnaik, 1990; Sreekumar *et al*., 1996; Idahosa *et al*., 2010; Nwosu *et al*., 2013; Thorat and Gadewar, 2013
		High	Moderate	Khanpara *et al*., 2016; Belay and Fisseha, 2020
		Moderate	Moderate	Shanko *et al*., 2014; Devi and Jayamani, 2018
		Low	Low	Olayiwola and Soremi, 2014
	100 seed weight (g)	High	High	Idahosa *et al*., 2010; Nwosu *et al*., 2013; Thorat and Gadewar, 2013; Olayiwola and Soremi, 2014; Shanko *et al*., 2014; Khanpara *et al*., 2016; Sharma *et al*., 2017; Devi and Jayamani, 2018; Belay and Fisseha, 2020;
		High	-	Gerrano *et al*.,2015
	Seed yield per plant(g)	High	High	Nwosu *et al*., 2013;Thorat and Gadewar, 2013; Khan *et al*., 2015; Belay and Fisseha, 2020
		High	-	Gerrano *et al*.,2015
		High	High	Roquib and Patnaik, 1990;Vineeta *et al*., 2003; Sharma *et al*., 2017
		Moderate	High	Olayiwola and Soremi, 2014; Singh *et al*., 2018; Devi and Jayamani, 2018
	Plant height (cm)	High	High	Gupta and Lodhi, 1979;Roquib and Patnaik, 1990; Vardhan and Savithramma,1998; Malarvizhi *et al*., 2005;Singh *et al*., 2010; Idahosa *et al*., 2010; Nath and Tajane, 2013; Thorat and Gadewar, 2013; Khanpara *et al*.,

				2016; Sharma *et al*., 2017; Phogat *et al.*, 2017; Singh *et al*., 2018; Devi and Jayamani, 2018; Belay and Fisseha, 2020
		High	-	Gerrano *et al*.,2015
		Moderate	High	Nwosu *et al*., 2013; Shanko *et al*., 2014
	Days to maturity	High	High	Vineeta *et al*., 2003; Thorat and Gadewar, 2013;Singh *et al*., 2018
		High	Moderate	Nwosu *et al*., 2013; Shanko *et al*., 2014; Belay and Fisseha, 2020
		High	Low	Idahosa *et al*., 2010; Khan *et al*., 2015; Sharma *et al*., 2017; Devi and Jayamani, 2018
		Low	Low	Phogat *et al.*, 2017
	Crude protein	High	Moderate	Malarvizhi *et al*., 2005
		High	Low	Nath and Tajane, 2013

2.3. CORRELATION STUDIES

Green fodder yield is a complicated trait that is heavily influenced by a number of yield component characters which are ruled by polygenes and are also highly influenced by environment. Therefore, direct selection alone is not that much effective. Correlation analysis is a useful tool for determining how one character's selection affects the progress of other positively associated characters. When highly heritable traits are linked to an important attribute like yield, correlation studies become extremely useful in selection programmes.

Correlation study in 20 genetically diverse lines of fodder cowpea was done by Dangi and Paroda (1974) and found that number of leaves/plant, number of branches/plant and stem girth were highly correlated with both green and dry matter yield.

Imran *et al*. (2010) recorded that number of branches per plant of cowpea showed a significant positive correlation with green fodder yield per plant (r =0.503) and leaf area (r =0.585). Leaf area showed a negative and significant correlation (r = -0.583) with pod length.

Correlation of different traits in fodder cowpea was studied by Singh *et al*. (2010) and reported that dry matter yield, stem weight and leaves weight were positively correlated to green fodder yield per plant. Leaf weight positively correlated with stem weight; plant height with days of 50per cent flowering. They also reported that leaf: stem ratio negatively correlated to plant height and leaf weight.

Correlation analysis in 10 cowpea genotypes revealed a high positive association between grain yield and number of peduncles per plant, number of pods per plant, pod length and 100-seed weight. However, grain yield was negatively correlated with days to 50 per cent flowering (Manggoel *et al*., 2012).

Sahai *et al.* (2013) evaluated 168 accessions of cowpea in augmented design to estimate the association among characters viz., early plant vigour, plant growth habit, plant height, length of main shoot per branch, number of nodes, number of primary branches, number of secondary branches, number of leaves per plant, leaf length, leaf width, leaf weight per plant, stem weight per plant, biomass per plant, fresh leaf per stem ratio, dry leaf weight, dry stem weight, dry weight per plant and dry leaf per stem ratio, days to 50 per cent flowering, days to total maturity, number of pods per plant, pod length, seeds per pod, 100 seed weight, seed weight per plant and number of seeds per plant. Correlation analysis revealed highest significant positive correlation between dry weight per plant and dry stem weight per plant followed by number of seeds per plant and number of pods per plant and between biomass per plant and stem weight per plant. Biomass per plant also had highly significant positive correlation with dry weight per plant and days to maturity initiation. Stem weight per plant had highly significant positive correlation with dry leaf weight per plant, dry stem weight per plant, biomass per plant and dry weight per plant.

Nath and Tajane (2013) reported that green forage yield showed highly significant positive correlation with dry matter yield per plant, plant height, days of 50 per cent flowering, leaf stem ratio and number of leaves per plant.

Correlation analysis conducted by Gerrano *et al*. (2015) reported significant correlation among cowpea genotypes for different vegetative and grain yield traits. High significant positive correlation observed between fresh weight and dry weight and also with number of seeds per pod and pod length. Fresh biomass weight, dry biomass weight, plant height, and pod length showed a moderate positive correlation with days to 50 per cent flowering. A significant positive correlation was observed by fresh weight, dry weight with plant height. Number of leaves had a moderate positive correlation with fresh biomass weight and plant height and negatively correlated with leaf length and number of seeds per pod. Leaf length showed a moderate positive correlation with leaf area index and a weak positive correlation with number of seeds per pod. Moderate positive correlation was showed by pod length, number of seeds per pod and grain yield per plant with leaf area index. Leaf width, leaf area index, and harvest index were all shown to be extremely significant and strongly correlated with grain yield per plant.

Lesly (2005) reported that plant height, number of clusters per plant, number of pods per plant, pod length, seeds per pod, hundred seed weight, and harvest index were positively correlated with seed yield per plant in cowpea.

Correlation studies in 30 fodder cowpea genotypes showed that green fodder yield and dry fodder yield per plant were found to have a high significant positive correlation, followed by days to 50 per cent flowering, days to maturity, number of branches per plant, plant height, and leaf: stem ratio, indicating the importance of these characteristics for green fodder yield. (Phogat *et al.,* 2017)

Navaselvakkumaran *et al.* (2019) assessed correlation coefficient in 136 fodder cowpea accessions and reported high positive significant correlation between green fodder yield and number of leaves per plant, leaf area, dry matter yield per plant and number of primary branches per plant at both genotypic and phenotypic levels. Dry matter yield per plant

showed a highly significant positive correlation at both the levels with number of leaves per plant and leaf area. While, number of primary branches per plant exhibited significant positive inter-correlation with plant height, number of leaves per plant and leaf area. Days to 50 per cent flowering was significantly correlated with days to maturity.

2.4. PATH COEFFICIENT ANALYSIS

Although correlation coefficients are useful for evaluating the strength among different traits, the direction of trait connections can be deceptive if a strong correlation between two qualities is due to the indirect effect of other traits (Bizeti *et al.,* 2004). Path coefficient analysis is a great tool which divide the correlation coefficients into direct and indirect effects of a set of independent factors on the dependent variable, resulting in a more realistic character connection and aiding in the identification of effective components. Although Wright (1921) invented this technique, Dewey and Lu (1959) were the first to apply it to plant selection. The available literature on path analysis of cowpea fodder yield with their contributing traits are briefly reviewed below.

Five cowpea cultivars were evaluated by Kumar *et al.* (2002) and reported that dry fodder yield had the highest positive direct effect on green fodder yield followed by number of days to 50 per cent flowering, leaf: stem ratio, number of branches, plant height, leaf breadth and leaf length respectively.

Belhekar *et al.* (2003) reported that the plant height and number of branches per plant had a strong positive direct effect and a direct negative effect was observed for 100 seed weight, days to maturity and leaf area per plant in cowpea.

Singh *et al*. (2010) observed in fodder cowpea that stem weight had maximum positive direct effect on green fodder yield followed by leaves weight. Leaves weight also showed a positive significant indirect effect on green fodder yield through stem weight and vice versa. The residual effect was very low which revealed most of important characters are included in the study. They concluded that the most important attributes for green fodder yield are stem weight and leaves weight followed by dry matter yield and plant height.

Path coefficient analysis done by Manggoel *et al*. (2012) in cowpea revealed high positive direct effects of number of peduncles per plant (p = 0.94), flowers per plant (p = 1.40), 100-seed weight (p = 1.45) and number of seeds per pod (p = 0.49) on grain yield. Days to 50 per cent flowering (p = -1.20) contributed negative direct effects on grain yield.

Sahai *et al.* (2013) studied 168 cowpea accessions in augmented block design and got a positive direct effect (0.4598) of dry weight per plant; stem girth (0.2336); and number of secondary branches (0.2005) over dry stem weight per plant. Biomass per plant showed a positive direct effect of number of leaves per plant (0.3251) and stem girth (0.2842). Number of seeds per plant had a direct positive effect on number of pods per plant (0.9059); and indirect effect on number of pod cluster per plant (0.7718). Thus this high impact of direct effect suggests selecting plant types with higher biomass per plant, dry weight per plant, stem girth, number of secondary branches, number of leaves per plant, number of pods per plant, and number of pod cluster per plant that would be effective for increasing fodder and seed yield in cowpea.

In fodder cowpea highest direct effect was observed between green fodder yield per plant and dry matter yield per plant by Nath and Tajane (2013). Number of leaves per plant, leaf stem ratio and days of 50 per cent flowering also showed a positive direct effect on green fodder yield per plant. Highly significant indirect effect was seen between days of 50 per cent flowering, plant height, number of leaves per plant *via* dry matter yield per plant.

Phogat *et al.* (2017) studied path analysis in 30 fodder cowpea genotypes and revealed that dry fodder yield per plant (0.802) had very high direct positive effect, followed by days to 50 per cent flowering (0.487), plant height (0.304). Number of branches per plant (0.198) and leaf: stem (0.032) showed a low and negligible positive direct effect on green fodder yield per plant. A high direct negative effect on green fodder yield was showed by days to maturity (-0.450).

The direct and indirect effects of different characters against green fodder yield per plant was analyzed in fodder cowpea by Navaselvakkumaran *et al.* (2019) in which leaf area showed the highest positive direct effect with green fodder yield per plant. The number of

leaves per plant recorded negative direct effect and dry matter per plant showed a negligible direct effect. Highest positive indirect effect was reported in number of leaves per plant and dry matter yield per plant *via* leaf area towards green fodder yield per plant

2.5. PRINCIPAL COMPONENT ANALYSIS

Gerrano *et al*. (2015) conducted principal component analysis of twenty-five cowpea genotypes for sixteen quantitative character and revealed that only the first five principal component had eigenvalues greater than one and contributed 79.30 per cent of the total variation. Leaf area and leaf area index showed maximum loading score in PC1 followed by pod length and number of seeds per plant which together contributed 30.42 per cent of total variation. Characters that contributed more strongly to PC2 were leaf number, plant height, and dry and fresh biomass weight contributed 21.24 per cent of total variation. Highest positive loadings to PC3 were yield per plant, hundred-seed weight, and number of branches, which contributed 12.77 per cent of the total variation. All the genotypes were scattered in all the four quadrant of PCA biplot which showed its genetic diversity among them.

Principal component analysis of thirty fodder cowpea genotypes was done by Jindal *et al*. (2018) in which the five principal components having eigen values >1 amounted to 90.64 per cent of total variability. Green fodder yield, stem weight, leaf weight had the maximum loading score in PC1 accounted for 32.11per cent of total variation. PC2 showed maximum value for dry matter character which contributed 17.1 per cent total variation. Leaf length and leaf width had high absolute value on PC-3. PC4 and PC5 could be regarded as yield contributing factors collectively since it contributed for diversity in plant height, number of branches per plant, LSR and days of 50 per cent flowering.

Principal Component Analysis was performed on 102 cowpea germplasm samples based on twelve quantitative characteristics viz., plant height, days to fifty per cent flowering, days to maturity, number of primary branches, peduncle length, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and single plant yield by Vijayakumar *et al*., (2020).

The PCA analysis separated the overall variance into five principle components whose eigen value was greater than one, which accounted for 76.53 per cent of the total variation. Biplot constructed using 1st two PC scattered all 102 genotypes apart with respect to its divergence. Single plant yield showed maximum absolute value in PC1 followed by number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, plant height, hundred seed weight, days to maturity contributed to the 26.4 per cent variation. Genotypes placed in same quadrant show similarity among each other for those traits which has highest absolute value in that quadrant

2.6. CLUSTER ANALYSIS

Genetic diversity analysis is a crucial step in crop development since it reveals genetic potential among the genotypes. According to Karuri *et al*. (2010) success of germplasm conservation is largely dependent on understanding its available diversity.

Multivariate analysis done by Rewale *et al*. (1996), categorised the cowpea genotypes into 19 clusters in which 11 clusters had only one genotype each. It was also concluded in this study that there is no link between genetic diversity and geographical origin.

Ushakumari *et al*. (2000) grouped fifty cowpea genotypes into 13 clusters using D^2 analysis and found that plant height (22.69 per cent) contributed highest towards genetic diversity followed by seeds per pod (17.63 per cent), number of branches per plant (16.82 per cent), number of pods per cluster (15.27 per cent).

Sixty genotypes of fodder cowpea were evaluated by Kapoor *et al.* (2000) and assessed genetic divergence for fourteen traits viz. green fodder yield, seed yield and their component traits using Mahalonobis's D^2 technique which grouped all the genotypes in to fifteen clusters.

Bakiyarani *et al.* (2000) revealed that 80 per cent of total genetic divergence in cowpea is accounted from the physiological traits like single plant yield, harvest index and earliness in flowering.

Genetic divergence analysis of sixty fodder cowpea cultivars was conducted by Borah and Khan (2002), and divide it in to 10 clusters groups. The biggest contribution to overall genetic divergence was recorded for dry matter production, green fodder yield, and plant height. These characters could be useful for parent selection. The clustering pattern revealed that geographic diversity was not an indicator of genetic diversity.

Narayanankutty *et al.* (2003) investigated the genetic variability and divergence of 37 vegetable cowpea genotypes and grouped them into eleven clusters using D^2 technique.

45 cowpea genotypes from indigenous and exotic sources were grouped into five clusters using Mahalanobis D^2 statistics by Nigude *et al.* (2004), in which cluster I had the maximum genotypes (28) followed by cluster II (11 genotypes) and cluster-III (4 genotypes). The clusters IV and V were singleton. Highest contribution towards divergence was by number of branches per plant, test weight, dry weight and number of pods per plant.

Magloire (2005) calculated the genetic divergence of 20 genotypes and found that for most of the morphological traits showed significant level of dissimilarity across the accessions, especially from different nations.

100 cowpea genotypes for 11 quantitative traits was analysed by Girish *et al*. (2006) and grouped them into 11 cluster using Mahalanois D^2 statistics in which fodder yield contributed highest towards the divergence followed by plant height and seed yield.

Bhandari and Verma (2007) compared twenty advanced generation forage cowpea genotypes along with two released varieties for genetic divergence and divided 22 genotypes into seven clusters. Cluster 1 included maximum number of genotypes (10 genotypes) followed by clusters II with 5 genotypes and cluster III with three genotypes. The major contributors towards divergence are crude protein content, dry matter digestibility, dry matter yield and number of leaves per plant.

Hierarchical clustering of twenty-five cowpea genotypes using UPGMA method was employed by Gerrano *et al*. (2015). The pair-wise combinations showed genetic distances ranging from 0.47 to 1.85 among the cowpea genotypes indicated the diversity of

phenotypic traits under study. Based on these traits, the dendrogram was constructed and grouped genotypes into three main clusters and a singleton. Maximum number of genotypes were included in cluster 2 (9 genotypes) followed by cluster 1 (8 genotypes) and cluster 3 (7 genotypes).

Lesly (2005) classified 169 cowpea genotypes using cluster analysis into 51 clusters and 46 clusters during Kharif 2004 and summer 2005 respectively and also reported that the number of pods per plant showed maximum contribution to divergence.

Thirty fodder cowpea genotypes were grouped into five major clusters by Jindal *et al*. (2018) using UPGMA method and dendrogram was prepared using the rescaled distances. Cluster II, with 17 genotypes, was the largest group, followed by Cluster III (6 genotypes), and Cluster I (5 genotypes). Clusters IV and V with one genotype each. Genotypes within cluster found to be closest to cluster mean).

Arya *et al.* (2019) classified KBC 9 and DC 7-15 as medium fodder-medium grain yield producing genotypes that may be used for both fodder and grain production in a meteroglyph research of 30 cowpea genotypes.

2.7. CORE ANALYSIS

The germplasm of a species is the total amount of hereditary material or genes present in that species. The goal of germplasm collections was to preserve the genetic variety of crop species and their wild relatives. The first one who identified the relevance of genetic diversity for crop improvement and organized huge germplasm collections of numerous crops from their "Center of Origin" was Nikolai Ivanovich Vavilov in 1951 (Brown, 1989). But the vast number of accessions acquired in gene banks are frequently under-documented, could become an obstacle for their full exploitation, assessment, and use breeding programmes. It would also be impractical to assess such big collections in depth because it would be both costly and time-consuming. Thus, subsets of the entire collection called "core set" could be developed to make this work easier to complete.

The concept of "core collection" was proposed by Frankel and Brown (1984) to describe a collection that includes a representative sample of the complete collection with minimal repetitiveness and maximal genetic diversity of a crop species and its relatives. Core collection (10 per cent of the entire collection), should represent at least 70 per cent of the genetic variation in the whole collection of the species (Brown, 1989).

Frankel and Brown (1984) and Brown (1989) described the procedure to build a core collection utilizing information about the accessions' origins and attributes. The guiding criteria for the formation of a core collection given by them are a) the entire collection is a major taxonomic entity b) the core collection is a genuine representative of the entire collection and has reduced size c) the core should be as diverse as the whole collection.

Several sampling strategies have been proposed, ranging from random sampling to stratified sampling based on identified groups with constant, logarithmic, or proportional sample sizes to group size (Brown *et al.,* 1987). Hu *et al.* (2000) studied different methods for the construction of core set in cotton and concluded that cluster approaches should be used with diverse sampling strategies for a better representation of the core collection. The Power Core was used to do a heuristic search which compute Mean Difference (MD, per cent), Variance Difference (VD, per cent), Variable Rate (VR, per cent) and Coincidence Rate (CR per cent) for continuous variables and frequency distribution for each variable.

Brown *et al*. (1987) established the first core collection for perennial Glycine, in which the core was made up of 111 accessions derived from a collection of 1400 Glycine accessions collected from Australia.

In 1995, the Vigna Crop Germplasm Committee developed a core collection comprised of 700 accessions from 7698 USDA cowpea accessions based on origin, taxonomic traits, and pest and disease resistance. The subset's lines represent the genetic diversity of the USDA cowpea collection as a whole (VCGC, 1996).

A core subset with 1956 accessions of chickpea germplasm was developed by Upadhyaya *et al*. (2001) based on country of origin and data on 13 quantitative characters from 16991

base accessions of ICRISAT chickpea germplasm collection. Clustering was done by using Ward's method. Entire collection and core set predominantly contained accessions from Asia followed by Africa, America and Europe. The variance (Levene's test) and frequency distribution (chi square test) showed homogeneity in both core and base for all the traits except tertiary branches and seeds per pod.

1704 accessions in the peanut core set were grouped into 77 clusters to form a mini core set of 184 accessions. Individual cluster ranged from 1 to 76 accessions. All the six botanical varieties of groundnut were included in the mini core set. The mini core subset's composition resembled that of core set and entire collection in terms of geographic distribution, mean, variance and got a Mean Difference per cent of 2.12per cent, Variable Difference of 8.51per cent, Variance Rate of 107.35per cent and Coincidence Rate of 89.3 per cent which indicated that mini core set truly represent the core set. Upadhyaya *et al*. (2002).

A core set comprising 1704 groundnut accessions was formed from 14310 base accessions available in ICRISAT genebank by Upadhyaya *et al*. (2003). The base accessions were stratified on the basis of country of origin and data on 14 morphological descriptor traits viz., stem color, stem hair, branching pattern, leaf color, leaf shape, leaf hair, flower color, cluster color, peg color, pod beak, pod constriction, pod, number of seeds per pod, and seed color. Clustering of these accessions was done using Ward's method and from each cluster approximately 10 per cent accessions were randomly selected to constitute a core collection. Mean values of quantitative traits using 't' test and frequency distribution of qualitative traits using chi-square test were compared for core and base accessions and found that the genetic variation available for these traits in the entire collection has been preserved in the core collection. The Shannon-Weaver diversity index (H') in the core collection was comparable to that of the total collection, indicating that the core collection reflected the full diversity of the entire collection. This core also preserves the co-adapted gene complexes represented in the entire collection.

Reddy *et al*. (2005) developed a core collection in pigeon pea based on 14 qualitative traits in the 12,153 accessions held in the ICRISAT gene bank. The germplasm accessions from 56 nations were divided into 14 clusters depending on their geographic origin. The comparison on mean, variance, frequency distribution of the core collection comprising 1290 accession (10.6 per cent of entire collection) indicated that the core collection was similar to that of the entire collection for various traits and the genetic variability available in the entire collection is preserved in the core collection. The Shannon–Weaver diversity index for different traits was also similar for both entire and core collection. All the important phenotypic associations between different traits available in the entire collection were preserved in the core collection.

The world largest germplasm of cowpea was maintained in the International Institute for Tropical Agriculture (IITA), Nigeria which contains over 15,000 cultivated cowpea accessions from 89 countries (Fatokun *et al*., 2018). A core collection of cowpea consisting of 2062 accessions based on origin and 28 agrobotanical descriptors from the entire collection of 15,003 accessions held at IITA genebank was developed by Mahalakshmi *et al.* (2007). The comparison of mean, variances, Shannon-Weaver diversity index (H') indicated that the core subset represents the entire collection. For the qualitative characters, all the descriptors showed similar frequency distribution in both core set and base collection.

Cho *et al.* (2008) used molecular profiling and UPGMA clustering to create a core set of 260 Korean soybean accessions from 2765 accessions. Seven quantitative and three qualitative variables were used to assess phenotypic diversity in the core set and found that core set as a good subset of base collection.

In numerous crops, core and mini core (10 per cent of core) collections have been recorded, and when analysed, they revealed new sources of diversity for agronomic traits such as resilience to biotic and abiotic stress. The most effective and reliable method of conducting an initial search of germplasm collections for desirable features, especially in legumes, has been suggested as evaluating core and mini-core collections (Upadhyaya *et al*., 2009).

Bhattacharjee *et al*. (2012) constructed a cassava core collection comprised of 428 accession from the international collection maintained at IITA. The core represented accessions mainly from Nigeria (45.5 per cent) followed by Ghana (11.2 per cent), Benin (9.5 per cent), Togo (6.0 per cent), and Guinea and Cameroon (both 5.8 per cent). The results revealed that the average, variances, and ranges of the variables under examination did not differ significantly between the total collection and the core. For continuous variables, the core subset recovered 81 per cent of the means and 63 per cent of the variances. The core set truly represented the base collection, in which it retained all the phenotypic diversity based on Gower's distance.

