GENETIC ANALYSIS OF YIELD AND QUALITY IN FODDER COWPEA

(*Vigna unguiculata* (L.) Walp)

by

PRAVEENA V.S.

(2015-21-030)

THESIS

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Dedicated to

Heroes (God, Father, Husband)
and

Heroines (Mother and Teachers)

in my life

DECLARATION

I, hereby declare that this thesis entitled **"Genetic analysis of yield and quality in fodder cowpea (*Vigna unguiculata* (L.) Walp)"** is a bonafide record of research work done by me during the course of research and that 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.

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CERTIFICATE

Certified that this thesis, entitled **"Genetic analysis of yield and quality in fodder cowpea (*Vigna unguiculata* (L.) Walp)"** is a record of research work done independently by Mrs. **Praveena V. S.** (2015-21-030) 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.

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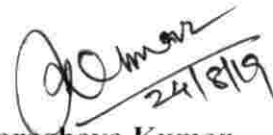Department of Plant Breeding and Genetics
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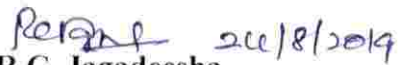College of Agriculture, Vellayani

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LISTOF ABBREVIATIONS

%	per cent
μ	Mean
μl	Micro litre
$\chi 2$	Chi-Square
ANOVA	Analysis of Variance
bp	base pairs
CD	Critical difference
cm	Centimetre
cv-grs	cultivar groups
d.f	degrees of freedom
DNA	Deoxyribonucleic acid
et al.	and co-workers/co-authors
F_1	First filial generation
Fig.	Figure
GDP	Gross Domestic Product
g	Gram
GoI	Government of India
Gca	General combining ability
GCV/gcv	Genotypic coefficient of variation
ha	Hectare
i.e.	that is
ISSR	Inter-simple sequence repeats
kg	Kilogram
m	Meter
mg	Milligram
min	Minutes
mt	Metric tonnes
Nacl	Sodium chloride
Ng	Nanogram

PCA	principal component analysis
PCR	Polymerase Chain Reaction
PCV	Phenotypic coefficient of variation
QTL	Quantitative Trait Loci
RFLP	Restriction Fragment Length Polymorphism
RAPD	Random amplified polymorphic marker
RNA	Ribonucleic acid
RNase	Ribonuclease
RPG	Recurrent parent genome
Rpm	revolutions per minute
Sca	specific combining ability
S.E(d)	Standard Error deviation
SE	Standard Error
SNP	Single nucleotide polymorphism
spp.	Species
ssp	Subspecies
SSR	simple sequence repeat
var	Variety
via	Namely
Viz.,	Namely
ng	Nanogram
μl^{-1}	Microliter
UV	Ultraviolet

INTRODUCTION

1. INTRODUCTION

Agriculture and animal husbandry in India are interwoven with the intricate fabric of society in cultural, religious and economical trout as mixed farming and livestock rearing forms an integral part of rural living. The agriculture and livestock sector still provides employment to 52 per cent of the work force. Livestock sector plays a crucial role in rural economy and livelihood. Milk production alone involves more than 30 million small producers, each raising one or two cows or buffaloes. The organic fertilizer produced by the sector is an important input to crop production, and dung from livestock is widely used as fuel in rural areas. Livestock also serves as an insurance substitute, especially for poor rural households; it can easily be sold during time of distress. Further, global energy crisis will lead to utilization of livestock-based bioenergy as well as waste recycling for organic manure and organic forage production for quality animal products.

As per 19th Livestock census (2012), India's livestock sector is one of the largest in the world with a holding of 11.6 per cent of world livestock population. Contribution of livestock sector to the national economy in terms of Gross Domestic Product (GDP) is 4 per cent. Agriculture and allied sector contributed about 15.1 per cent to the total GDP. Out of the total agricultural GDP, livestock sector contributed about 27.25 per cent during 2012-13. Global market for animal products is expanding fast, and it is an opportunity for India to improve its participation in global market.

One of the major challenges of animal husbandry sector is shortage of feed and fodder, which needs to be, addressed (Annual report 2016-17, GoI).

The nutritive value of feed and fodder has a significant bearing on productivity of livestock. The major reasons for shortage of feed and fodder are; increasing pressure on land for growing food grains, oil seeds and pulses and hence adequate attention has not been given to the production of fodder crops. Majority of the grazing lands have either been degraded or encroached upon restricting

their availability for livestock grazing. The area under fodder cultivation is only about 4 per cent of the cropping area, and it has remained static for long periods of time. Though the availability of feed and fodder has improved in the last decade, still a lot is required to be done to bridge the gap between the demand and availability of fodder in the country, particularly during the lean periods and crisis situations.

Kerala has a large livestock population of 27.35 lakh (Livestock Census, 2012). One of the main constraints in this sector is the non-availability of quality fodder in sufficient quantity. The land devoted for fodder cultivation is less than one per cent of the cultivable area, which produces 94.5 lakh mt of fodder compared to the required quantity of 232 lakh mt (FIB, 2011).

Roughage of lesser quality is straw. Straw from rice, barley, wheat, sorghum etc. are widely used in feeding ruminants. Their protein content is zero and their energy content low because of their largely lignified cell-walls. Rice or paddy straw has a high silica content in the cell walls which makes it difficult to digest.

Legumes provide potential to enhance forage quality of grass. Protein is required for growth, tissue repair and milk production among other desirable characters. Good sources of protein are leguminous forage, grain and oil-seed-cakes. For better health and yield of milk, livestock requires a balanced diet of three parts of green grass and one part of leguminous fodder (Vendramini *et al.,* 2012). Hence the cultivation of fodder legumes is very important.

Considering the land availability, cropping systems and climatic factors of Kerala, fodder cowpea is the best option. Cowpea (*Vigna unguiculata* L. Walp.) is a self-pollinating annual herbaceous legume belonging to the family Fabaceae which originated in West Africa. It is grown for vegetable, grain, as fresh cut and carry forage, and for hay and silage. It can be grown throughout the year and suitable for inter, mixed and relay cropping systems. It has a narrow genetic base (Asare *et al.,* 2010). This legume is well known for its inherent abilities like shade tolerance, drought tolerance, quick growth, rapid ground cover and protein content (Fatokun *et al.,* 2009). As a fodder crop, it's

short duration and multicut nature (KAU, 2018) makes it attractive to farmers. It requires very few inputs, as the plant's root nodules are able to fix atmospheric nitrogen. The whole plant used as an important nutritious legume for livestock (Singh and Tarawali, 1997). The nutritive value of cowpea leaves and haulms is very high. The crude protein content ranges from 22 to 30 per cent in the grain and leaves (Bressani, 1985; Nielsen *et al.*, 1997) and from 13 to 17 per cent in the haulms with high digestibility (Tarawali *et al.*, 1997) while fiber content is about 6 per cent (Bressani, 1985).

Not much systematic research work appears to have been conducted on cowpea for its utility as a fodder crop in Kerala.

Genotype x environment interaction remained always a serious problem in crop production while recommending a variety for some region/area in the developing countries. Environment for commercial cultivation cannot be changed but genotype can be modified by hybridization and bio-tech methods to suit the available soil and climate related environmental conditions. For this purpose breeders collect and create genetic variability in crops for development of varieties suitable for diverse agro-climatic zones. Crop outcome is a product of the genotype and the environment in which crop has been grown. Ideal variety is always one, which passes general adaptation with higher yield potential (Finlay and Wilkinson, 1963).

The study of genetic diversity is important in a crop breeding program for the selection of suitably diverse parents to obtain heterotic hybrids as well as for germplasm characterization. Various morphological, biochemical and molecular markers are used for the characterization of germplasm. The nature and magnitude of gene action involved in expression of quantitative traits is important for successful development of crop varieties and cultivars through proper choice of parents for hybridization (Griffings, 1956; Baker, 1978; Falconer, 1989). Diallel analysis is an effective means of understanding the genetic nature of quantitatively inherited traits and their inheritance (Ayo-Vaughan *et al.*, 2011). It has been used in cowpea to provide important information on general combining

ability (*gca*) and specific combining ability (*sca*), determine genetic variances, estimate heritability, and maternal effects (Hazra *et al.,* 1994).

Traditional selection mainly depends on the phenotypic variation. However, morphological markers are easily influenced by the environment, and some of them have epistatic effects. Molecular characterization of germplasm is important, especially in the changing scenario with regard to Plant Biodiversity Act (2002). Compared with morphological markers and biochemical markers, DNA molecular markers have some unique advantages. Its multi-locus nature as well as high reproducibility makes it particularly attractive for analyzing a large number of samples with narrow genetic variation. The use of molecular markers provides a much more reliable approach to distinguish cowpea genotypes for germplasm conservation, and for the identification of parental lines for use in breeding for improved cultivars in both countries, and to remove varieties which are duplicated. They are widely used in genetic diversity research. Inter-simple sequence repeat markers are considered more discriminating (Qian *et al.,* 2001).

Therefore, the present study was designed with the following objectives

- Genetic analysis of fodder yield and quality in 30 fodder cowpea accessions

- Evaluation of F_2 progenies to identify superior recombinants.

REVIEW OF

LITERATURE

2. REVIEW OF LITERATURE

A brief analysis of literature on various aspects of fodder cowpea is attempted. Despite its importance in animal husbandry, very little consideration has been volunteered to the improvement of this crop. In inheritance studies for various characters in cowpea was reviewed in early 1900s by Harland (1919, 1920 and 1922). However relevant literature available has been pooled under the following headings.

2.1. ORIGIN AND DOMESTICATION

Cowpea (*Vigna unguiculata* (L.) Walp.), is a highly self-pollinated herbaceous annual pulse crop known as black eye pea, (Ehlers and Hall, 1997) grown in Africa, Latin America and South Asia. It belongs to the family Fabaceae, tribe - Phaseoleae, genus - Vigna and section - Catiang (Marechal *et al.*, 1978). There are four subspecies in *Vigna unguiculata*, three of them are wild and a cultivated subspecies *unguiculata*; this one includes, in its turn, four *cv-grs*: *unguiculata* (cowpea), *sesquipedalis* (asparagus bean), *biflora* (catjang bean) and *textilis* (Marechal *et al.*, 1981).

Pasquet (1993, 1997 and 1998) divided *V. unguiculata* into thirteen subspecies. Out of theses, eleven were perennial subspecies and an annual subspecies (*ssp. unguiculata*) and another was a wild form (*var. spontanea*) which is treated as the wild progenitor of cultivated cowpea. Pasquet (1998) grouped cultivated cowpea into five cultigroups *via. Textilis, Unguiculata* and *Melanophthalmus* which grows in Africa, *Sesquipedalis* is seen in Asia and *Biflora* is found in northern Africa, on the Arabian Peninsula and in Asia (Pasquet, 2000).

Cowpea was domesticated in Africa (Padulosi and Ng, 1997) and is one of the oldest crops to be domesticated. A second domestication event probably occurred in Asia, before they spread into Europe and America (Chevalier, 1944; Sanjeev *et al.*, 2018). Vavilov considered India as the primary centre of origin and

Africa and China as secondary centers of origin. Ng and Marechal (1985) concludes that, the centre of origin of cowpea seems to be in central-southern Africa, while West Africa is considered the most probable primary centre of domestication and India the secondary one. The two *cv-grs biflora* and *sesquipedalis* evolved from *unguiculata* in India and south-east Asia respectively (Ng and Marechal, 1985). Harlan (1971), Rachie and Roberts (1974) considered Nigeria as centre of origin or domestication, where the wild and weedy species of cowpea co-exist with cultivated types. Menssen *et al.* (2017) concluded that even now the center of domestication is quiet unclear.

Cowpea has small genome size of 613 million base pairs and total nuclear DNA content of 1.27pg/2C (Arumuganathan and Earle, 1991), consisting of $2n = 2x = 22$ chromosomes (Rao, 1929; Yarnell, 1965; Sen and Bhowal, 1962; Faris, 1964; Leliveld, 1965). Vaillancourt and Weeden (1992) postulated Nigeria as another center of domestication, due to chloroplast DNA polymorphisms observed in wild (*var. spontanea*) and cultivated cowpea (*var. unguiculata*).

Lush and Evans (1981) referred *Vigna unguiculata* ssp. *dekindtiana* as the progenitor of modern cowpea. Singh *et al.* (1981) reported wild cowpea with chromosome structure similar to that of *Vigna unguiculata* ssp. *dekindtiana* in Tanzania.

2.2. VARIABILITY STUDIES

Assessment of variability in the available germplasm is the primary step for any crop improvement programme (Allard, 1960). It gives a better understanding of the breeding procedure and efficiency of selection (Zelleke, 2000). The most important studies on the variability related to the present study are cited below.

Variability present in eight quantitative characters traits in hundred and fifty four varieties of cowpea from five diverse regions of world was studied by

Kohli *et al.* (1971). Mehndiratta and Singh (1971) also researched the interrelationships existing among a few components of production in relation with regions of origin of the material.

Kumar and Mishra (1981) conducted variability studies in fifty diverse accessions for green fodder yield in cowpea. They reported higher environmental coefficient of variation than genetic variance for seed yield, dry matter yield and forage yield.

Pandita *et al.* (1982) experimented with forty genotypes of cowpea and found variability for characters days to flowering and plant height.

Studies on character association conducted by Obisesan (1985) also reported high range of genetic variability for days to flowering.

Pal (1988) also reported significant variation for plant height, weight, leaf number, dry matter production and branch number of eighteen cultivars of fodder cowpea.

Kandasamy *et al.* (1989) also reported highly significant variability for character days to fifty per cent flowering in cowpea. Thiyagarajan *et al.* (1989) observed high variability in plant height in a study with thirty six Nigerian cowpea types.

Roquib and Patnaik (1990) reported highly significant phenotypic variances for maturity and plant height followed by green fodder yield and area of terminal leaflet in fodder cowpea.

Gopalan and Balasubramanian (1993) reported high genetic variability for plant height in sixteen cowpea genotypes.

Perrino *et al.* (1993) studied three hundred and seventy six accessions of cowpea from ten countries of origin using both univariate and multivariate analysis.

Wide range of genetic variability was observed for plant height in cowpea by Hazra *et al.* (1996) also. High magnitude of genetic variability was

noticed by Mehta and Zaveri (1998) for character number of primary branches plant[-1] in segregating generations of cowpea.

Resmi (1998) observed high range of variation for several characters in cowpea. Significant variability was observed in cowpea for days to fifty per cent flowering, number of branches plant[-1] and plant height by Shoba and Vahab (1998).

Backiyarani *et al.* (2000) observed significant variability among thirty two genotypes of cowpea for days to fifty per cent flowering and plant height.

Panicker (2000) in a study involving fifty one cowpea types, reported high variability for days to flowering in cowpea.

Anbuselvam *et al.* in 2000 reported significant variability between fifty cowpea genotypes for plant height, primary branches and days to fifty per cent flowering.

High range of variability for the characters *viz.* days to fifty per cent flowering, plant height and branches plant[-1] were also reported in cowpea by Vidya (2000), Ajith (2001) and Philip (2004). Jyothi in 2001 reported broad spectrum variability for branches plant[-1] and plant height in cowpea.

Protein content in cowpea exhibited wide range of genetic variability (Kalaiyarasi and Palanisamy, 2001).

Mishra *et al.,* in 2003 studied seven hundred and forty exotic and indigenous accessions for twenty four descriptors in cowpea and found wide range of variation in almost all characters studied.

Malarvizhi *et al.* (2005) studied variability in sixty genotypes of fodder cowpea and reported significant difference between all the genotypes for days to fifty per cent flowering, plant height, number of branches plant[-1], number of leaves plant[-1], dry matter yield, green fodder yield, dry weight of leaves, dry weight of stem and crude protein content.

Lesly (2005) conducted an experiment in cowpea with the objective to assess the genetic variability, genetic divergence of genotypes and to study the

magnitude of association consisting of genetic material collected from various divergent environments. The genotypes revealed high significant variability for all the tested traits such as germination percentage, plant height, days to flower initiation, days to flower termination, days to physiological maturity, number of branches plant[-1], number of clusters plant[-1], number of pods plant[-1], pod length, seeds pod[-1], hundred seed weight, harvest index and seed yield plant[-1]. High variation was recorded for all the characters except plant height, days to flower initiation, days to flower termination, days to physiological maturity and number of branches plant[-1].

In a collection of twenty five cowpea genotypes Gerrano *et al.* (2015) recorded sixteen phenotypic markers and reported highly significant differences among genotypes.

Variations were observed with respect to plant height, leaf length, number of leaves and other growth parameters evaluated in a study conducted with ten cultivars of cowpea in 2015 by Animasaun *et al.*

Sunil *et al.*, (2015), characterized twenty fodder cowpea genotypes based on various morphological traits, mentioned in cowpea germplasm catalogue of IITA, Nigeria. All genotypes expressed indeterminate growth habit of axial branch and raceme type of layer in canopy; whereas accessions *viz.*, IC 249141, KBC 2, CO 4, HC 46, EC 101980, EC 3941-1, CO 5 and Kohinoor showed exclusive state of expression among nine traits *viz.*, seed crowding, occurrence of cowpea mosaic, texta structure, pod shape, eye color, terminal leaflet shape, pod attachment to peduncle, flower pigmentation and twining tendency, respectively.

Gerrano *et al.* (2015) estimated the level of phenotypic variability among a collection of twenty five cowpea genotypes. Sixteen phenotypic markers were recorded. Analysis of variance for the phenotypic traits revealed that differences among genotypes were highly significant for all traits. This indicated the high level of genetic variability among the cowpea genotypes studied.

Olayiwola *et al.* (2015) aimed to find the magnitude of genetic variability among cowpea genotypes for further use in cowpea improvement. Eleven cowpea genotypes were sourced from GLIP-IITA. Data were collected on pod, seed and dry fodder yield and subjected to combined ANOVA. The genotypic and phenotypic variances and coefficients of variation were determined. Broad-sense heritability and expected genetic advance were estimated. Genotypic effect was highly significant for all traits.

Sunil *et al.* (2017) experimented with twenty fodder cowpea genotypes and reported significant variability for all the genotypes for fodder yield plant^{-1}, weight of total leaf in plant, weight of stem, number of main branches plant^{-1}, plant height and protein content.

According to Sanjeev *et al.* (2018) highly significant diversity was observed within the species with large variations in the size, structure and shape of the plant. He also reported growth habit of cowpea can be erect, semi erect (trailing) or climbing.

Gerrano *et al.* (2018a) determined the variability and heritability of mineral and crude protein contents in the leaves of selected twenty five accessions of cowpea for two cropping seasons. The combined mean values of mineral elements showed wide genetic variation in the mineral elements evaluated. Significant association was observed among and between total protein and mineral elements in correlation analysis. Biometrical analysis revealed that the phenotypic variances were higher than the genotypic variances. High values of heritability estimates were also recorded for most of the evaluated traits. The principal component analysis (PCA) showed that the first three principal components contributed 71.93 per cent of total variation among the genotypes. The study revealed that there is an ample genetic variability that can be exploited for use in breeding for nutritional quality in cowpea leaves.

2.3. GENETIC PARAMETERS, HERITABILITY AND GENETIC ADVANCE

High GCV was reported for thirty five genotypes of cowpea for plant height, dry matter yield, pods plant^{-1} and green forage by Sharma *et al.* (1988).

Plant height and pods plant^{-1} had high GCV and PCV in cowpea (Siddique and Gupta, 1991).

Ushakumari and Chandrasekharan (1992) conducted genetic variability studies in fodder lablab and reported significant variability and high genetic advance for dry matter for fodder.

High variability for green fodder yield and nutrient composition was reported by Thaware *et al.* (1992) in thirty varieties of fodder cowpea.

In fodder cowpea, high estimates of GCV and PCV were observed for leaf number, dry weight of leaf, branch number, dry matter and green fodder yield and fifty per cent flowering and crude protein content had considerable heritability and low genetic advance (Borah and Fazlullahkhan, 2000).

High PCV and GCV for green fodder yield, in a study of ten diverse genotypes of fodder cowpea along with high genetic advance for fresh fodder yield and high heritability for days to fifty per cent flowering (Manonmani *et al.* 2000).

In seventy two genotypes of cowpea, variability for nine characters related to yield was studied by Kumar and Sangwan (2000). They stated that height of plants and number of branches plant^{-1} exhibited moderate to high genetic advance and heritability.

Withanage (2005) reported high values for PCV than the GCV for yield of seed plant^{-1}, weight of hundred seeds, harvest index, number of pods plant^{-1} and germination percentage. Low GCV and PCV values were recorded in days to flower initiation, flower termination and physiological maturity. Both GCV and PCV values showed similar pattern of changing over the characters. All characters showed high heritability except seeds pod^{-1} and length of pod. The highest heritability recorded by hundred seed weight. High genetic advance was observed

for germination percentage, plant length, clusters plant[-1], pods plant[-1], weight of hundred seed, harvest index and yield of seeds plant[-1].