Core set of rice comprised of 34 accession (21.25 per cent) was developed by Saini (2012) based on 24 quantitative traits using Power core software from a base collection of 160 short duration germplasm accessions. The core set possessed a mean difference (MD) of 6.98 per cent, a variance difference (VD) of 41.99 per cent, a variable rate (VR) of 128.37 per cent, and a coincidence rate of 96.34 per cent (CR). The core and base collection were compared with respect to mean (t test), variance (homogeneity test) and revealed that both population are at par for all the traits. Qualitative traits are compared using chi square test and reported that there is no significant difference between the population for these descriptors. The phenotypic diversity in core set and base collection were compared using Shannon – Weaver diversity index (H‟) and presented that both indices are similar with respect to each other.

Egbadzor *et al.* (2014) conducted a diversity analysis on 113 cowpea accessions using SNP marker and recognized 48 accession as core collection from it, each of which is morphologically unique and has certain unique alleles found exclusively in elite lines.

The core and mini core collections, which represent variability in the complete collection of germplasm of a given species conserved in the gene bank, are suitable resources for efficient conservation and use of plant genetic resources in crop improvement programmes (Upadhyaya, 2015).

Core set of wheat was developed using Power Core Software and validated using Shannon-Diversity Index by Dutta *et al.* (2015). There were 2,208 accessions in the core set, with 1,770 *T. aestivum*, 386 *T. durum*, and 52 *T. dicoccum*.

Fatokun *et al.* (2018) genotyped 298 mini core subset lines of cowpea maintained in IITA. On this subset, Ward's minimal variance hierarchical cluster analysis, model-based ancestry analysis, and discriminant analysis of principal component (DAPC) were performed and identified three clusters each. Cluster one has the most gene diversity and polymorphic information content (PIC) values, which contained 115 accessions from the most countries.

Pahuja *et al*. (2019) evaluated 61 forage sorghum mini core accession for genetic diversity of 30 characters, including both quantitative and qualitative aspects. The accessions were divided into six clusters using hierarchical cluster analysis. Cluster I contained the tallest genotypes with high green fodder production, dry fodder yield, plant height, crude protein, DDM, K, and low zonate leaf spot intensity. This small core collection can be used in combination breeding programmes to create transgressive segregants with desirable characteristics and high green and dry fodder yield.

Materials and Methods

3. MATERIALS AND METHODS

The present study entitled “Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions” was conducted in Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Trivandrum 695522 located at a latitude of 8.4407º N and longitude of 76.9888º E with an altitude of 29 m above MSL. Two experiments were conducted between 2019-2021. Experiment 1 was evaluation of seedlings and Experiment 2 was field evaluation of fodder cowpea variability and identification of core set.

3.1 EXPERIMENTAL MATERIAL

The experimental material comprised of 143 fodder cowpea (*Vigna unguiculata* (L.) Walp) genotypes collected from NBPGR, New Delhi and released bush type cowpea varieties of KAU with 3 checks. The 3 check varieties were Aiswarya (State check), KBC-1 (Zonal check) and EC- 4216 (National check). The list of 146 germplasm accessions evaluated are given in table 3 which forms the “Base Collection”.

Table3. List of Accessions used for the study

Treatment	Accession name	Institute	Source
1	CS-88	NBPGR	UNKNOWN
2	NR/18-105	NBPGR	UNKNOWN
3	NR/18-112	NBPGR	UNKNOWN
4	NR/18-99	NBPGR	UNKNOWN
5	NR/18-74	NBPGR	UNKNOWN
6	NR/18-62	NBPGR	UNKNOWN
7	SNAR-12-11	NBPGR	UNKNOWN
8	SNAR-12-08	NBPGR	UNKNOWN
9	IC553515	NBPGR	UNKNOWN
10	IC546525	NBPGR	TELANGANA
11	IC546523	NBPGR	TELANGANA

Table 3. List of Accessions used for the study (Contd…)

12	IC546516	NBPGR	TELANGANA
13	IC536723	NBPGR	UNKNOWN
14	IC519621	NBPGR	ANDRA PRADESH
15	IC398992	NBPGR	ANDRA PRADESH
16	IC372642	NBPGR	UNKNOWN
17	IC372130	NBPGR	UNKNOWN
18	IC548288	NBPGR	UTTARAKHAND
19	IC402125	NBPGR	NEW DELHI
20	IC402115	NBPGR	NEW DELHI
21	IC402111	NBPGR	NEW DELHI
22	IC394237	NBPGR	ASSAM
23	IC363962	NBPGR	ARUNACHAL
24	IC337387	NBPGR	UTTARAKHAND
25	IC259069	NBPGR	NEW DELHI
26	IC97787	NBPGR	KERALA
27	EC244217	NBPGR	PHILIPPINES
28	EC244211	NBPGR	PHILIPPINES
29	EC244021	NBPGR	PHILIPPINES
30	EC241058	NBPGR	PHILIPPINES
31	EC241056	NBPGR	PHILIPPINES
32	EC241037	NBPGR	PHILIPPINES
33	EC241023	NBPGR	PHILIPPINES
34	EC241022	NBPGR	PHILIPPINES
35	EC240801	NBPGR	PHILIPPINES
36	EC240796-1	NBPGR	PHILIPPINES
37	EC240755	NBPGR	PHILIPPINES
38	EC240925	NBPGR	PHILIPPINES

Table 3. List of Accessions used for the study (Contd…)

39	EC240891	NBPGR	PHILIPPINES
40	EC148711	NBPGR	USA
41	EC110599	NBPGR	UNKNOWN
42	EC109968	NBPGR	UNKNOWN
43	EC109112	NBPGR	UNKNOWN
44	EC107183	NBPGR	USA
45	EC98668	NBPGR	UNKNOWN
46	EC43203	NBPGR	PHILIPPINES
47	EC42956	NBPGR	UNKNOWN
48	EC42726	NBPGR	UNKNOWN
49	EC14966-1	NBPGR	UNKNOWN
50	EC14966	NBPGR	UNKNOWN
51	EC4862	NBPGR	USA
52	EC4208	NBPGR	USA
53	EC4190	NBPGR	USA
54	EC4185	NBPGR	USA
55	EC2791	NBPGR	COSTA RICA
56	EC2790	NBPGR	COSTA RICA
57	EC4218	NBPGR	USA
58	EC10734	NBPGR	UNKNOWN
59	EC14702	NBPGR	UNKNOWN
60	EC99566	NBPGR	NIGERIA
61	EC99569	NBPGR	NIGERIA
62	EC100090	NBPGR	NIGERIA
63	EC101967	NBPGR	NIGERIA
64	EC101970	NBPGR	NIGERIA
65	EC101973	NBPGR	NIGERIA

Table 3. List of Accessions used for the study (Contd…)

66	EC101978	NBPGR	NIGERIA
67	EC101997	NBPGR	NIGERIA
68	EC107119	NBPGR	USA
69	EC107127	NBPGR	USA
70	EC107185	NBPGR	USA
71	EC107189	NBPGR	USA
72	EC109493/3427-2	NBPGR	UNKNOWN
73	EC148714	NBPGR	USA
74	EC149345	NBPGR	NIGERIA
75	EC240630	NBPGR	PHILIPPINES
76	EC240635	NBPGR	PHILIPPINES
77	EC240671-1	NBPGR	PHILIPPINES
78	EC240744-A	NBPGR	PHILIPPINES
79	EC240856-1	NBPGR	PHILIPPINES
80	EC240878	NBPGR	PHILIPPINES
81	EC240885-2	NBPGR	PHILIPPINES
82	EC240905	NBPGR	PHILIPPINES
83	EC240912-1	NBPGR	UNKNOWN
84	EC239662	NBPGR	UNKNOWN
85	EC343036	NBPGR	USA
86	EC343047	NBPGR	USA
87	EC367714	NBPGR	USA
88	EC390207	NBPGR	USA
89	EC390241	NBPGR	USA
90	IC3016	NBPGR	UNKNOWN
91	IC20647	NBPGR	MADHYA PRADESH
92	IC20672	NBPGR	MADHYA PRADESH

Table 3. List of Accessions used for the study (Contd…)

93	IC20678	NBPGR	MADHYA PRADESH
94	IC20682/P3	NBPGR	MADHYA PRADESH
95	IC20696	NBPGR	CHATTISGARH
96	IC20698	NBPGR	MADHYA PRADESH
97	IC20703	NBPGR	CHATTISGARH
98	IC26012	NBPGR	KARNATAKA
99	IC26048	NBPGR	KARNATAKA
100	IC39908	NBPGR	GUJARATH
101	IC249140	NBPGR	ANDRA PRADESH
102	IC253278	NBPGR	NEW DELHI
103	IC257410	NBPGR	KERALA
104	IC257413	NBPGR	KERALA
105	IC257414	NBPGR	KERALA
106	IC257422	NBPGR	UNKNOWN
107	IC257447	NBPGR	UNKNOWN
108	IC259061	NBPGR	NEW DELHI
109	IC259076	NBPGR	NEW DELHI
110	IC259084	NBPGR	NEW DELHI
111	IC259087	NBPGR	KERALA
112	EC723987	NBPGR	SENEGAL
113	EC723990	NBPGR	AUSTRALIA
114	EC724033	NBPGR	BOSTWANA
115	EC724051	NBPGR	BOSTWANA
116	EC724352	NBPGR	HONDURUS
117	EC724382	NBPGR	USA
118	EC724498	NBPGR	INDIA
119	EC724564	NBPGR	HUNGARY

Table 3. List of Accessions used for the study (Contd…)

120	EC724591	NBPGR	NIGERIA
121	EC724313	NBPGR	CHAD
122	EC723836	NBPGR	UGANDA
123	EC724768	NBPGR	NIGERIA
124	EC724773	NBPGR	UGANDA
125	EC724774	NBPGR	UGANDA
126	EC724778	NBPGR	SOUTH AFRICA
127	EC724779	NBPGR	INDIA
128	EC724780	NBPGR	INDIA
129	EC724787	NBPGR	NIGERIA
130	EC724796	NBPGR	TANZANIA
131	EC724807	NBPGR	NIGERIA
132	EC724818	NBPGR	TANZANIA
133	EC724824	NBPGR	LIBERIA
134	EC734794	NBPGR	UNKNOWN
135	EC966551	NBPGR	UNKNOWN
136	EC99682	NBPGR	UNKNOWN
137	IC1255	NBPGR	UNKNOWN
138	EC546491	NBPGR	UNKNOWN
139	EC738173	NBPGR	ITALY
140	DC-15	KAU	KARNATAKA
141	DCS-47-1	KAU	KARNATAKA
142	KBC-4	KAU	KARNATAKA
143	KANAKAMONY	KAU	KERALA
C1	AISWARYA	KAU	KERALA
C2	KBC-1	KAU	KARNATAKA
C3	EC 4216	NBPGR	USA

Field Preparation

10 days after sowing

Plate 1. General Field View

20 days after sowing

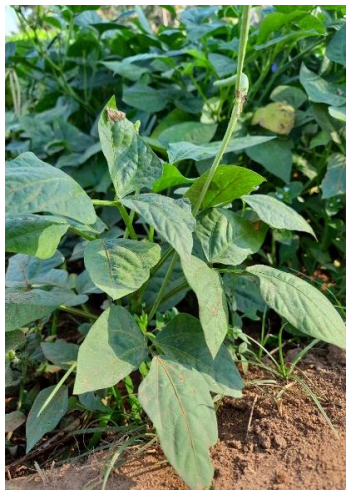
30 days after sowing

Plate 1. General Field View

40 days after sowing

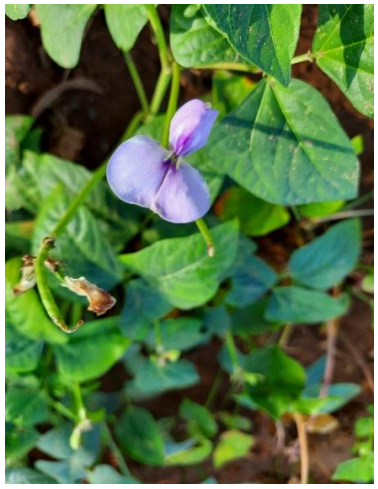
50 days after sowing

Plate 1. General Field View




Check Variety 1- Aiswarya


Check variety 2- KBC 1

Check Variety 3- EC 4216

Plate 2. Check Varieties

3.2 METHODS

3.2.1. Layout of the Experiments

Experiment 1 : Evaluation of seedlings

Design : CRD (Completely Randomized Design)

Treatments : 143 + 3 Check varieties

Replication : 2

Experiment 2 : Evaluation of Variability

Design : Augmented block design

Treatments : 143 + 3 check varieties

Spacing : 30 cm x 15 cm

Block Size : 12.6 m^2

No. of Blocks : 13

14 accessions including 3 checks were planted in each block comprising 10 plants of each accession in 2 rows. i.e., 280 plants/block. The cultural operations were done according to the recommendation of KAU Package of Practices (KAU,2016)

3.3 MORPHOLOGICAL CHARACTERISATION AND EVALUATION OF FODDER COWPEA ACCESSIONS

3.3.1 Evaluation of Seedlings

Seeds of all the genotypes along with the checks sown in germination paper in 2 replication and quantitative traits were recorded at particular interval.

3.3.1.1. Germination Percentage

Germination test was conducted by following between paper method as per the International Seed Testing Authority (ISTA) guidelines. Two replications with 100 seeds were maintained and count of germinated seeds taken on 7^{th} day after sowing.

3.3.1.2. Root Length

Measured from the base of the root to the tip of main root on 7^{th} day after sowing. Root length of 10 randomly selected seedlings were taken and computed the average value.

3.3.1.3. Shoot Length

Measured from the base of the shoot to the tip of the tallest leaf on 7^{th} days after sowing. Shoot length of 10 randomly selected seedlings were taken and computed the average value.

3.3.1.4. Seedling Length

Ten randomly selected normal seedlings were taken. Seedling length was measured from root tip to the tip of the tallest leaf. Then the mean seedling length was calculated.

3.3.1.5. Seedling Fresh Weight

100 seedlings fresh weight taken using an electronic weight machine on 10^{th} day after sowing

3.3.1.6. Seedling Dry Weight

Seedling were dried in an oven at 60℃ for 24 hours and weighed.

3.3.1.7. Vigour Index

Seedling vigour index calculated using the formula given by Abdul-Baki and Anderson (1973).

Vigour index I = Germination per cent * Seedling length

3.3.1.8. Relative growth index

Relative Growth Rate of seedling were estimated using the formula

$$RGR = \frac{\ln S2 - \ln S1}{t2 - t1}$$

Where, S_1 and S_2 are the seedling size at time t_1 and t_2 respectively

3.3.2 Evaluation of Variability in Base Collection

Average of 5 randomly selected representative plants of each treatment were taken for quantitative character statistical analysis. Observation for traits were taken at 50 per cent flowering stage. Observations on qualitative characters were taken as per the descriptors of fodder cowpea given by Roy *et al*. (2017)

3.3.2.1. *Biometric Characters*

3.3.2.1.1. *Plant Height*

Plant height was measured from ground to the tip of the main branch using a measuring scale at 50 per cent flowering. Mean value was estimated.

3.3.2.1.2. *Leaflet Length*

Leaflet length was measured on mid leaflet of 5th fully grown leaf from the base at 50 per cent flowering and mean value was taken.

3.3.2.1.3. *Leaflet Width*

Leaflet width was measured on mid leaflet of 5th fully grown leaf from the base at widest point during 50 per cent flowering and mean value was calculated.

3.3.2.1.4. *Number of Leaves Plant^{-1}*

Total number of leaves from each representative samples were recorded at 50 per cent flowering and calculated its mean.

3.3.2.1.5. *Number of Primary Branches Plant^{-1}*

Total number branches on the main stem was counted at 50 per cent flowering stage in the selected five plant samples and taken its average.

3.3.2.1.6. *Number of Secondary Branches Plant^{-1}*

Number of branches arising from primary branches was counted at 50 per cent flowering and worked out the average value.

3.3.2.1.7. *Stem Girth*

Stem girth was measured between 3rd and 4th node from the ground on the main stem and calculated its average.

3.3.2.1.8. *Number of Nodes Plant^{-1}*

Total number of nodes of the selected plants were counted on main shoots from ground level to the apex and worked out its mean.

3.3.2.1.9. *Internode Length*

Internodal length was recorded between 3rd and 4th node on the main shoot from base at 50 per cent flowering

3.3.2.1.10. *Days to 50 per cent Flowering*

Recorded the number of days taken from sowing to when the plants shown 50 per cent flowering

3.3.2.1.11. *Green Fodder Yield Plant^{-1}*

Recorded as average fresh weight of total foliage including stem of 5 plants at 50 per cent flowering.

3.3.2.1.12. *Dry Matter Yield Plant^{-1}*

Representative 5 plant samples were oven dried at 60°C till it reached a constant weight. The weight of these were taken and calculated its mean.

3.3.2.1.13. *Leaf Dry Weight Plant^{-1}*

Dry weight of oven dried leaves of 5 plant samples were taken and calculated its mean value.

3.3.2.1.14. *Stem Dry Weight Plant^{-1}*

Recorded dry weight of stems of 5 plants which was oven dried at 60°C and worked out its average.

3.3.2.1.15. *Leaf Stem Ratio (LSR)*

Dry weight of leaves and stems were taken separately and calculated the ratio by dividing leaf dry weight by stem dry weight.

3.3.2.1.16. *Leaf Area Index*

Leaf area of the 5th matured leaf from tip was measured using a graph paper. Then calculated the total leaf area by multiplying it with total number of leaves per plant. The Leaf Area Index were estimated using the formula given below (Watson,1962)

$$LAI = \frac{\text{Total leaf area}(cm^2)}{\text{Ground area of a plant}(cm^2)}$$

3.3.2.1.17. *Number of Seeds Pod^{-1}*

Counted the total number of seeds from 5 matured, threshed pods and calculated its average.

3.3.2.1.18. *1000 Seed Weight*

Recorded the weight of 1000 random seeds of each plants.

3.3.2.1.19. *Seed Yield Plant^{-1}*

Measured the weight of matured seeds from each plant at the time of harvest and calculated its average.

3.3.2.1.20. *Days to Maturity*

Counted the number of days from sowing to 90 per cent maturation of plants in an accession.

3.3.2.2. *Biochemical Characters*

3.3.2.2.1. *Crude Protein*

Crude protein content was calculated from the nitrogen content of the plant dry matter following the modified kjeldahl method (Jackson, 1973) and then multiplying it with 6.25.

3.3.2.2.2 *Crude Fibre*

Crude fibre content was estimated using acid & alkali digestion method on powdered plant sample (Kanwar and Chopra, 1976).

3.3.2.3. *Qualitative Characters*

Scoring based on the descriptors by Roy *et al.* (2017) was adopted for assessment of qualitative characters which is given in table 4.

Table 4. Descriptor for qualitative traits (Roy *et al*., 2017)

Sl. No.	Traits	Recording of observation	Score	Descriptors state
1	Early plant vigour	After 25 days of sowing	1 2 3	Poor Good Very good
2	Plant growth habit	At initiation of flowering	1 2 3 4 9	Erect Semi erect Spreading Bushy Others(Specify)
3	Leaf texture	Classified by appearance and feel of upper leaf surface	1 2	Rough Smooth
4	Leaf colour	At 50 per cent flowering	1 2 3 9	Light green Green Dark green Others (specify)

Table 4. Descriptor for qualitative traits (Roy *et al*., 2017) (Contd..)

5	Stem solidness	At 50 per cent flowering	1 2	Hollow Solid
6	Flower colour	At full blossom stage	1 2 3 4 9	White Pink Red Purple Others (specify)
7	Seed colour	After harvest of pods	1 2 3 4 5 6 9	White Brown Black Red Grey Mottled Others (specify)

3.4 STATISTICAL ANALYSIS

3.4.1. Analysis of Variance

Analysis of variance was worked out for both experiment 1 and 2. For experiment 1 it is calculated using replicated data, while for experiment 2 it is done for non-replicated data. The statistical analysis was carried out using "GRAPES" software of Kerala Agricultural University.

3.4.1.1. *Experiment 1- One-Way ANOVA*

Experiment 1 was carried out in CRD (Completely Randomized Design) with 2 replications. PCA (Principal Component Analysis) was done with the data to arrive at a valuable interpretation.

Source of variation	df	SS	MSS	'F' value
Treatment	t-1	TrSS	TrMSS	TrMSS/EMSS
Error	n-t	ESS	EMSS	
Total	n-1	TSS	TMSS	

Where, t = No. of Treatments

n = Total No. of Observation

The significance was checked by referring to the table F value.

3.4.1.2. Experiment 2- ANOVA

Experiment 2 was carried out in Augmented Randomized Block Design, where checks are replicated in all blocks.

Source of variation	df	SS	MSS	'F'
Blocks	b-1	BSS	BMSS	BMSS/EMSS
Checks	c-1	CSS	CMSS	CMSS/EMSS
Treatments Test	t-1	TrSS	TrMSS	TrMSS/EMSS
Test v/s Checks	1	ISS	IMSS	IMSS/EMSS
Error	(b-1) (c-1)	ESS	EMSS	

Where, b = No. of blocks BMSS – Block Mean Sum of Square

c = No. of Check Variety CMSS – Check Mean Sum of Square

t = No. of Treatments TrSS – Treatment Mean Sum of Square

IMSS – Interaction Mean Sum of Square

EMSS – Error Mean Sum of Square

3.4.1.3. *Biochemical Evaluation – One –Way ANOVA*

Biochemical characters such as crude protein and crude fibre was estimated for the best thirty genotypes which showed high Green fodder yield along with checks. Estimation was carried out in CRD with 2 replications.

Source of variation	df	SS	MSS	'F' value
Treatment	t-1	TrSS	TrMSS	TrMSS/EMSS
Error	n-t	ESS	EMSS	
Total	n-1	TSS	TMSS	

Where, t = No. of Treatments

n = Total No. of Observation

The significance was checked by referring to the table F value.