Malarvizhi *et al.* (2005) reported additive genetic effect and scope for selection for characters branches and number of leaves plant[-1], dry matter yield and plant height in cowpea.

In this context, Sarutayophat *et al.*, (2007), characterized thirteen cowpea accessions based on growth habit, fifty per cent flowering, color, length, pods plant[-1] and seed yield plant[-1].

Ayan *et al.* (2012) evaluated nine cowpea genotypes for forage yield and quality features at two locations. Their forage yield and quality were desirable in experiment conditions. Forage yield significantly affected by genotype, year and location. No differences were found in crude protein among cultivars and years.

Basavaraj, *et al.*, 2013, conducted an experiment to characterize thirty five cowpea accessions using standard descriptors at plant level. Highly significant differences were obtained among the genotypes for the characters studied. All characters except pods peduncle[-1] and seed yield hectare[-1] were reliable.

Shanko *et al.* (2014) tested forty-nine cowpea accessions in 7 x 7 triple lattice design. High phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance estimated for the characters *viz.*, yield plant[-1], number of pods plant[-1], and 100-seed weight indicated that selection is effective.

Magashi *et al.* (2014) identified two varieties ITO6K-128, IT07K-291-92 which showed significant difference in terms of yield and root parameters as compared with others.

Gerrano *et al.* 2015 reported that the first five principal components expressed 79.30 per cent variability among the genotypes.

Sunil *et al.* (2017) found out GCV, PCV, high heritability along with high genetic advance and additive gene action was reported for the characters green

fodder yield plant^{-1}, leaf and stem weight, number of main branches plant^{-1} and plant height.

2.4. CORRELATION STUDIES AND PATH ANALYSIS

Correlation coefficients between yield and attributing characters help the plant breeder in indirect selection. Hence, these coefficients among various morphological and agronomic characters have been determined in cowpea. The term "path coefficient" was coined by Wright (1921) to indicate direct and indirect influence of one variable (cause) upon another (effect) as measured by the standard deviation remaining in the effects, after all other possible path influence are eliminated except that one cause. The technique of path coefficient to plant breeding was first applied by Dewey and Lu (1959). Lia (1956) gave a detailed account of both basic and applied aspects of path coefficient analysis. He suggested the formulation of path diagram to show cause and effect relationship.

The analysis was used to identify the components of seed production in crested wheat grass *(Agropyron cristatum)*. The complete correlation coefficient was divided into direct and indirect effects. And values were assigned for path coefficients which gives an idea of the complex association. This in turn helps in further selection procedures.

Doku (1970) reported higher genotypic correlation coefficients than phenotypic correlation coefficients in cowpea. Trehan *et al.* (1970) observed positive and significant correlation between height of plant, branches plant^{-1}, days to fifty per cent flowering, seeds pod^{-1} and length of peduncle.

Fodder yield was positively correlated with leaf and branch number, height and branch length, stem girth, protein content and digestibility in cowpea (Chopra and Singh, 1977 and Tyagi *et al.* 1978).

In a study of interrelationship between yield and its component in F$_3$ progenies of a cross (T44 x K 851) in *Vigna radiata,* Singh *et al.* (1988) found that seed yield plant^{-1} was positively and significantly correlated with pods plant^{-1}, plant

height, primary branches plant^{-1}, clusters plant^{-1}, pod length, seeds pod^{-1} and 100 seed weight.

Sharma *et al.* (1988) reported that seed yield, green forage yield and pod yield had significant correlation with pods plant^{-1}, seeds pod^{-1}, days to fifty per cent flowering and days to maturity in cowpea.

Path coefficient analysis in fodder cowpea was studied by Jindal (1989). He reported that plant height, leaf weight, leaf number, fodder yield, stem girth, stem weight and number of branches were significantly and positively correlated among them.

Roquib and Patniak (1990) recorded that green forage and dry matter yield were correlated with nodule number at thirty and sixty days after sowing, plant height, lateral and terminal leaflet area and leaf stem ratio.

Ushakumari and Chandrasekharan (1992) conducted correlation studies in fodder lablab and reported significant and positive correlation of green fodder yield with plant height, dry matter production, dry weight of leaf and dry weight of stem.

Sawant (1994) reported that pods plant^{-1} exhibited highest positive direct bearing on seed yield followed by seeds pod, days to fifty per cent flowering, plant height and pod length in cowpea.

Sharma and Gupta (1994) recorded maximum direct positive effect of biological yield followed by pods plant^{-1}, days to maturity, days to flowering and pod length on seed yield in interspecific generation of *Vigna*. In inter-specific derivatives of *Vigna* species, they found that seed yield was positively correlated with biological yield plant^{-1}, harvest index, clusters plant^{-1} and pods plant^{-1}.

Reddy *et al.* (1994) noted a strongly positive association of pods plant^{-1}, pods cluster $^{-1}$ and seeds pod^{-1} with seed yield.

In thirty six hybrids of fodder lablab, correlation and path analysis for dry weight of leaf and stem were the selection criteria for green fodder yield (Vasanthi and Das, 1995).

Arvindhan and Das (1995) reported that dry matter and leaf area index were the main contributors to green fodder yield in fifty nine genotypes of fodder cowpea with significant and positive correlation with specific leaf yield, branches plant[-1], leaf area index, leaf/stem ratio, dry forage yield and crude protein content.

Srinivasan and Das (1996) suggested an ideal plant type in fodder cowpea will be late flowering tall plants with plenty of larger leaves with high protein.

Oluwatosin (1997) reported that yield was negatively correlated with protein content in fifteen genotypes of cowpea grown in three locations. Vardhan and Savithramma (1998) noted that pod length, pod width and number of branches were the major traits contributing to green pod yield plant[-1] in cowpea. Niazi *et al.* (1999) found that pods plant[-1] is the major reliable yield component and it can be served as a selection criterion in breeding for high yielding genotypes of *Vigna radiata.*

Olusola (1999) experimented with fifteen cultivars of cowpea in three locations and indicated that yield was negatively correlated to protein content.

Rajeswari and Kamalam (1999) studied correlation between yield plant[-1] and its component characters in twenty five genotypes of *Vigna radiata* and reported that yield of grains plant[-1] was positively correlated with the days to final harvest, plant height, branches plant[-1], pods plant[-1], clusters plant[-1], pod length, grain pod ratio, harvest index and dry matter accumulation at flowering and formation. Similar results were observed by Manonmani *et al.* (2000) in cowpea.

In five cowpea cultivars, Santosh kumar *et al.* (2002) reported that dry fodder yield had the highest direct positive contribution towards green fodder yield

along with days to fifty per cent flowering, leaf: stem ratio, branch number, plant height, leaf length and breadth respectively.

Yadav *et al.* (2003), indicated that studying green pod yield plant[-1] had positive and significant association with plant height, pods cluster[-1], pod length, seed pod[-1] and pod dry matter in all the hybrid generations. Path analysis revealed that dry matter in pod, pods plant[-1], seeds pod[-1] and plant height was the main components of green pod yield in the early generation of cowpea.

A field study was conducted by Kamara *et al.* (2010) to determine the rate of genetic improvement in grain and fodder yields of cowpea genotypes. The study showed that selection was effective for dual-purpose cowpea varieties with better fodder and grain yield.

Leaf area index, leaf number, plant length, dry and fresh biomass contributed to the divergence according to Gerrano *et al.* (2015).

Monica *et al.* (2017) provided an insight that number of leaves plant[-1], number of branches plant[-1], crude protein yield plant[-1], crude protein yield plant[-1] day^{-1}, dry matter yield plant[-1], dry matter yield plant[-1] day^{-1}, leaf stem ratio and plant height at both genotypic and phenotypic levels in rice bean. Path coefficient analysis revealed crude protein yield plant[-1], dry matter yield plant[-1] day^{-1}, days to fifty per cent flowering, days to flower initiation and plant height were effective in increasing fodder yield in rice bean.

Positive and significant correlation between green fodder yield and leaf weight was observed by Sunil *et al.* (2017). Negative correlation was found between protein content and branches plant[-1]. Genotypic correlation coefficient was found to be positive and highly significant between fodder yield plant[-1] and leaf weight, stem weight, and number of branches plant[-1]. Negative and highly significant correlation was found between protein content and plant height.

An experiment was conducted by Mahesh *et al.* (2016) using sixty genotypes of cowpea showed that selection for biological yield plant[-1], harvest index,

number of pods plant^{-1}, days to fifty per cent flowering, number of flowers cluster^{-1}, number of primary branches plant^{-1}, number of seeds pod^{-1}, test weight and plant height can improve the seed yield plant^{-1}.

2.5. DIVERGENCE

Predominant dominant gene action was found for plant height, total leaf area, stem weight and green fodder yield in Indian bean (Ushakumari and Chandrasekharan, 1992). The frequency and level of heterosis are related more to specific combining ability than to the genetic divergence of the parents as estimated by Mahalanobis's, D^2 statistics in cowpea (Hazra *et al.*, 1993).

Nagalakshmi *et al.*, (2010) reported wide genetic diversity among sixty six genotypes of cowpea by the formation of twenty three clusters in *Vigna unguiculata*. The study indicated that days to maturity contributed maximum to the total divergence followed by 100 seed weight and days to fifty per cent flowering. There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the environmental influences over the character. Regarding the least contribution, number of branches plant^{-1} and petiole length contributed the least.

Leaf area index, leaf number, plant height, dry biomass and fresh biomass contributed to the biomass in a study conducted by Gerrano *et al.*, (2015).

Asoontha and Mareen (2017) studied twelve yard long bean and the genotypes were grouped into five clusters using Mahalanobis's D^2 statistics.

2.6. HETEROSIS

As early as in 18th and 19th century, Koelreuter, Gartner (1849) and Darwin (1876) reported hybrid vigour in crops. However, East (1908) and Shull (1911) started systematic work on heterosis in maize. Shull (1914 and 1948) introduced the term heterosis for the special stimulus of heterozygosis and defined

heterosis to cover the real observable phenomena when unlike genetics are brought together to form a hybrid. In this sense, heterosis is synonymous to hybrid vigour.

In plant breeding programmes, heterosis is referred to denote expression of increased vigour of hybrids over better parent but it was also expressed over mid parent and check parent values. There is, therefore, need to use distinguished word for each heterosis. The term heterobeltiosis has been proposed by Fonesoca and Patterson (1968) to describe the improvement of F_1 hybrids over mid parent as well as better parent value. Analysis of variance revealed significant differences among the genotypes, parents and hybrids for all characters except pod length in parents in a study conducted by Raut *et al.* (2017). Presently the term heterobeltiosis, relative heterosis and standard heterosis are being used to express heterosis over better parent, mid parent and check parent, respectively.

Heterosis is being utilized successfully now a days in cross pollinated crops and vegetables. However, commercial exploitation of heterosis in self pollinated crop is locked up due to difficulties in large scale emasculation as well as lack of suitable restorer genetic system. Efforts are in progress to remove the barriers and to search out the extent of heterosis for economic traits for successful utilization of hybrid vigour in self pollinated crops.

The first report of heterosis in cowpea is of Hoffmann who reported heterosis for plant height and stem diameter. Later on, Hawthorne (1944) reported heterosis for yield and its components in cowpea. Roy and Richharia (1948) recorded average heterosis of 0.52 to 18.0 per cent for seeds pod^{-1} which was higher than better parent value of 16.0 per cent seeds pod^{-1} in cowpea. Brittingham (1950) also recorded heterosis for seed yield and its determining characters in cowpea.

The systematic work on studies of heterosis in cowpea began in 1970s. Singh and Jain (1972) recorded heterobeltiosis ranging from -15.0 to 27.20 per cent, -15.30 to 14.00 per cent, -28.60 to 24.10 per cent and- 44.8 to 89.20 per cent for pod length, seeds pod^{-1}, seed weight and grain weight pod^{-1}, respectively.

They further observed that heterosis in yield seemed to be influenced by heterosis in pod length and seeds pod[-1].

Ojomo (1974) much of the genetic variation for days to flowering is due to dominance or epistasis.

Kheradnam *et al.*(1975) observed least heterosis was expressed by number of branches plant[-1] (2.6 per cent) which also showed least inbreeding depression.

Tikka *et al.*, (1976) recorded significant negative heterosis in four crosses and significant positive heterosis in two crosses for days to flowering in cowpea. Eraskin and Khan (1978) reported heterosis for earliness in cowpea.

Several authors concluded that additive gene action is responsible for much of the genetic variation for earliness (Mak and Yap, 1980; Zaveri *et al.*, 1980).

Jain (1982) studied line X tester analysis in cowpea and found a significant variation among parents and hybrids for fodder yield. He also observed heterosis over the better parent ranging between 68.53 and 181.48 per cent for green fodder yield plant[-1] and 132.98 and 79.70 per cent for dry matter yield plant[-1]. Heterosis was higher in one environment than that of the other for most of characters in majority of crosses.

Zaveri *et al.* (1983) recorded heterosis over mid parent and better parent for days to fifty per cent flowering and days to maturity.

Other reports, however, indicate that action by non-additive genes and interactions between genotype and environment are important in some instances (Singh and Rachie, 1985). They also reported broad sense heritability estimate of 48.3 per cent for days to flowering and 47.8 per cent for days to pod maturity.

Lodhi *et al.* (1990) studied the extent of heterosis for days to fifty per cent flowering, stem length, stem girth, number of branches plant[-1], leaf length, leaf breadth, green fodder yield plant[-1], dry matter yield plant[-1], protein content and *in vitro* dry matter digestibility using line x tester crosses in two environments. They

observed that the range of heterosis was very high in both the environments over both better parent and better check for most of the characters.

Supaporn (1992) recorded marked heterobeltiosis for lateral branches plant^{-1}. Damarany (1994) observed that plant height, number of branches plant^{-1} exhibited medium heterosis.

Sawant *et al.* (1994) studied forty five diallel hybrids of cowpea along with their ten parents and reported that characters, branches plant^{-1} (85.60 per cent) and plant height (73.40 per cent) exhibited heterosis.

Vasanthi and Das (1995) found highest positive heterosis over the better parent for dry matter yield (57.3 per cent) in the cross MS9448 X C01, while heterosis for crude protein content of the dry matter was highest (15.05 per cent) in cross PLS966 X C01 of Dolichos bean.

Aravindhan and Das (1996) studied heterosis and combining ability for fodder yield and seed yield in fodder cowpea. Predominant effect of *sca* over *gca* was reported which indicate pre-dominance of non-additive gene action.

Panmariammal and Das (1996) reported that majority of the hybrids show superiority over their parents except for days to fifty per cent flowering in cowpea. The variability studies on ten yield related characters in thirty four genotypes of cowpea was observed by Backiyarani and Natarajan (1996) and they reported high PCV and GCV for leaf area index

Bhore *et al.* (1997) studied F_1 and F_2 plants in fourteen crosses of cowpea for five yield related traits and observed that heterosis over better parent ranged from 4.33 to 92.3 per cent for plant height. Hybrids exhibiting high heterosis also showed high inbreeding depression. They also obtained heterosis over better parents for days to fifty per cent flowering, number of primary branches plant^{-1} and plant height in cowpea.

Withanage (2005) reported highly significant positive genotypic association was recorded between seed yield and harvest index. Hundred seed weight, seeds pod^{-1}, pod length, number of pods plant^{-1}, number of clusters plant^{-1}, branches plant^{-1} and days to flower initiation recorded positive genotypic association with seed yield. High positive association was observed between days to flower initiation and days to physiological maturity, clusters plant^{-1} and number of pods plant^{-1} and pod length and seeds pod^{-1}. Highly significant variation was present among the genotypes and significant variation was present between environments except for germination percentage. Based on D^2 values, genotypes were grouped into fifty one clusters. In general, crosses showing high heterosis also exhibited high inbreeding depression for most of the characters with some exception.

Heterosis and combining ability analysis were carried out by Ushakumari *et al.* (2010) in line x tester model using five lines. The ratio of specific combining ability component of variance to the general combining ability variance was found to be high for all the characters *viz.*, plant height, clusters plant^{-1}, pods plant^{-1}, length of pod, fifty per cent flowering, number of seed pod^{-1} and single plant yield indicating the preponderance of non-additive gene action governing the characters.

A work was conducted to estimate of some genetic parameters to understand the inheritance of yield and its components of cowpea crosses by Rashwan (2010). Dominance gene action (h) was the main types of gene effects for all studied traits in both crosses. The additive gene effects were found to be significant positive for days to flowering, number of pods plant^{-1}, weight seeds plant^{-1}, total seed yield per kilogram fodder, suggesting the potential for obtaining further improvement of these traits by using pedigree selection program. Duplicate epistasis was found for all studied traits in the two crosses. Heterosis per cent over mid-parent value ranged from 4.45 per cent for days to flowering to 23.75 per cent for

number of seeds pod^{-1} trait. The inbreeding depression per cent value ranged from 12.87 per cent for days to flowering to 17.02 per cent for number of pods plant^{-1}.

Anitha *et al.* (2016) conducted a study to estimate the level of heterosis for yield and its contributing traits in fodder cowpea. Three lines and twelve testers were crossed in a line × tester mating design. A total of thirty six F$_1$ hybrids along with fifteen parents were evaluated for days to fifty per cent flowering, plant height, number of branches plant^{-1}, number of leaves plant^{-1}, leaf : stem ratio, green fodder yield, dry fodder yield, crude protein content, crude fibre content and crude fat content and recorded significantly higher standard heterosis for fodder yield and its contributing characters. Early flowering is a desirable feature of a genotype. Therefore negative heterosis for days to fifty per cent flowering was considered desirable by Anitha *et al.* (2016).

2.8. COMBINING ABILITY

The knowledge of gene action and combining ability of parents and their hybrids is important for planning a sound breeding programme. The combining ability analysis helps the breeder in identifying the potential parents and also throws light on genetic system governing the various characters in the study. Thus, combining ability analysis is essential for deciding the breeding methods for genetic amelioration in a particular crop. Griffing (1956) described the methods of analyses for combining ability considering Eberhart's model I (fixed effect) and model II (random effect). This method has been widely used to know the genetics of various yield component characters and to recognize the desirable parents for hybridization in cowpea.

Kherdanam and Niknejad (1971) were the first to estimate combining ability in cowpea. They found that both general and specific combining ability effects were significant for yield plant^{-1}, cluster plant^{-1}, seed per twenty five pods,

seed weight and flowering date by Singh and Jain (1972) also observed that both general and specific combining ability variances were important for yield plant[-1].

Rodrigo and Adams (1972) analyzed recurrent selection in F3 and F4 families in a multi-location trial. Leaf number and size were associated with in families with high, medium, and low levels of expression of these two components.

Aryeetey and Laing (1973) reported that yield component characters in cowpea were mainly under polygenic control showing transgressive segregation in F_2 generation.

Ojomo (1974) observed that specific combining ability was more important than general combining ability in cowpea and postulated that most of the genetic variation for days to flowering was due to dominance or epitasis.

Lal et al. (1975) recorded that general combining ability variances were more important than specific combining ability variances for majority of the characters.

Zaveri et al. (1980) studied the genetics of days to flowering and maturity using a diallel cross involving six parents in cowpea and reported that both additive and dominant gene actions controlled the inheritance of days to flowering. Both general and specific combining ability variances were significant for days to fifty per cent flowering (Zaveri et al., 1980), but former was more important than the latter in a study conducted by them.

Mak and Yap (1980) reported that dominance variances were more important than additive variances for crude protein. The crude protein appeared to be controlled by over dominance, whereas partial dominance determined the flowering date. High protein content was associated with recessive genes.

Combining ability analysis was carried out in ten parental diallel by Jain et al. (1981) for fodder yield and related characters in cowpea. They reported that genotypes HFC 388 were good general combiner for vine length; FDC 354, HFC 617 and HFC 627 for leaf breadth, leaves plant[-1], leaf weight, branches plant[-1]

and stem girth; HFC 354, HFC 388 and HFC 617 for dry matter in pod, yield plant^{-1} and HFC 354, HFC 388, HFC 617and HFC 627 for green fodder yield in cowpea. They also reported additive genetic variance was predominant for days to fifty per cent flowering, branches palnt^{-1} and stem girth were as, non-additive genetic variance was more important for vine length, leaf length, leaf breadth and number of leaves plant^{-1}.

Jain (1982) studied the heterosis and combining ability in cowpea and reported that HFC 617 and HFC 637 were good combiners for forage and quality characters, while HFC 322 and FOS 1 were good combiners for most of the seed characters. The best specific combiner were HFC 617 x HFC 42-1, HFC 136 x FOS I and HFC 638 x FOS 1 for seed yield and its component characters in cowpea.

Imrie and Bray (1983) reported that general combining ability variances were significant for all the characters in cowpea. Zaveri *et al.* (1983) noted predominance of non-additive gene actions in controlling days to fifty per cent blooming. In a ten parental diallel cross Patil and Bhapkar (1986) found that additive effects alone were involved in determining days to flowering.

Patil and Shete (1986) concluded that in cowpea, additive effects alone were involved in determining days to flower but non-additive effects were of minor importance for the other characters. The yield of the parents was clearly associated with their general combining ability.