3.4.2. Estimation of Genetic Parameters

3.4.2.1. *Genetic Components of Variance*

By equating expected value of mean squares (MS) with the respective variance components, the phenotypic and genotypic components can be estimated (Jain, 1982).

i) Genotypic variance $(V_G) = \frac{MST-MSE}{r}$

ii) Environmental variance $(V_E) = MSE$

iii) Phenotypic variance $(V_p) = V_G + V_E$

3.4.2.2. *Coefficient of variation*

Genotypic, Environmental and Phenotypic Coefficient of variance were estimated from V_G, V_E, V_P respectively. The values were expressed in percentage for each trait.

i) Genotypic coefficient of variation $(GCV) = \frac{\sqrt{VG}}{X} \times 100$

ii) Environmental coefficient of variation $(ECV) = \frac{\sqrt{VE}}{X} \times 100$

iii) Phenotypic coefficient of variation $(PCV) = \frac{\sqrt{VP}}{X} \times 100$

Where, X is the grand mean

Range of coefficient of variation was classified according to the scale of variation given by Sivasubramanian and Menon (1973) are given below:

Low : less than 10 per cent

Medium : 10 – 20 per cent

High : more than 20 per cent

3.4.2.3. *Heritability (Broad Sense)*

Broad sense heritability (h^2) is the ratio between genotypic variance to the total variance (phenotypic variance) in a population and it is calculated by using the formula given by Burton (1952) and Johnson *et al*. (1955)

$h^2 = \frac{VG}{VP} \times 100$

Range of heritability (Johnson *et al*.,1955)

Low : 0-30 per cent

Medium : 30- 60 per cent

High : > 60 per cent

3.4.2.4. *Genetic Advance*

Genetic advance is the expected genetic gain or improvement in the following generation by the selection of superior genotype under certain selection pressure. Johnson *et al*. (1955) suggested formula for genetic advance is given below:

$GA = k.h^2.\sqrt{vp}$

Where, k = selection differential

k= 2.06 at 5 per cent selection intensity (Miller et al., 1958)

h^2= Heritability

V_p = Phenotypic variance

Genetic advance as per mean (GAM) = $\frac{GA}{X} \times 100$

Where, GA = Genetic Advance

X = Grand Mean

Range of Genetic Advance (Johnson *et al*., 1955)

Low : < 10 per cent

Medium : 10-20 per cent

High : > 20 per cent

3.4.3. Correlation Analysis

The degree and direction of the character associations are represented by correlation coefficient between different pairs of characters at the genotypic and phenotypic levels and it is estimated from genotypic, phenotypic and environmental variances and covariance. Here phenotypic correlation matrix was made using Indostat software

Genotypic correlation coefficient $\mathbf{r_{g12}} = \frac{\mathbf{Cov\ g12}}{\sqrt{\sigma^2_{g1}.\sigma^2_{g2}}}$

Where, Cov $_{g12}$ is the genotypic covariance between two traits, $\sigma^2 g_1$ and $\sigma^2 g_2$ are the genotypic variance of first trait and second trait respectively.

Phenotypic correlation coefficient $r_{P12} = \frac{\text{Cov p12}}{\sqrt{\sigma^2_{p1} \cdot \sigma^2_{p2}}}$

Cov $_{p12}$ is the phenotypic covariance between the two traits, $\sigma^2 p_1$ and $\sigma^2 p_2$ are the phenotypic variance for each trait.

Values of correlation coefficient and its scale suggested by Searle (1965)

≥ 0.65	– very strong
0.50 to 0.64	– moderately strong
0.30 to 0.49	– moderately weak
< 0.30	– very weak

3.4.4. Path Coefficient Analysis (Dewey and Lu, 1959)

Path coefficient analysis was performed using the phenotypic and genotypic correlation coefficients to know the direct and indirect effect of independent variable over dependent variable. In this study, green fodder yield per plant was taken as dependent variable along with selected component characters and subjected to path analysis to find out its cause and effect relationships and path diagram was also constructed. Residual effect was measured using the formula;

Residual effect PRy= $\sqrt{1 - r^2}$

Where, $r2 = (P_{1y}r_{1y} + P_{2y}r_{2y} + \ldots\ldots\ldots\ldots\ldots\ldots + P_{ny}r_{ny})$

P_{iy} = direct effect of X_i on y

r_{iy} = correlation coefficient of X_i on y

Score values of direct and indirect effect by Lenka and Mishra (1973)

0.0 – 0.09 : Negligible

0.1 – 0.19 : Low

0.2 – 0.29 : Moderate

0.3 – 1.0 : High

> 1.0 : Very high

3.4.5. Cluster Analysis

Cluster analysis was done using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method formulated by Sokal and Michener,1958

3.4.6. Core Analysis

3.4.6.1. *Identification of core set*

A subset of base collection which capture most of the available genetic diversity was formed using "Power Core" (v.1.0) software developed by Genetic Resource Division, Rural Development Administration, Republic of Korea. This use Advanced M (Maximization) strategy implemented through a modified Heuristic Algorithm.

3.4.6.2. *Core Set v/s Base Collection comparison*

To find out that the core set possess most of all the variability in base collection different statistical test were carried out which are mentioned below.

3.4.6.2.1. *Percentage Geographical Distribution of Accessions*

The accessions in core set and base collection were classified according to its place of origin and percentage distribution compared for both.

Per cent distribution = (No. of accessions from Place A/ Total no. of accessions) * 100

3.4.6.2.2. *Goodness of Fit Test*

To find the extent of diversity retained in core w.r.t. base, frequencies of distribution of accessions in core set and base collection were carried out using chi square ($\chi 2$) test for qualitative characters.

$$\chi 2 = \sum (O_i - E_i)^2 / E_i,$$

where, O_i = observed value (actual value) and E_i = expected value.

Degrees of freedom: n-1 (n is the number of classes in each trait)

For quantitative character mean, range, variance was compared using two sample t test and homogeneity test of variance (F test)

3.4.6.2.3. Two Sample t Test

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{(s^2(\frac{1}{n_1} + \frac{1}{n_2}))}}$$

where, t is the t-value, x_1 and $\bar{x}_2$ are the means of the two groups

s^2 is the pooled standard error of the two groups

n_1 and n_2 are the number of observations in each of the groups

n_1-1 and n_2-1 are the degrees of freedom

3.4.6.2.4. *Homogeneity Test of Variance (F test)*

$$F = \frac{\sigma_1^2}{\sigma_2^2}$$

$$where\ \sigma^2 = \frac{\sum (x - \mu)^2}{n}$$

3.4.6.2.5. *Shannon – Weaver Diversity Index (H')*

The phenotypic diversity among core and the base also assessed using Shannon and Weaver diversity index (H').

It was estimated using the formula:

$$H = \sum_{i=1}^{n} pi \log_e pi$$

Where, n = Number of phenotypic classes

pi = The proportion of individuals of a given species the total number of individuals in the community

Percentage genetic diversity can be calculated by using the formula:

Per cent diversity = (Core set mean/ Base collection mean) * 100

Results

4. RESULTS

The results of the present investigation "Identification of Core Set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions" are presented in this chapter under following titles.

4.1. Evaluation of seedling characters

4.1.1 Variability studies in Base Collection for seedling characters

4.1.2. Principal Component Analysis of seedling characters

4.2. Evaluation of variability in Base Collection

4.2.1. Variability studies in Base Collection for quantitative traits

4.2.2. Variability for biochemical characters

4.3. Estimation of genetic parameters of the Base Collection

4.4. Correlation studies of different characters in the Base accessions

4.5. Path coefficient analysis

4.6. Cluster analysis

4.7. Core analysis

4.7.1. Identification of Core Set

4.7.2. Comparisons of Core Set and Base Collection

4.7.2.1. Percentage geographical distribution of accessions

4.7.2.2. Frequency distribution of qualitative traits in Core Set and Base Collection

4.7.2.3. Variability in Core Set and Base Collection with respect to quantitative traits

4.7.2.4. Diversity in Core Set & Base Collection

4.7.3. Evaluation of Core Set accessions

4.1. EVALUATION OF SEEDLING CHARACTERS

One hundred and forty-six accessions in Base Collection were evaluated for their seedling characters in Completely Randomized Design with 2 replications. Observations like germination per cent, shoot length, root length, seedling length, fresh weight, dry weight, vigor index and relative growth index were taken. The data collected were subjected to statistical analysis and result are given below.

4.1.1. Variability Studies in Base Collection for Seedling Characters

Analysis of variance revealed that there was significant difference among all accessions for all the seedling characters under study. The mean values for different seedling character studied is depicted in table 5.

Table 5. Analysis of variance of different seedling characters

Sl. No.	Source of variation	Mean±SE	Calculated F value
1	Germination percentage	91.44 ±1.202	21.37*
2	Root length(cm)	8.75±0.333	13.89*
3	Shoot length(cm)	6.73±0.286	18.86*
4	Seedling length (cm)	15.46±0.576	20.21*
5	Seedling fresh weight(g)	79.82±1.706	75.26*
6	Seedling dry weight (g)	11.84±0.441	30.33*
7	Vigour index	1447±61.017	29.79*
8	Relative growth index (per cent)	0.389±0.022	13.46*

EC109493/3427-2

IC398992

Plate 3. Evaluation of seedlings

IC39908

IC402125

EC723987

Plate 3. Evaluation of seedlings

4.1.1.1. *Germination percentage*

The genotypes differed significantly for germination percentage with a mean value of 91.4 per cent. 36 genotypes recorded less germination per cent than average value.

4.1.1.2. *Root length*

Significant difference was observed among the genotypes for seedling root length. It ranged from 2 cm to 20.2 cm with an average value of 8.75 cm. The accession EC723987 showed the maximum root length and EC240878 had the minimum value.

4.1.1.3. *Shoot length*

Shoot length differed significantly among the genotypes and ranged between 0.5 and 15 cm with an average of 6.7 cm. The genotype IC398992 recorded highest shoot length among the accessions.

4.1.1.4. *Seedling length*

Significant variation was observed among the genotypes for seedling length with a range between 2.8 and 33.25 cm and a mean value of 15.5 cm. The genotype IC398992 showed the highest seedling length followed by genotype EC723987. The lowest seedling length was for EC240878.

4.1.1.5. *Seedling fresh weight*

Seedling fresh weight for 100 seedlings significantly differed among all the genotypes with an average value of 79.8 g. The values ranged from 26.8g to 165.7 g. Maximum fresh weight was for EC724787 and minimum for NR/18-105.

4.1.1.6. *Seedling dry weight*

The genotypes differed significantly for seedling dry weight and ranged from 2.9 to 32.9g with an average value of 11.84 g taken for oven dried 100 seedlings. The highest dry weight was recorded for IC402125 and lowest for EC2791.

4.1.1.7. *Vigour index*

Vigour index among the genotypes ranged from 185 to 3325 with a mean of 1447. All the genotypes significantly differed among each other. The highest vigour index was estimated for IC398992 which was on par with EC723987and lowest for NR/18-105.

4.1.1.8. *Relative growth index*

Significant variation was observed among all the genotypes for relative growth index with an average value of 39 per cent. The highest value was observed for IC372642 and lowest for IC553515.

4.1.2. Principal Component Analysis of Seedling Characters

Principal Component Analysis (PCA) was done for eight seedling characters to understand genetic diversity among the traits.

Total variances were distributed in to eight principal component (PC) group which is depicted in fig1. 86.5 per cent of total variance was contributed from first three PC groups. The PC1 had an eigen value of 4.413 and included 55.2 per cent of total variance. PC 2 showed second highest eigen value (1.589) and contributed 19.9 per cent of total variance.

The loading plot diagram (fig 2) depicted the distribution of different characters in various quadrants. The character like germination per cent found closer to the origin had lower loading score with least contribution towards divergence while the characters such as seedling length, fresh weight, seedling vigor which are away from the origin had the maximum loading score which contributed highest towards genetic divergence.

Biplot constructed (fig 3) using first two PC showed the arrangements of accessions in different quadrates. In the present study, genotypes *viz*., NR/18-105, IC398992, IC402125, EC101967, EC240878, IC39908, EC723987 are scattered apart in all the four quadrates of the biplot representing maximum genetic divergence among the genotypes. The genotypes placed in 1st quadrant were similar for seedling fresh weight, root length and germination per cent. Genotypes in 2nd quadrant were similar for shoot length, seedling length and

seedling vigour. Genotypes in 3rd quadrant differ from each other for all the characters. Genotypes present in 4th quadrant were similar for dry weight and RGR.

The interaction among the characters and the PC groups are geometrically represented in squared cosine diagram (fig 4). Seedling vigour and seedling length possessed highest absolute value in the first principal component followed by root length, shoot length which depicted that 55.2 per cent genetic divergence among the genotypes was mainly based on these characters. Seedling fresh weight and dry weight showed maximum value in PC 2 which accounted for the 19.85 per cent total variation. In 3rd PC germination percentage showed the maximum value.

4.2. EVALUATION OF VARIABILITY IN BASE COLLECTION

The field experiment was conducted in augmented block design with 143 treatments and 3 checks. The check varieties were Aiswarya from Kerala, KBC-1 from Karnataka, and EC-4216 from USA. The three check varieties were replicated in all the 13 blocks. Each block has 11 accessions planted in two rows of ten plants each. The seeds were sown in the field on 15th January 2021.

4.2.1. Variability Studies in Base Collection for Quantitative Traits

Analysis of variance for biometric characters in Base Collection revealed that highest significant difference was seen between accessions for all the characters except number of secondary branches per plant and stem girth (Table 6).

Principal Component Analysis of seedling characters

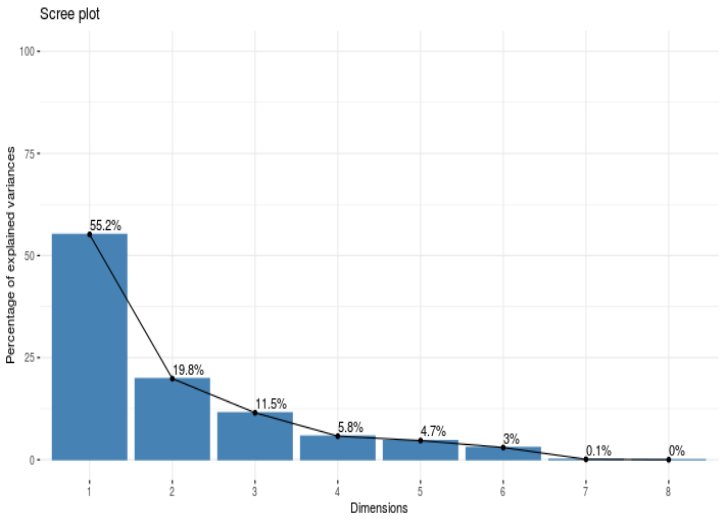


Fig. 1. Scree plot showing contribution of various principal components towards divergence.

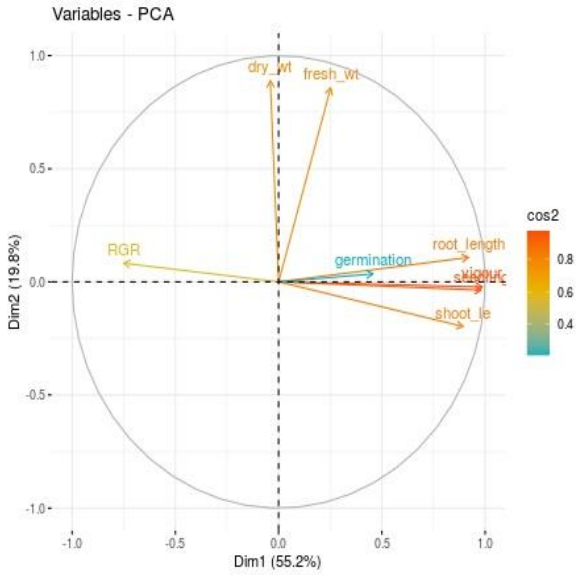


Fig. 2. Loadings plot of eight seedling characters based on principal components

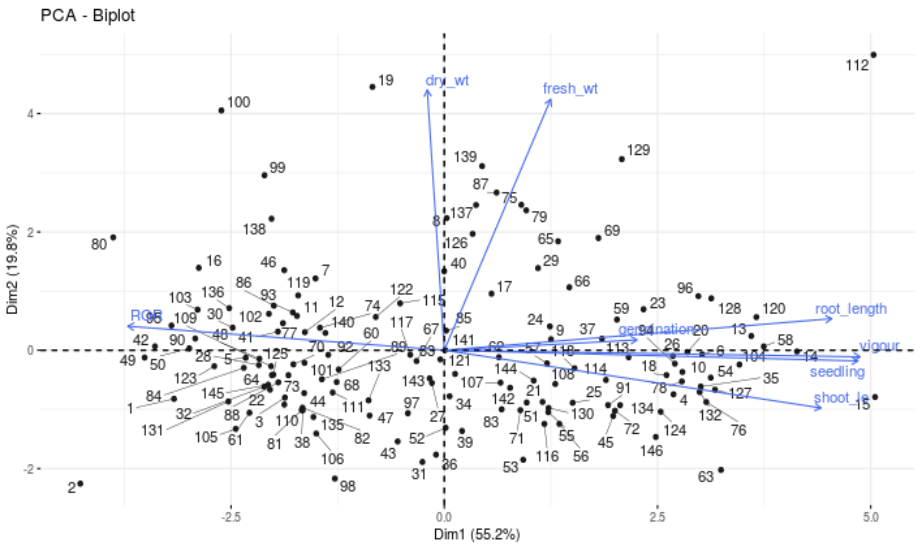


Fig 3. Biplot showing variation among 146 fodder cowpea genotypes along with eight seedling characters

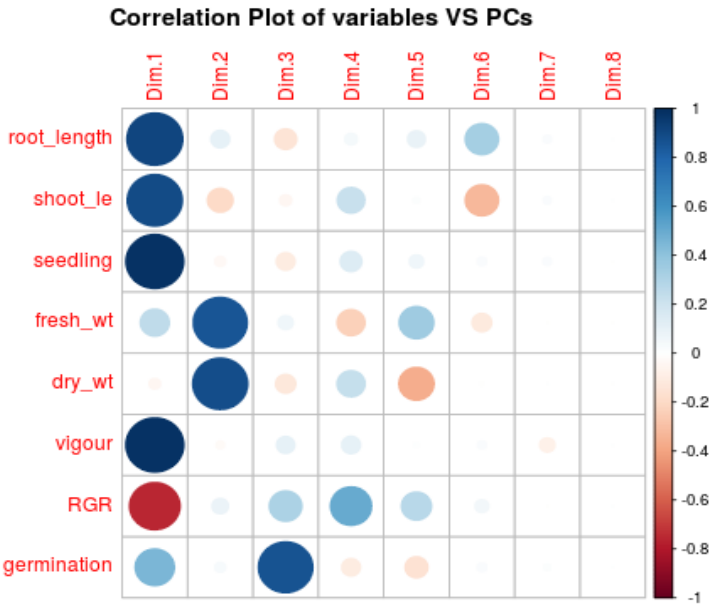


Fig. 4. Squared cosine variables of major principal components

4.2.1.1. *Number of primary branches plant^{-1}*

Number of primary branches per plant ranged from 1 to 5 with a mean value of 2.85.

4.2.1.2. *Number of secondary branches plant^{-1}*

There is no deviation seen in any genotypes in case of number of secondary branches per plant. None of the genotypes had any secondary branches in them.

4.2.1.3. *Number of leaves plant^{-1}*

All the genotypes differ significantly for number of leaves per plant with a mean value of 15.8 and ranged from 5 (IC519621) to 35 (EC14702)

4.2.1.4. *Leaflet length*

Leaflet length ranged from 7.1 cm (IC402111) to 15.7 cm (EC101978) with a mean value of 10.3 cm. All the genotypes significantly differed for leaflet length.

4.2.1.5. *Leaflet width*

All the genotypes differed significantly for leaflet width with a mean value of 5.9 cm and ranged from 2.1 cm (IC1255) to 9.3 cm (EC724352).

4.2.1.6. *Stem girth*

Stem girth showed a non-significant difference among the genotype with a mean value of 3.4 cm and ranged from 1 cm (KBC-4) to 4.9 cm (IC253278)

4.2.1.7. *Number of nodes plant^{-1}*

Number of nodes per plant significantly differed among all the genotypes with an average value of 8.6 and ranged from 4 (SNAR-12-08) to 16 (EC101970)

4.2.1.8. *Internode length*

Internode length ranged from 0.5 cm (EC244021) to 5.4 cm (EC10734) with a mean value of 2.6 cm. All the genotypes significantly differ from each other for internode length.

4.2.1.9. *Days to 50 per cent flowering*

All the genotypes significantly differed from each other for days to 50 per cent flowering with a mean value of 43 days and ranged from 30 (EC244021) to 56 (KBC-4) days.

4.2.1.10. *Green fodder yield plant^{-1}*

Green fodder yield per plant showed a significant difference with a mean value of 98.4g and a range of 16 g (EC724787) to 260 g (EC241037)

4.2.1.11. *Dry matter yield plant^{-1}*

Dry matter yield per plant ranged from 2.2 g (EC724787) to 36.7 g (EC241037) with an average value of 15.4. Significant deviation was observed among the genotypes for dry matter yield per plant.

4.2.1.12. *Leaf Stem Ratio (LSR)*

The mean value of leaf stem ratio was 1.46 and ranged from 0.29 (EC101978) to 3.01 (EC546491). All the genotypes significantly differ from one another.

4.2.1.13. *Leaf dry weight plant^{-1}*

All the genotypes significantly differed from each other for leaf dry weight per plant with a mean value of 8.9 g and ranged from 1.6 g (EC724787) to 19.6 g (EC241037).

4.2.1.14. *Stem dry weight plant^{-1}*

Stem dry weight per plant showed a significant difference among accessions with a mean value of 6.5 g and a range of 1.08 g (KBC-4) to 17.02 g (EC241037)

4.2.1.15. *Leaf Area Index (LAI)*

Significant difference among genotypes was observed for LAI with a mean value of 4.63 and ranged from 0.5 (IC1255) to 15.5 (IC257413).

4.2.1.16. *Number of seeds pod^{-1}*

Number of seeds per pod differed significantly among the accessions with a mean value of 12 and a range of 6 (IC257410) to 17 (EC98668)

4.2.1.17. *1000 seed weight*

Significant variation was observed among genotypes for 1000 seed weight with a mean value of 124 g and ranged from 54g (IC26012) to 237g (IC39908).

4.2.1.18. *Seed yield plant^{-1}*

Seed yield per plant showed an average of 12.3 g and ranged from 4 g (IC546523) to 29.9 g (EC546491). All the genotypes significantly differed from each other for this trait.

4.2.1.19. *Plant height*

All the genotypes significantly differed for plant height with a mean value of 30 cm and ranged from 13.6 cm (EC2791) to 111.6 cm (EC101970).

4.2.1.20. *Days of maturity*

All the genotypes significantly differed from each other for days of maturity. A mean value of 62 days as observed for this trait and it ranged from 50 (EC244021) to 77 (Kanakamony) among the genotypes studied.

Table 6. Analysis of variance for quantitative traits in Base collection

Source of variation	Df	Number of primary branches per plant	Number of secondary branches per plant	Number of leaves per plant	Leaflet length (cm)	Leaflet width (cm)
Blocks	12	3.012**	NA	3.216**	1.128	1.715
Checks	2	1.783	NA	1.886	0.526	1.229
Treatment Test	142	1.888*	NA	12.416**	1.849*	1.822*
Test v/s Check	1	44.242**	NA	324.31**	2.612	0.330
Error	24	NA	NA	NA	NA	NA

Table 6. Analysis of variance for quantitative traits in Base collection (Contd…)

Source of variation	Df	Stem girth(cm)	Number of nodes per plant	Internode length (cm)	Days to 50% flowering	Leaf Area Index
Blocks	12	2.032	3.676**	1.757	3.49**	1.629
Checks	2	6.154**	6.152**	7.583**	121.421**	2.183
Treatment Test	142	1.514	3.331**	2.207**	9.357**	5.701**
Test v/s Check	1	31.19**	39.030**	5.479*	279.346**	82.461**
Error	24	NA	NA	NA	NA	NA

***P= 0.05 and P ** =0.01**

Table 6. Analysis of variance for quantitative traits in Base collection (Contd….)

Source of variation	Df	Green fodder yield per plant (g)	Dry matter yield per plant(g)	Leaf Stem Ratio (LSR)	Leaf dry weight per plant(g)	Stem dry weight per plant(g)
Blocks	12	5.311**	4.659**	3.333**	3.496**	6.885**
Checks	2	4.335*	3.552*	3.562*	4.188*	1.766
Treatment Test	142	4.212**	4.012**	1.47	3.116**	5.835**
Test v/s Check	1	64.922**	68.502**	16.077**	37.893**	118.87***
Error	24	NA	NA	NA	NA	NA

Table 6. Analysis of variance for quantitative traits in Base collection (Contd…)

Source of variation	Df	Number of seeds per pod	1000 seed weight (g)	Seed yield per plant(g)	Plant height (cm)	Days to maturity
Blocks	12	1.094	1.226	1.149	3.526**	5.071**
Checks	2	0.545	222.199**	24.23**	4.61*	22.22**
Treatment Test	142	1.962*	50.011**	10.051**	7.832**	3.782**
Test v/s Check	1	3.251	86.377**	169.59**	3.065	46.96**
Error	24	NA	NA	NA	NA	NA

***P= 0.05 and P ** =0.01**

4.2.2. Variability for Biochemical Characters

Biochemical characters such as crude protein content and crude fibre content (%) were estimated for best thirty genotypes including check varieties which showed high green fodder yield per plant. The design was Completely Randomized Design with 2 replications. The mean performance of these characters is given in table 7.

Table 7. Mean performance of crude protein & crude fibre content in fodder cowpea

Treatment	**CP mean**	**CF mean**	**Treatment**	**CP mean**	**CF mean**
T5	21.215	18.13	T57	24.01	19.89
T8	20.55	18.95	T58	16.99	19.76
T9	18.65	18.43	T59	21.265	19.21
T11	18.35	18.04	T63	19.03	21.855
T23	15.875	18.3	**T64**	20.96	**22.5**
T24	17.71	**16.945**	T73	22.885	19.59
T26	20.775	20.165	T74	19.01	22.31
T30	20.27	19.41	T76	18.605	22.485
T31	19.97	20.46	T81	24.36	20.77
T32	19.005	18.995	**T89**	**26.73**	17.585
T33	17.58	19.525	T100	23.94	21.605
T40	22.22	22.2	T124	18.74	21.41
T44	22.41	22.28	C1	20.33	18.56
T46	21.615	18.12	C2	22.63	22.165
T49	19.23	22.125	C3	20.44	20.495

Biochemical characters	**Mean**	**SE**	**CD (5 per cent)**
Crude protein	**20.512**	**0.297**	**0.859**
Crude fibre	**20.082**	**0.186**	**0.537**

Table 8. ANOVA for Crude protein and Crude fibre content

Source of variation	df	F calculated		F critical
		CP	CF	
Treatment	29	66.508**	83.739**	1.62
Error	30	NA	NA	-

4.2.2. *Crude protein content*

All the thirty genotypes significantly differed from each other for crude protein content with a mean value of 20.5 per cent. The maximum crude protein content was shown by EC390241 with 26.73 per cent followed by EC240885-2 with 24.36 per cent which is on par to EC4218 with 24.01 per cent. Minimum crude protein content was obtained in IC363962 with 15.875 per cent.

4.2.2.2. *Crude fibre content*

Highest crude fibre content was recorded for EC101970 with 22.5 per cent which is on par to EC240635 with 22.48 per cent and the least crude fibre content was reported for IC337387 with 16.95per cent. All the thirty genotypes showed significant difference from each other with a mean value of 20 per cent.

4.3. ESTIMATION OF GENETIC PARAMETERS OF THE BASE COLLECTION

Genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance for 20 biometric characters were estimated and are given in table 9.

High PCV and GCV was recorded for number of primary branches per plant, number of leaves per plant, internode length, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight, seed yield per plant and plant height.

Low PCV and GCV was seen for days of maturity. For all the characters, PCV showed greater value than GCV indicating the environmental effects on expression of these characters.

High heritability accompanied with high genetic advance as per cent of mean observed for number of leaves per plant, number of nodes per plant, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight and plant height, which indicated that this heritability is due to additive gene action and selection may be effective for these characters.

For characters like number of primary branches per plant, internode length, leaf stem ratio has high genetic advance as per cent of mean with a moderate heritability. These characters can also be used for selection since this medium heritability is due to environmental effect.

1000 seed weight had highest heritability (98 per cent) and leaf stem ratio had the lowest (32 per cent). Genetic advance as per cent of mean was moderate for leaflet length, leaflet width, stem girth, days of 50 per cent flowering, number of seeds per pod and days of maturity. All the other characters showed high genetic advance.

PCV, GCV, heritability and genetic advance were highest for number of leaves per plant, number of nodes per plant, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight and plant height revealed that these characters are very much effective for selection and crop improvement programmes.

Table 9. Genetic parameters for quantitative traits in Base collection

Sl. No.	Traits	Mean±SE	Range		Variance		Coefficient of Variability		h^2 (Broad sense) (%)	GA
			Min	Max	PV	GV	PCV (%)	GCV (%)		
1	Number of primary branches per plant	2.83±0.084	1	5	1.004	0.472	35.70	24.49	47.03	34.64
2	Number of secondary branches per plant	0	0	0	0	0	NA	NA	NA	NA
3	Number of leaves per plant	15.80±0.574	5	35	47.09	43.3	43.80	42.01	91.95	83.09
4	Leaflet length (cm)	10.31±0.143	7.1	15.7	2.91	1.34	16.56	11.22	45.92	15.69
5	Leaflet width (cm)	5.91±0.100	2.1	9.3	1.44	0.65	20.29	13.63	45.12	18.89
6	Stem girth(cm)	3.37±0.058	1	4.9	0.47	0.16	20.48	11.93	33.93	14.34
7	Number of nodes per plant	8.55±0.172	4	16	4.22	2.95	24.09	20.16	69.98	34.79
8	Internode length (cm)	2.58±0.101	0.5	5.4	1.45	0.79	46.45	34.35	54.69	52.40
9	Days to 50% flowering	43.43±0.372	30	56	19.75	17.64	10.21	9.65	89.31	18.82
10	Green fodder yield per plant (g)	98.37±4.252	16	260	2584.8	1971	51.93	45.35	76.26	81.70

Table 9. Genetic parameters for quantitative traits in Base collection (Contd…)

Sl. No.	Traits	Mean±SE	Range		Variance		Coefficient of Variability		h^2 (Broad sense) (%)	GA
			Min	Max	PV	GV	PCV (%)	GCV (%)		
11	Dry matter yield per plant(g)	15.43±0.618	2.22	36.7	54.55	40.95	48.12	41.70	75.07	74.53
12	Leaf Stem Ratio (LSR)	1.47±0.042	0.29	3.01	0.26	0.08	34.31	19.41	31.99	22.64
13	Leaf dry weight per plant(g)	8.93±0.367	1.6	19.6	19.28	13.09	49.33	40.65	67.90	69.10
14	Stem dry weight per plant(g)	6.50±0.282	1.08	17.02	11.33	9.39	52.09	47.41	82.86	89.04
15	Leaf Area Index	4.63±0.230	0.5	15.53	7.59	6.26	60.04	54.52	82.46	102.13
16	Number of seeds per pod	12.18±0.176	6	17	4.43	2.17	17.30	12.11	49.03	17.50
17	1000 seed weight (g)	124.16±2.76	54	237	1087.4	1065.7	26.59	26.33	98	53.77
18	Seed yield per plant(g)	12.29±0.400	4	29.9	22.87	20.59	39.15	37.15	90	72.73
19	Plant height (cm)	30.13±1.272	13.6	111.6	231.40	201.90	50.55	47.22	87.23	90.97
20	Days to maturity	61.46±0.435	50	77	27.11	19.90	8.46	7.26	73.56	12.84

4.4. CORRELATION STUDIES OF DIFFERENT CHARACTERS IN THE BASE COLLECTION

The association between twenty characters was worked out in all possible combination and phenotypic correlation matrix for green fodder yield and its contributing characters are depicted in table 10.

Green fodder yield per plant showed a highly significant positive phenotypic correlation with dry matter yield per plant (0.981), stem dry weight per plant (0.938), leaf dry weight per plant (0.936), number of leaves per plant (0.559), leaf area index (0.525), stem girth (0.449), number of nodes per plant (0.439), plant height (0.373) and a negative significant correlation with leaf stem ratio (-0.208). It showed no correlation with days to 50 per cent flowering.

Significant positive phenotypic correlation was recorded in between days to 50 per cent flowering and leaf stem ratio (0.185) and a negative significant correlation with stem girth (-0.163).

Highly significant positive phenotypic correlation was seen in between dry matter yield per plant and green fodder yield per plant (0.981) followed by leaf dry weight per plant (0.966), stem dry weight per plant (0.942), leaf area index (0.483), plant height (0.386) and a negative significant correlation with leaf stem ratio (-0.179).

Plant height had a positive significant phenotypic correlation with number of nodes per plant (0.494), stem dry weight per plant (0.419), green fodder yield per plant (0.373), dry matter yield per plant (0.386), number of leaves per plant (0.359), leaf dry weight per plant (0.329) and leaf area index (0.286).

Stem dry weight per plant and leaf dry weight per plant showed a significant high positive phenotypic correlation (0.824). Both stem and leaf dry weight per plant had a significantly high positive correlation with dry matter yield per plant (0.942) ;(0.966), green fodder yield per plant (0.938); (0.936), number of leaves per plant (0.578); (0.416), leaf area index (0.544); (0.399), stem girth (0.467); (0.356), number of nodes per plant (0.445); (0.376) and plant height (0.419); (0.329) respectively.

Table 10. Phenotypic correlation matrix of yield and yield contributing characters of fodder cowpea

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1													
X2	0.183*	1												
X3	0.102	0.407**	1											
X4	0.451**	0.151	0.099	1										
X5	0.541**	0.171*	0.211**	0.351**	1									
X6	0.037	0.016	0.068	-0.058	-0.101	1								
X7	0.041	0.101	0.089	-0.163*	-0.048	0.150	1							
X8	0.509**	0.168*	0.223**	0.423**	0.425**	-0.019	0.029	1						
X9	-0.341	-0.139	-0.049	-0.306	-0.258	0.162	0.185*	-0.179*	1					
X10	0.359**	0.147	0.130	0.164*	0.494**	0.047	0.116	0.386**	-0.178*	1				
X11	0.828**	0.547**	0.465**	0.416**	0.470**	0.0534	0.091	0.483**	-0.287	0.286**	1			
X12	0.578**	0.195*	0.219**	0.467**	0.445**	-0.053	-0.026	0.942**	-0.445	0.419**	0.544**	1		
X13	0.416**	0.134	0.209*	0.356**	0.376**	0.009	0.071	0.966**	0.041	0.329**	0.399**	0.824**	1	
X14	0.559**	0.176*	0.225**	0.449**	0.439**	-0.025	0.065	0.981**	-0.208*	0.373**	0.525**	0.938**	0.936**	1

* significant at 5%

** significant at 1%

X1 : Number of leaves per plant
X2 : Leaflet length
X3 : Leaflet width
X4 : Stem girth
X5 : Number of nodes per plant
X6 : Internode length
X7 : Days to 50% flowering
X8 : Dry matter yield per plant
X9 : Leaf Stem Ratio
X10 : Plant height
X11 : LAI
X12 : Stem dry weight per plant
X13 : Leaf dry weight per plant
X14 : Green fodder yield per plant

4.5. PATH COEFFICIENT ANALYSIS

Path coefficient analysis provides information on direct and indirect effect of different characters on green fodder yield per plant since it was taken as the dependent variable. The independent variables studied were number of leaves per plant, leaflet length, leaflet width, stem girth, number of nodes per plant, internode length, days of 50 per cent flowering, dry matter yield per plant, leaf stem ratio, plant height, leaf area index, stem dry weight per plant and leaf dry weight per plant. The path matrix of green fodder yield per plant is presented in table 11 and the direct and indirect effect scored using the scale values given Lenka and Mishra (1973)

4.5.1. Direct Effects

Leaf dry weight per plant showed highest direct effect on green fodder yield per plant (4.38) followed by stem dry weight per plant (3.52). All other characters showed negligible direct effect on green fodder yield per plant. Negative direct effect was observed in dry matter yield per plant on green fodder yield per plant. Thus, Indirect effects of dry matter yield per plant on green fodder yield per plant need to be considered for effective selection.

4.5.2. Indirect Effects

High indirect effect on green fodder yield was observed for many characters. Highest positive indirect effect was seen with dry matter yield per plant *via* leaf dry weight per plant (4.23) followed by stem dry weight per plant *via* leaf dry weight per plant (3.6). Dry matter yield per plant also showed a high indirect effect on green fodder yield per plant *via* stem dry weight per plant (3.32) and *via* leaf stem ratio (1.186).

Table 11. Direct and indirect effects of different characters on Green fodder yield/plant

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	**0.0818**	0.0150	0.0084	0.0369	0.0442	0.0031	0.0033	0.0416	-0.0279	0.0294	0.0677	0.0472	0.0340
X2	0.0004	**0.0021**	0.0009	0.0003	0.0004	0.0000	0.0002	0.0004	-0.0003	0.0003	0.0011	0.0004	0.0003
X3	0.0013	0.0050	**0.0124**	0.0012	0.0026	0.0008	0.0011	0.0028	-0.0006	0.0016	0.0058	0.0027	0.0026
X4	0.0118	0.0040	0.0026	**0.0263**	0.0092	-0.0015	-0.0043	0.0111	-0.0080	0.0043	0.0109	0.0123	0.0094
X5	0.0048	0.0015	0.0019	0.0031	**0.0088**	-0.0009	-0.0004	0.0038	-0.0023	0.0044	0.0042	0.0039	0.0033
X6	-0.0004	-0.0002	-0.0007	0.0006	0.0011	**-0.0105**	-0.0016	0.0002	-0.0017	-0.0005	-0.0006	0.0006	-0.0001
X7	0.0020	0.0049	0.0043	-0.0079	-0.0023	0.0073	**0.0485**	0.0014	0.0090	0.0056	0.0044	-0.0013	0.0034
X8	-3.3629	-1.1093	-1.4745	-2.7953	-2.8039	0.1267	-0.1935	**-6.6030**	1.1861	-2.5458	-3.1917	-6.2224	-6.3779
X9	-0.0058	-0.0024	-0.0008	-0.0052	-0.0044	0.0028	0.0031	-0.0031	**0.0170**	-0.0030	-0.0049	-0.0076	0.0007
X10	-0.0124	-0.0051	-0.0045	-0.0056	-0.0170	-0.0016	-0.0040	-0.0133	0.0061	**-0.0345**	-0.0099	-0.0144	-0.0114
X11	-0.0188	-0.0124	-0.0106	-0.0094	-0.0107	-0.0012	-0.0021	-0.0110	0.0065	-0.0065	**-0.0227**	-0.0123	-0.0091
X12	2.0333	0.6872	0.7708	1.6429	1.5652	-0.1871	-0.0931	3.3168	-1.5675	1.4735	1.9130	**3.5197**	2.8987
X13	1.8240	0.5854	0.9152	1.5615	1.6458	0.0376	0.3075	4.2326	0.1760	1.4442	1.7472	3.6090	**4.3821**
X14	0.5590	0.1757	0.2252	0.4492	0.4389	0.0246	0.0647	0.9803	0.2076	0.3730	0.5246	0.9377	0.9361

Residual effect = 0.176

X1 : Number of leaves per plant
X2 : Leaflet length
X3 : Leaflet width
X4 : Stem girth
X5 : Number of nodes per plant
X6 : Internode length
X7 : Days to 50% flowering
X8 : Dry matter yield per plant
X9 : Leaf Stem Ratio
X10 : Plant height
X11 : LAI
X12 : Stem dry weight per plant
X13 : Leaf dry weight per plant
X14 : Green fodder yield per plant

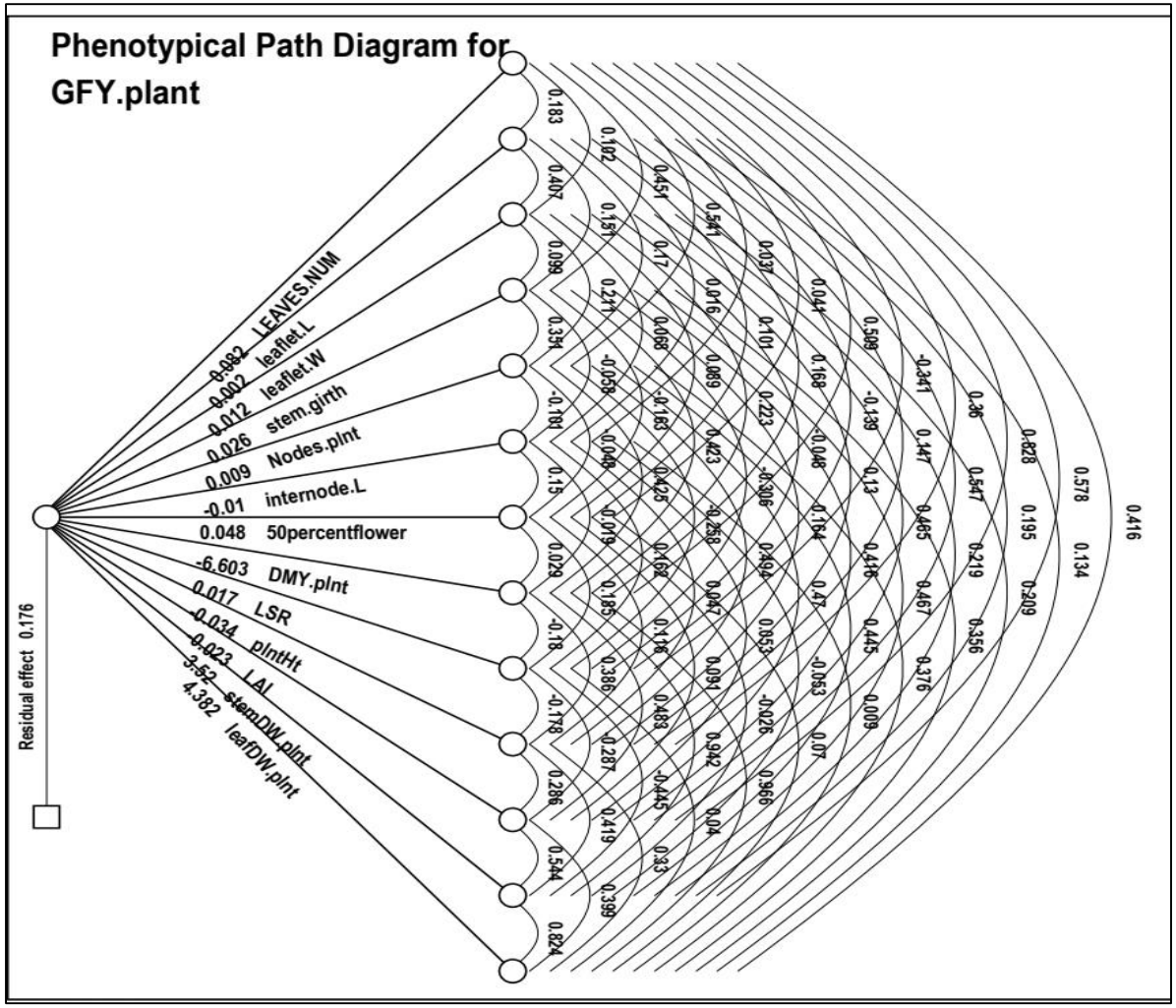


Fig. 5. Path diagram for green fodder yield per plant

Leaf area index showed a negligible negative direct effect on green fodder yield (-0.027). However, it had a high positive indirect effect on green fodder yield *via* stem dry weight per plant (1.91) and leaf dry weight per plant (1.75). Most of the other characters also showed a positive indirect effect on green fodder yield per plant *via* stem dry weight per plant and leaf dry weight per plant.

The residual effect obtained was 17.6 per cent which indicated that 82.4 per cent variation on green fodder yield per plant was contributed by the characters under study.

4.6. CLUSTER ANALYSIS

Cluster analysis was done using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method. The 146 accessions were grouped into 30 clusters shown in (table 12). Cluster X with 21 genotypes was the largest followed by cluster XI (20 genotypes), cluster XIV (13 genotypes), cluster I (12 genotypes), cluster VII (10 genotypes), cluster II (8 genotypes), cluster IV (7 genotypes), cluster XII and cluster XXVI1 (6 genotypes each), cluster XVII (5 genotypes), cluster VI, cluster VIII, cluster XIX and cluster XXIX (4 genotypes each), cluster XIII (3 genotypes), cluster IX, cluster XV, cluster XVIII and cluster XXIV (2 genotypes each) and the remaining were solitary clusters.

Table 12. Accessions in different cluster group

Cluster number	Number of accessions	Accessions in each cluster
1	12	IC553515, EC148714, EC2790, EC240635, NR/18-105, IC259069, EC244217, EC107183, NR/18-112, NR/18-99, NR/18-74, EC14966-1
2	8	EC98668, EC240744-A, IC257413, EC99569, EC4185, IC97787, IC546525, EC244211
3	1	EC241056

Table 12. Accessions in different cluster group (Contd….)

4	7	EC149345, EC109493/3427-2, EC107189, EC4190, EC42956, EC724773, EC109112
5	1	EC101967
6	4	EC239662, EC240630, EC107185, IC372642
7	10	IC253278,EC240671-1,EC99566, IC402125, IC548288, IC20678, EC42726, SNAR-12-11, NR/18-62, CS-88
8	4	EC241023, IC363962, EC241058, IC337387
9	2	IC546523, SNAR-12-08
10	21	EC240905, IC536723, EC724780, AISWARYA, EC723836, EC724591, EC724051, EC343036, IC20698, EC724807, EC724564, EC99682, EC724774, IC398992, IC546516, EC724779, EC723990, IC20682/P3, EC724033, EC107127, IC372130
11	20	EC4208, EC14966, IC402111, EC724768, IC402115, IC519621, EC4862, EC240891, IC249140, EC240755, EC240796-1, EC240912-1, EC240801, EC241022, KBC-1, IC259087, EC107119, IC20672, EC101997, IC20647
12	6	EC240925, IC394237, EC724382,EC724352, IC257414, IC257447
13	3	EC966551, IC257422, EC 4216
14	13	IC259084, IC20703, EC390207, EC724796, IC259061, EC734794, IC259076, DC-15, EC724818, KBC-4, EC724313, EC2791, DCS-47-1
15	2	EC724787, EC724498
16	1	IC26012
17	5	IC26048, EC244021, EC724778, EC110599, EC240856-1
18	2	IC1255, EC724824

Table 12. Accessions in different cluster group (Contd….)