Mishra *et al.* (1987) reported in a line x tester analysis involving four tester and ten lines of *Vigna unguiculata,* that gca was more important for days to fifty per cent blooming, *gca* was more important for days to fifty per cent flowering. The higher magnitude of *gca* variance compared to *sca* variance reveal additive type gene action in expression.

Patil and Patil (1987) reported that additive gene effect was more pronounced in the expression of many of the yield component traits in cowpea. They also observed the existence of partial dominance or over dominance for most of the

characters. Emebiri (1989) observed that both parental and maternal genomes influenced the protein content in cowpea.

Additive gene action is seen in the inheritance of plant height and it also recorded high heritability in narrow sense for the character (Supaporn, 1992).

Naidu and Satyanarayana (1993) observed the major role of additive genetic variance in the inheritance of days to fifty per cent flowering whereas non-additive gene action was mainly responsible for plant height and shoot dry matter in *Vigna* species. Biradar *et al.* (1993) reported that the additive x dominance component was significant for protein content in a cross involving C 152 X Russian Giant.

Golasangi *et al.* (1995) studied variance component, heritability and genetic gain from selection in cowpea and reported that additive components of genetic variance was predominant for most of the characters in all the four crosses, while dominance component was predominant for length of peduncle and grain yield plant^{-1}. Madhusudan *et al.* (1995) and Sawant (1995) reported that both additive and non-additive variances were highly significant for most of the characters in cowpea.

Sharma and Pandey (1996) observed that both additive and non-additive components were involved in the expression of yield traits with predominance of former in urdbean. Arvindhan and Das (1996) also reported more or less similar results in cowpea.

Non-additive gene action contributes to plant height. Ponmariammal and Das (1997) recorded predominance of additive gene action for days to flowering, number of leaf, leaf area index and dry matter yield. The nonadditive gene action was important in the expression of plant height, number of branches and crude protein.

Mehta and Zaveri (1997) carried out genetic analysis in cowpea and reported that additive (d) and dominance (h) effects were significant for days to fifty per cent flowering, plant height and branches plant^{-1} in four crosses except for days

to fifty per cent flowering in GC 1 x RC 8 and branches plant^{-1} in GC 2 x V 16. All the three types of digenic interactions were significant for days to fifty per cent flowering in GC 2 x V 240 and plant height in all the crosses except Pusa Phalguni x V 269. Duplicate type of gene action was noticed for almost all the traits in four crosses namely, Pusa Phalguni x V 269, GC 1 x RC 8, GC 2 x V 16 and GC 2 x V 240.

Bhor and Dumbre (1998) reported that the magnitude of additive gene effect was higher in most of the crosses for number of days to maturity and number of days to fifty per cent flowering, while for rest of the characters i.e. number of primary branches plant^{-1}, plant height, number of clusters plant^{-1}, number of pods per cluster, pod length, number of pods plant^{-1}, seed yield plant^{-1} and 100-seed weight showed predominance of dominant (h) gene effect.

Sangwan *et al.* (1998) studied three crosses of cowpea *(Vigna unguiculata* L. Walp) to elucidate gene effects for plant length, branch number, leaf length and breadth, green fodder yield and dry matter yield. For most of the traits an additive dominance model was inadequate. Additive gene effect was more important for leaf length and leaf breadth, whereas dominance gene effect was predominant for number of branches, green fodder yield and dry matter yield. Both additive and non-additive gene effects were equally important for plant height. Among epistatic interactions, dominance x dominance appeared to be most important for all characters except leaf length and leaf breadth. There was predominance of duplicate type of epistasis for green fodder yield, dry matter yield and number of branches.

Chaudhari *et al.* (1998) reported that both additive and non-additive gene effects were involved in the inheritance of the characters like plant height, branches plant^{-1}, pod length, pods plant^{-1}, seeds pod^{-1} and grain yield with predominant role of non-additive gene action in cowpea. They also reported that parent GC 940 was good general combiner for grain yield, plant height, branches plant^{-1} and pods plant^{-1}. Parent GC 3 was good combiner for grain yield, pods plant^{-}

[1], pod length and seeds pod[-1] and Pusa Phalguni and RC 8 was also good combiners for early flowering, maturity and plant height.

Sobha *et al.* (1998) studied combining ability in a 10×10 diallel cross in cowpea for nine important characters. The variance due to general combining ability and specific combining ability showed both additive and non-additive gene action for plant height, primary branches and days to flowering.

The magnitude of the specific combining ability variance was higher than the general combining ability variance for all the traits indicating the predominance of non-additive gene action in cowpea (Bhushana *et al.*, 2000).

Dokashi and Mohamed (2002) conducted a field experiment to study the genetic analysis of variability in earliness and yield among five local and exotic cowpea varieties each by using 5 X 5 half-diallel cross and suggested that both additive and non-additive gene effects were involved in variation.

Manivannan and Sekar (2005) observed significant *sca* variance for all traits in cowpea.

Patil and Navale (2006) recorded the best mean performance and *sca* effect for green yield plant[-1] and its contributing characters among the hybrids of cowpea. All the crosses including parents had significant *sca* effects with high x high, high x low and low x low combining ability suggesting presence of allelic as well as non-allelic interaction in the expression of these characters.

Pal *et al.* (2007) observed significant differences among parents and hybrid for days to fifty per cent flowering in cowpea. The variance due to *gca* and *sca* were highly significant denoting importance of additive and non additive gene action for the traits. Additive genetic variance was predominant for days to fifty per cent flowering.

Ayo-Vaughan *et al.* (2011) conducted a study on the inheritance and genetic control of earliness in cowpea using diallel procedures. Eight cowpea genotypes and their twenty eight F[1] generations (excluding reciprocals) were

evaluated. *GCA* was significant for days to flowering and maturity (P <0.01), while specific combining ability (*SCA*) were significant (P < 0.01) for days to maturity only indicating that days to flowering is influenced by additive genetic effects and days to maturity by additive-dominance gene actions. Estimates of narrow sense heritability were low (<20 per cent) for both earliness traits.

Efforts have been made by Adeyanju *et al.* (2012) to improve either the fodder or the grain productivity separately. Transgressive segregants for high and low fodder yield were observed, suggesting that the fodder yielding genes were dispersed among the parents. Frequency analysis showed that all the F_2 populations for fodder yield exhibited a continuous distribution, suggesting that inheritance of fodder yield is quantitative in nature and may involve more than two genes. Fodder yield plant[-1], appeared to be influenced by both additive and non additive gene effects.

Idahosa and Alika (2013) conducted a diallel study involving eight genomic cowpea cultivars from diverse geographical origin to identify superior germplasm and develop high yielding varieties. The eight populations and their twenty eight crosses were evaluated in two locations. Data obtained for grain yield, plant height, days to flowering, pod length, seed pod[-1] and seed weight were analyzed with Gardner and Eberhart model (1966). General and specific combining abilities effect were highly significant (P<0.05) for the characters except for plant height (GCA). There was a preponderance of dominance gene effects for most characters.

Maan (2014) experimented with fodder cowpea, nine parental lines and their thirty six crosses in half diallel fashion were evaluated. The estimate of variances due to combining ability showed that the general combining ability variances were higher for the characters like stem girth, leaf:stem ratio, days to flowering, leaf length, leaf breadth, number of leaves plant[-1], number of branches plant[-1], green fodder yield plot[-1], detergent fibre contents which indicated the

predominance of additive type of gene effects for these traits where as variances due to specific combining ability effects were higher for wine length, cowpea mosaic virus, dry matter yield plot[-1], crude protein content and *in vitro* dry matter digestibility indicating the predominance of non-additive types of gene effects for these traits.

Anitha *et al.* (2017) carried out a study to determine combining ability analysis among crosses derived from fifteen selected fodder cowpea genotypes. Three lines and twelve testers were crossed in L × T fashion and thirty six hybrids were synthesized. The analysis of variance revealed significant variation among the genotypes for all the characters. All the characters exhibited significant SCA variance that was higher than the GCA variance, indicating preponderance of non-additive genetic component for all the characters.

2.9. MOLECULAR DIVERSITY ANALYSIS

Sorrels and Wilson (1997) specifies the importance of integrating molecular techniques and methodology into conventional program to facilitate speedy identification, characterization and manipulation of genetic variation.

Naylor *et al.* (2004) described cowpea was a crop with limited genomic resources; however, since then, a consensus genetic map with high-density SNP markers has been developed from eleven mapping populations (Muchero *et al.*, 2009; Lucas *et al.*, 2011). Iwata-Otsubo *et al.* (2016) reported that cowpea has highly distinct chromosomal structures.

Ajibade *et al.* (2000) reported ISSR markers are useful in detecting differences between closely related cowpea lines and reveal the polymorphism in cowpea.

In a review of molecular markers applied in cowpea by Huaqiang Tan *et al.* (2012), he concludes that ISSR markers are linked better to morphological variation than RAPD markers.

Diversity in wild and cultivated cowpea germplasm has been done by morphological and physiological traits (Perrino *et al.*, 1993; Fery, 1985), allozymes (Pasquet, 1993, 1999, 2000; Vaillancourt *et al.*, 1993; Panella and Gepts, 1992), seed storage proteins (Fotso *et al.*, 1994), and chloroplast DNA polymorphisms (Vaillancourt and Weeden, 1992); random amplified polymorphic DNA (RAPD) (Zannou *et al.*, 2008; Diouf and Hilu, 2005; Xavier *et al.*, 2005; Ba *et al.*, 2004; Nkongolo, 2003; Fall *et al.*, 2003; Mignouna *et al.*, 1998); restriction fragment length polymorphisms (RFLP) (Fatokun *et al.*, 1993); amplified fragment length polymorphisms (AFLP) (Fang *et al.*, 2007); DNA amplification fingerprinting (Simon *et al.*, 2007) and analysis of simple sequence repeats (SSRs) (Uma *et al.*, 2009; Xu *et al.*, 2010; Asare *et al.*, 2010; Wang *et al.*, 2008; Ogunkanmi *et al.*, 2008) or sequence tagged microsatellite sites (Abe *et al.*, 2003; He *et al.*, 2003; Li *et al.*, 2004; Choumane *et al.*, 2000). SSRs studies is useful since these sequences, besides being abundant and distributed throughout eukaryotic genomes, are highly polymorphic, inherited co-dominantly and reproducible, with simple screening requirements (Dib *et al.*, 1996). Simple sequence repeats have also been extensively used in genotype identification, seed purity evaluation and variety protection (Brown *et al.*, 1996; Senior *et al.*, 1998), pedigree analysis (Bowers *et al.*, 1999; Ayres *et al.*, 1997), and genetic mapping of simple and quantitative traits and MAS (Weising *et al.*, 1998; Blair and McCouch, 1997; Chen *et al.*, 1997).

Six cowpea (*Vigna unguiculata* L.) genotypes were subjected to yield analysis to determine their genetic relationships by Sharawy and El-Fiky (2003). The presence of significant differences in morphological and quality traits among genotypes was observed with ten primers. Relationships among the six genotypes of the cowpea were determined by RAPDistance software package, version 1.04.

In Maan's (2014) experiment genetic diversity analysis among ten parental lines revealed that all the genotypes showed more than seventy per cent

similarity for all the forty one SSR markers used for investigation. The analysis revealed narrow genetic base among genotypes used in the study.

In a study by Mafakheri *et al.* (2017) thirty two cowpea genotypes were selected for characterization at molecular and morphological markers under normal irrigation and drought stress conditions separately, as an assisting tool for a reliable varietal selection in breeding programs. In this study, seventeen morphological characters and multivariable statistical methods were studied, followed by using a set of twenty two Simple Sequence Repeat (SSR) primer pairs for molecular characterizations. The analysis of variance for morphological traits revealed significant differences among accessions for all measured traits. In molecular (SSR) analysis, a total of hundred and eighty six alleles were detected with an average of two alleles for each locus.

MATERIALS AND

METHODS

3. MATERIALS AND METHODS

The research was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2016-2019. Thirty accessions of fodder cowpea were screened for yield and quality characters using selection index method. The genetic divergence was confirmed using four ISSR markers. Eight divergent parents were selected from the initial studies and crossed in half diallel pattern with eight parents and hybrids without reciprocals for estimating heterosis, gene action and combining ability. Twenty eight crosses were made and F_1 was raised. Four better crosses from the twenty eight crosses were selected and raised in compact family block design for analyzing the F_2 generation.

3.1. EXPERIMENT 1: EVALUATION OF FODDER COWPEA ACCESSIONS

3.1.1. Materials

This experiment consisted of thirty diverse accessions of fodder cowpea collected from experimental fields of State Agricultural Universities, All India Coordinated Research Project on Forage Crops and from local markets. The details are given in Table 1.

3.1.2. Method

The thirty accessions were raised in a randomized block design with three replications during kharif 2016 in the field attached to the Department of Plant Breeding and genetics, College of Agriculture, Vellayani, in plots of size 3m x 1.5m at a spacing of 30cm x 15cm. The cultural and manurial practices were done as per the Package of Practices Recommendations of Kerala Agricultural University (KAU, 2018).

3.1.2.1. Observations

Observations on plant height, number of primary branches, number of leaves plant[-1], leaf area index, crude protein and crude fibre were

Table 1. List of thirty accessions used in variability screening- experiment I

Sl. No.	Treatment	Accessions	Source/Origin
1	T_1	CO - 9	TNAU, Coimbatore
2	T_2	CO – 8	TNAU, Coimbatore
3	T_3	Vellayani-1	College of Agriculture, Vellayani
4	T_4	MFC - 09 - 1	AICRP on forage crops, Mandya
5	T_5	MFC - 08 - 14	AICRP on forage crops, Mandya
6	T_6	EC - 394779	AICRP on forage crops, Mandya
7	T_7	EC - 458489	AICRP on forage crops, Mandya
8	T_8	EC - 4216	AICRP on forage crops, Mandya
9	T_9	KBC - 2	UAS, Karnataka
10	T_{10}	IC - 1061	AICRP on forage crops, Mandya
11	T_{11}	IC - 1071	AICRP on forage crops, Mandya
12	T_{12}	IC - 9883	AICRP on forage crops, Mandya
13	T_{13}	IC - 25105	AICRP on forage crops, Mandya
14	T_{14}	IC – 39916	AICRP on forage crops, Mandya
15	T_{15}	IC- 97767	AICRP on forage crops, Mandya
16	T_{16}	IC – 201095	AICRP on forage crops, Mandya
17	T_{17}	IC – 202777	AICRP on forage crops, Mandya
18	T_{18}	IC – 202781	AICRP on forage crops, Mandya
19	T_{19}	IC – 202804	AICRP on forage crops, Mandya
20	T_{20}	IC – 253251	AICRP on forage crops, Mandya
21	T_{21}	IC – 402090	AICRP on forage crops, Mandya
22	T_{22}	IC – 402101	AICRP on forage crops, Mandya
23	T_{23}	IC- 402154	AICRP on forage crops, Mandya
24	T_{24}	IC – 402162	AICRP on forage crops, Mandya
25	T_{25}	IC – 458485	AICRP on forage crops, Mandya
26	T_{26}	IC – 394779	AICRP on forage crops, Mandya
27	T_{27}	IT – 38956-1	AICRP on forage crops, Mandya
28	T_{28}	IT – 37154999-38	AICRP on forage crops, Mandya
29	T_{29}	Pant Lobia – 2	College of Agriculture, Pantnagar
30	T_{30}	KBC – 5	UAS, Karnataka

recorded on ten randomly selected plants from each plot along with first harvest i.e. forty five days after sowing and averages recorded.

3.1.2.1.1. Plant Height (cm)

Height of the plant was measured in centimeters using a meter scale from the base of the plant to the tip of the longest stem and the mean plant height was estimated.

3.1.2.1.2. Number of Primary Branches Plant[-1]

The number of primary branches in each plant was counted and the mean recorded.

3.1.2.1.3. Number of Leaves Plant[-1]

Total number of leaves from each sample plant was counted and mean was recorded.

3.1.2.1.4. Days to First Flowering

Number of days from the date of sowing to opening of first flower was recorded and mean calculated.

3.1.2.1.5. Days to Fifty Percent Flowering

Number of days taken from sowing to fifty per cent of the plants to flower was recorded.

3.1.2.1.6. Leaf Area Index

The fifth matured leaf from the tip of each plant was measured using graph paper and approximate leaf area was calculated with number of leaves plant[-1]. Leaf area index was measured using the following equation (Watson, 1962).

$$LAI = \frac{\text{Total leaf area}}{\text{Land area occupied}}$$

3.1.2.1.7. Green Fodder Yield Plant^{-1} (g)

Green fodder was taken at three stages, forty five days after sowing and subsequent cuts at thirty days interval. The green fodder yield was estimated by summing up the three harvests.

3.1.2.1.8. Dry Matter Yield Plant^{-1} (g)

Green fodder taken at three stages was dried to a constant weight in hot air oven for three days and dry matter yield was estimated.

3.1.2.1.9. Leaf Fresh Weight Plant^{-1} (g)

The sample plants collected for recording green fodder yield were separated into stem and leaf and fresh weight of leaves was recorded.

3.1.2.1.10. Stem Fresh Weight Plant^{-1} (g)

The sample plants collected for recording green fodder yield were separated into stem and leaf and fresh weight of stem was recorded.

3.1.2.1.11. Leaf Dry Weight Plant^{-1} (g)

The sample plants collected for recording dry matter yield were separated into stem and leaf and dry weight of leaves was recorded.

3.1.2.1.12. Stem Dry Weight Plant^{-1} (g)

The sample plants collected for recording dry matter yield were separated into stem and leaf and dry weight of stem was recorded.

3.1.2.1.13. Crude Protein Content (mg g^{-1})

The nitrogen content of the plant samples was estimated following the modified Microkjeldhal method (Jackson, 1973). The crude protein content was calculated by multiplying the nitrogen content by the factor 6.25.

3.1.2.1.14. Crude Fibre Content (mg g^{-1})

Dried plant samples collected at the time of harvest was utilized for the estimation of crude fibre content by acid and alkali digestion method (Kanwar and Chopra, 1976).

3.1.2.2. Statistical analysis - Biometrical techniques applied

Mean, variance, standard error and coefficient of variation were the basic parameters estimated. The significance of the genotypic differences

was tested through analysis of variance technique. The character associations were estimated through correlation coefficient using analysis of covariance technique. Heritability coefficient and genetic advance as percentage of mean were estimated. The methodology for estimation of the parameters are given below. With two characters X and Y measured on 'g' genotypes raised in completely randomized design with 'r' replications, the variance – covariance analysis (ANACOVA) was as follows.

ANOVA for RBD analysis

Sources	df	Mean sum of Squares		
		X	Y	XY
Between treatments (genotypes)	t-1	GXX	GYY	GXY
Within treatments (Error)	(t-1) (r-1)	EXX	EYY	EXY
Total	tr-1			

Standard Error difference (SE(d)) $= \sqrt{\dfrac{2MSE}{ri}}$

C.D. = t X SE (d)

and t was the critical t value for error degrees of freedom at 5% level.

Estimates of components of variance and covariance

Variate	Genotypic variance	Environmental variance	Phenotypic variance
X	$\sigma^2 gx = \dfrac{Gxx - Exx}{r}$	$\sigma^2 ex = Exx$	$\sigma^2 px = \sigma^2 gx + \sigma^2 ex$
Y	$\sigma^2 gy = \dfrac{Gyy - Eyy}{r}$	$\sigma^2 ey = Eyy$	$\sigma^2 py = \sigma^2 gy + \sigma^2 ey$

| XY | $\sigma gxy = \dfrac{Gxy - Exy}{r}$ | $\sigma exy = Exy$ | $\sigma \, pxy = \sigma gxy + \sigma exy$ |

Coefficient of variation

Phenotypic and genotypic coefficient of variations (PCV and GCV) for a trait x were estimated as :

$$GCV = \frac{\sigma_{gx}}{x'} \times 100$$

$$PCV = \frac{\sigma_{px}}{x'} \times 100$$

Where, σ_{gx} was Genotypic standard deviation, σ_{px} was Phenotypic standard deviation and x' was mean of the character under study.

Heritability coefficient and Genetic Advance

Heritability (H^2) in broad sense was estimated as the proportion of heritable component of variation.

$$\text{Heritability coefficient } H^2 = \frac{\sigma_{gx^2}}{\sigma_{px^2}} \times 100$$

Heritability in broad sense as percentage was classified by Allard (1960) as low (10-30 per cent), medium (30-60 per cent) and high (above 60 per cent).

$$\text{Genetic advance as percentage of mean (GA)} = \frac{kH^2\sigma_{px}}{X'} \times 100$$

Where k was the selection differential =2.06 if five per cent selection was to be practiced (Miller *et al.*, 1958). Robinson *et al.* (1949) classified genetic advance of characters as high (>20 per cent) and low (<20 per cent).

Estimation of components of variation

Correlation analysis

The phenotypic, genotypic and environmental correlation coefficients were estimated as follows

$$\text{Genotypic correlation } (r_{gxy}) = \frac{\sigma_{gxy}}{\sigma_{gx} \times \sigma_{gy}}$$

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{\sigma_{pxy}}{\sigma_{px} \times \sigma_{py}}$$

$$\text{Environmental correlation } (r_{exy}) = \frac{\sigma_{exy}}{\sigma_{ex} \times \sigma_{ey}}$$

Path coefficient analysis

To study the cause and effect relationship of yield and its component attributes, direct and indirect effects were analyzed using path coefficient analysis.

The genotypic correlation between yield and selected component characters were subjected to path analysis and the direct effect of the character on yield as well as the indirect effect through other characters were estimated.

Genetic divergence

Genetic divergence was measured using the technique D^2 statistics developed by Mahalanobis in 1928. Grouping of genotypes into clusters was made based on the relative distances (D^2 values) from each other and it was based on the method suggested by Tocher (Rao, 1952).

Discriminant function analysis

The discriminant function based on a number of variables was used for the formulation of selection indices to discriminate thirty genotypes. The genetic worth of the plant was defined by Smith (1936) as

$$H = a_1G_1 + a_2G_2 + \ldots\ldots + a_nG_n$$

Where G_1, G_2,.........,G_n are the genotypic values with respect to n characters of the individual genotypes and a_1, a_2, ..., a_n was the economic weight assigned to each. As G-values are not measurable, another function I,

which describes the phenotypic performance of an individual based on 'n' characters x_1, x_2, ..., x_n was defined as

$$I = b_1x_1 + b_2x_2 + ... + b_nx_n$$

Where b_1, b_2, ..., b_n are the corresponding coefficients. The 'b' coefficients are calculated such that the correlation between H and I was maximum and the selection of genotypes using I gives maximum gain.

The genetic advance that can be expected at a selection intensity of 5 percent was calculated as follows:

$$GA = \frac{ia'G b}{\sqrt{b'Pb}}$$

Where a' is the vector of weights attached to each character, b' is the vector of b-coefficients in the discriminant function, G is the genotypic variance – covariance matrix, P was the phenotypic variance – covariance matrix and i was the selection differential at a given selection intensity, which at five per cent is 2.06.

3. 2. Experiment 2- Molecular characterization of genotypes

Diversity analysis of thirty genotypes/varieties was done using identified molecular markers. The following steps were followed:

3.2.1. DNA isolation using NucleoSpin® Plant II Kit (Macherey-Nagel)

About 100 mg of the tissue was homogenized using liquid nitrogen and the powdered tissue was transferred to a microcentrifuge tube. Four hundred microlitres of buffer PL1 was added and vortexed for 1 minute. Ten microlitres of RNase A solution was added and inverted to mix. The homogenate was incubated at 65°C for 10 minutes. The lysate was transferred to a Nucleospin filter and centrifuged at 11000 x g for 2 minutes. The flow through liquid was collected and the filter was discarded. Four hundred and fifty microlitres of buffer PC was added and mixed well. The solution was transferred to a Nucleospin Plant II column, centrifuged for 1 minute and the flow through liquid was discarded. Four hundred microlitre buffer PW1 was added to the column, centrifuged at 11000 x g for 1 minute and flow though liquid was discarded.

Then 700 µl PW2 was added, centrifuged at 11000 x g and flow through liquid was discarded. Finally 200 µl of PW2 was added and centrifuged at 11000 x g for 2 minutes to dry the silica membrane. The column was transferred to a new 1.7 ml tube and 50 µl of buffer PE was added and incubated at 65°C for 5 minutes. The column was then centrifuged at 11000 x g for 1 minute to elute the DNA. The eluted DNA was stored at 4°C.

3.2.2. Quantification of DNA

The quantity of DNA is necessary before it is subjected to amplification. The quantification of DNA was carried out with the help of UV spectrophotometer.

The buffer in which the DNA was already dissolved, was taken in a cuvette to calibrate the spectrophotometer at 260 and 280 nm wavelengths. The optical density (OD) of the DNA samples dissolved in the buffer was recorded both at 260 and 280 nm. The concentration of the DNA was found using the formula

$$\text{Amount of DNA } (\mu g/\mu l) = \frac{A_{260} \; X \; 50 \; X \; dilution \; factor}{1000}$$

where A_{260} is the absorbance at 260nm.

The quality of the DNA could be judged from the ratio of the OD values recorded at 260 and 280 nm. The ratio between 1.8 and 2.0 indicates best quality of DNA. A_{280} is the absorbance at 280 nm.

3.2.3. Agarose Gel Electrophoresis

The quality of the DNA isolated was checked using agarose gel electrophoresis. 1µl of 6X gel-loading buffer (0.25% bromophenol blue, 30% sucrose in TE buffer pH-8.0) was added to 5µl of DNA. The samples were loaded to 0.8 per cent agarose gel prepared in 0.5X TBE (Tris-Borate-EDTA) buffer containing 0.5 µg ml^{-1} ethidium bromide. Electrophoresis was performed with 0.5X TBE as electrophoresis buffer at 75 V until bromophenol dye front has migrated to the bottom of the gel. The gels were visualized in a UV

transilluminator (Genei) and the image was captured under UV light using Gel documentation system (Bio-Rad).

3.2.4. ISSR PCR Analysis

3.2.4.1. Primers used

No.	Primer Name	Sequence (5' → 3')
1	UBC-811	GAGAGAGAGAGAGAGAC
2	UBC-812	GAGAGAGAGAGAGAGAA
3	UBC-823	TCTCTCTCTCTCTCTCC
4	UBC-834	AGAGAGAGAGAGAGAGTT

PCR amplification reactions were carried out in a 20 µl reaction volume.

2x DyNAzyme II PCR Master Mix	:	10 µl
Primer (10 µM)	:	1 µl
DW	:	7 µl
DNA	:	2 µl

The PCR amplification was carried out in a PCR thermal cycler (GeneAmp PCR System 9700, Applied Biosystems).

3.2.4.2. PCR amplification profile

95 °C	-	5.00 min	
94 °C	-	0.45 min	
42 °C	-	1.00 min	35 cycles
72 °C	-	1.30 min	
72 °C	-	10.00 min	
4 °C	-	∞	

3.2.4.3. Agarose Gel electrophoresis of PCR products

The PCR products were checked in 1.2 per cent agarose gels prepared in 0.5X TBE buffer containing 0.5 µg ml^{-1} ethidium bromide. 1 µl of 6X loading dye was mixed with 5 µl of PCR products. It was loaded and electrophoresis was performed at 75V power supply with 0.5X TBE as

electrophoresis buffer for about 1-2 hours, until the bromophenol blue front had migrated to almost the bottom of the gel. The molecular standard used was 2-log DNA ladder (NEB). The gels were visualized in a UV transilluminator (Genei) and the image was captured under UV light using Gel documentation system (Bio-Rad) (Figure 2).

3.2.4.4. Data Analysis

The reproducible bands were scored for their presence (1) or absence (0) for all the genotypes studied. A genetic similarity matrix was constructed using the Jaccard's coefficient method (Jaccard, 1908).

$$Sj = a/(a+b+c)$$

Where, a= Number of bands present in both the genotypes in a pair

b= Number of bands present in the first genotype but not in the second one

c= Number of bands present in the second genotype but not in the first

Based on the similarity coefficient a dendrogram was constructed with the help of the software package 'NTSYS' (version 2.02). Association between the genotypes was found out from the dendrogram.

3.3. Experiment 3 - Production of hybrid seeds

Eight divergent parents selected based on cluster analysis were raised in field for the production of hybrid seeds. The design for hybridization was half diallel with parents. Each individual parent was crossed with each other without reciprocals (Griffing, 1956). Hybrids were produced by artificial pollination as suggested by Krishnaswamy (1970). Mature flowers in the female parent plants that would open the next day were emasculated and covered with butter paper cover. Emasculation was done by holding the bud between the thumb and fore finger with the keel petal on the upper side. The corolla was split using a needle, along the two edges of standard petal. One side of the standard petal was brought down and held in position with the thumb. The wing petal was also held similarly. The exposed keel petals were split on the exposed side and

held as above. The immature stamens were removed by seizing the filaments using a forceps. The petals were released and covered with a leaflet to avoid dessication. Butter paper covers were used to secure the emasculated flowers. Next day morning between 6.30 am and 9.00 am pollination was done using pollen collected from male parent. The pollen was collected from the pollen parent by removing the standard and wing petals. The keel petal was pressed gently to expose the stamens covered with pollen grains. The detached flower was used as a brush to dust the pollen on to the stigma of the female parent. Proper tagging was done with required data. The pollinated flower was then covered again. The cover was retained for two days and then removed.

3.4. EXPERIMENT 4 - EVALUATION OF PARENTS AND F_1 HYBRID

The eight parents along with the twenty eight hybrids were raised in the field in RBD with three replications for evaluation. The crop was raised as per the package of practices (KAU, 2018) recommendations. Observations were recorded on yield, yield attributes and quality parameters as in experiment - 1. The data collected were used to estimate the general combining ability of parents and specific combining ability of the crosses. The mode of gene action involved in the inheritance of different characters was studied. The parents and hybrids were allowed to self pollinate naturally.

3.4.1. Statistical analysis

3.4.1.1. Analysis of Variance

Analysis of variance (ANOVA) for individual character was carried out on the basis of mean value per entry per replication as suggested by Panse and Sukhatme (1985) for Randomized Block Design (RBD). The model of analysis of variance is as given below.

ANOVA for each character

Source	d.f.	Mean squares	Expectation of mean squares

Replications	(r-1)	M_r	$\sigma^2e + g\sigma^2r$
Genotypes	(g-1)	M_g	$\sigma^2e + r\sigma^2g$
Parents	(p-1)	M_p	
Hybrid	(h-1)	M_h	
Parent Vs hybrids	1	M_p Vs M_h	
Error	(r-1)(g-1)	M_e	σ^2e

Where,

r = number of replications

g = number of genotypes

p = number of parents

h = number of hybrids

Significance of the treatments was tested at 5 and 1 per cent level of probability.

3.4.1.2. Test of Significance

Test of significance of various components was carried out by 'F' test. The 'F' values were calculated as under.

$$\text{Genotypes} = \frac{M_g}{M_e}$$

$$\text{Parents} = \frac{M_p}{M_e}$$

$$\text{Hybrids} = \frac{M_h}{M_e}$$

$$\text{Parents Vs. hybrids} = \frac{M_p \, Vs \, M_h}{M_e}$$

M_g = mean squares of genotypes

M_p = mean squares of parents

M_h = mean squares of hybrids

M_e = mean squares of error

3.4.1.3. Critical Difference of the Estimates

To test the significance of differences of the estimates, critical difference was calculated as.

$$S.E.D = \sqrt{\frac{2M_e}{r}} \text{ and S.E.M.} = \sqrt{\frac{M_e}{r}}$$

$$C.D. = S.E.D \times t$$

Where,

t = Table 't' value for error degree of freedom at 0.01 and 0.05 levels of probability.

3.4.1.4. Coefficient of Variation

The coefficient of variation for each character was calculated as under,

$$C.V.\% = \frac{\sqrt{M_e}}{X} \times 100$$

Where,

M_e = error mean square

X = general mean for the character

3.4.1.5. Combining Ability Analysis

Combining ability analysis was performed with the data obtained for parents and hybrids according to Model –I, Method –II proposed by Griffing (1956). This includes partitioning of variation among sources attributable to general combining ability (gca) and specific combining ability (sca) components.

The analysis of variance for the combining ability was based on the following statistical model.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + \varepsilon_{ij}$$

Where,

Y_{ijk} = mean value of hybrid involving i^{th} and j^{th} parent in the kth replication

μ = general mean

g_i = gca effect of ith parent

g_j = gca effect of jth parent

s_{ij} = sca effect for the cross between i^{th} and j^{th} parents such that $s_{ij} = s_{ji}$

ε_{ij} = uncontrolled variation associated with ijk^{th} observation

$i,j = 1,2,\ldots\ldots\ldots p$ (p = number of parents)

$k = 1,2,\ldots\ldots\ldots b$ (b=number of blocks)

The form of ANOVA for combining ability and expectation of mean square are given in below table.

Analysis of variance for combining ability

Source	d.f.	S.S.	M.S.	Expectation of mean squares
GCA	(p-1)	S_g	M_g	$\sigma^2 e + \frac{(p+2)}{(p-1)} \Sigma_i\, g^2{}_i$
SCA	$\dfrac{p(p-1)}{2}$	S_s	M_s	$\sigma^2 e + \frac{(2)}{p(p-1)} \Sigma_i\, \Sigma_j\, s^2{}_{ij}$
Error	(r-1)(g-1)	S_e	M_e	$\sigma^2 e$

Sum of squares due to various sources were calculated as follows:

$$S_g = \frac{1}{(p+2)}\left((\Sigma_i\, (Xi.+Xii)^2) - \frac{4}{p}x^2 \right)$$

$$S_s = \sum_i \sum_j \left(X_{ij}^2 - \frac{1}{(p+2)} \left(\sum_i (Xi. + Xii)^2 \right) + \frac{2}{(p+1)(p+2)} x^2 \dots \dots \dots \right)$$

S_g = Sum of square due to general combining ability

S_s = Sum of square due to specific combining ability

p = number of parents

$X_{i.}$ = mean value of ith parent

$X_{..}$ = grand total of all the progenies and parental mean values

M_e = error mean square (M_e/r)

Further, the components of variance determining the additive and non-additive gene actions were computed using the following formula.

$$\sigma^2 gca = \frac{M_g - M_e}{p+2}$$

$$\sigma^2 sca = M_s - M_e$$

Where,

M_g = mean sum of square due to gca effect

M_s = mean sum of square due to sca effect

M_e = M_e /b = Error mean square

3.4.1.5.1. Test of Significance of Combining Ability

The error mean square for combining ability (M_e) was obtained by dividing error mean square (M_e) in ANOVA for each character by number of replications.

The following F ratios were used to test gca and sca variances

gca mean square : F = M_g/M_e

sca mean square : $F = M_s/M_e$

3.4.1.5.2. Estimation of General and Specific Combining Ability Effects

The general and specific combining ability effects were estimated as follows

Population mean $(\mu) = \dfrac{2}{p(p+1)} Y..$

gca effect $= (g_i) = \dfrac{1}{(p+2)} \left\{ \sum (Y_{i.} + Y_{ii}) - \dfrac{2}{p} Y.. \right\}$

sca effect $= (s_{ij}) = Y_{ij} - \dfrac{1}{(p+2)} (Y_{i.} + Y_{ii} + Y_{.j} + Y_{jj}) + \dfrac{2}{(p+1)(p+2)} Y..$

where,

p = number of parents

g_i = gca effect of ith parent

s_{ij} = sca effect of the cross involving i^{th} and j^{th} parent

$Y_{i.}$ = total of array involving i^{th} parent

$Y_{.j}$ = total of array involving j^{th} parent

Y_{ii} = Parental value of the ith parent

Y_{jj} = Parental value of the jth parent

$Y..$ = total of all $\dfrac{p(p+1)}{2}$ items of the Diallel table

Various standard errors required to test the significance of gca and sca effects and differences between them are calculated as

S.E.$(g_i) = \sqrt{\dfrac{(p-1)}{p(p+2)} M_e}$

$$S.E. (s_{ij}) = \sqrt{\frac{(p^2+p+2)}{(p+1)(p+2)}}\, M_e$$

3.4.5.3. Test of Significance

The 't' test used to test the significance of individual gca and sca effects as under.

To test g_i : $t = |g_i|/(S.E.(g_i))$

To test s_{ij} : $t = |s_{ij}|/(S.E.(s_{ij}))$

To test the significance of differences of two estimates, critical differences (CD) was calculated as product of the 't' for error degrees of freedom and the standard error of two estimates.

3.5. Experiment 5 - Evaluation of F_2 population

F_2 seeds of four superior F_1 hybrids were raised in the field experiment in Compact Family Block Design. Even though the pants were raised in compact family design, replications were not taken, since it is a segregating F_2. The data were recorded from all the two hundred plants planted and mean values and variance were calculated to find the best superior recombinant. The crop was raised as per the package of practices (KAU, 2018) recommendations. Observations were taken for the characters *viz.* plant height, number of primary branches plant[-1], number of leaves plant [-1], days to first flowering, days to fifty per cent flowering, Leaf Area Index, green fodder yield plant [-1], dry matter yield plant [-1], leaf fresh weight plant [-1], stem fresh weight plant [-1], leaf dry weight plant [-1] and stem dry weight plant [-1].

3.4.2.1. Analysis of Variance

The Analysis of Variance was carried out for all the traits to find out whether there was any significant difference among the families and the progenies within the family.

Analysis of Variance for Families

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replications	(r-1)	SSR	MSR	MSR/MSE
Families	(f-1)	SSF	MSF	MSF/MSE
Error	(r-1)(f-1)	SSE	MSE	

Analysis of Variance for Progenies within the Family

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replications	(r-1)	SSR	MSR	MSR/MSE
Families	(p-1)	SSP	MSP	MSP/MSE
Error	(r-1)(p-1)	SSE	MSE	

Pooled Analysis of Variance

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replications	(r-1)	SSR	MSR	MSR/MSE
Families	(f-1)	SSF	MSF	MSF/MSE
Error	(r-1)(f-1)	SSE	MSE	
Progenies in i^{th} family	(p-1)	SSP_i	MSP_i	MSP_i/MSE
Pooled error	f(r-1)(p-1)	SSE	MSE	

Where, r = Number of replications,   f = Number of treatments

p = Number of progenies,   SSR = Replication sum of squares

MSE = Replication mean square   SSF = Family sum of square

MSP_i = Progeny mean sum of square and i range from 1 to 8

MSF = Family mean square

Test of significance for various components was carried out by 'F' test. The F values were calculated as under

Replication = MSR/MSE

Treatments = MST/MSE

MSR – Mean sum of replication

MST – Mean sum of treatments

When the treatments differed significantly by the F test, the pair wise comparison of the treatment means are made by using critical difference as

Critical difference (CD) = $t_\propto \times \sqrt{\dfrac{2MSE}{r}}$

Where, $t_\propto$ is the students 't' table value for $\propto$ (5 per cent or 1 per cent) level of significance corresponding to the error degree of freedom.

RESULTS

4. RESULTS

The results of the present investigation on "Genetic analysis of yield and quality in fodder cowpea (*Vigna unguiculata* (L.) Walp)" are presented under five major experiments.

1. Experiment I – Evaluation of fodder cowpea accessions
2. Experiment II – Molecular characterization of genotypes
3. Experiment III – Production of hybrid seeds
4. Experiment IV – Evaluation of parents and F_1 hybrids
5. Experiment V – Evaluation of F_2 population

4.1. EXPERIMENT I – EVALUATION OF FODDER COWPEA ACCESSIONS

Thirty accessions of fodder cowpea were evaluated in a replicated field trial at Instructional Farm, College of Agriculture, Kerala Agricultural University, Vellayani during Kharif 2016 (Plate-1, 2, 3 and 4). The accessions were replicated thrice in plots of size 3m x 1.5m with a spacing of 30 cm x 15 cm. Other cultural operations were carried out as per KAU packages of practices recommendations. The data from experiment I were subjected to statistical analysis and the results are presented in the following subheads.

4.1.1. Estimation of mean and variability components

4.1.2. Estimation of genetic parameters

4.1.3. Estimation of heritability and genetic advance

4.1.4. Correlation between different characters

4.1.5. Path coefficient analysis

4.1.6. Cluster analysis

4.1.7. Discriminant function analysis

4.1.1. Estimation of Mean and Variability Components

Analysis of variance (ANOVA) revealed significant differences for all accessions evaluated (Table – 2). The mean performance of the accessions and the CD values are presented in Table – 3.