19	4	EC546491, EC738173, EC367714, EC101978
20	1	IC3016
21	1	EC101970
22	1	KANAKAMONY
23	1	IC20696
24	2	EC10734, EC14702
25	1	EC241037
26	1	EC43203
27	6	EC109968,EC100090,EC101973,EC240878,EC240885-2, EC343047
28	1	EC723987
29	4	EC148711, EC4218, IC257410, EC390241
30	1	IC39908

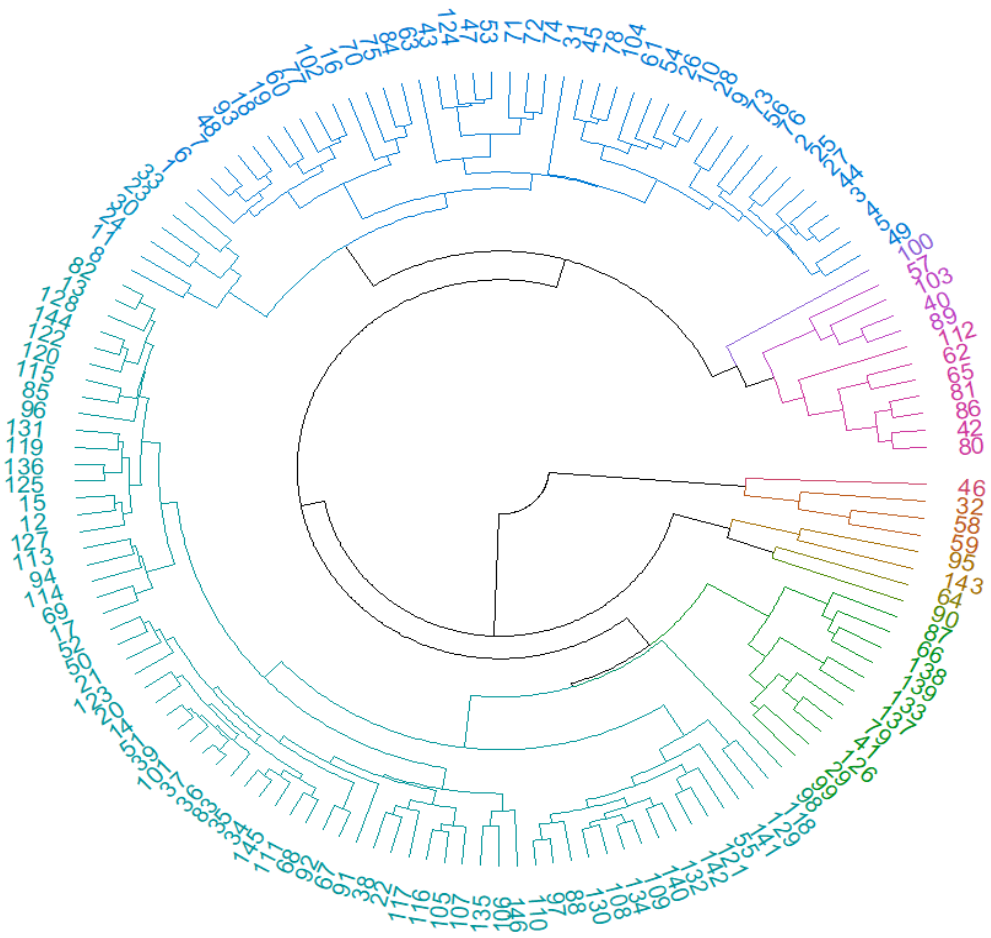


Fig. 6. Cluster Diagram

4.7. CORE ANALYSIS

Core Set is the subset of Base Collection which captures most of the available genetic diversity in it with negligible repetitiveness. Core analysis was carried out using Power Core (v.1.0) software using 20 quantitative characters of fodder cowpea.

4.7.1. Identification of Core Set

The Core Set identified comprised of 24 accessions out of 143 accessions in the Base Collection. The Core Set represented 16.8 per cent of the Base Collection which has a low mean difference (MD) value of 10.5 per cent, 42.8 per cent variable difference (VD), high coincidence ratio (CR) of 96.3 per cent and a high variable rate (VR) of 121.8 per cent. MD value less than 20 per cent is considered as a good one. While the CR greater than 80 per cent indicates the homogeneous distribution of quantitative traits in Core Set with respect to Base Collection. Variable rate more than 100 per cent is required to consider the identified Core Set as a true representation of Base Collection.

The Core Set obtained from the study included landraces, elite lines, breeding lines and released variety in it. The Core Set formation details and list of accessions identified as Core Set are given in table 13 respectively.

Table 13. Details pertaining to Core Set

Sl. No.	Accessions	Treatment number	Source	Sl. No.	Accessions	Treatment number	Source
1	SNAR-12-11	7	Unknown	13	EC101978	66	Nigeria
2	IC546523	11	Andhra Pradesh	14	EC367714	87	USA
3	IC363962	23	Arunachal Pradesh	15	IC20703	97	Chattisgarh
4	EC244217	27	Philippines	16	IC26012	98	Karnataka
5	EC244021	29	Philippines	17	IC39908	100	Gujarat

Table 13. Details pertaining to Core Set (Contd…)

Sl. No.	Accessions	Treatment number	Source	Sl. No.	Accessions	Treatment number	Source
6	EC241037	32	Philippines	18	IC257447	107	India
7	EC241023	33	Philippines	19	EC724564	119	Hungary
8	EC43203	46	Philippines	20	EC724313	121	Chad
9	EC4218	57	USA	21	EC966551	135	Unknown
10	EC10734	58	Unknown	22	IC1255	137	India
11	EC101970	64	Nigeria	23	DCS-47-1	141	Karnataka
12	EC101973	65	Nigeria	24	Kanakamony	143	Kerala

Table 14. Core Set formation details

Sl. No.	Particulars	Entries
1.	Number of accessions	143
2.	Number of variables	20
3.	Core Set	
a)	Maximum possible entries	143
b)	Power Core	24
4.	Mean Difference (MD)	10.5 per cent
5.	Coincidence Rate (CR)	96.3 per cent
6.	Variance Difference (VD)	42.85 per cent
7.	Variable Rate (VR)	121.84 per cent

4.7.2. Comparison of Core Set and Base Collection

Validation of the Core Set and ascertaining that the Core Set possessed most of all the variability in Base Collection was done using different statistical tools in these two population.

4.7.2.1. *Percentage geographical distribution of accessions*

The accessions in both Base Collection and Core Set were categorized based on their place of origin and their frequencies compared. Percentage geographical distribution of accessions in Core Set and Base Collection is presented in table 15.

The Base Collection comprised of accessions from most of all continents *viz*., Asia, Africa, North America, Europe, Australia. Most of the accessions are from India (34 per cent), followed by Philippines (15 per cent), USA (13 per cent), Nigeria (10 per cent), Uganda (2 per cent), Botswana, Chad, Tanzania, Liberia, South Africa, Senegal, Costa Rica, Honduras, Italy, Hungary, Australia (1 per cent) each.

Statewide distribution of Indian accessions included genotypes from New Delhi, Kerala, Karnataka, Telangana, Andhra Pradesh, Uttarakhand, Chhattisgarh, Gujarat, Arunachal Pradesh, Assam and Haryana.

In Core Set also majority of accessions are from India (9 out of 24, 38 per cent), which included accessions from Karnataka (2 accessions), Kerala, Chhattisgarh, Gujarat, Arunachal Pradesh and Andhra Pradesh (1 accession each). Second highest accessions in Core Set are from Philippines (21 per cent) followed by Nigeria (13 per cent), USA (8 per cent), Chad (4 per cent) and Hungary (4 per cent).

Table 15. Geographical distribution of accessions in Core Set & Base Collection

Sl. No.	Contin-ent	Country	State	Accessions Base	Per-cent distrib ution	Core Set	Per cent distributio n
1	Asia	India	Andhra Pradesh	3	2.097	1	4.167
			Arunachal Pradesh	1	0.699	1	4.167

Table 15. Geographical distribution of accessions in Core Set & Base Collection (Contd)

Sl. No.	Contin-ent	Country	State	Accessions Base	Per-cent distribution	Core Set	Per cent distribution
			Assam	1	0.699	0	-
			Chattisgarh	2	1.398	1	4.167
			Gujarat	1	0.699	1	4.167
			Haryana	1	0.699	0	-
			Karnataka	5	3.497	2	8.33
			Kerala	6	4.195	1	4.167
			Madhya Pradesh	5	3.497	0	-
			New Delhi	8	5.594	0	-
			Telangana	3	2.097	0	-
			Uttarakhand	2	1.398	0	-
			Others	11	7.692	2	8.33
			Total (India)	**49**	**34.266**	**9**	**37.5**
		Philippines		21	14.685	5	20.83
			Total (Asia)	**70**	**48.95**	**14**	**58.3**
2	North America	USA	USDA	18	12.587	2	8.33
		Costa Rica		2	1.398	0	-
		Honduras		1	0.699	0	-
			Total (North America)	**21**	**14.685**	**2**	**8.33**

Table 15. Geographical distribution of accessions in Core Set & Base Collection (Contd)

Sl. No.	Contin-ent	Country	State	Accessions Base	Per-cent distribution	Core Set	Per cent distribution
3	Africa	Nigeria	IITA, Nigeria	14	9.79	3	12.5
		Bostwana		2	1.398	0	-
		Chad		1	0.699	1	4.167
		Uganda		3	2.097	0	-
		Tanzania		2	1.398	0	-
		Liberia		1	0.699	0	-
		South Africa		1	0.699	0	-
		Senegal		1	0.699	0	-
			Total (Africa)	**25**	**17.48**	**4**	**16.67**
4	Europe	Italy		1	0.699	0	-
		Hungary		1	0.699	1	4.167
			Total (Europe)	**2**	**1.398**	**1**	**4.167**
5	Australia	Australia		1	0.699	0	-
6		Unknown		24	16.78	3	12.5
			Total	**143**		**24**	

4.7.2.2. ***Frequency distribution of qualitative traits in Core Set and Base Collection***

Fodder cowpea accessions in Core Set and Base Collection were classified according to seven qualitative characters as per descriptors given by Roy *et al.* (2017). A comparison of

frequency distribution for qualitative characters of accessions in Core Set and Base Collection were carried out using chi square test and depicted in table 16.

Table 16. Frequency distribution of qualitative traits in Core Set & Base Collection

Sl. No.	**Descriptors**	**Descriptor state**	**Score code**	**B**	**C**	χ^2
1	Early plant vigour	Poor Good Very good	1 2 3	42 65 36	2 13 9	4.944 NS
2	Plant growth habit	Erect Semi erect Spreading Bushy Others(Specify)	1 2 3 4 9	10 20 15 97 1	3 2 4 14 1	4.33 NS
3	Leaf texture	Rough Smooth	1 2	32 111	4 20	0.396 NS
4	Leaf colour	Light green Green Dark green Others	1 2 3 9	16 112 15 0	1 22 2 0	0.813 NS
5	Stem solidness	Hollow Solid	1 2	14 129	1 23	0.794 NS
6	Flower colour	White Pink Red Purple Violet	1 2 3 4 9	7 5 0 109 22	1 1 0 20 2	0.893 NS

Table 16. Frequency distribution of qualitative traits in Core Set & Base Collection (Contd)

Sl. No.	Descriptors	Descriptor state	Score code	B	C	χ^2
7	Seed colour	White	1	13	2	5.601
		Brown	2	63	8	NS
		Black	3	5	3	
		Red	4	10	2	
		Grey	5	14	4	
		Mottled	6	13	1	
		Others	9	25	4	

NS : Non-significant

4.7.2.2.1. *Early plant vigour*

In Base Collection, 42 accessions out of 143 (29.3 per cent) showed poor early plant vigour while 65 accessions (45 per cent) had a good early plant growth and 36 accessions (25 per cent) showed highest early plant vigour. Similarly, in Core Set out of 24 accessions, 13 accessions (54.2 per cent) showed good early vigour followed by nine accessions (37.5 per cent) which exhibited very good early plant vigour. Only two accessions (8.3 per cent) showed poor early plant vigour in Core Set.

4.7.2.2.2. *Plant growth habit*

Among the accessions in Base Collection, 97 out of 143 (67.8 per cent) were bushy followed by semi erect growth habit (20 accessions, 14 per cent), spreading (15 accessions, 10.5 per cent), erect (10 accessions, 7 per cent) and others (1 accession, 0.7 per cent). In Core Set also most of the accessions obtained were bushy type (14 accessions, 58.3 per cent). 4 accessions were spreading type (16.6 per cent) followed by erect type (3 accessions, 12.5 per cent).8.3 per cent were semi spreading (2 accessions) and 4.16 per cent (1 accession) belonged to other growth habit.

4.7.2.2.3. *Leaf texture*

Leaf texture in Base Collection varied between rough one (32 accessions out of 143, 22.4 per cent) to smooth one (111 accessions, 77.6 per cent). Similarly, in Core Set also possessed rough (4 out of 24, 16.7 per cent) and smooth (20, 83.3 per cent) textured leaves.

4.7.2.2.4. *Leaf colour*

The intensity of leaf colour in Base Collection was green in most of accessions (112 accessions, 78.3 per cent). 16 accessions (11.2 per cent) had light green colour and 15 accessions (10.5 per cent) had dark green leaves. In Core Set also majority of accessions showed green coloured leaves (22 accessions, 91.7 per cent) followed by dark green leaves (2 accessions, 8.3 per cent) and light green (1 accession, 4.16 per cent).

4.7.2.2.5. *Stem solidness*

Majority of accession in Base Collection had solid stem (129 accessions, 90.2 per cent) and the rest had hollow stem (14 accessions, 9.79 per cent). Similarly, most of the Core Set accession possessed solid stem (23 accessions, 95.8 per cent) and only one accession has hollow stem (4.16 per cent).

4.7.2.2.6. *Flower colour*

The flower colour in Base Collection was purple for 109 accessions (76.2 per cent) followed by violet coloured flower (22 accession, 15.4 per cent). Seven accessions showed white coloured flower (4.89 per cent) and pink flower colour was seen in five accessions (3.49 per cent). In Core Set, 20 accessions (83.3 per cent) showed purple flower colour followed by violet flower colour (2 accessions, 8.3 per cent). White and pink flower colour was showed only by one accession each (4.16 per cent) in Core Set.

4.7.2.2.7. *Seed colour*

In Base Collection, majority of accessions possessed brown coloured seed (63 accessions, 44 per cent) while 14 accessions (9.79 per cent) had grey coloured seed. Some genotypes also showed mottled (13 accessions, 9.09 per cent), white (13 accessions, 9.09 per cent),

and red (10 accessions, 7 per cent) coloured seeds. Remaining 25 accessions (17.5 per cent) showed a varied coloured seed which doesn't belong to above categories. Seed colour in Core Set also varied between brown (8 accessions, 33.3 per cent), grey (4 accessions, 16.7 per cent), black (3 accessions, 12.5 per cent), white (2 accessions, 8.3 per cent), red (2 accessions, 8.3 per cent), mottled (1 accession, 4.16 per cent) and the remaining 4 accessions (16.7 per cent) belong to other category.

Chi square ($\chi 2$) test was performed between Base Collection and Core Set collection to check the frequency distribution of accessions for qualitative traits. For all the qualitative characters, chi square ($\chi 2$) test value was non-significant for base and core population. This reveals that the Core Set possessed a proportional representation of accession with respect to Base Collection.

4.7.2.3. *Variability in Core Set and Base Collection with respect to quantitative traits*

Comparison of Core Set and Base Collection was done for the statistical parameters viz., range, mean and variance of twenty quantitative characters. Two sample t-test to compare the mean and homogeneity test for variance (F test) to compare the variance of two populations was carried out and the results are depicted in table 17.

The results of two sample t-test revealed that mean values of Core Set and Base Collection for quantitative characters didn't differ significantly from each other. The range values are also on par with each other in these two populations, which represent that the diversity of biometric traits in Base Collections are fully included in the Core Set.

Homogeneity test (F test) conducted to compare the variance of quantitative characters also showed a non-significant result in both Core Set and Base Collection.

Table 17. Comparison of mean, range and variance for the quantitative traits in core set & Base collection

Sl. No.	Traits	Mean±SE		T test	Range		Variance		F test
		Base	Core set		Base	Core set	Base	Core set	
1	Number of primary branches per plant	2.83±0.08	2.75±0.25	0.329^{NS}	1-5	1-5	1.004	1.50	0.67 ^{NS}
2	Number of secondary branches per plant	0	0	NA	0	0	0	0	NA
3	Number of leaves per plant	15.79±0.57	17.46±1.72	-1.06 ^{NS}	5-35	7-33	47.09	71.13	0.662 ^{NS}
4	Leaflet length (cm)	10.31±0.14	10.733±0.41 1	-1.096 ^{NS}	7.1-15.7	7.2-15.7	2.91	4.06	0.716 ^{NS}
5	Leaflet width (cm)	5.91±0.10	5.93±0.30	-0.082 ^{NS}	2.1-9.3	2.1-9.2	1.44	2.10	0.684 ^{NS}
6	Stem girth(cm)	3.37±0.06	3.29±0.17	0.539 ^{NS}	1-4.9	1.4-4.6	0.47	0.71	0.671^{NS}
7	Number of nodes per plant	8.55±0.17	8.67±0.57	-0.238 ^{NS}	4-16	4-16	4.22	7.88	0.535 ^{NS}
8	Internode length (cm)	2.58±0.10	2.40±0.26	0.686 ^{NS}	0.5-5.4	0.5-5.4	1.43	1.59	0.91 ^{NS}
9	Days to 50% flowering	43.43±0.37	43.33±1.28	0.096 ^{NS}	30-56	30-54	19.75	39.19	0.504^{NS}
10	Green fodder yield per plant (g)	98.37±4.25	111.4±14.60	-1.09 ^{NS}	16-260	18-260	2584.87	5120.61	0.505 ^{NS}

Table 17. Comparison of mean, range and variance for the quantitative traits in core set & Base collection (contd..)

Sl. No.	Traits	Mean±SE		T test	Range		Variance		F test
		Base	Core set		Base	Core set	Base	Core set	
11	Dry matter yield per plant(g)	15.43±0.62	17.60±2.09	-1.255 NS	2.22-36.7	3.8-36.7	54.55	104.91	0.52 NS
12	Leaf Stem Ratio (LSR)	1.47±0.04	1.41±0.13	0.452 NS	0.29-3.01	0.29- 3.0	0.26	0.42	0.606 NS
13	Leaf dry weight per plant(g)	8.93±0.37	9.91±1.24	-0.946 NS	1.6-19.6	2.1-19.6	19.28	37.14	0.519 NS
14	Stem dry weight per plant(g)	6.50±0.28	7.69±0.94	-1.524 NS	1.08-17.02	1.16-17.02	11.33	21.36	0.531 NS
15	Leaf Area Index	4.63±0.23	5.72±0.84	-1.652 NS	0.5-15.53	0.5-15.4	7.60	16.96	0.448 NS
16	Number of seeds per pod	12.18±0.18	11.63±0.48	1.179 NS	6-17	7-17	4.43	5.55	0.799 NS
17	1000 seed weight (g)	124.16±2.76	134.33±9.25	-1.319 NS	54-237	54-237	1087.43	2053.36	0.53 NS
18	Seed yield per plant(g)	12.29±0.40	13.27±1.42	-0.864 NS	4-29.9	4-28.4	22.87	48.08	0.476 NS
19	Plant height (cm)	30.13±1.27	38.25±5.13	-2.173 NS	13.6-111.6	15.4-111.6	231.43	631.63	0.366 NS
20	Days to maturity	61.46±0.44	62.71±1.48	-1.027 NS	50-77	50-77	27.11	52.39	0.517 NS

4.7.2.4. *Diversity in Core Set & Base Collection (Shannon- Weaver Index)*

Phenotypic diversity among Core Set and Base Collection was assessed using Shannon-Weaver diversity index (H'). It measures allelic richness and evenness among accessions. High H' value indicates more diversity among the genotypes. Shannon - Weaver index for the twenty quantitative characters studied is given in table 18.

Highest H' value in Core Set as well as Base Collection was observed for leaf dry weight per plant (C=2.39, B=2.36) followed by dry matter yield per plant, stem dry weight per plant, green fodder yield per plant, internode length, number of leaves per plant etc. For all characters except internode length (C= 2.31, B= 2.38), has highest H' index value in Core Set compared to Base Collection which reveals that the Core Set sustained most of all diversity in Base Collection. H' value was zero for number of secondary branches per plant in both populations. The mean values of H' index for twenty quantitative traits in Base Collection and Core Set are comparable to one another with an overall mean of 2.008±0.11 and 2.138±0.12 respectively.

Percentage of diversity in Core Set over Base Collection was 101.5 per cent.

Table 18. Diversity index (H‟) in Core Set & Base Collection

Traits	SW index		Genetic Diversity per cent
	Base Collection	Core Set	
Number of primary branches plant^{-1}	1.84	1.95	106.22
Number of secondary branches plant^{-1}	0	0	0
Number of leaves plant^{-1}	2.27	2.33	102.93
Leaflet length (cm)	2.18	2.29	105.13
Leaflet width (cm)	2.09	2.17	103.77
Stem girth (cm)	2.11	2.15	102.32
No. of nodes plant^{-1}	2.03	2.25	110.97

Table 18. Diversity index (H‟) in Core Set & Base Collection (Contd)

Traits	SW index		Genetic Diversity per cent
	Base	Core	
Internode length (cm)	2.38	2.31	97.088
Days to 50 per cent flowering	2.06	2.26	109.76
Green fodder yield plant^{-1} (g)	2.20	2.35	106.72
Dry matter yield plant^{-1}(g)	2.28	2.37	104.22
Leaf stem ratio (LSR)	2.13	2.23	104.74
Leaf dry weight plant^{-1}(g)	2.36	2.39	101.20
Stem dry weight plant^{-1}(g)	2.21	2.37	107.41
Leaf area index	2.05	2.20	107.35
Number of seeds pod^{-1}	2.16	2.21	102.26
1000 seed weight (g)	2.054	2.24	109.17
Seed yield plant^{-1}(g)	2.10	2.25	106.77
Plant height (cm)	1.65	2.05	124.03
Days to maturity	2.03	2.37	117.21
Mean ± SE	**2.008±0.11**	**2.138±0.12**	**101.46**

4.7.3. Evaluation of Core Set Accessions

The study of the Core Set revealed the presence of potential accessions that could be relevant in future crop improvement efforts. Values of Core Set accession for green fodder yield and other economic traits are given in table 19.

Genotypes such as EC241037, EC10734, EC43203 showed maximum green fodder yield. Core Set also included genotypes which had least green fodder yield *viz.,* DCS-47-1, IC1255, EC724313 etc.

Genotypes like EC244021, IC26012, EC244217 were early flowering types while EC724313, EC724564, EC10734 were the few late flowering accessions.

Core Set also included accessions which are dwarf - bushy type to tall - spreading types. EC724564, IC20703, IC1255 were short bushy ones and EC101970, Kanakamony were tall spreading ones.

IC39908, EC101978, EC367714 were observed for high seed yield per plant while IC546523, EC10734, EC724564 had the least seed yield per plant.

Accessions EC43203, EC101973, EC241037 recorded higher LAI while IC1255, SNAR-12-11, EC966551 recorded least value for this trait.

EC241037 showed highest value for stem dry weight per plant, leaf dry weight per plant and dry matter yield per plant while IC26012 showed least value for dry matter yield per plant and stem dry weight per plant.