Plate 1 : Field view of Experiment I – Evaluation of fodder cowpea accessions

Table – 2 Abstract of analysis of variance of 14 characters in experiment I

Sl. No.	Characters	Character notation	Mean square	
			Genotypes df = 30	Error df = 30
1	Plant height at harvest (cm)	X_1	2716.27**	494.23
2	No. of primary branches plant^{-1}	X_2	1.17*	0.32
3	No. of leaves plant^{-1}	X_3	51.44**	5.31
4	Days to first flowering (days)	X_4	17.19**	4.55
5	Days to 50% flowering (days)	X_5	37.31**	6.38
6	Leaf area index	X_6	206.07**	10.45
7	Green fodder yield plant^{-1} (g)	X_7	7902.55**	1272.20
8	Dry matter yield plant^{-1} (g)	X_8	126.74**	9.51
9	Leaf fresh weight plant^{-1} (g)	X_9	2711.68**	443.13
10	Stem fresh weight plant^{-1} (g)	X_{10}	1634.36**	217.17
11	Leaf dry weight plant^{-1} (g)	X_{11}	40.80**	2.95
12	Stem dry weight plant^{-1} (g)	X_{12}	20.87**	1.97
13	Crude protein content (mg g^{-1})	X_{13}	19.04**	0.97
14	Crude fibre content (mg g^{-1})	X_{14}	10723.95**	156.30

*Significant at five per cent level

**Significant at one per cent level

Table 3 – Mean value of fourteen characters in experiment I

Sl. No.	Accession No.	Plant height (cm)	No. of primary branches	No. of leaves plant^{-1}	Days to first flowering	Days to 50% flowering	Leaf Area Index	Green fodder yield (g plant^{-1})
1.	T_1	247.83	2.72	17.82	40.58	48.67	18.63	274.07
2.	T_2	199.78	2.33	17.64	44.40	53.33	28.14	284.48
3.	T_3	156.03	1.41	14.67	43.47	50.33	18.32	96.68
4.	T_4	183.75	1.86	12.31	46.92	51.67	19.14	144.20
5.	T_5	191.33	1.72	16.86	42.67	47.67	24.15	131.65
6.	T_6	172.83	3.50	21.25	42.09	46.00	28.43	184.51
7.	T_7	189.42	1.58	13.50	42.80	48.67	21.96	161.55
8.	T_8	189.06	1.83	17.08	46.58	55.67	20.96	166.77
9.	T_9	189.17	2.91	20.94	43.07	50.33	21.06	184.05
10.	T_{10}	176.50	2.22	24.44	42.20	47.67	40.41	170.18
11.	T_{11}	182.13	1.91	15.50	39.58	46.00	21.77	146.10
12.	T_{12}	171.03	1.91	16.61	40.33	48.67	22.00	143.50
13.	T_{13}	201.75	1.75	17.67	41.53	46.67	17.59	121.64
14.	T_{14}	187.58	2.41	19.39	43.73	50.33	25.42	248.23
15.	T_{15}	193.42	1.75	20.56	40.60	45.33	24.25	236.94
16.	T_{16}	175.20	1.52	19.06	45.20	54.67	36.59	153.71
17.	T_{17}	184.17	1.75	15.67	42.90	55.67	24.44	112.85
18.	T_{18}	172.83	2.00	16.42	46.56	54.00	19.70	178.47
19.	T_{19}	151.50	0.58	11.67	39.31	45.00	16.75	99.95
20.	T_{20}	166.75	1.08	20.42	37.60	42.67	23.05	86.31
21.	T_{21}	171.42	2.05	15.33	37.93	44.33	24.40	111.85
22.	T_{22}	172.89	2.08	16.53	44.35	54.00	23.43	149.27
23.	T_{23}	183.50	1.58	15.08	41.99	45.00	25.21	122.79
24.	T_{24}	171.17	2.89	27.25	40.60	45.67	35.24	167.78
25.	T_{25}	133.00	1.75	14.92	45.04	51.67	23.16	177.63
26.	T_{26}	202.33	2.52	16.69	40.73	49.00	30.12	174.60
27.	T_{27}	159.17	2.41	25.08	43.37	51.00	28.76	244.51
28.	T_{28}	188.00	2.58	24.08	44.30	49.33	54.59	183.94
29.	T_{29}	57.28	3.25	22.53	42.40	48.33	40.85	179.41
30.	T_{30}	191.39	1.61	27.10	41.07	47.67	30.96	110.54
Mean		171.65	2.05	18.47	42.46	49.17	26.32	164.74
SE		12.84	0.32	1.33	1.23	1.46	1.87	20.59
CD (5%)		36.49	0.92	3.78	3.50	4.15	5.31	58.54

T_1 to T_{30} represents 30 accessions as in Table 1

Table-3 Mean value of fourteen characters in experiment I continued......

Sl. No.	Accession No.	Dry matter yield plant^{-1} (g)	Leaf fresh weight plant^{-1} (g)	Stem fresh weight plant^{-1} (g)	Leaf dry weight plant^{-1} (g)	Stem dry weight plant^{-1} (g)	Crude protein content (mgg^{-1})	Crude fiber content (mgg^{-1})
1.	T$_1$	26.38	168.56	105.51	12.86	13.51	19.51	142.33
2.	T$_2$	24.19	155.36	129.12	12.62	11.57	22.67	132.67
3.	T$_3$	7.71	61.09	35.59	4.45	3.26	21.32	94.00
4.	T$_4$	10.47	90.24	53.96	5.81	4.65	22.37	98.67
5.	T$_5$	10.02	83.80	47.84	6.03	4.11	18.49	219.67
6.	T$_6$	12.89	105.20	79.31	6.37	6.52	26.40	142.67
7.	T$_7$	24.33	89.57	71.99	12.97	11.36	24.34	401.67
8.	T$_8$	14.68	97.58	69.19	8.55	6.13	19.70	170.67
9.	T$_9$	17.68	97.61	86.44	9.35	8.32	21.15	244.00
10.	T$_{10}$	12.80	99.89	70.29	5.87	6.94	24.17	112.33
11.	T$_{11}$	10.98	90.69	55.41	6.58	4.40	23.14	175.67
12.	T$_{12}$	16.73	92.66	50.84	10.94	5.79	22.73	194.33
13.	T$_{13}$	12.18	62.94	58.70	5.54	6.65	25.21	156.67
14.	T$_{14}$	16.72	151.65	96.58	10.81	5.90	20.32	195.00
15.	T$_{15}$	17.12	128.66	108.27	8.45	8.67	24.17	145.33
16.	T$_{16}$	10.43	91.16	62.55	5.33	5.09	19.07	184.00
17.	T$_{17}$	8.57	67.25	45.60	4.70	3.87	19.69	245.33
18.	T$_{18}$	17.62	103.27	75.20	8.71	8.90	28.77	145.33
19.	T$_{19}$	8.69	57.14	42.80	5.00	3.69	22.57	127.00
20.	T$_{20}$	8.49	56.47	29.84	4.82	3.67	24.81	166.67
21.	T$_{21}$	8.85	68.56	43.29	4.23	4.61	21.34	228.33
22.	T$_{22}$	11.25	76.15	73.12	5.19	6.06	23.36	152.00
23.	T$_{23}$	14.34	77.91	44.88	8.73	5.61	23.34	209.00
24.	T$_{24}$	12.35	92.50	75.28	6.66	6.47	22.26	149.00
25.	T$_{25}$	17.03	121.66	55.96	12.17	4.87	20.13	143.33
26.	T$_{26}$	17.82	103.34	71.27	9.50	8.31	21.94	130.00
27.	T$_{27}$	37.43	155.94	88.57	21.52	11.48	26.42	132.67
28.	T$_{28}$	15.32	101.16	82.78	7.60	7.72	21.34	213.67
29.	T$_{29}$	9.46	113.19	66.22	7.50	5.93	25.88	95.00
30.	T$_{30}$	10.53	71.78	38.76	5.74	4.79	19.30	182.00
Mean		14.77	97.77	67.17	8.15	6.63	22.53	170.97
SE		1.78	12.15	8.51	0.99	0.80	0.57	7.22
CD (5%)		5.06	34.55	24.19	2.82	2.27	1.62	20.52

T$_1$ to T$_{30}$ represents 30 accessions as in Table 1

MFC-09-1   CO - 9

Vellayani - 1   CO - 8
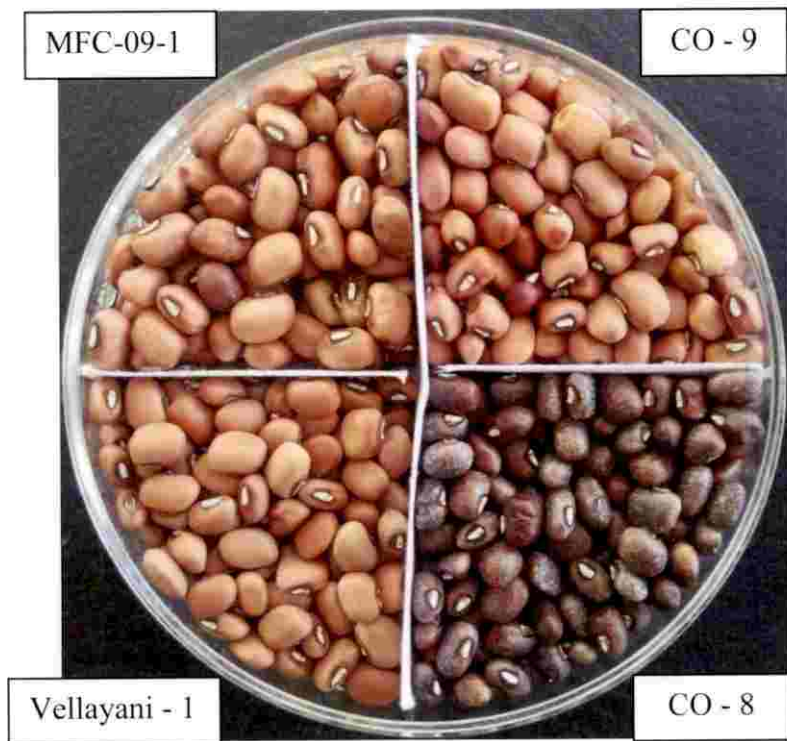
Plate 2 Variability of seeds in accessions

EC - 4216   MFC-08-14

EC - 458489   EC - 394779

IC - 9883
KBC - 2
IC - 1071
IC - 1061

Plate 3 Variability of seeds in accessions

IC – 201095
IC - 25105
IC- 97767
IC – 39916

IC – 253251

IC – 202777

IC – 202804

IC – 202781

Plate 3 Variability of seeds in accessions

IC – 402162

IC – 402090

IC- 402154

IC – 402101
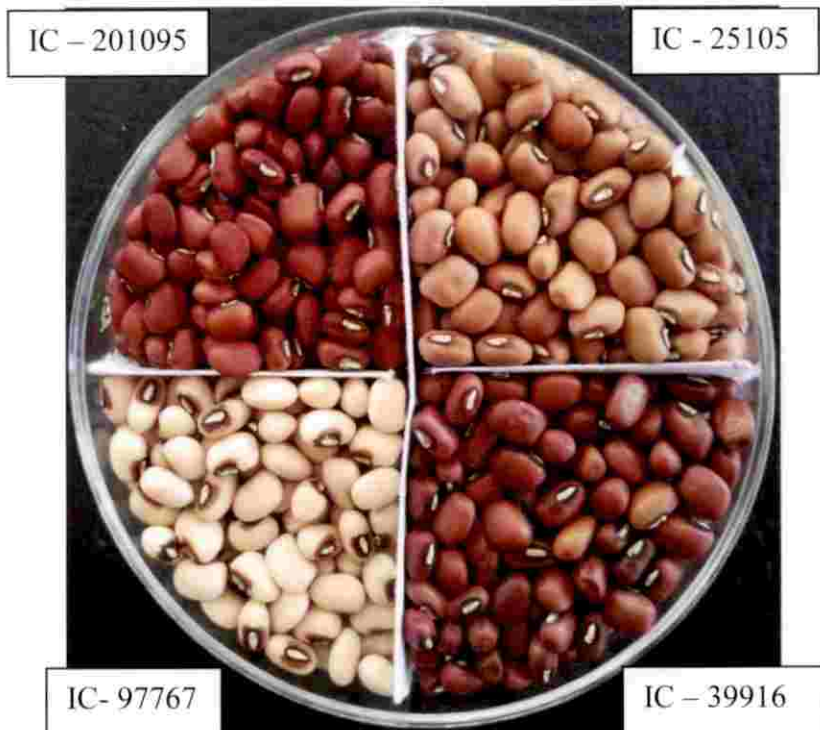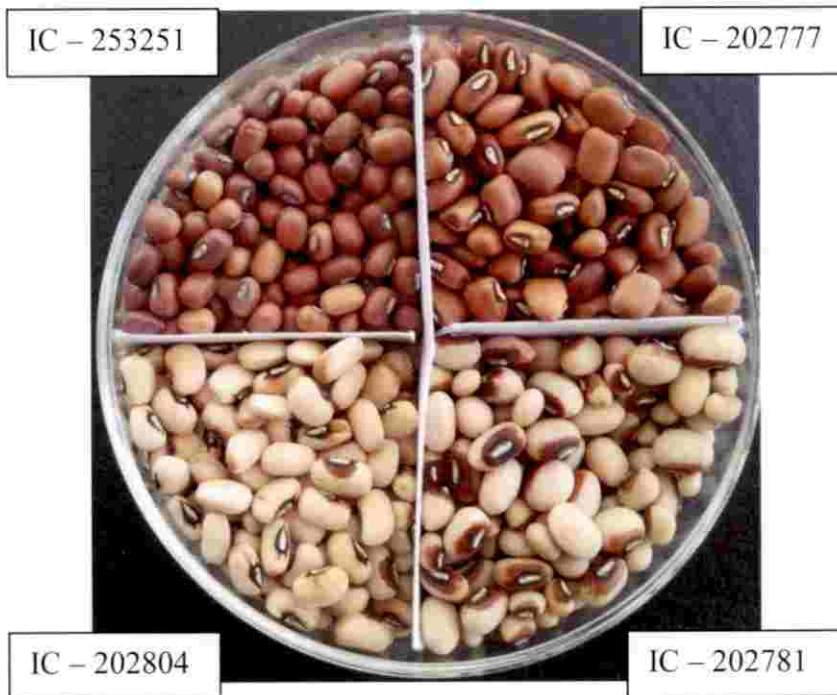
IT – 37154999-38

IC – 458485
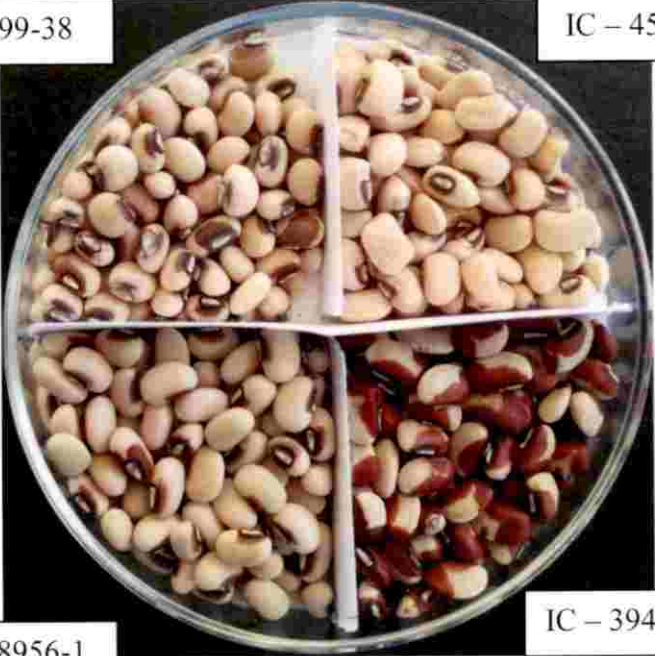
IT – 38956-1

IC – 394779

Plate 4 Variability of seeds in accessions

Pant Lobia – 2

KBC – 5

4.1.1.1. Plant Height at Harvest (cm)

Plant height ranged from 57.28cm to 247.83cm. T_{29} (57.28cm) was the shortest accession. T_{29} was followed by T_{25} (133cm), T_{19} (151.5cm), T_3 (156.03cm), T_{27} (159.17cm) and T_{20} (166.75cm). T_1 (247.83cm) was the longest accession. T_1 is followed by T_{26} (202.33cm). Twenty two other accessions were on par with T_{26}.

4.1.1.2. Number of Primary Branches Plant^{-1}

Number of primary branches plant^{-1} ranged from 3.50 (T_6) to 0.58 (T_{19}). T_{29} with 3.25 branches was followed by T_9 (2.91), T_{24} (2.89), T_1 (2.72) and T_{28} (2.58).

4.1.1.3. Number of Leaves Plant^{-1}

Number of leaves plant^{-1} ranged from 11.67 to 27.25. Maximum number of leaves plant^{-1} was recorded in T_{24} (27.25) and was on par with T_{30} (27.10), T_{27} (25.08), T_{10} (24.44) and T_{28} (24.08). T_{19} (0.58) had the minimum number of leaves plant^{-1}.

4.1.1.4. Days to First Flowering

T_{20} (37.60 days) flowered the earliest and T_4 (46.92 days) was late in flowering. Days to first flowering ranged from 37.60 days to 46.92 days.

4.1.1.5. Days to Fifty Per Cent Flowering

Days to fifty per cent flowering ranged from 42.67 days (T_{20}) to 55.67 days (T_8). T_{20} (42.67) was followed by T_{21} (44.33 days), T_{19} (45.00 days) and T_{23} (45.00 days)

4.1.1.6. Leaf Area Index (LAI)

Leaf area index ranged from 16.75 to 54.59. It was maximum for T_{28} (54.59) followed by T_{29} (40.85), T_{10} (40.41) and T_{16} (36.59). T_{19} (16.75) had the minimum value and was followed by T_{13} (17.59), T_3 (18.32), T_1 (18.63), T_4 (19.14) and T_{18} (19.70).

4.1.1.7. Green Fodder Yield Plant^{-1} (g)

Green fodder yield plant^{-1} ranged from 86.31g to 284.48g. Maximum value recorded in T_2 (284.48g) and minimum in T_{20} (86.31g). T_{20} was on par with T_1 (274.07g), T_{14} (248.23g), T_{27} (244.51g) and T_{15} (236.94g).

4.1.1.8. Dry Matter Yield Plant^{-1} (g)

Dry matter yield plant^{-1} ranged from 7.71g to 37.43g. T_{27} (37.43g) recorded maximum value and T_3 (7.71g) recorded minimum value. T_{27} (37.43g) was on par with T_1 (26.38g) and T_7 (24.33g), T_{26} (17.82g), T_9 (17.68g), T_{18} (17.62g), T_{15} (17.12g) and T_{25} (17.03g) followed by T_7.

4.1.1.9. Leaf Fresh Weight Plant^{-1}(g)

Leaf fresh weight plant^{-1} ranged from 56.47g to 168.56g. T_1 (168.56g) had maximum leaf fresh weight. T_{27} (155.94g), T_2 (155.36g) and T_{14} (151.65g) were on par with T_1. T_{20} (56.47g) recorded minimum value and was on par with T_{19} (57.14g), T_3 (61.09g) and T_{21} (68.56g).

4.1.1.10. Stem Fresh Weight Plant^{-1}(g)

Stem fresh weight plant^{-1} ranged from 29.84g to 129.12g. Highest stem fresh weight was observed in T_2 (129.12g). T_2 was followed by T_{15} (108.27g) and T_1 (105.51g). Lowest value was obtained by T_{20} (29.84g) followed by T_3 (35.59g) and T_{30} (38.76g).

4.1.1.11. Leaf Dry Weight Plant^{-1}(g)

Maximum leaf dry weight plant^{-1} was recorded by T_{27} (21.52g) followed by T_7 (12.97g), T_1 (12.86g) and T_2 (12.62g). Minimum leaf dry weight plant^{-1} was recorded by T_{21} (4.23g) followed by fourteen other accessions which were on par with T_{21}.

4.1.1.12. Stem Dry Weight Plant^{-1}(g)

Highest stem dry weight plant^{-1} was recorded in T_1 (13.51g) which was on par with T_2 (11.57g), T_{27} (11.48g) and T_7 (11.36g). Lowest stem dry weight plant^{-1} was recorded in T_3 (3.26g) which was on par with T_{20} (3.67g) and T_{19} (3.69g).

4.1.1.13. Crude protein content (mg g^{-1})

Crude protein content was maximum for T_{18} (28.77mg g^{-1}) followed by T_{27} (26.42mg g^{-1}) and T_6 (26.40mg g^{-1}). T_6 was followed by T_{29} (25.88mg g^{-1}), T_{13} (25.2 mg g^{-1}) and T_{20} (24.81 mg g^{-1}). Minimum crude protein was reported by T_5 (18.49 mg g^{-1}) followed by T_{16} (19.07 mg g^{-1}), T_{30} (19.30 mg g^{-1}), T_1 (19.51 mg g^{-1}) and T_{17} (19.69 mg g^{-1}).

4.1.1.14. Crude Fibre Content (mg g^{-1})

Crude fibre content is least in T_3 (94.00mg g^{-1}) followed by T_{29} (95mg g^{-1}), T_4 (98.67mg g^{-1}) and T_{10} (112.33mg g^{-1}). Highest crude fibre content was recorded in T_7 (401.67mg g^{-1}) followed by T_{17} (245.33mg g^{-1}), T_9 (244mg g^{-1}), T_{21} (228.33mg g^{-1}), T_5 (219.67mg g^{-1}) and T_{23} (209mg g^{-1}).

4.1.1.15. Growth Habit and Leaf Pubescence

Growth habit and leaf pubescence of the thirty genotypes was visually observed and given in table 4.

4.1.2. Genetic Parameters

The phenotypic, genotypic and environmental variances for the various characters were evaluated. Estimation of variances showed that for most of the characters studied, genotypic variance contributed more than the environmental variance to phenotypic variance (Fig.1).

4.1.2.1. Coefficients of Variation

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were worked out and given in Table 5.

PCV was highest for leaf dry weight plant^{-1} (48.38 per cent) followed by dry matter yield plant^{-1} (47.20 per cent), stem dry weight plant^{-1} (43.27 per cent), stem fresh weight plant^{-1} (39.09 per cent), number of primary branches plant^{-1} (37.75 per cent), green fodder yield plant^{-1} (35.78 per cent), leaf fresh weight plant^{-1} (35.42 per cent), crude fibre content (35.35 per cent) and leaf area index (33.05 per cent).

Table 4 - Growth habit and pubescence of the thirty genotypes in experiment I

Treatments	Accessions	Growth habit	Pubescence
T_1	CO - 9	Spreading type	Glabrous
T_2	CO – 8	Spreading type	Glabrous
T_3	Vellayani-1	Spreading type	Glabrous
T_4	MFC - 09 - 1	Spreading type	Glabrous
T_5	MFC - 08 - 14	Spreading type	Glabrous
T_6	EC - 394779	Spreading type	Glabrous
T_7	EC - 458489	Spreading type	Glabrous
T_8	EC - 4216	Spreading type	Glabrous
T_9	KBC - 2	Spreading type	Glabrous
T_{10}	IC - 1061	Spreading type	Glabrous
T_{11}	IC - 1071	Spreading type	Glabrous
T_{12}	IC - 9883	Spreading type	Glabrous
T_{13}	IC - 25105	Spreading type	Glabrous
T_{14}	IC – 39916	Spreading type	Glabrous
T_{15}	IC- 97767	Spreading type	Glabrous
T_{16}	IC – 201095	Spreading type	Glabrous
T_{17}	IC – 202777	Spreading type	Glabrous
T_{18}	IC – 202781	Spreading type	Glabrous
T_{19}	IC – 202804	Spreading type	Glabrous
T_{20}	IC – 253251	Spreading type	Glabrous
T_{21}	IC – 402090	Spreading type	Glabrous
T_{22}	IC – 402101	Spreading type	Glabrous
T_{23}	IC- 402154	Spreading type	Glabrous
T_{24}	IC – 402162	Spreading type	Glabrous
T_{25}	IC – 458485	Spreading type	Glabrous
T_{26}	IC – 394779	Spreading type	Glabrous
T_{27}	IT – 38956-1	Spreading type	Glabrous
T_{28}	IT – 37154999-38	Spreading type	Glabrous
T_{29}	Pant Lobia – 2	Erect type	Glabrous
T_{30}	KBC – 5	Spreading type	Glabrous

Fig. 1 Components of total variance – PCV and GCV for 14 traits
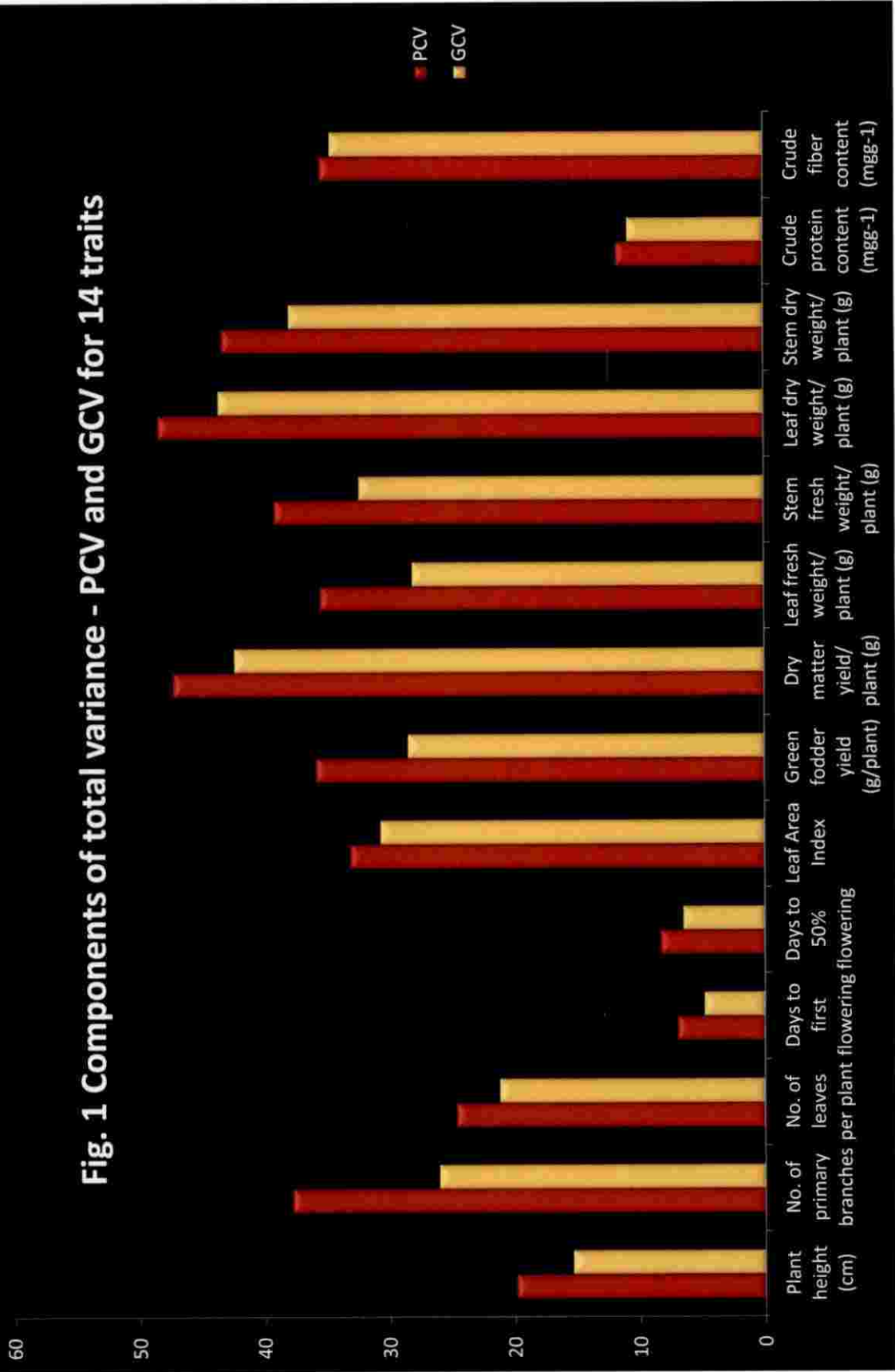
Table 5 Components of variance for 14 characters in fodder cowpea in experiment I

Sl No.	Characters	Genotypic variance	Phenotypic variance	Environmental variance	GCV	PCV
1	X_1	740.68	1234.91	494.23	15.37	19.85
2	X_2	0.29	0.60	0.31	26.04	37.75
3	X_3	15.37	20.69	0.53	21.23	24.63
4	X_4	4.21	8.76	4.55	4.83	6.97
5	X_5	10.31	16.69	6.38	6.53	8.31
6	X_6	65.21	75.66	10.45	30.69	33.05
7	X_7	2210.11	3482.32	1272.20	28.50	35.78
8	X_8	39.08	48.59	9.51	42.33	47.20
9	X_9	756.18	1199.31	443.13	28.13	35.42
10	X_{10}	472.39	689.57	217.17	32.36	39.09
11	X_{11}	12.62	15.56	2.95	43.56	48.38
12	X_{12}	6.32	8.22	1.91	37.93	43.27
13	X_{13}	6.02	6.99	0.97	10.89	11.74
14	X_{14}	3522.55	3678.85	156.30	34.59	35.35

X_1 to X_{14} represents 14 characters as given in Table 2

PCV – Phenotypic coefficient of variation

GCV – Genotypic coefficient of variation

Lowest PCV values were recorded for characters days to first flowering (6.97 per cent) and days to fifty percent flowering (8.31 per cent).

GCV was highest for leaf dry weight plant^{-1} (43.56 per cent) followed by dry matter yield plant^{-1}(42.33 per cent), stem dry weight plant^{-1} (37.93 per cent), crude fibre content (34.59 per cent), stem fresh weight plant^{-1} (32.36 per cent) and leaf area index (30.69 per cent). Lowest GCV values were recorded for characters days to first flowering (4.83 per cent) and days to fifty per cent flowering (6.53 per cent).

ECV was low in all the studied characters as compared to GCV and PCV.

4.1.3. Estimation of Heritability and Genetic Advance

In the present study heritability was high for most of the characters under study (Table 6) (Fig.2). Heritability was high for crude fiber content (96 per cent) followed by crude protein content (86 per cent), leaf area index (86 per cent), leaf dry weight plant^{-1}(81 per cent), dry matter yield plant^{-1}(80 per cent), stem dry weight plant^{-1} (77 per cent), number of leaves plant^{-1} (74 per cent), stem fresh weight plant^{-1} (69 per cent), leaf fresh weight plant^{-1} (63 per cent), green fodder yield plant^{-1} (63 per cent) followed by days to fifty per cent flowering (62 per cent). Medium heritability was recorded for number of primary branches (48 per cent) and days to first flowering (48 per cent) followed by plant height (59 per cent).

Genetic advance was also estimated as percentage of mean and given in table 6 and fig.2. Based on Robinson *et al.* (1949) classification, high genetic advance was recorded for leaf dry weight plant^{-1} (80.80 per cent), dry matter yield plant^{-1} (78.20 per cent), crude fiber content (69.73 per cent), stem dry weight plant^{-1} (68.47 per cent), leaf area index (58.68 per cent), stem fresh weight plant^{-1}(55.17 per cent), green fodder yield plnat^{-1} (46.78 per cent), leaf fresh weight plant^{-1} (46.01 per cent), number of leaves plant^{-1} (37.70 per cent), number of primary branches (37.01 per cent), plant height (25.52 per cent) and crude protein content (20.83 per cent).

Fig. 2 Heritability and Genetic advance for 14 characters

Legend:
- HERITABILITY (%)
- GENETIC ADVANCE (as % of mean)

Characters (top to bottom):
- Crude fiber content (mgg-1)
- Crude protein content (mgg-1)
- Stem dry weight/ plant (g)
- Leaf dry weight/ plant (g)
- Stem fresh weight/ plant (g)
- Leaf fresh weight/ plant (g)
- Dry matter yield (g/plant)
- Green fodder yield (g/plant)
- Leaf Area Index
- Days to 50% flowering
- Days to first flowering
- No. of leaves per plant
- No. of primary branches
- plant height (cm)
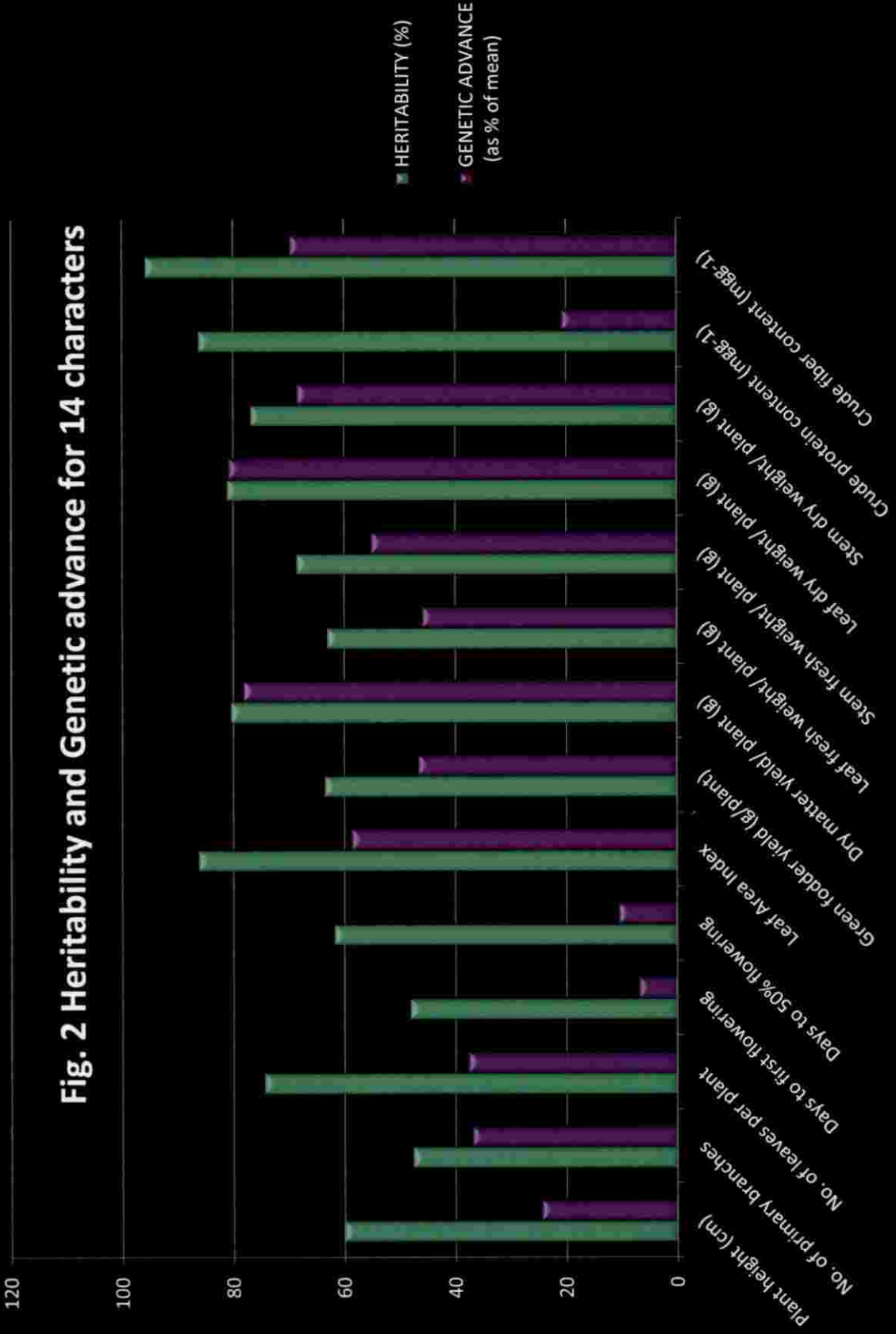
Table 6 - Heritability and genetic advance for 14 characters in cowpea in experiment I

Sl No.	Characters	Heritability %	Genetic advance as percentage of mean
1	Plant height	59.98	24.52
2	No. of primary branches	47.59	37.01
3	No. of leaves plant^{-1}	74.32	37.70
4	Days to first flowering	48.09	6.91
5	Days to 50% flowering	61.77	10.57
6	Leaf Area Index	86.19	58.68
7	Green fodder yield plant^{-1}	63.47	46.78
8	Dry matter yield plant^{-1}	80.42	78.20
9	Leaf fresh weight plant^{-1}	63.05	46.01
10	Stem fresh weight plant^{-1}	68.51	55.17
11	Leaf dry weight plant^{-1}	81.08	80.80
12	Stem dry weight plant^{-1}	76.81	68.47
13	Crude protein content	86.14	20.83
14	Crude fiber content	95.75	69.73

Low genetic advance was observed for days to first flowering (6.91 per cent) followed by days to fifty per cent flowering (10.57 per cent).

4.1.4. Correlation Between Different Characters

The phenotypic, genotypic and environmental coefficients of correlations among the various characters were estimated and results are given in the Table 7, Table 8 and Table 9 respectively.

4.1.4.1. Correlation Among Yield Component Characters

4.1.4.1.1. Green Fodder Yield Plant $^{-1}$

Green fodder yield plant^{-1} had highly significant positive phenotypic correlation with leaf fresh weight plant^{-1} (0.9767), followed by stem fresh weight plant^{-1} (0.9591), stem dry weight plant^{-1} (0.8254), dry matter yield plant^{-1} (0.7829), leaf dry weight plant^{-1} (0.7408) and number of primary branches plant^{-1}(0.4555). Number of leaves plant^{-1} (0.2904) had significant positive phenotypic correlation with green fodder yield plant^{-1}. Green fodder yield plant^{-1} exhibited no significant correlation with plant height (0.1996), days to first flowering (0.1955), leaf area index (0.1807) and days to fifty per cent flowering (0.1309), crude protein content (0.0726) and crude fiber content (-0.1310). The above phenotypic correlations are represented in Fig.3.

Green fodder yield plant^{-1} had highly significant positive genotypic correlation with leaf fresh weight plant^{-1} (0.9646), followed by stem fresh weight plant^{-1} (0.9426), stem dry weight plant^{-1} (0.7745), dry matter yield plant $^{-1}$ (0.7325), number of primary branches plant $^{-1}$ (0.6860), leaf dry weight plant^{-1} (0.6786), days to fifty per cent flowering (0.3650) and days to first flowering (0.3550). Number of leaves plant^{-1} (0.2660) and plant height (0.2630) had significant positive correlation with green fodder yield plant^{-1}. Green fodder yield plant^{-1} had no significant correlation with leaf area index (0.1741), crude protein content (0.1014) and crude fiber content (-0.1500). The above genotypic correlations are represented in Fig.4.

Table 7 - Phenotypic correlation coefficients among fourteen characters in experiment I

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7
X_1	1	-0.0108	-0.0216	-0.0381	0.0240	-0.1746	0.1996
X_2	-0.0108	1	0.4811**	0.0234	-0.0091	0.3938**	0.4555**
X_3	-0.0216	0.4811**	1	-0.1217	-0.1588	0.6868**	0.2904*
X_4	-0.0381	0.0234	-0.1217	1	0.7209**	0.0291	0.1955
X_5	0.0240	-0.0091	-0.1588	0.7209**	1	-0.0308	0.1309
X_6	-0.1746	0.3938**	0.6868**	0.0291	-0.0308	1	0.1807
X_7	0.1996	0.4555**	0.2904*	0.1955	0.1309	0.1807	1
X_8	0.2460	0.2677*	0.1897	0.2420	0.1125	0.0048	0.7829**
X_9	0.1446	0.4344**	0.2742*	0.1866	0.1211	0.1626	0.9767**
X_{10}	0.2578*	0.4508**	0.2910*	0.1933	0.1344	0.1917	0.9591**
X_{11}	0.0947	0.2475	0.1615	0.1407	0.1190	0.0000	0.7408**
X_{12}	0.3306*	0.3627**	0.2207	0.0945	0.0671	0.0848	0.8254**
X_{13}	-0.2520	0.1550	0.0975	-0.0333	-0.1587	0.0050	0.0726
X_{14}	0.2003	-0.1013	-0.1325	-0.0772	0.0012	-0.0341	-0.1310

X_1 to X_{14} represents 14 characters as given in Table 2.

*Significant at 5% level.   **Significant at 1% level.

Table 7 - Phenotypic correlation coefficients among fourteen characters in experiment I continued....

Charac ters	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	0.2460	0.1446	0.2578*	0.0947	0.3306*	-0.2520	0.2003
X_2	0.2677*	0.4344**	0.4508**	0.2475	0.3627**	0.1550	-0.1013
X_3	0.1897	0.2742*	0.2910*	0.1615	0.2207	0.0975	-0.1325
X_4	0.2420	0.1866	0.1933	0.1407	0.0945	-0.0333	-0.0772
X_5	0.1125	0.1211	0.1344	0.1190	0.0671	-0.1587	0.0012
X_6	0.0048	0.1626	0.1917	0.0000	0.0848	0.0050	-0.0341
X_7	0.7829**	0.9767**	0.9591**	0.7408**	0.8254**	0.0726	-0.1307
X_8	1	0.7940**	0.7123**	0.9629**	0.8900**	0.1948	0.0958
X_9	0.7940**	1	0.8761**	0.7914**	0.7729**	0.0370	-0.1643
X_{10}	0.7123**	0.8761**	1	0.6211**	0.8355**	0.1143	-0.0771
X_{11}	0.9629**	0.7914**	0.6211**	1	0.7707**	0.1627	0.0827
X_{12}	0.8900**	0.7729**	0.8355**	0.7707**	1	0.2305	0.1040
X_{13}	0.1948	0.0370	0.1143	0.1627	0.2305	1	-0.1791
X_{14}	0.0958	-0.1640	-0.0770	0.0827	0.1040	-0.1791	1

X_1 to X_{14} represents 14 characters as given in Table 2.

*Significant at 5% level.   **Significant at 1% level.