Table 19. Green fodder yield and other economic traits of genotypes in core set

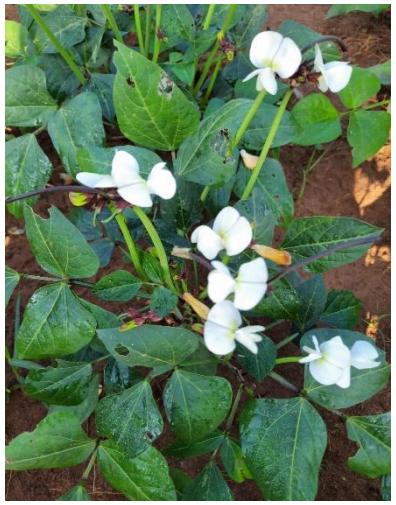
Treatment	Green fodder yield per plant	Dry matter yield per plant	Leaf Stem Ratio	Leaf dry weight per plant	Stem dry weight per plant	LAI	Seed yield per plant	Plant height	No. of leaves per plant	Days of 50% flowering
7	118	22.96	1.07	11.88	11.08	1.59	12.54	28.5	8	40
11	162	28.1	1.68	17.62	10.48	4	**4**	41.8	17	45
23	170	27.72	1.51	16.7	11.02	5.75	13.34	63.4	26	49
27	142	24.18	1.64	15.02	9.16	3.6	12.6	28	14	35
29	62	8.98	0.43	2.72	6.26	3.35	26.2	18.6	9	**30**
32	**260**	**36.68**	1.15	**19.66**	**17.02**	10.79	9.92	80.4	26	47
33	152	21.08	1.73	13.36	7.72	8.56	15.59	62	25	44
46	218	32.6	1.2	17.84	14.76	**15.44**	18.82	39.9	31	49
57	178	26.38	1.83	17.06	9.32	11.66	17.23	23.4	29	45
58	232	33.16	1.22	18.24	14.92	9.73	6.84	27.8	24	50
64	174	26.06	1	13.08	12.98	6.96	7.7	**111.6**	**33**	46
65	108	17.66	0.59	6.6	11.06	13.04	15.12	33	30	46
66	53.6	9.32	**0.29**	**2.12**	7.2	10.09	25.86	27.2	18	43
87	72	11.32	1.58	6.94	4.38	3.08	22.47	24	12	37
97	32	5.66	0.66	2.26	3.4	1.94	9.63	17.2	11	37
98	18	**3.84**	2.31	2.68	1.16	3.96	7.18	24.6	16	33
100	150	20.58	1.81	13.28	7.3	4.89	**28.44**	26.4	15	48
107	77	14.28	1.7	9	5.28	5.81	7.74	32.6	18	40
119	52	7.68	0.96	3.78	3.9	3.4	6.16	**15.4**	15	50
121	31	5.4	2.6	4.24	**1.16**	2.01	7.56	19	8	**54**
135	51	8.88	**3**	6.96	1.92	1.76	9.22	24.8	**7**	38
137	30	7.28	1.58	4.46	2.82	**0.5**	17.1	17.6	8	37
141	**25**	4.48	1.26	2.5	1.98	2.75	8.04	41.8	9	48

SNAR-12-11

IC546523

IC363962

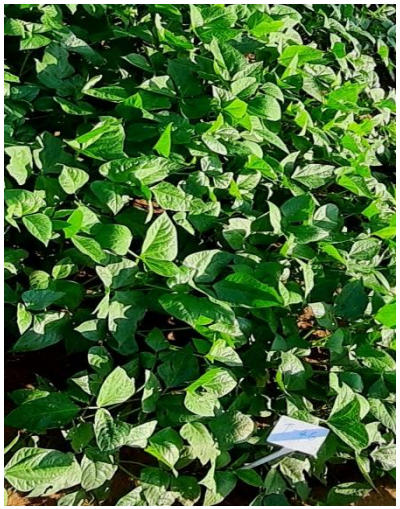
EC244217



EC244021

EC241037

EC241023



EC43203

Plate 4. Accessions included in Core collection

EC4218

EC10734

EC101970 & EC101973

EC101978

EC367714

IC20703

IC26012

Plate 4. Accessions included in Core collection

IC39908

IC257447

EC724564

EC724313

EC966551

IC1255

DCS-47-1

Kanakamony

Plate 4. Accessions included in Core collection

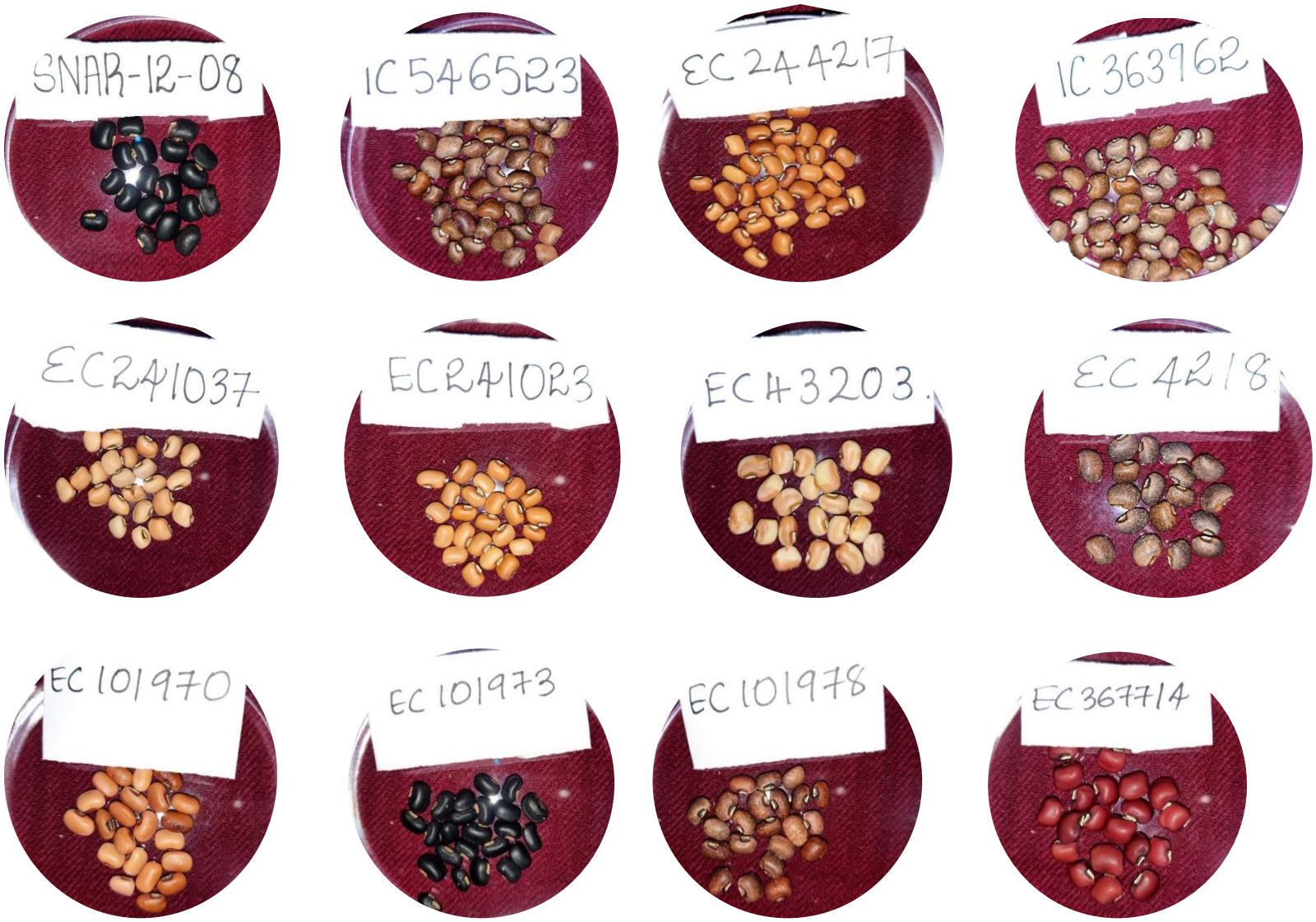


Plate 5. Variability of Seeds in Core set

Plate 5. Variability of Seeds in Core set

Discussion

5. DISCUSSION

Cowpea (*Vigna unguiculata* (L.) Walp, 2n=2x=22) is one of the most prominent tropical legume which has the potential to serve as food as well as a fodder crop. Characterization and evaluation of cowpea germplasm collections becomes an important aspect since it forms the base for further crop improvement programmes. Full utilization of all these accessions in a study is a cumbersome task, which showcases the importance of core set development in this crop. Kerala has got an ideal condition with respect to climate, topography and consumer preference for cowpea which is consumed as grain, vegetable and fodder purpose.

Therefore, in the present investigation, a base population comprising of 143 fodder cowpea accessions were evaluated for its variability, association of different pivotal characters and subsequently a core set of 24 accessions were identified. The most important findings from this study are discussed below.

5.1. Evaluation of seedlings

5.1.1. Variability studies in Base Collection for seedling characters

5.1.2. Principal Component Analysis of seedling characters

5.2. Evaluation of variability in Base Collection

5.2.1. Variability studies in Base Collection for quantitative traits

5.2.2. Variability studies for biochemical characters

5.3. Estimation of genetic parameters in Base Collection

5.4. Correlation Studies of different characters in Base Collection

5.5. Path coefficient analysis

5.6. Cluster analysis

5.7. Core analysis

5.7.1. Identification of Core set

5.7.2. Comparisons of Core set and Base Collection

5.7.2.1. Percentage geographical distribution of accessions

5.7.2.2. Frequency distribution of qualitative traits in Core set and Base Collection

5.7.2.3. Variability in Core set &Base Collection with respect to quantitative traits

5.7.2.4. Diversity in Core set vs Base Collection (Shannon- Weaver Index)

5.7.3. Future line of work

5.1. EVALUATION OF SEEDLINGS

High quality and viable seeds are the prerequisite for the production of vigorous seedling and establishment of successful crop stand (Mia and Shamsuddin, 2009). Seeds are enriched with all the qualities present in an embryo. Therefore, the seeds largely determine the traits of seedling that later develop into a crop.

5.1.1. Variability Studies in Base Collection for Seedling Characters

According to Ajala *et al*. (2003), crop improvement is highly dependent on the amount of genetic variability present in the base population. Variability studies of seedlings provide us an idea about the quality of seeds and the vigour of different genotypes.

In the present study 146 accessions of fodder cowpea genotype were evaluated for seedling characters in Completely Randomized Design with two replications. Observations like germination per cent, shoot length, root length, seedling length, fresh weight, dry weight, vigor index and relative growth index were taken. Analysis of variance revealed that there is significant difference among the accessions for all the seedling characters under study. The findings are in agreement with the works of Ajala *et al.* (2003) in cowpea, Shaibu and Ibrahim (2016) in common bean, Akshitha *et al.* (2020) in rice and Panwar *et al.* (2020) in vegetable pea which is in tune with the results obtained in this study.

Seedling vigour has always been recognised as a complex trait influenced by a number of factors, including genetic makeup and environmental influences during seed development and storage (Sun *et al.,* 2007). Highly vigourous seeds are a desirable character for optimum crop establishment in the field. Seedling vigour comprehend all those properties of seeds which help them for germination and potential seedling emergence (Perry, 1984). In this study the vigour index among the genotypes ranged from 185 to 3325 with a mean of 1446, which was in accordance with the result of Akshitha *et al.* (2020) and Panwar *et al.* (2020).

5.1.2. Principal Component Analysis of seedling characters

Principal component analysis approach is the oldest and most recognized statistical method which aids breeders to identify important phenotypic traits useful for selection (Vijayakumar *et al*., 2020). In this study, principal component analysis (PCA) was done for eight seedling characters to understand genetic diversity among the traits. The total variance in the population was distributed into eight principal component (PC) group. 86.5 per cent of total variance was contributed from first three PC group. The PC 1 has an eigen value of 4.413 and included 55.2 per cent of total variance. PC 2 showed 2nd highest eigen value (1.589) and contributed 19.9per cent of total variance. Similar findings were reported by Gerrano *et al.* (2015) in cowpea where first five principal component contributed 79.30per cent of the total variation and by Jindal *et al*. (2018) in fodder cowpea where first five principal component contributed 90.64per cent of total variability. The eigen values can be used as a criterion for determining important principal components which contributed most to the variation. Principal components with eigen value greater than 1 are considered as crucial while variables with eigen values smaller than one can be omitted because the variation they generate is insignificant and negligible (Walle *et al*., 2019).

Biplot constructed using first two PC shows the arrangements of accessions in different quadrant. The accessions which showed maximum diversity scattered away from origin and accessions near origin had similar characteristics (Sharma *et al.*, 2016). In the present analysis, genotypes NR/18-105, IC398992, IC402125, EC101967, EC240878,

IC39908, EC723987 showed maximum scattering, hence they are the most diverse ones among all the genotypes. The genotypes placed in first quadrant were similar for seedling fresh weight, root length and germination per cent. Genotypes in second quadrant were similar for shoot length, seedling length and seedling vigour. Genotypes in third quadrant differed from each other for all the characters. Genotypes present in fourth quadrant were similar for dry weight and RGR. Characters in same quadrant have positive interaction and characters in opposite quadrant have opposite interaction (Molosiwa *et al*., 2016).

The interaction among the characters and the PC groups are geometrically represented in squared cosine diagram. Seedling vigour and seedling length possess highest absolute value in the first principal component followed by root length, shoot length depicts that 55.2 per cent genetic divergence among the genotypes was mainly based on these characters. Seedling fresh weight and dry weight showed maximum value in PC 2 which accounts for the 19.85 per cent total variation. Characters which had highest absolute value in the principal component contributed largest towards divergence in that group (Singh *et al*., 2017).

5.2. EVALUATION OF VARIABILITY IN BASE COLLECTION

5.2.1. Variability Studies in Base Collection for Quantitative Traits

Analysis of variance for twenty biometric characters in Base Collection revealed a high significant difference among 143 fodder cowpea accessions for all the characters except number of secondary branches per plant and stem girth. Similar wide variability in cowpea yield and yield contributing attributes are reported by several researchers in their work (Khanpara *et al*.,2016; Lesly, 2005; Sharma *et al*., 2017; Singh *et al*., 2018; Devi and Jayamani, 2018 and Belay and Fisseha, 2020).

Green fodder yield per plant varied widely from 16g to 260g with a mean value of 98.4g. Genotypes EC241037 and EC724787 recorded highest and lowest value for green fodder yield per plant respectively. Existence of high diversity in cowpea germplasm for

green fodder yield has been reported by Girish *et al*. (2006), Singh *et al*. (2010) and Sanjeev *et al*. (2015).

The days to 50 per cent flowering ranged from 30 to 56 days in this study. The genotype EC244021 flowered earliest (30 days) and genotype KBC-4 flowered late (54 days) to attain 50 per cent flowering. Different cowpea genotypes had reported varying numbers for days to 50 per cent flowering. Hadley *et al*. (1983) have opined that flowering is highly controlled by environmental factors of which mainly temperature and photoperiod plays a very significant role.

One of the key techniques plant breeders had used to tackle the challenge of increasing yield is to utilize the genetic diversity available in germplasm for the selection of high yielding genotypes that may provide a satisfactory yield under diverse soil and environmental circumstances (Kaur *et al*., 2007). The results showed that the Base Collection used in this study was widely diverse, a best population that allow for the selection of exceptional and desirable genotypes for further breeding programmes.

5.2.2. Variability Studies for Biochemical Characters

Biochemical characters namely crude protein content and crude fibre content (per cent) were estimated for best thirty genotypes which showed high green fodder yield per plant. All the thirty genotypes significantly differed from each other for crude protein content and crude fibre content. The mean crude protein obtained was 20.5 per cent and crude fibre was 20 per cent which is in agreement with the findings of Sultan *et al.* (2018) and Gondwe *et al.* (2019).

5.3. ESTIMATION OF GENETIC PARAMETERS OF THE BASE ACCESSIONS

The genetic parameters like phenotypic and genotypic coefficients of variation, broad sense heritability and genetic advance are most important ones which are used for the selection of best parents from the population (Ubi *et al.*,2001 and Denton and Nwangburuka, 2011).

In the present study genetic parameters for twenty biometric characters were estimated and for all the traits PCV had higher value than GCV indicating the environmental influence on these quantitative characters which is in accordance with the result obtained by Nwosu *et al.* (2013). However, the difference between them was minimal indicating a higher influence of the genes in the expression of the characters. Graphical representation of PCV and GCV were given in fig 7 and heritability and genetic advance in fig 8. High PCV and GCV was observed for number of primary branches per plant, number of leaves per plant, internode length, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight, seed yield per plant and plant height. Similar result was reported for number of primary branches per plant by (Khan *et al*., 2015 and Sharma *et al*., 2017), for number of leaves per plant by (Nath and Tajane, 2013 and Gerrano *et al*.,2015). As the difference between PCV and GCV for number of leaves per plant, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight, seed yield per plant and plant height is low, a reliable selection using these characters can guarantee consistent results.

Gerrano *et al*. (2015), Phogat *et al.* (2017) and Singh *et al*. (2018) got similar high PCV and GCV for green fodder yield per plant and dry matter yield per plant. For leaf dry weight per plant and stem dry weight per plant, Malarvizhi *et al*. (2005) and Singh *et al*. (2010) obtained comparable result. High value of PCV and GCV was also reported by Thorat and Gadewar (2013) and Gerrano *et al*. (2015) for Leaf Area Index.

Highest PCV and GCV for cowpea seed yield per plant obtained in this study was in agreement with the reports of Singh *et al*. (2018), Devi and Jayamani (2018) and Belay and Fisseha (2020) and for plant height by Khanpara *et al*. (2016), Khan *et al*. (2015), Sharma *et al*. (2017) and Singh *et al*. (2018).

Lower value for both PCV and GCV was observed only for 90 per cent maturity in the current study. Sharma *et al*. (2017), Devi and Jayamani (2018) and Belay and Fisseha (2020) reported similar result in their respective studies.

High heritability accompanied with high genetic advance as per cent of mean was observed for number of leaves per plant, number of nodes per plant, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight and plant height. Manggoel *et al.* (2012) and Rashwan (2010) suggested that high broad sense heritability values showcase the preponderance of additive gene action in that trait. It provides an idea about the extent of genetic control for the expression of a particular character (Chopra, 2000). But according to Johnson *et al.* (1955) and Ubi *et al.* (2001) high broad sense heritability accompanied with high genetic advance confirm additive gene effect and are more reliable indexes for selection.

Malarvizhi *et al*. (2005) reported high heritability and genetic advance for number of leaves per plant, number of nodes per plant, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant and plant height as in the present study results.

High heritability and genetic advance estimates for green fodder yield per plant and dry matter yield per plant were earlier reported by Nath and Tajane (2013) and Phogat *et al.* (2017).

Characters like number of primary branches per plant, internode length, leaf stem ratio has high genetic advance with a moderate heritability. These characters can also be used for selection since this medium heritability is due to environmental effect. Days of 50 per cent flowering showed high heritability with moderate genetic advance. Results from this study are in accordance with observations by Malarvizhi *et al*. (2005) and Nwosu *et al*. (2013).

PCV, GCV, heritability and GA were highest for number of leaves per plant, number of nodes per plant, green fodder yield per plant, dry matter yield per plant, leaf dry weight per plant, stem dry weight per plant, leaf area index, 1000 seed weight and plant height revealed these characters are very much effective for selection and further crop improvement study.

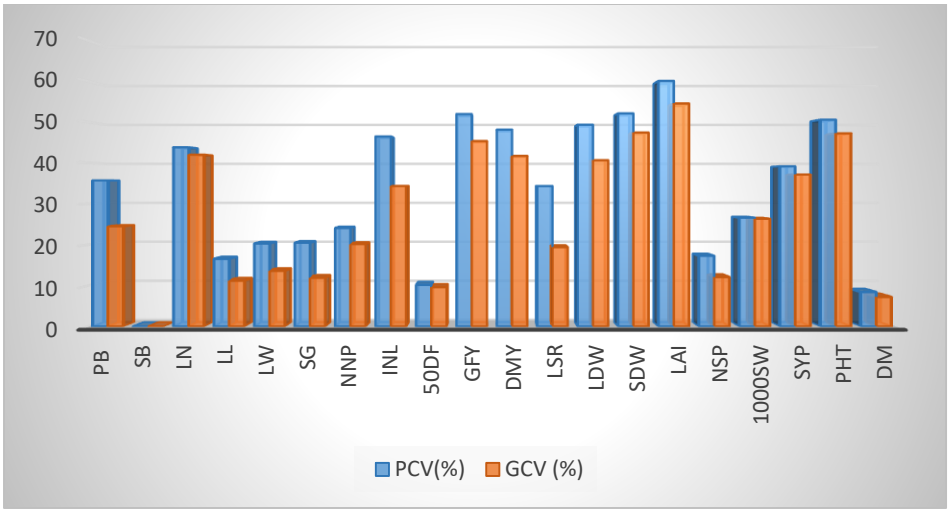


Fig.7. PCV & GCV for twenty biometric characters

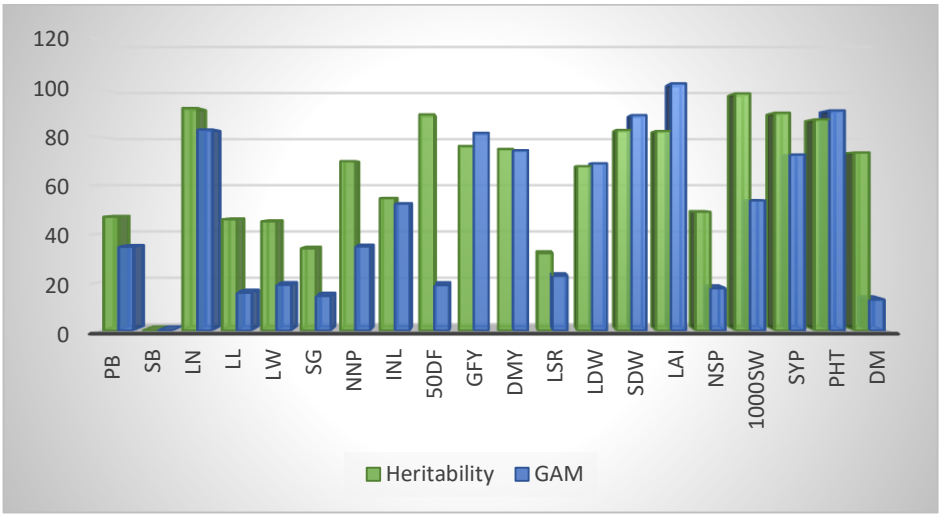


Fig. 8. Heritability & Genetic Advance for twenty biometric characters

PB	Number of primary branches plant^{-1}	InL	Internode length (cm)	1000SW	1000 seed weight (g)
SB	Number of secondary branches plant^{-1}	DM	Days to maturity	DMY	Dry matter yield plant^{-1}(g)
LN	Number of leaves plant^{-1}	NNP	No. of nodes per plant	SYP	Seed yield per plant (g)
LL	Leaflet length	NSP	No. of seeds per pod	LSR	Leaf Stem Ratio
PHt	Plant height (cm)	GFY	Green fodder yield per plant (g)	LAI	Leaf Area Index
SG	Stem girth	LDW	Leaf dry wt plant^{-1} (g)	SDW	Stem dry wt plant^{-1} (g)
LW	Leaflet width	50DF	Days of 50% flowering		

5.4. CORRELATION STUDIES OF DIFFERENT CHARACTERS IN THE BASE ACCESSIONS

Correlation analysis is an effective tool for determining how one character's selection affects the progress of other positively associated characters. Correlation coefficients are used to determine the size and direction of association between traits, it can be positive or negative. Like seed yield, green fodder yield is also a complex character controlled by polygenes, and hence a correlation study provides a clear picture of other associated characters which can be utilized for the improvement of green fodder yield. Correlation pattern is also a reflection of the genetic makeup of the population, it is predicted to vary depending on the material investigated (Lesly,2005).

In the present investigation, association between fourteen characters were worked out in all possible combination and constructed the phenotypic correlation matrix for green fodder yield. Green fodder yield per plant showed a highly significant positive phenotypic correlation with dry matter yield per plant (0.981), stem dry weight per plant (0.938), leaf dry weight per plant (0.936), number of leaves per plant (0.559), leaf area index (0.525), stem girth (0.449), number of nodes per plant (0.439), plant height (0.373). Singh *et al.* (2010) reported a similar result in fodder cowpea that dry matter yield, stem weight and leaves weight were positively correlated to green fodder yield per plant. Dangi and Paroda (1974) also found that number of leaves/plant, number of branches/plant and stem girth were highly correlated with green fodder yield. High significant positive correlation of dry matter yield per plant, plant height, leaf stem ratio, number of leaves per plant with green fodder yield was earlier identified by Nath and Tajane (2013). The positive correlation of green fodder yield with dry matter yield per plant, number of leaves per plant, leaf area index, plant height was also reported by Imran *et al.* (2010 Gerrano *et al*. (2015), Phogat *et al.* (2017) and Navaselvakkumaran *et al.* (2019).

Stem dry weight per plant showed a significant high positive phenotypic correlation with leaf dry weight per plant and both had a positive correlation with dry matter yield per plant, green fodder yield per plant, number of leaves per plant which are in agreement with the reports of Singh *et al.* (2010) and Sahai *et al.* (2013).

Dry matter yield per plant and green fodder yield per plant (0.981) had a significant positive correlation followed by leaf dry weight per plant (0.966), stem dry weight per plant (0.942), leaf area index (0.483), plant height (0.386) and a negative significant correlation with leaf stem ratio (-0.179) in this work. Similar reports were also published by Phogat *et al.* (2017), Sunil *et al*. (2017) and Navaselvakkumaran *et al.* (2019) in cowpea.

Plant height had a positive significant phenotypic inter correlation with number of nodes per plant (0.494), stem dry weight per plant (0.419), green fodder yield per plant (0.373), dry matter yield per plant (0.386), number of leaves per plant (0.359), leaf dry weight per plant (0.329) and leaf area index (0.286). Similar results were reported by Alege and Mustapha (2007), Gerrano *et al.* (2015), Lesly (2005) and Navaselvakkumaran *et al.* (2019)

Thus it is evident that traits viz., dry matter yield per plant, leaf dry weight per plant and stem dry weight per plant are highly associated with green fodder yield per plant, which can be considered for selection to improve green fodder yield.

5.5. PATH COEFFICIENT ANALYSIS

Correlation coefficients greatly aid to understand the bilateral relationship between two characters. However, they do not give precise information on the dynamic interconnection that occurs between a set of characters and yield. Path analysis untangles this complicated relationship between the traits by splitting the correlation coefficient into direct and indirect effect which help to understand the contribution of independent variable to dependent one (i.e. yield) in a realistic way. If the characters which are positively correlated with each other and had a positive significant direct effect, it specifies the genuine relationship between the characters where direct selection would be effective. But for characters which had a positive correlation and negative direct effect, the high correlation is due to indirect effect *via* other character, so indirect selection through that character would be appropriate.

In the current analysis, leaf dry weight per plant showed highest direct effect on green fodder yield per plant (4.38) followed by stem dry weight per plant (3.52). Green fodder yield per plant also had a high positive correlation with stem dry weight per plant and leaf dry weight per plant reveals the true relationship between these traits. So direct selection through these two traits will surely improve green fodder yield in fodder cowpea. This was in congruence with the result given by Singh *et al*. (2010). Traits like number of leaves per plant, days to 50 per cent flowering, stem girth had a positive direct effect on green fodder yield per plant. Similar findings were reported by, Nath and Tajane (2013) Sahai *et al*. (2013) and Phogat *et al.* (2017). Dry matter yield per plant showed negative direct effect on green fodder yield, but this result was in contradiction to the finding of Kumar *et al.* (2002), Nath and Tajane (2013) and Phogat *et al*. (2017). But in this present study, the highest positive indirect effect to green fodder yield was exhibited by dry matter yield per plant *via* leaf dry weight per plant (4.23) followed by stem dry weight per plant *via* leaf dry weight per plant (3.6). Dry matter yield per plant also showed a high indirect effect on green fodder yield per plant *via* stem dry weight per plant (3.32) and *via* leaf stem ratio (1.186). The positive correlation between green fodder yield per plant and dry matter yield per plant was due to these indirect effects. Nath and Tajane (2013) and Singh *et al.* (2010) reported similar findings about high indirect effect of dry matter yield *via* other character on green fodder yield. Navaselvakkumaran *et al.* (2019) observed a negligible direct effect of dry matter per plant on green fodder yield.

5.6. CLUSTER ANALYSIS

The magnitude of diversity present in a crop determines the effectiveness of any crop improvement program, for that estimation of divergence in germplasm, is necessary. UPGMA is one of the methods used for cluster analysis of genotypes in a population.

In the present study, 146 fodder cowpea accessions were subjected to divergence analysis using UPGMA method and divided into 30 clusters. Cluster diagram depicted the presence of high diversity among genotypes. Cluster X with 21 genotypes was the largest followed by cluster XI (20 genotypes), cluster XIV (13 genotypes), cluster I (12

genotypes), cluster VII (10 genotypes), cluster II (8 genotypes), cluster IV (7 genotypes), cluster XII and cluster XXVI1 (6 genotypes each), cluster XVII (5 genotypes), cluster VI, cluster VIII, cluster XIX and cluster XXIX (4 genotypes each), cluster XIII (3 genotypes), cluster IX, cluster XV, cluster XVIII and cluster XXIV (2 genotypes each) and the remaining were solitary clusters. Similar divergence analysis and grouping of genotypes into various cluster was also done by Rewale *et al*. (1996) who categorized cowpea genotypes into 19 clusters, Ushakumari *et al*. (2000) who grouped fifty cowpea genotypes into 13 clusters, Kapoor *et al.* (2000) who classified sixty genotypes of fodder cowpea into fifteen clusters and Borah and Khan (2002) who grouped sixty fodder cowpea genotypes into ten clusters.

5.7. CORE ANALYSIS

One of the most difficult tasks faced by genebank curators is the conservation of all genotypes available in crops in a cost-effective and efficient manner. Duplication and redundancy present in germplasm collection have been big concerns for conservators. Core collections subset of total germplasm accessions that represent the total diversity of that crop. (Mahalakshmi *et al*., 2007).

5.7.1. Identification of Core set

In the present investigation, a core set of fodder cowpea consisting of 24 accessions out of 143 base accession were identified using powercore software. The Base Collection comprised of accessions from NBPGR, New Delhi and bush type cowpea from KAU. Here the core set represent 16.8 per cent of Base Collection. According to Brown (1989), a core collection (10 per cent of the entire collection), should represent at least 70 per cent of the genetic variation in the whole collection of the species. But Xiao-ling *et al.* (2011) reported that the percentage of core set with respect to Base Collection is dependent on size of initial collection. When there is higher number of accessions in Base Collection the ratio will be smaller because as size of Base Collection increase duplication and redundancy in them also increases.

"Power Core v.1" was used to analyze four statistical parameters *viz.*, Mean difference MD (per cent), Variable rate VR (per cent), Variable difference VD (per cent) and Coincidence ratio CR (per cent) to compare variance and mean ratio between base and core collection. Hu *et al*. (2000), suggested that the core result should possess the MD per cent (mean difference) less than 20 per cent, the VR per cent (variable rate) more than 100 per cent and CR per cent (coincidence rate) greater than 80 per cent. The variable rate compares coefficient of variation of quantitative traits in core and Base Collection. While the CR greater than 80 per cent indicates the homogeneous distribution of quantitative traits in core set with respect to Base Collection. Variable rate more than 100 per cent required to consider core set as a true representation of Base Collection. In the present study, core result got a low mean difference (MD) value of 10.5 per cent, 42.8 per cent variable difference (VD), high coincidence ratio (CR) of 96.3 per cent and a high variable rate (VR) of 121.8 per cent. This was in accordance with the result obtained by Upadhyaya *et al*. (2002), Kim *et al.* (2007) and Agrama *et al.* (2009).

5.7.2. Comparisons of Core Set and Base Collection

To validate the core set, percentage geographical distribution, frequency distribution of seven qualitative characters and variability studies of twenty quantitative traits were performed. Frequency distribution of qualitative characters in core and Base Collection were tested using chi square test. In case of quantitative traits mean, range and variance were compared using two sample t test and homogeneity test for variance (F test). The phenotypic diversity was evaluated using Shannon- Weaver diversity index.

5.7.2.1. *Percentage Geographical Distribution of Accessions*

The Base Collection comprised of accessions from most of all continents viz., Asia, Africa, North America, Europe, Australia. Most of the accessions are from India (34 per cent), followed by Philippines (15 per cent), USA (13 per cent), Nigeria (10 per cent), Uganda (2 per cent), Botswana, Chad, Tanzania, Liberia, South Africa, Senegal, Costa Rica, Honduras, Italy, Hungary, Australia (1 per cent) each depicted in fig 9.

Statewide distribution of Indian accessions included genotypes from New Delhi, Kerala, Karnataka, Telangana, Andhra Pradesh, Uttarakhand, Chhattisgarh, Gujarat, Arunachal Pradesh, Assam and Haryana is given in fig 11.

In core set also majority of accessions are from India (9 out of 24, 38 per cent), which included accessions from Karnataka (2 accessions), Kerala, Chhattisgarh, Gujarat, Arunachal Pradesh and Andhra Pradesh (1 accessions each). 2nd highest accessions in core set are from Philippines (21 per cent) followed by Nigeria (13 per cent), USA (8 per cent), Chad (4 per cent) and Hungary (4 per cent) given in fig 10 and 12. Accessions from all the African countries are not included in core set. Core set only possessed accessions from Nigeria and Chad. This exclusion might be due to redundancy or duplication of accessions because of close geographic origin. Rewale *et al*. (1996) and Bhandari and Verma (2007) reported that geographic diversity was not a measure of genetic diversity.

5.7.2.2. *Frequency Distribution of Qualitative Traits in Core Set and Base Collection*

Qualitative traits are useful for determining the genotype of any organism, since it is governed by oligo genes which are not under environmental influence. Qualitative traits are stable and are highly heritable. So it can be used as a marker for selection if we found any interlinking of quantitative character on them.

Fodder cowpea accessions in Core Set and Base Collection were classified according to seven qualitative characters as per descriptors given by Roy *et al.* (2017) and a comparison of frequency distribution were carried out using chi square test. For all the seven qualitative characters, chi square ($\chi 2$) test value was non-significant for base and core population. This reveals that the core set possessed a proportional representation of accession with respect to Base Collection and captured all the variability in it. Lesly (2005) classified genotypes on the basis qualitative character in which flower colours were grouped into four viz., white (8.89 per cent), violet (3.59 per cent) mauve pink (85 .78 per cent) and others (1.77 per cent), which had higher variability. Genotypes also showed high variability in plant type. Sixty-one germplasm lines showed determinate plant type, seventy-four was intermediate bush type and thirty-four lines were intermediate spreading,

not climbing types. Kumar *et al*. (2015) classified fodder cowpea on the basis plant growth habit, flower colour, seed eye colour, plant pigmentation and determinacy.

5.7.2.3. *Variability in Core Set and Base Collection with respect to Quantitative Traits*

Large diversity among the accessions were observed within the Base Collection and Core Set for the twenty quantitative traits studied. Green fodder yield showed high genetic variance in both core and base followed by 1000 seed weight, plant height, dry matter yield per plant, number of leaves per plant and seed yield per plant. These characteristics could be effectively used to develop new plant varieties.

Two sample t test was used to compare the mean values of different quantitative characters between core and base population, and to check whether any deviation in mean exist between two populations. The results of two sample t-test revealed that mean values of core set and base population for quantitative character didn't differ significantly from each other. The range values are also on par with each other in these 2 populations, which represent that the diversity of biometric traits in Base Collections are fully included in the core set. Homogeneity test (F test) conducted to compare the variance of quantitative characters also showed a non-significant result in both core set and Base Collection. These result point out that core set captured as much variability in Base Collection which has the potential to form a great population. Several researchers had identified and documented the utility of core set in capturing the diversity of base population in various crops. Few among them are Hu *et al*. (2000) in cotton, Upadhyaya *et al*. (2001) in chickpea, Upadhyaya *et al*. (2002) in peanut, Reddy *et al.* (2005) in pigeon pea, Mahalakshmi *et al.* (2007) in cowpea, Cho *et al*. (2008) in soybean, Bhattacharjee *et al*. (2012) in cassava, Saini (2012) in rice, Dutta *et al.* (2015) in wheat and Pahuja *et al.* (2019) in forage sorghum.

5.7.2.4. *Diversity in Core Set & Base Collection (Shannon- Weaver Index)*

In the Core Set and Base Collection, the Shannon-Weaver diversity index (H') (Shannon and Weaver, 1949) was computed using phenotypic frequency and is used to compare the phenotypic diversity among species. This index provides a handy measure of

allelic richness and allelic evenness. High H' value indicates more diversity among the genotypes whereas low H' showcase the unbalance class distribution and lack of diversity.

Highest H' value in core set as well as Base Collection was observed for leaf dry weight per plant (C=2.39, B=2.36) followed by dry matter yield per plant, stem dry weight per plant, green fodder yield per plant, internode length, number of leaves per plant etc. For all characters except internode length (C= 2.31, B= 2.38), has highest H' index value in core set compared to Base Collection which reveals that the core set sustained most of all diversity in Base Collection. However, H' value was zero for number of secondary branches per plant in both populations. The mean values of H' index for twenty quantitative traits in Base Collection and core set are comparable to one another with an overall mean of 2.008±0.11 and 2.138±0.12 respectively. Percentage of diversity in core set over Base Collection was 101.5 per cent which revealed that the Base Collection's richness was very well captured in the core set. This results were in agreement with the findings of Upadhyaya *et al*. (2003) in groundnut, Reddy *et al*. (2005) in pigeon pea, and Xiao-ling *et al.* (2011) and Saini (2012) in rice, Dutta *et al.* (2015) in wheat

So, from this study we can conclude that the identified Core Set appears to be a good subset of Base Collection, which inculcated most of the diversity present in the actual population.

5.7.3. Future line of work

This core set can be further used for minicore development using genetic markers, it can be utilized for identification of superior parents for hybridization and development of new variety. The best accessions from this population can be taken forward for direct varietal release after yield trials. Abiotic and biotic stress tolerance studies can also be conducted using these diverse accessions.

Fig 9. Geographic distribution of accessions in base collection

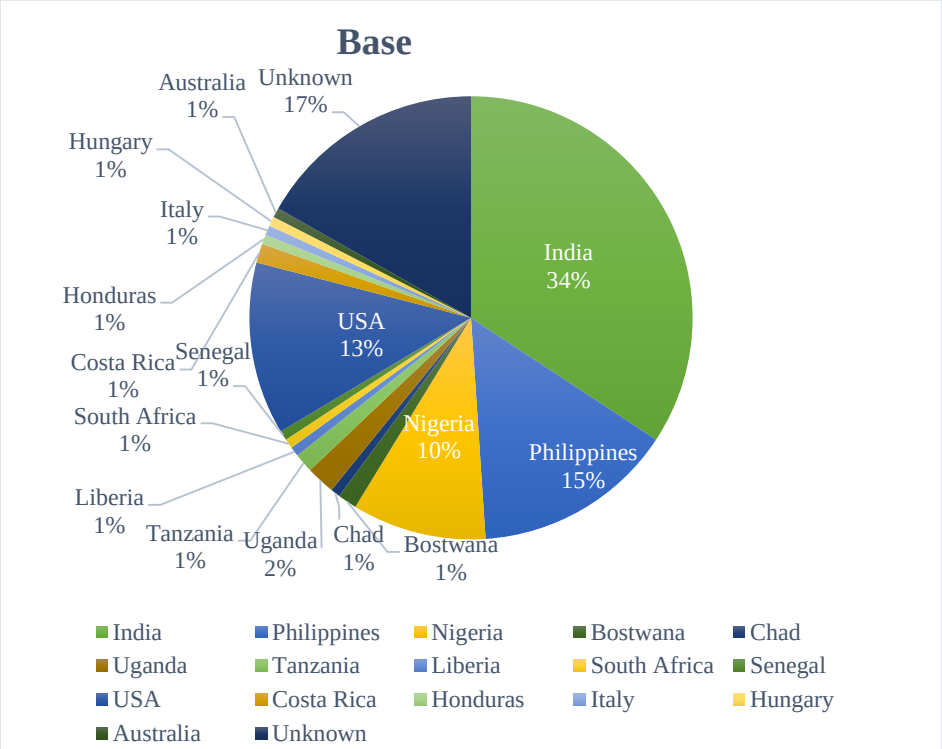


Fig 10. Geographic distribution of accession in core collection

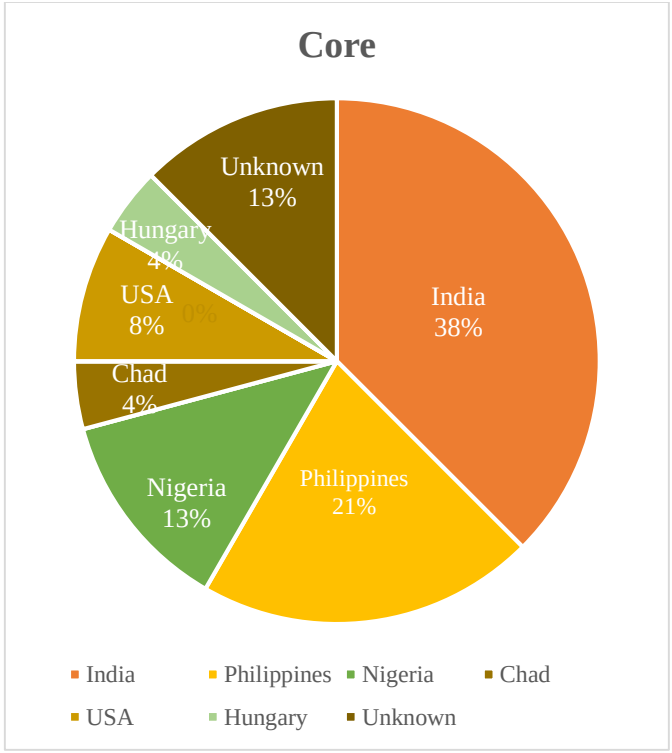


Fig 11. Geographic distribution of accession in base collection from India

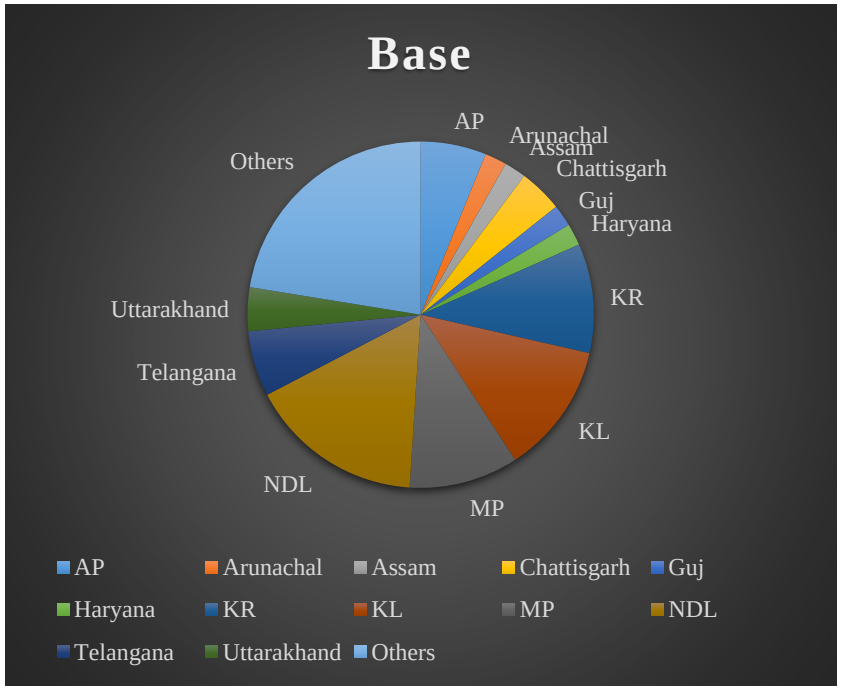
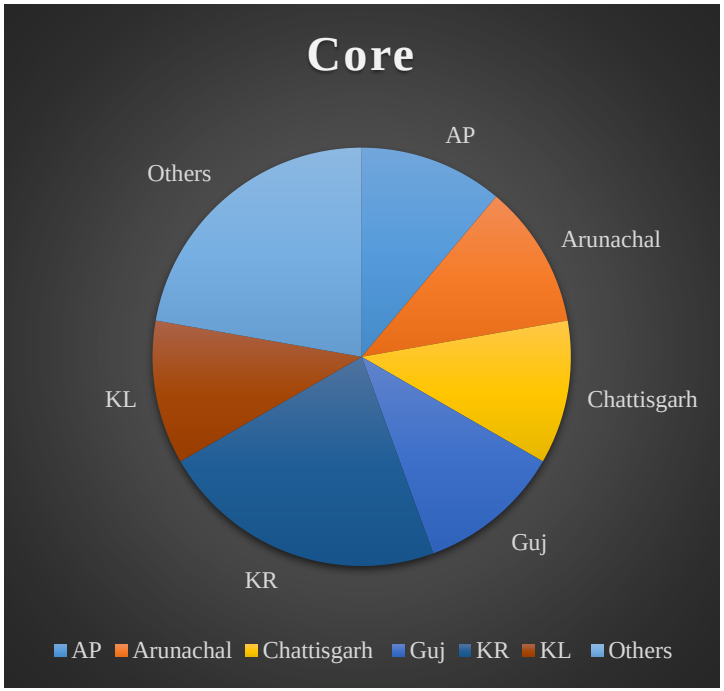


Fig12. Geographic distribution of accession in core collection from India



Summary

6. SUMMARY

Animal husbandry is one among the highly dynamic sectors of agriculture. India as a country holds the topmost position for livestock rearing and milk production, which account for 4.11 per cent of GDP and 25.6% of overall agricultural GDP (Economic Review, 2020). The livestock sector is anticipated to become a major driver of agricultural expansion since it possesses a multi-dimensional role in the upliftment of rural lives. The scarcity of good feed is one of the major challenges faced by sector. Legume fodder is considered as 'Natural Protein Banks' as they synthesize and supply the majority of the world's plant protein to livestock. Fodder cowpea is reported to be a better fodder legume than others in terms of both quantity and quality in semiarid areas.

The present study entitled "Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions" was envisaged for the assessment of variability in the fodder cowpea germplasm, constitution of a representative core set from the base collection, and evaluate the representativeness of the core set vis a vis base collection. Two experiment were conducted in Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during 2020-2021. Experiment 1 was evaluation of seedlings and Experiment 2 was field evaluation of fodder cowpea variability and identification of core set. The experimental material comprised of 143 fodder cowpea (*Vigna unguiculata* (L.) Walp) genotypes collected from NBPGR, New Delhi and released bush type cowpea varieties of KAU with 3 checks. The 3 check varieties were Aiswarya (State check), KBC-1 (Zonal check) and EC- 4216 (National check).

Seedling evaluation of 146 accessions was carried out in Completely Randomized Design with 2 replications. Various seedling characters such as germination %, shoot length, root length, seedling length, fresh weight per plant, dry weight per plant, vigor index and relative growth index were observed. One-way ANOVA and Principal Component Analysis were also carried out using GRAPES software of KAU. All the genotypes significantly differ each other in all the character. The biplot was constructed using the first two PC's, in which genotypes like EC723987, IC39908, IC402125, IC398992, NR/18-105

showed maximum scattering and demonstrated maximum genetic divergence among the accessions.