Fig. 3 - Phenotypic correlation of green fodder yield with other characters

Table 8- Genotypic correlation coefficients among fourteen characters in experiment I

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7
X_1	1	-0.1253	-0.1316	-0.0438	0.0560	0.0560	0.2630*
X_2	-0.1253	1	0.5379**	0.2155	0.1281	0.4771**	0.6860**
X_3	-0.1316	0.5379**	1	-0.1061	-0.1642	0.6603**	0.2660*
X_4	-0.0438	0.2155	-0.1061	1	0.9381**	0.1174	0.3550**
X_5	0.0560	0.1281	-0.1642	0.9381**	1	0.0007	0.3650**
X_6	0.0560	0.4771**	0.6603**	0.1174	0.0007	1	0.1741
X_7	0.2630*	0.6860**	0.2660*	0.3550**	0.3650**	0.1741	1
X_8	0.3086*	0.3288*	0.1517	0.2316	0.2666*	-0.0360	0.7325**
X_9	0.1706	0.6417**	0.2457	0.3343*	0.3459**	0.1517	0.9646**
X_{10}	0.3529**	0.6718**	0.2650*	0.3448**	0.3518**	0.1847	0.9426**
X_{11}	0.0892	0.2960*	0.1180	0.2471	0.2668*	-0.0390	0.6786**
X_{12}	0.4400**	0.5009**	0.1886	0.1811	0.2246	0.0580	0.7745**
X_{13}	-0.3754**	0.2155	0.1088	-0.0763	-0.2766*	-0.0220	0.1014
X_{14}	0.2677*	-0.1439	-0.1582	-0.0930	-0.0306	-0.0350	-0.1500

X_1 to X_{14} represents 14 characters as given in Table 2.

*Significant at 5% level.   **Significant at 1% level.

Table 8- Genotypic correlation coefficients among fourteen characters in experiment I continued…..

Characters	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	0.3086*	0.1706	0.3529**	0.0892	0.4400**	-0.3754**	0.2677*
X_2	0.3288*	0.6417**	0.6718**	0.2960*	0.5009**	0.2155	-0.1439
X_3	0.1517	0.2457	0.2650*	0.1180	0.1886	0.1088	-0.1582
X_4	0.2316	0.3343*	0.3448**	0.2471	0.1811	-0.0763	-0.0930
X_5	0.2666*	0.3459**	0.3518**	0.2668*	0.2246	-0.2766*	-0.0306
X_6	-0.0358	0.1517	0.1847	-0.0390	0.0580	-0.0223	-0.0348
X_7	0.7325**	0.9646**	0.9426**	0.6786**	0.7745**	0.1014	-0.1504
X_8	1	0.7479**	0.6382**	0.9557**	0.8656**	0.2361	0.1215
X_9	0.7479**	1	0.8211**	0.7472**	0.7015**	0.0475	-0.1960
X_{10}	0.6382**	0.8211**	1	0.5225**	0.7877**	0.1593	-0.0773
X_{11}	0.9557**	0.7472**	0.5225**	1	0.7200**	0.1905	0.1051
X_{12}	0.8656**	0.7015**	0.7877**	0.7200**	1	0.2908*	0.1378
X_{13}	0.2361	0.0475	0.1593	0.1905	0.2908*	1	-0.1989
X_{14}	0.1215	-0.1960	-0.0770	0.1051	0.1378	-0.1989	1

X_1 to X_{14} represents 14 characters as given in Table 2.

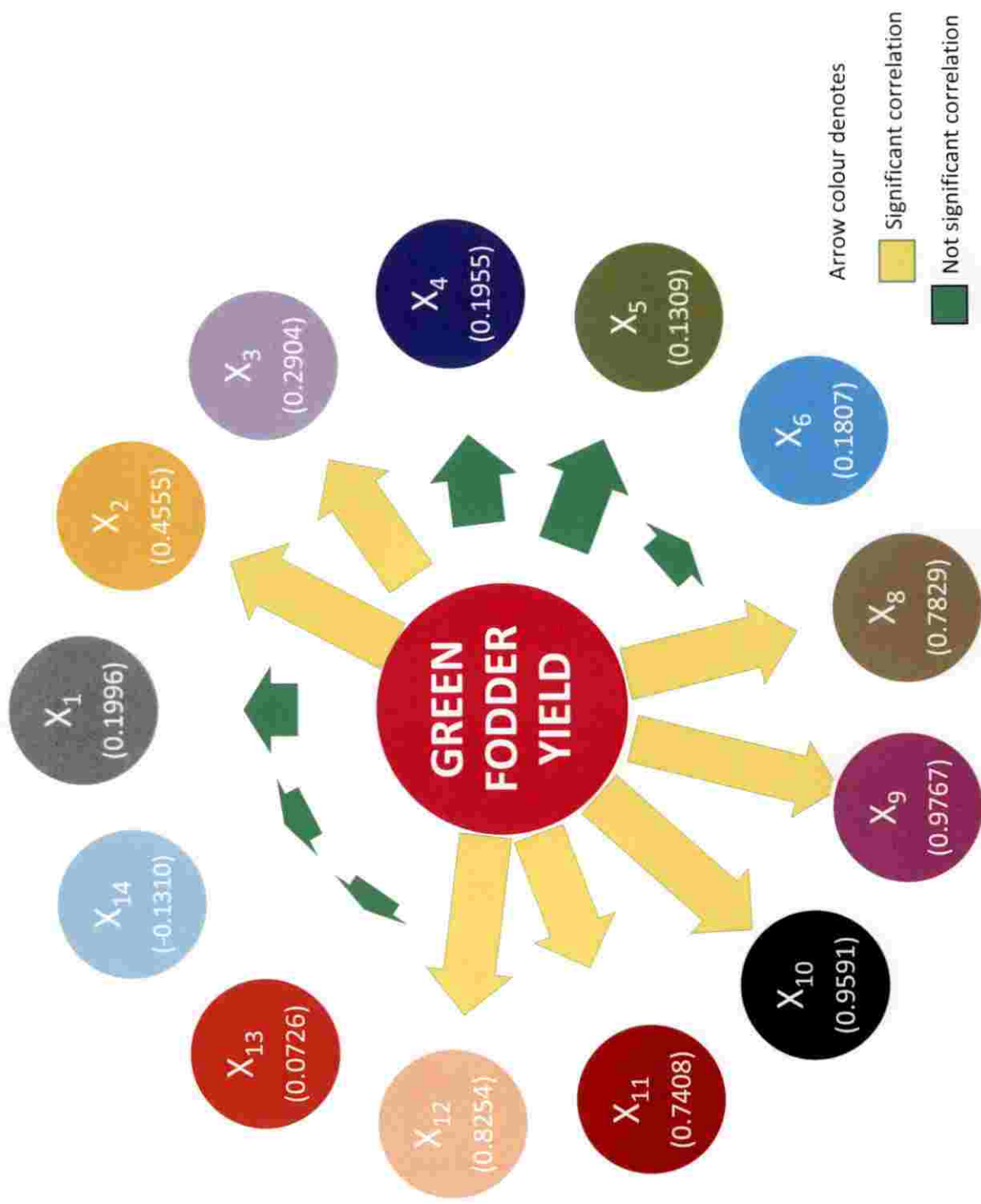*Significant at 5% level.   **Significant at 1% level.
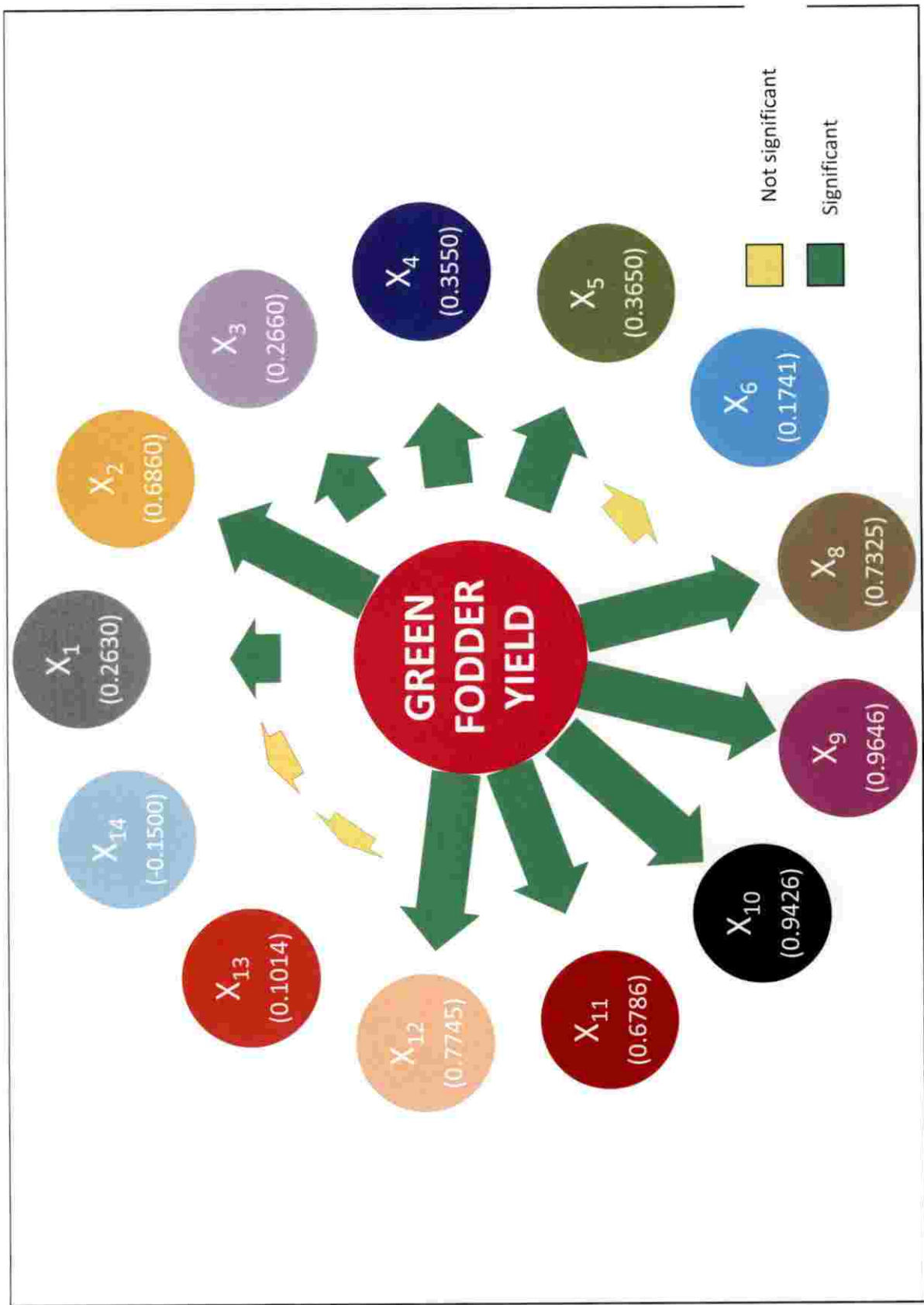
Fig. 4 - Genotypic correlation of green fodder yield with other characters

Table 9 - Environmental correlation coefficients among fourteen characters in experiment I

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7
X_1	1	0.1255	0.2065	-0.0319	-0.0259	0.1849	0.0976
X_2	0.1255	1	0.4395**	-0.1527	-0.1754	0.3280*	0.1796
X_3	0.2065	0.4395**	1	-0.1595	-0.1518	0.8410**	0.3516**
X_4	-0.0320	-0.1530	-0.1600	1	0.4704**	-0.1735	-0.0015
X_5	-0.0260	-0.1750	-0.1520	0.4704**	1	-0.1363	-0.2613*
X_6	0.1849	0.3280*	0.8410**	-0.1735	-0.1363	1	0.2312
X_7	0.0976	0.1796	0.3516**	-0.0015	-0.2613*	0.2312	1
X_8	0.1130	0.2007	0.3232*	-0.0622	-0.2754*	0.2108	0.9707**
X_9	0.1032	0.1884	0.3440**	0.0057	-0.2521	0.2246	0.9977**
X_{10}	0.0889	0.1655	0.3596**	-0.0115	-0.2722*	0.2387	0.9952**
X_{11}	0.1181	0.2023	0.3168*	-0.0435	-0.2594	0.2016	0.9660**
X_{12}	0.1050	0.1716	0.3205*	-0.0448	-0.2943*	0.2099	0.9788**
X_{13}	0.0757	0.0633	0.0553	0.0591	0.1870	0.1756	-0.0107
X_{14}	-0.0200	-0.0280	0.0094	-0.0949	0.1943	-0.0326	-0.1083

X_1 to X_{14} represents 14 characters as given in Table 2.

*Significant at 5% level.   **Significant at 1% level.

Table 9 - Environmental correlation coefficients among fourteen characters in experiment I continued….

Characters	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	0.1130	0.1032	0.0889	0.1181	0.1050	0.0757	-0.0202
X_2	0.2007	0.1884	0.1655	0.2023	0.1716	0.0633	-0.0282
X_3	0.3232*	0.3440*	0.3596**	0.3168*	0.3205*	0.0553	0.0094
X_4	-0.0622	0.0057	-0.0115	-0.0435	-0.0448	0.0591	-0.0949
X_5	-0.2754*	-0.2521	-0.2722*	-0.2594	-0.2943*	0.1870	0.1943
X_6	0.2108	0.2246	0.2387	0.2016	0.2099	0.1756	-0.0326
X_7	0.9707**	0.9977**	0.9952**	0.9660**	0.9788**	-0.0107	-0.1083
X_8	1	0.9722**	0.9607**	0.9935**	0.9841**	-0.0102	-0.1181
X_9	0.9722**	1	0.9863**	0.9725**	0.9727**	0.0090	-0.0958
X_{10}	0.9607**	0.9863**	1	0.9489**	0.9771**	-0.0386	-0.1252
X_{11}	0.9935**	0.9725**	0.9489**	1	0.9667**	0.0217	-0.1108
X_{12}	0.9841**	0.9727**	0.9771**	0.9667**	1	-0.0335	-0.1427
X_{13}	-0.0102	0.0090	-0.0386	0.0217	-0.0335	1	0.0199
X_{14}	-0.1181	-0.0958	-0.1252	-0.1108	-0.1427	0.0199	1

X_1 to X_{14} represents 14 characters as given in Table 2.

*Significant at 5% level.   **Significant at 1% level.

Green fodder yield had high significant positive environmental correlation with leaf fresh weight plant^{-1}(0.9977), followed by stem fresh weight plant^{-1} (0.9952), stem dry weight plant^{-1}(0.9788), dry matter yield plant^{-1} (0.9707), leaf dry weight plant^{-1}(0.9660) and number of leaves plant^{-1}(0.3516). Days to fifty per cent flowering (-0.2613) had significant negative correlation with green fodder yield plant^{-1}. Green fodder yield plant^{-1} had no significant environmental correlation with leaf area index (0.2312), number of primary branches plant^{-1} (0.1796), plant height (0.0976), crude fiber content (-0.1083), crude protein content (-0.0107) and days to first flowering (-0.0015).

4.1.4.1.2. Dry Matter Yield Plant $^{-1}$

Phenotypic correlation of dry matter yield with other characters is depicted in Fig.5. Dry matter yield plant^{-1} had positive genotypic correlation with all other characters except for leaf area index (-0.0358), which had an insignificant negative correlation. Dry matter yield plant^{-1} had highly significant positive correlation with leaf dry weight plant^{-1} (0.9557), followed by stem dry weight plant^{-1} (0.8656), leaf fresh weight plant^{-1}(0.7479), green fodder yield plant^{-1}(0.7325) and stem fresh weight plant^{-1} (0.6382). Number of primary branches plant^{-1}(0.3288), plant height (0.3086) and days to fifty per cent flowering (0.2666) had significant genotypic correlation coefficient with dry matter yield plant^{-1}. Dry matter yield plant^{-1} had no significant phenotypic correlation with crude protein content (0.2361), days to first flowering (0.2316), number of leaves plant^{-1} (0.1517) and crude fiber content (0.1215).

Genotypic correlation of dry matter yield plant^{-1} with other characters is represented in the Fig.6. Dry matter yield had highly significant positive phenotypic correlation with leaf dry weight plant^{-1} (0.9629), followed by stem dry weight plant^{-1} (0.8900), leaf fresh weight plant^{-1} (0.7940), green fodder yield plant^{-1} (0.7829) and stem fresh weight plant^{-1}(0.7123). Number of primary branches plant^{-1} (0.2678) had significant positive correlation with dry matter yield plant^{-1}. Dry matter
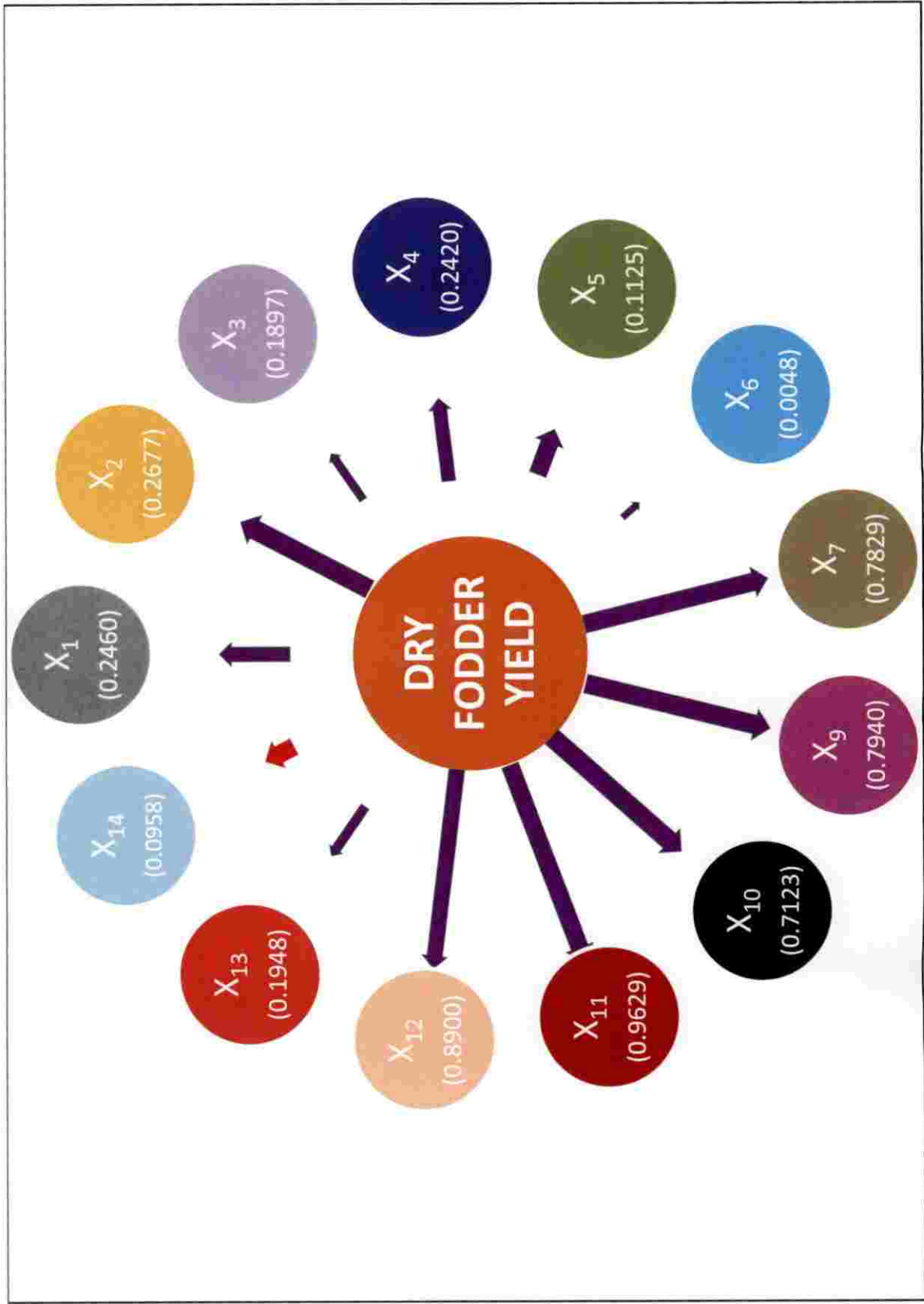
Fig. 5 - Phenotypic correlation of dry fodder yield with other characters
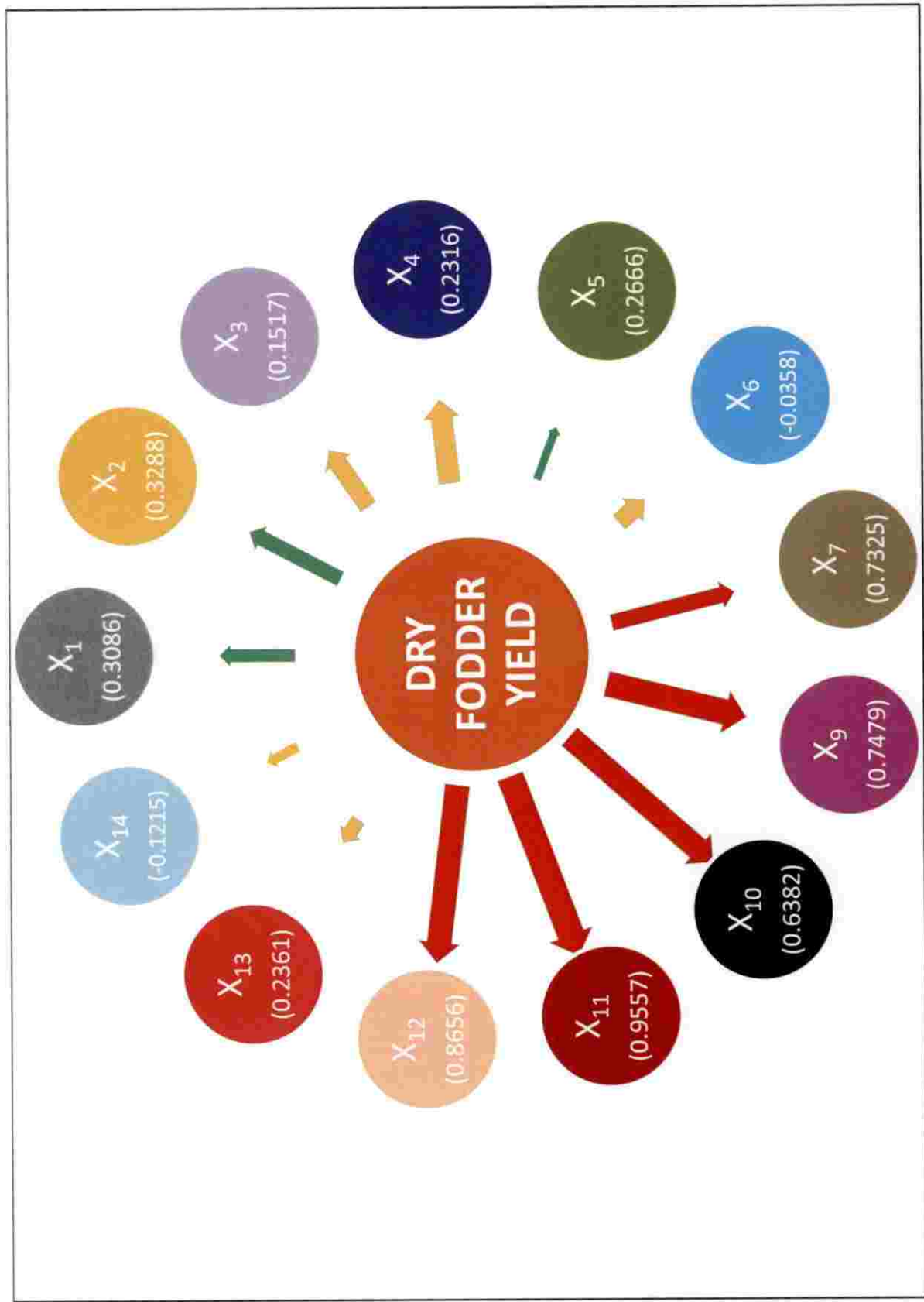
Fig. 6 - Genotypic correlation of dry fodder yield with other characters

yield plant^{-1} showed no significant phenotypic correlation with other characters like plant height (0.2460), days to first flowering (0.2420), crude protein content (0.1948), number of leaves plant^{-1} (0.1897), days to fifty per cent flowering (0.1125), crude fiber content (0.0958) and leaf area index (0.0048).