Evaluation of variability was carried out in the field using Augmented Block Design. The seeds were sown at a spacing of 15 cm x 30 cm during January 2021. Every accessions were sown in two rows of ten plants each and the check varieties were replicated in all the 13 blocks.

The genotypes were evaluated for 20 biometric characters and seven qualitative characters. Analysis of variance showed significant differences among genotypes for all the characters except secondary branches per plant and stem girth. Biochemical character such as crude protein and crude fibre content for top genotypes which showed high green fodder yield per plant was estimated and all the treatments significantly differ from each other. Genetic parameter viz., PCV, GCV, heritability and genetic advance were estimated for twenty biometric characters. The phenotypic and genotypic coefficient of variation were maximum for Leaf Area Index (LAI), green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, seed yield per plant etc. and minimum for days to maturity. Heritability and genetic advance was high for number of leaves per plant, LAI, green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, plant height, seed yield per plant etc.

The correlation studies revealed positive correlation of leaf dry weight, stem dry weight, dry matter yield, LAI with green fodder yield per plant. A negative significant correlation was seen in between stem girth and days of 50% flowering. Significant high positive phenotypic inter correlation was observed between leaf area index and number of leaves per plant. Plant height had a positive significant phenotypic correlation with number of nodes per plant, stem dry weight per plant, green fodder yield per plant, dry matter yield per plant, number of leaves per plant, leaf dry weight per plant and leaf area index.

The path analysis provides information on contribution of traits by partitioning the total correlation into direct and indirect effects. Path analysis of fourteen characters revealed high and positive direct effect of stem dry weight, leaf dry weight, primary

branches per plant, days of 50% flowering on green fodder yield. High indirect effect on green fodder yield was observed for many characters. Residual effect obtained was 17.6% which indicates that 82.4% variation in yield was contributed by characters under study.

Cluster analysis was done using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method. The 146 accessions were grouped into 30 clusters. Cluster X with 21 genotypes was the largest followed by cluster XI (20 genotypes), cluster XIV (13 genotypes), cluster I (12 genotypes), cluster VII (10 genotypes), cluster II (8 genotypes), cluster IV (7 genotypes), cluster XII and cluster XXVI1 (6 genotypes each), cluster XVII (5 genotypes), cluster VI, cluster VIII, cluster XIX and cluster XXIX (4 genotypes each), cluster XIII (3 genotypes), cluster IX, cluster XV, cluster XVIII and cluster XXIV (2 genotypes each) and the remaining were solitary clusters.

Core set is the subset of base collection which captures most of the available genetic diversity in it with negligible repetitiveness. Core analysis was carried out using power core (v.1.0) software using 20 quantitative characters of fodder cowpea. The core set identified comprised of 24 accessions out of 143 accessions in the base collection. The core set represented 16.8% of the base collection which has got a low mean difference (MD) value of 10.5%, 42.8% variable difference (VD), high coincidence ratio (CR) of 96.3% and a high variable rate (VR) of 121.8%.

Validation of the Core Set and ascertaining that the Core Set possessed most of all the variability in Base Collection, different comparative study was done in these two population. The accessions in both Base Collection and Core Set were categorized based on their place of origin and their frequencies compared. The base collection comprised of accessions from most of all continents viz., Asia, Africa, North America, Europe, Australia. Most of the accessions are from India (34%), followed by Philippines (15%), USA (13%), Nigeria (10%), Uganda (2%), Botswana, Chad, Tanzania, Liberia, South Africa, Senegal, Costa Rica, Honduras, Italy, Hungary, Australia (1%) each. In core set also majority of accessions are from India (9 out of 24, 38%), which included accessions from Karnataka (2 accessions), Kerala, Chhattisgarh, Gujarat, Arunachal Pradesh and Andhra Pradesh (1

accessions each). 2nd highest accessions in core set are from Philippines (21%) followed by Nigeria (13%), USA (8%), Chad (4%) and Hungary (4%).

A comparison of frequency distribution of seven qualitative traits viz., early plant vigour, plant growth habit, leaf texture, leaf colour, stem solidness, flower colour, seed colour in core and base collection were estimated using chi square test and all the characters showed non significance among each other indicated the true representation of core with respect to qualitative characters. Comparison of statistical parameters viz., mean, range and variance with respect to 20 quantitative traits in both core set and base collection were also done using two tailed t-test for comparing mean and homogeneity test (F test) for comparison of variance. In this case also all the character showed no significant difference between the two population revealed that the core set included as much genetic diversity as possible. Phenotypic diversity among core and base was assessed using Shannon-Weaver diversity index (H‟). All character has obtained higher H‟ value with comparable overall mean of 2.008±0.11 and 2.138±0.12 respectively. Percentage of diversity in core set over base collection was 101.5%.

The core set seems to be a good subset of fodder cowpea germplasm accessions which covers most of all existing diversity in base collection and eliminated the duplicates. This can form a great population which can further utilize for various breeding aspects like best accession from this study can be taken forward for direct varietal release after yield trials, the diverse core set can be utilized for identifying suitable parents in future breeding programs, formation of mini core using molecular markers can be made to further clarifications, abiotic and biotic stress tolerance studies can be done among these genotypes.

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IDENTIFICATION OF CORE SET IN FODDER COWPEA (*Vigna unguiculata* (L.) WALP) GERMPLASM ACCESSIONS

by
AMRITHA VARANYA
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ABSTRACT OF THE THESIS

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DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM - 695522
KERALA, INDIA
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ABSTRACT

The study entitled "Identification of core set in fodder cowpea (*Vigna unguiculata* (L.) Walp) germplasm accessions" was carried out at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during December 2020-May 2021 with the objective of assessing variability in the fodder cowpea germplasm accessions, constitute a representative core set and to evaluate the representativeness of the core set vis a vis base collection.

143 fodder cowpea (*Vigna unguiculata* (L.) Walp) genotypes collected from NBPGR, New Delhi and bush type cowpea varieties of KAU along with 3 check varieties formed the base collection. There were 2 experiments, in which experiment 1 was evaluation of seedlings and experiment 2 was field evaluation of fodder cowpea variability and identification of core set. Experiment 1 i.e., seedling evaluation of 146 accessions was carried out in Completely Randomized Design with 2 replications. Various seedling characters such as germination %, shoot length, root length, seedling length, fresh weight per plant, dry weight per plant, vigor index and relative growth index were observed. One-way ANOVA and Principal Component Analysis were also carried out using GRAPES software of KAU. All the genotypes significantly differ each other in all the character. The biplot was constructed using the first two PC's, in which genotypes like EC723987, IC39908, IC402125, IC398992, NR/18-105 showed maximum scattering and demonstrated maximum genetic divergence among the accessions.

Evaluation of variability was carried out in the field using Augmented Block Design. The seeds were sown at a spacing of 15 cm x 30 cm during January 2021. Every accessions were sown in two rows of ten plants each and the check varieties were replicated in all the 13 blocks. The cultural operations were done according to the recommendation of KAU Package of Practices.

The genotypes were evaluated for 20 biometric characters and seven qualitative characters. The genotypes showed significant differences for all the characters except secondary branches per plant and stem girth. Biochemical character such as crude protein

and crude fibre content for top genotypes which showed high green fodder yield per plant was estimated and all the treatments significantly differ from each other. Genetic parameter analysis was performed for twenty biometric characters and for all the characters PCV values were higher than GCV values indicating the influence of environment. The phenotypic and genotypic coefficient of variation were maximum for Leaf Area Index (LAI), green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, seed yield per plant etc. and minimum for days to maturity. Heritability and genetic advance was high for number of leaves per plant, LAI, green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, plant height, seed yield per plant etc.

The correlation studies revealed positive correlation of leaf dry weight, stem dry weight, dry matter yield, LAI with green fodder yield per plant. A negative significant correlation was seen in between stem girth and days of 50% flowering.

The path analysis provides information on contribution of traits by partitioning the total correlation into direct and indirect effects. Path analysis of fourteen characters revealed high and positive direct effect of stem dry weight, leaf dry weight, primary branches per plant, days of 50% flowering on green fodder yield. High indirect effect on green fodder yield was observed for many characters. Residual effect obtained was 17.6% which indicates that 82.4% variation in yield was contributed by characters under study.

Cluster analysis was done using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) method. The 146 accessions were grouped into 30 clusters. Cluster X with 21 genotypes was the largest followed by cluster XI (20 genotypes), cluster XIV (13 genotypes), cluster I (12 genotypes), cluster VII (10 genotypes), cluster II (8 genotypes), cluster IV (7 genotypes), cluster XII and cluster XXVI1 (6 genotypes each), cluster XVII (5 genotypes), cluster VI, cluster VIII, cluster XIX and cluster XXIX (4 genotypes each), cluster XIII (3 genotypes), cluster IX, cluster XV, cluster XVIII and cluster XXIV (2 genotypes each) and the remaining were solitary clusters.

Core analysis was carried out using power core (v.1.0) software. The core set formed comprised of 24 accessions (16 per cent) of the entire collection. A comparison of

geographical distribution of accessions in core set and base collection were done. The base collection comprised of accessions from India- 34%, Philippines- 14%, Nigeria, USA, African countries, Europe, Australia etc. The core collection contained accession mostly from India with representation from Philippines, Nigeria, USA, Chad, Hungary. A comparison of frequency distribution of qualitative traits in core and base collection were estimated using chi square test and all the characters showed non significance among each other indicated the true representation of core with respect to qualitative characters. Comparison of statistical parameters viz., mean, range and variance with respect to 20 quantitative traits in both core set and base collection were also done using two tailed t-test for comparing mean and homogeneity test (F test) for comparison of variance. In this case also all the character showed no significant difference between the two population revealed that the core set included as much genetic diversity as possible. Phenotypic diversity among core and base was assessed using Shannon-Weaver diversity index (H‟). All character has obtained higher H‟ value with comparable overall mean of 2.008±0.11 and 2.138±0.12 respectively. Percentage of diversity in core set over base collection was 101.5%.

The core set seems to be a good subset of fodder cowpea germplasm accessions which covers most of all existing diversity in base collection and eliminated the duplicates. This can form a great population which can further utilize for various breeding aspects.

സംഗ്രഹം

"കാലിത്തീറ്റ വൻപയറിന്റെ ജനിതക ദ്രവ്യ സമാഹാരത്തിൽ നിന്നും കോർ ശേഖരണ രൂപീകരണം" എന്ന ഗവേഷണ പദ്ധതി 2019 - 2020 കാലയളവിൽ വെള്ളായണി കാർഷിക കോളേജിലെ സസ്യ പ്രജനന ജനിതകശാസ്ത്ര വിഭാഗത്തിൽ നടത്തുകയുണ്ടായി. ജനിതക ദ്രവ്യ സമാഹാരത്തിലെ വ്യതിയാനം മനസിലാക്കി ഒരു കാതൽ ശേഖരണം രൂപീകരിക്കുകയും, അതിന്റെ പ്രാതിനിധ്യം വിലയിരുത്തുകയുമായി- രുന്നു പഠന ലക്ഷ്യം.

ന്യൂഡൽഹിയിലെ എൻ.ബി.പി.ജി. ആറിൽ നിന്ന് ശേഖരിച്ച 143 കാലിത്തീറ്റ പയർ ജനിതക ഇനങ്ങളും, കേരളം കാർഷിക സർവകലാശാലയിലെ കുറ്റി പയർ ഇനങ്ങളും, 3 ചെക്ക് ഇനങ്ങളും ഉൾക്കൊണ്ടതാണ് അടിസ്ഥാന ശേഖരണം.

രണ്ട് പരീക്ഷണങ്ങളിലായാണ് പഠനം നടന്നത്. ആദ്യ പരീക്ഷണം, 146 ജനിതക ഇനങ്ങളുടെ തൈ മൂല്യനിർണ്ണയമായിരുന്നു. രണ്ട് തവണ ആവർത്തിച്ചു കംപ്ലീറ്റിലി റാൻറ്റമൈസിഡ് ബ്ലോക്ക് ഡിസൈൻ എന്ന രീതിയിലാണ് ഈ പഠനം നടത്തിയത്. അങ്കുരണ ശതമാനം, വേരിന്റെ നീളം,തണ്ടിന്റെ നീളം, തൈകളുടെ നീളം, ഓരോ ചെടിയുടെയും മൊത്തഭാരം, ഉണങ്ങിയ തൂക്കം, വീര്യസൂചിക, ആപേക്ഷിക വളർച്ചാ സൂചിക എന്നിവ പഠിച്ചതിൽ, എല്ലാ പ്രതീകങ്ങൾക്കും ജനിതകയിനങ്ങൾ ഗണ്യമായി വ്യത്യാസപ്പെട്ടിരിക്കുന്നതായി കണ്ടെത്തി. തൈകളുടെ പ്രിൻസിപ്പൽ ഘടക വിശകലനത്തിൽ, EC723987, IC39908, IC402125, IC398992, NR/18-105 എന്നിങ്ങനെയുള്ള ജനിതകരൂപങ്ങൾ ബിപ്ലോട്ട് ഗ്രാഫിൽ കൂടുതൽ ചിന്നി ചിതറുകയും തൽഫലമായി പരമാവധി വൈവിധ്യം കാട്ടുന്ന ഇനങ്ങൾ ഇവ ആണെന്നും മനസിലാക്കാൻ സാധിച്ചു.

ഓഗ്മെന്റഡ് ബ്ലോക്ക് ഡിസൈൻ ക്രമീകരണത്തിലാണ് രണ്ടാമത്തെ പരീക്ഷണം നടത്തിയത്. 15 സെ. മീ. x 30 സെ. മീ. അകലത്തിൽ വിത്തുകൾ പാകി, വിളപരിപാലനം, സസ്യ സംരക്ഷണ നടപടികൾ എന്നിവ കേരള കാർഷിക സർവ്വകലാശാലയുടെ ശുപാർശ അനുസരിച്ചു ചെയ്യുകയുണ്ടായി. പത്ത് ചെടികൾ വീതമുള്ള രണ്ട് വരികളിലായി എല്ലാ ജനിതക ഇനങ്ങളും വിതയ്ക്കുകയും ചെക്ക് ഇനങ്ങൾ മാത്രം 13 ബ്ലോക്കുകളിലും ആവർത്തിക്കുകയും ചെയ്തു. 20 ബയോമെട്രിക് പ്രതീകങ്ങൾക്കും ഏഴ് ഗുണപരമായ പ്രതീകങ്ങൾക്കും

ജനിതകവ്യതിയാനം വിലയിരുത്തി. ഓരോ ചെടിയുടെയും തണ്ടിന്റെ ചുറ്റളവ്, ദ്വിതീയ ശാഖകളുടെ എണ്ണം എന്നിവ ഒഴികെയുള്ള എല്ലാ പ്രതീകങ്ങൾക്കും ജനിതകഇനങ്ങൾ തമ്മിൽ കാര്യമായ വ്യത്യാസങ്ങൾ കാണിച്ചു. ഒരു ചെടിയിൽ നിന്ന് ഉയർന്ന പച്ചപ്പുല്ല് വിളവ് കാണിക്കുന്ന മുൻനിര ജനിതകഇനങ്ങളുടെ അസംസ്കൃത മാംസ്യം, നാര് എന്നിവയും കണക്കാക്കി.

ഇരുപത് പ്രതീകങ്ങളുടെ ജനിതക സ്വഭാവ വിശകലനം നടത്തിയതിൽ നിന്നും എല്ലാത്തിനും പരിസ്ഥിതിയുടെ സ്വാധീനവും, ഉയർന്ന പൈതൃക ക്ഷമതയും ഉള്ളതായി കണ്ടെത്തി. ഇലയുടെ വിസ്തീർണ സൂചിക, ഒരു ചെടിയിൽ നിന്നുള്ള പച്ചപ്പുല്ല് വിളവ്, ഒരു ചെടിയുടെ ഉണങ്ങിയ ഇലകളുടെ ഭാരം, തണ്ടിന്റെ ഉണങ്ങിയ ഭാരം, ഓരോ ചെടിയുടെയും വിത്ത് വിളവ് മുതലായവയ്ക്ക് ഉയർന്ന ജനിതകമുന്നേറ്റം രേഖപ്പെടുത്തി.

പ്രതീകങ്ങൾ തമ്മിലുള്ള പരസ്പര ബന്ധം വിശകലനം ചെയ്തപ്പോൾ ഒരു ചെടിയുടെ ഉണങ്ങിയ ഇലകളുടെ ഭാരം, തണ്ടിന്റെ ഉണങ്ങിയ ഭാരം, ഓരോ ചെടിയുടെയും ഉണങ്ങിയ പദാർത്ഥത്തിന്റെ വിളവ്, ഇലയുടെ വിസ്തീർണ സൂചിക എന്നിവ പച്ചപ്പുല്ല് വിളവുമായി നേരിട്ട് ബന്ധപ്പെട്ടിരിക്കുന്നതായി കണ്ടെത്തി. ഈ പ്രതീകങ്ങളുടെ പരസ്പര ബന്ധം വിളവിനെ എങ്ങനെയാണ് പ്രത്യക്ഷവും പരോക്ഷവുമായി ബാധിക്കുന്നതെന്നു വിശകലനം ചെയ്തപ്പോൾ തണ്ടിന്റെ ഉണങ്ങിയ ഭാരം, ഇലകളുടെ ഉണങ്ങിയ ഭാരം തുടങ്ങിയവ വിളവിൽ നേരിട്ട് പ്രഭാവം ചെലുത്തുന്നതായി മനസിലാക്കാൻ സാധിച്ചു.

ജനിതക അകലം കണ്ടെത്തി വിവിധ ഇനങ്ങളെ ക്ലസ്റ്ററാക്കി തിട്ടപ്പെടുത്തുന്ന രീതി അവലംബിക്കുകയുണ്ടായി. യു.പി.ജി.എം.എ രീതി ഉപയോഗിച്ച് 146 ജനിതക ഇനങ്ങളെ 30 ക്ലസ്റ്ററുകളായി ഗണപ്പെടുത്തി. 21 ജനിതകഇനങ്ങളുള്ള ക്ലസ്റ്റർ X ആണ് ഏറ്റവും വലുത്, തുടർന്ന് ക്ലസ്റ്റർ XI (20 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ XIV (13 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ I (12 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ VII (10 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ II (8 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ IV (7 ജനിതകഇനങ്ങൾ) , ക്ലസ്റ്റർ XII, ക്ലസ്റ്റർ XXVI1 (6 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ XVII (5 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ VI, ക്ലസ്റ്റർ VIII, ക്ലസ്റ്റർ XIX, ക്ലസ്റ്റർ XXIX (4 ജനിതകഇനങ്ങൾ വീതം), ക്ലസ്റ്റർ XIII (3 ജനിതകഇനങ്ങൾ), ക്ലസ്റ്റർ IX, ക്ലസ്റ്റർ IX ക്ലസ്റ്റർ XVIII, ക്ലസ്റ്റർ XXIV

എന്നിവ (2 ജനിതകഇനങ്ങൾ വീതം), ബാക്കിയുള്ളവയിൽ ഓരോ ഇനവും ഉൾപ്പെടുന്നതായി കണ്ടെത്തി.

പവർ കോർ (v.1.0) സോഫ്റ്റ്വെയർ ഉപയോഗിച്ചാണ് കോർ വിശകലനം നടത്തിയത്. മൊത്തം ശേഖരത്തിന്റെ 24 ജനിതകഇനങ്ങൾ (16 ശതമാനം) ഉൾക്കൊള്ളുന്നതായിരുന്നു കോർ ശേഖരണം. കോർ ശേഖരണത്തിലെയും, അടിസ്ഥാന ശേഖരണത്തിലെയും ജനിതകഇനങ്ങളുടെ ഭൂമിശാസ്ത്രപരമായ വിതരണം താരതമ്യം ചെയ്തു. അടിസ്ഥാന ശേഖരത്തിൽ ഇന്ത്യ- 34%, ഫിലിപ്പീൻസ്- 14%, നൈജീരിയ, യുഎസ്എ, ആഫ്രിക്കൻ രാജ്യങ്ങൾ, യൂറോപ്പ്, ഓസ്ട്രേലിയ മുതലായവയിൽ നിന്നുള്ള ഇനങ്ങൾ ഉൾപ്പെട്ടിരുന്നു. കോർ ശേഖരത്തിൽ കൂടുതലും ഇന്ത്യയിൽ നിന്നുള്ള ഇനങ്ങൾ ആയിരുന്നു. ഫിലിപ്പീൻസ്, നൈജീരിയ, യുഎസ്എ, ചാഡ്, ഹംഗറി എന്നിവിടങ്ങളിൽ നിന്നുള്ള പ്രാതിനിധ്യം കോർ ശേഖരത്തിൽ അടങ്ങിയിരിക്കുന്നു. രണ്ടു ശേഖരണത്തിലെയും ഗുണപരമായ പ്രതീകങ്ങളുടെ ആവർത്തന വിഭജനം $\chi 2$ ടെസ്റ്റ് ഉപയോഗിച്ച് കണക്കാകുക്കയും ഇവ തമ്മിൽ വ്യത്യാസം കാണിക്കുന്നില്ല എന്ന നിഗമനത്തിൽ എത്തുകയും ചെയ്തു. കോർ ശേഖരണത്തിലെ ജനിതകഇനങ്ങളുടെ പ്രാതിനിധ്യം മനസിലാക്കാൻ രണ്ടു ശേഖരണത്തിന്റെയും ശരാശരികളുടെ താരതമ്യം, എഫ് ടെസ്റ്റ്, ടി ടെസ്റ്റ് എന്നിവ കണക്കാക്കുകയുണ്ടായി. ഈ സാഹചര്യത്തിലും രണ്ട് സമാഹാരങ്ങൾ തമ്മിൽ കാര്യമായ വ്യത്യാസമൊന്നും കാണിച്ചില്ല, തൽഫലമായി കോർ ശേഖരത്തിൽ കഴിയുന്നത്ര ജനിതക വൈവിധ്യം ഉൾപ്പെടുന്നുവെന്ന് വെളിപ്പെടുത്താൻ സാധിച്ചു. ഷാനൺ-വീവർ വൈവിധ്യ സൂചിക (H') ഉപയോഗിച്ച് കോറും അടിസ്ഥാന ശേഖരണവും തമ്മിലുള്ള ഭാഹിക വൈവിധ്യം വിലയിരുത്തി. എല്ലാ പ്രതീകങ്ങൾക്കും യഥാക്രമം 2.008±0.11, 2.138±0.12 എന്നിങ്ങനെ താരതമ്യപ്പെടുത്താവുന്ന മൊത്തത്തിലുള്ള ശരാശരിയിൽ ഉയർന്ന H' മൂല്യം ലഭിച്ചു. അടിസ്ഥാന ശേഖരണത്തേക്കാൾ കോർ ശേഖരത്തിൽ 101.5 ശതമാനം വൈവിധ്യം ലഭിച്ചു.

കാലിത്തീറ്റ വൻ പയറിന്റെ ജനിതക ദ്രവ്യ സമാഹാരത്തിന്റെ അടിസ്ഥാന ശേഖരണത്തിലെ നിലവിലുള്ള എല്ലാ വൈവിധ്യങ്ങളെയും ഉൾക്കൊള്ളുന്ന നല്ലൊരു ഉപവിഭാഗമാണ് ഈ കോർ ശേഖരണം എന്ന് വിലയിരുത്താം. ഇത് വിവിധ സസ്യ പ്രജനന വശങ്ങൾക്കായി കൂടുതൽ പ്രയോജനപ്പെടുത്താൻ കഴിയും.