Dry matter yield plant^{-1} had highly significant positive environmental correlation with leaf dry weight plant^{-1} (0.9935) followed by stem dry weight plant^{-1} (0.9841), leaf fresh weight plant^{-1} (0.9722), green fodder yield plant^{-1}(0.9707) and stem fresh weight plant^{-1}(0.9607), significant positive correlation was estimated for dry matter yield plant^{-1} with number of leaves plant^{-1} (0.3232). Leaf area index (0.2108), number of primary branches plant^{-1} (0.2007), plant height (0.1130), crude fiber content (-0.1181), days to first flowering (-0.0622) and crude protein content (-0.0102) had no significant correlation with dry matter yield plant^{-1}. Dry matter yield plant^{-1} had significant negative environmental correlation with days to fifty per cent flowering (-0.2754).

4.1.4.2. Correlation Among Yield Related Characters

4.1.4.2.1. Plant Height

Plant height had significant positive phenotypic correlation with stem dry weight plant^{-1} (0.3306) and stem fresh weight plant^{-1} (0.2578). Dry matter yield plant^{-1}(0.2460),crude fiber content (0.2003), green fodder yield plant^{-1} (0.1996), leaf fresh weight plant^{-1} (0.1446), leaf dry weight plant^{-1}(0.0947), days to fifty percent flowering (0.0240), number of primary branches plant^{-1}(-0.0108), number of leaves plant^{-1} (-0.0216), days to first flowering (-0.0381), leaf area index(-0.1746) and crude protein content (-0.2520) had no significant correlation with plant height.

Plant height had highly significant positive genotypic correlation with stem dry weight plant^{-1} (0.4400) and stem fresh weight plant^{-1} (0.3529). Dry fodder yield plant^{-1} (0.3086), crude fiber content (0.2677) and green fodder yield plant^{-1} (0.2630) had significant positive correlation with plant height. Leaf fresh weight plant^{-1} (0.1706), leaf dry weight plant^{-1} (0.0892), days to fifty percent flowering

(0.0560), leaf area index (0.0560), days to first flowering (-0.0438), number of primary branches plant^{-1} (-0.1253) and number of leaves plant^{-1} (-0.1316) had no significant correlation with plant height. Plant height had highly significant negative genotypic correlation with crude protein content (-0.3754).

Plant height had no significant environmental correlation with any trait. Number of leaves plant^{-1} (0.2065), leaf area index (0.1849), number of primary branches plant^{-1} (0.1255), leaf dry weight plant^{-1} (0.1181), dry matter yield plant^{-1} (0.1130), stem dry weight plant^{-1} (0.1050), leaf fresh weight plant^{-1} (0.1032), green fodder yield plant^{-1} (0.0976), stem fresh weight plant^{-1} (0.0889), crude protein content (0.0757), crude fiber content (-0.0200), days to fifty per cent flowering (-0.0260) and days to first flowering (-0.0320) were the environmental correlation coefficients.

4.1.4.2.2. Number of Primary Branches Plant^{-1}

Number of primary branches plant^{-1} had highly significant positive phenotypic correlation with number of leaves plant^{-1} (0.4811), green fodder yield plant^{-1} (0.4555), stem fresh weight plant^{-1} (0.4508), leaf fresh weight plant^{-1} (0.4344), leaf area index (0.3938), stem dry weight plant^{-1} (0.3627) and dry matter yield plant^{-1} (0.2677). Leaf dry weight plant^{-1} (0.2475), days to first flowering (0.0234), crude protein content (0.1550), days to fifty percent flowering (-0.0091), plant height (-0.0108) and crude fiber content (-0.1013) had insignificant phenotypic correlation with number of primary branches plant^{-1}.

Number of primary branches plant^{-1} had highly significant positive genotypic correlation with green fodder yield plant^{-1} (0.6860), stem fresh weight plant^{-1} (0.6718), leaf fresh weight plant^{-1} (0.6417), number of leaves plant^{-1} (0.5379), stem dry weight plant^{-1} (0.5009) and leaf area index (0.4771). Dry matter yield plant^{-1} (0.3288) and leaf dry weight plant^{-1} (0.2960) had significant positive genotypic correlation with number of primary branches plant^{-1}. Days to first flowering (0.2155), crude protein content (0.2155) and days to fifty percent

flowering (0.2155), plant height (-0.1253) and crude fiber content (-0.1439) were insignificant.

   Number of primary branches plant[-1] had highly significant positive environmental correlation with number of leaves plant[-1] (0.4395). Leaf area index (0.3280) had significant positive environmental correlation with number of primary branches plant[-1]. Leaf dry weight plant[-1] (0.2023), dry matter yield plant[-1] (0.2007), leaf fresh weight plant[-1] (0.1884), green fodder yield plant[-1] (0.1796), stem dry weight plant[-1] (0.1716), stem fresh weight plant[-1] (0.1655), plant height (0.1255), crude protein content (0.0633), crude fiber content (-0.0280), days to first flowering (-0.1530) and days to fifty per cent flowering (-0.1750) had insignificant environmental correlation with number of primary branches plant[-1].

4.1.4.2.3. Number of Leaves Plant[-1]

   Number of leaves plants[-1] had highly significant positive phenotypic correlation with leaf area index (0.6868) and number of primary branches plant[-1] (0.4811), stem fresh weight plant[-1] (0.2910), green fodder yield plant[-1] (0.2904), leaf fresh weight plant[-1] (0.2742) had significant positive phenotypic correlation. Stem dry weight plant[-1] (0.2207), dry matter yield plant[-1] (0.1897), leaf dry weight plant[-1] (0.1615), crude protein content (0.0975), plant height (-0.0216), days to first flowering (-0.1217), crude fibre content (-0.1325), and days to fifty per cent flowering (-0.1588) had insignificant phenotypic correlation with number of leaves plant[-1].

   Number of leaves plant[-1] had highly significant positive genotypic correlation with leaf area index (0.6603) and number of primary branches plant[-1] (0.5379). Green fodder yield plant[-1] (0.2660) and stem fresh weight plant[-1] (0.2650), show significant positive genotypic correlation. Leaf fresh weight plant[-1] (0.2457), stem dry weight plant[-1] (0.1886), dry matter yield plant[-1] (0.1517), leaf dry weight plant[-1] (0.1180), crude protein content (0.1088), days to first flowering (-0.1061), plant height (-0.1316), crude fiber content (-0.1582) and days to fifty per cent

flowering (-0.1642) had no significant genotypic correlation with number of leaves plant^{-1}.

Number of leaves plant^{-1} had highly significant positive environmental correlation with leaf area index (0.8410), number of primary branches plant^{-1} (0.4395), stem fresh weight plant^{-1} (0.3596), green fodder yield plant^{-1} (0.3516) and leaf fresh weight plant^{-1} (0.3440). Stem dry weight plant^{-1} (0.3205), dry matter yield plant^{-1} (0.3232) and leaf dry weight plant^{-1} (0.3168) had significant positive environmental correlation.

4.1.4.2.4. Days to First Flowering

Days to first flowering expressed highly significant positive phenotypic correlation with days to fifty per cent flowering (0.7209). Characters like dry matter yield plant^{-1} (0.2420), green fodder yield plant^{-1} (0.1955), stem fresh weight plant^{-1} (0.1933), leaf fresh weight plant^{-1} (0.1866), leaf dry weight plant^{-1} (0.1407), number of primary branches plant^{-1} (0.0234), stem dry weight plant^{-1} (0.0945), leaf area index (0.0291), plant height (-0.0381), crude fiber content (-0.0772), crude protein content (-0.0333) and number of leaves plant^{-1} (-0.1217) had no significance.

Days to first flowering expressed high significantly positive genotypic correlation with days to fifty per cent flowering (0.9381), green fodder yield plant^{-1} (0.3550) and stem fresh weight plant^{-1} (0.3448). Significant positive genotypic correlation was seen between days to first flowering and leaf fresh weight plant^{-1} (0.3343). Leaf dry weight plant^{-1} (0.2471), dry matter yield plant^{-1} (0.2316), number of primary branches plant^{-1} (0.2155), stem dry weight plant^{-1} (0.1811), leaf area index (0.1174), and number of leaves plant^{-1} (-0.1061), crude fiber content (-0.0930), plant height (-0.0438) and crude protein content (-0.0763) had not expressed any significant genotypic correlation with days to first flowering.

Days to first flowering had highly significant positive environmental correlation with days to fifty per cent flowering (0.4704) only. All other characters were insignificant.

4.1.4.2.5. Days to Fifty Per Cent Flowering

Days to fifty per cent flowering had highly significant positive phenotypic correlation with days to first flowering (0.7209). All other characters had no significant correlation with days to fifty per cent flowering.

Days to fifty per cent flowering exhibited highly significant positive genotypic correlation with days to first flowering (0.9381), stem fresh weight plant^{-1} (0.3518) and leaf fresh weight plant^{-1} (0.3459). Significant positive genotypic correlation was observed for leaf dry weight plant^{-1} (0.2668). Stem dry weight plant^{-1} (0.2246), number of primary branches plant^{-1} (0.1281), plant height (0.0560), leaf area index (0.0007), crude fiber content (-0.0306) and number of leaves plant^{-1} (-0.1642) had no significant correlation with days to fifty per cent flowering. Crude protein content (-0.2766) had significant negative genotypic correlation with days to fifty per cent flowering.

Highly significant positive environmental correlation coefficient was obtained for days to fifty per cent flowering with days to first flowering (0.4704). Stem dry weight plant^{-1} (-0.2943), dry matter yield plant^{-1} (-0.2754), stem fresh weight plant^{-1} (-0.2722), green fodder yield plant^{-1} (-0.2613) had significant negative correlation with days to fifty per cent flowering.

4.1.4.2.6. Leaf Area Index

Leaf area index had highly significant positive phenotypic correlation with number of leaves plant^{-1} (0.6868) and number of primary branches plant^{-1} (0.3938). Leaf area index had highly significant positive genotypic correlation with number of leaves plant^{-1} (0.6603) and number of primary branches plant $^{-1}$ (0.4771). Leaf area index had highly significant positive environmental correlation with number of leaves plant^{-1} (0.8410) and significant positive correlation with number of

primary branches plant[-1] (0.3280). No other characters had significant genotypic correlation with leaf area index.

4.1.4.2.7. Leaf Fresh Weight Plant [-1]

Leaf fresh weight plant[-1] had highly significant positive phenotypic correlation with green fodder yield plant[-1] (0.9767), stem fresh weight plant [-1] (0.8761), dry matter yield plant [-1] (0.7940), leaf dry weight plant[-1](0.7914), stem dry weight plant[-1](0.7729) and number of primary branches plant[-1](0.4344). Significant positive correlation was observed with number of leaves plant [-1](0.2742).

Leaf fresh weight plant[-1] had highly significant positive genotypic correlation with green fodder yield plant[-1] (0.9646), stem fresh weight plant[-1] (0.8211), dry matter yield palnt[-1] (0.7479), leaf dry weight plant[-1] (0.7472), stem dry weight plant[-1] (0.7015), number of primary branches plant[-1] (0.6417) and dry to fifty percent flowering (0.3459). Significant positive genotypic correlation was observed with days to first flowering (0.3343).

Leaf fresh weight plant[-1] had highly significant positive environmental correlation with green fodder yield plant[-1] (0.9977), stem fresh weight plant[-1] (0.9863), dry matter yield plant[-1] (0.9722) stem dry weight plant[-1] (0.9727) and leaf dry weight plant[-1] (0.9725). Significant positive environmental correlation was observed with number of leaf plants [-1] (0.3440).

4.1.4.2.8. Stem Fresh Weight Plant[-1]

Stem fresh weight plant[-1] had highly significant positive phenotypic correlation with green fodder yield plant[-1] (0.9591), leaf fresh weight plant[-1] (0.8767), stem dry weight plant[-1] (0.8355), dry matter yield plant[-1] (0.7123), leaf dry weight plant[-1] (0.6211) and number of primary branches plant[-1] (0.4508).

Stem fresh weight plant[-1] had highly significant positive genotypic correlation with green fodder yield plant[-1] (0.9426), leaf fresh weight plant[-1] (0.8211), stem dry weight plant[-1] (0.7877), and number of primary branches plant[-1] (0.6718), dry matter yield plant[-1] (0.6382), leaf dry weight plant[-1] (0.5225), plant

height (0.3529), days to fifty per cent flowering (0.3518) and days to first flowering (0.3448). Significant positive genotypic correlation was observed between stem fresh weight plant^{-1} and number of leaves plant^{-1} (0.2650).

Stem fresh weight plant^{-1} had highly significant positive environmental correlation with green fodder yield plant^{-1} (0.9952), leaf fresh weight plant^{-1} (0.9863), stem dry weight plant^{-1} (0.9771), dry matter yield plant^{-1} (0.9607), leaf dry weight plant^{-1} (0.9489) and number of primary branches plant^{-1} (0.3596). Days to fifty per cent flowering (-0.2722) showed significant negative correlation with stem fresh weight plant^{-1}.

4.1.4.2.9. Leaf Dry weight Plant^{-1}

Leaf dry weight plant^{-1} had highly significant positive phenotypic correlation with dry matter yield plant^{-1} (0.9629), leaf fresh weight plant^{-1} (0.7914), stem dry weight plant^{-1} (0.7707), green fodder yield plant^{-1} (0.7408) and stem fresh weight plant^{-1}(0.6211).

Leaf dry weight plant^{-1} had highly significant positive genotypic correlation with dry matter yield plant^{-1} (0.9557), leaf fresh weight plant^{-1} (0.7472), stem dry weight plant^{-1} (0.7200), green fodder yield plant^{-1} (0.6786) and stem fresh weight plant^{-1} (0.5225). Leaf dry weight plant^{-1} had significant positive phenotypic correlation with number of primary branches plant^{-1} (0.2960) and days to fifty per cent flowering (0.2668).

Leaf dry weight plant^{-1} had highly significant positive environmental correlation with dry matter yield plant^{-1} (0.9935), leaf fresh weight plant^{-1} (0.9725), stem dry weight plant^{-1} (0.9667), green fodder yield plant^{-1} (0.9660) and stem fresh weight plant^{-1} (0.9489). Leaf dry weight plant^{-1} had significant positive environmental correlation with number of leaves plant^{-1} (0.3596).

4.1.4.2.10. Stem Dry Weight Plant^{-1}

Stem dry weight plant^{-1} had highly significant positive phenotypic correlation with dry matter yield plant^{-1} (0.8900), stem fresh weight plant^{-1} (0.8355),

green fodder yield plant^{-1} (0.8254), leaf fresh weight plant^{-1} (0.7729), leaf dry weight plant^{-1} (0.7707) and number of primary branches plant^{-1} (0.3627). Significant genotypic correlation of stem dry weight was observed with plant height (0.3306).

Stem dry weight plant^{-1} had highly significant positive genotypic correlation with dry matter yield plant^{-1} (0.8656), stem fresh weight plant^{-1} (0.7877), green fodder yield plant^{-1} (0.7745), leaf dry weight plant^{-1} (0.7200), leaf fresh weight plant^{-1} (0.7015), number of primary branches plant^{-1} (0.5009) and plant height (0.4400). Significant genotypic correlation was observed between stem dry weight and crude protein content (0.2908).

Stem dry weight plant^{-1} had highly significant positive environmental correlation with dry matter yield plant^{-1} (0.9841), green fodder yield plant^{-1} (0.9788), stem fresh weight plant^{-1} (0.9771), leaf fresh weight plant^{-1} (0.9727) and leaf dry weight plant^{-1} (0.9667). Significant positive environmental correlation was observed between stem dry weight and number of leaves plant^{-1} (0.3168). Significant negative environmental correlation was observed between stem dry weight and days to fifty per cent flowering (-0.2943).

4.1.2.3 Correlation Among the Quality Parameters

4.1.2.3.1. Crude Protein Content and Crude Fiber Content

Crude protein content had no significant phenotypic correlation with any other character. It had highly significant negative genotypic correlation with plant height (-0.3754). Significant positive genotypic correlation was observed between crude protein content and stem dry weight plant^{-1} (0.2908). Significant negative genotypic correlation was observed between crude protein content and days to fifty per cent flowering (-0.2766). No significant environmental correlation existed between crude protein content and any other characters. Crude fiber content had significant positive genotypic correlation with plant height only.

4.1.3. Path Coefficient Analysis

Green fodder yield was considered the dependent variable for path analysis. The component characters selected for analysis were plant height, number of primary branches plant^{-1}, number of leaves plant^{-1}, days to first flowering and dry matter yield plant^{-1}. The direct and indirect effect of these characters on yield plant^{-1} were presented in Table 10 and Fig. 7.

Number of primary branches plant^{-1} (0.566) and dry matter yield plant^{-1} (0.472) showed high and positive direct effect on yield followed by plant height (0.184) and days to first flowering (0.124). Number of leaves plant^{-1} had an indirect effect (0.305) through number of primary branches which was high and positive. The highest significant and positive total correlation was seen in the dry matter yield plant^{-1} (0.733). It was followed by number of primary branches plant^{-1} (0.686). The residual effect obtained was 19.28 per cent indicating that 80.72 per cent of the variation in yield was contributed by the characters selected for analysis.

4.1.4 .Cluster Analysis

The thirty fodder cowpea genotypes were grouped into eleven clusters (Table 11). The grouping of genotypes revealed that cluster I was the largest group (10 genotypes) followed by cluster II (5 genotypes), cluster III and IV (4genotypes each), clusters V, VI, VII, VIII, IX, X and XI (1 genotype each).

The intra and inter cluster D^2 values among six clusters are presented in Table 12 and Fig.8. The inter-cluster D^2 values were greater than the intra-cluster D^2 values, further indicating the considerable amount of diversity among the genotypes studied. The intra-cluster D^2 values ranged from 55.47 (cluster I) to 146.57 (cluster II). Moreover, the clusters V to XI were unimembered, as a result, its D^2 values were zero. The maximum inter-cluster D^2 values among genotypes existed between clusters VIII and X (1559.98), followed by clusters VIII and XI (1480.33), clusters II and VIII (1367.65), clusters IV and VIII (1309.08), clusters VI and VIII (1061.84), clusters V and VIII (1057.18), clusters V and IX (1050.25), clusters V and

Fig 7 Path Diagram
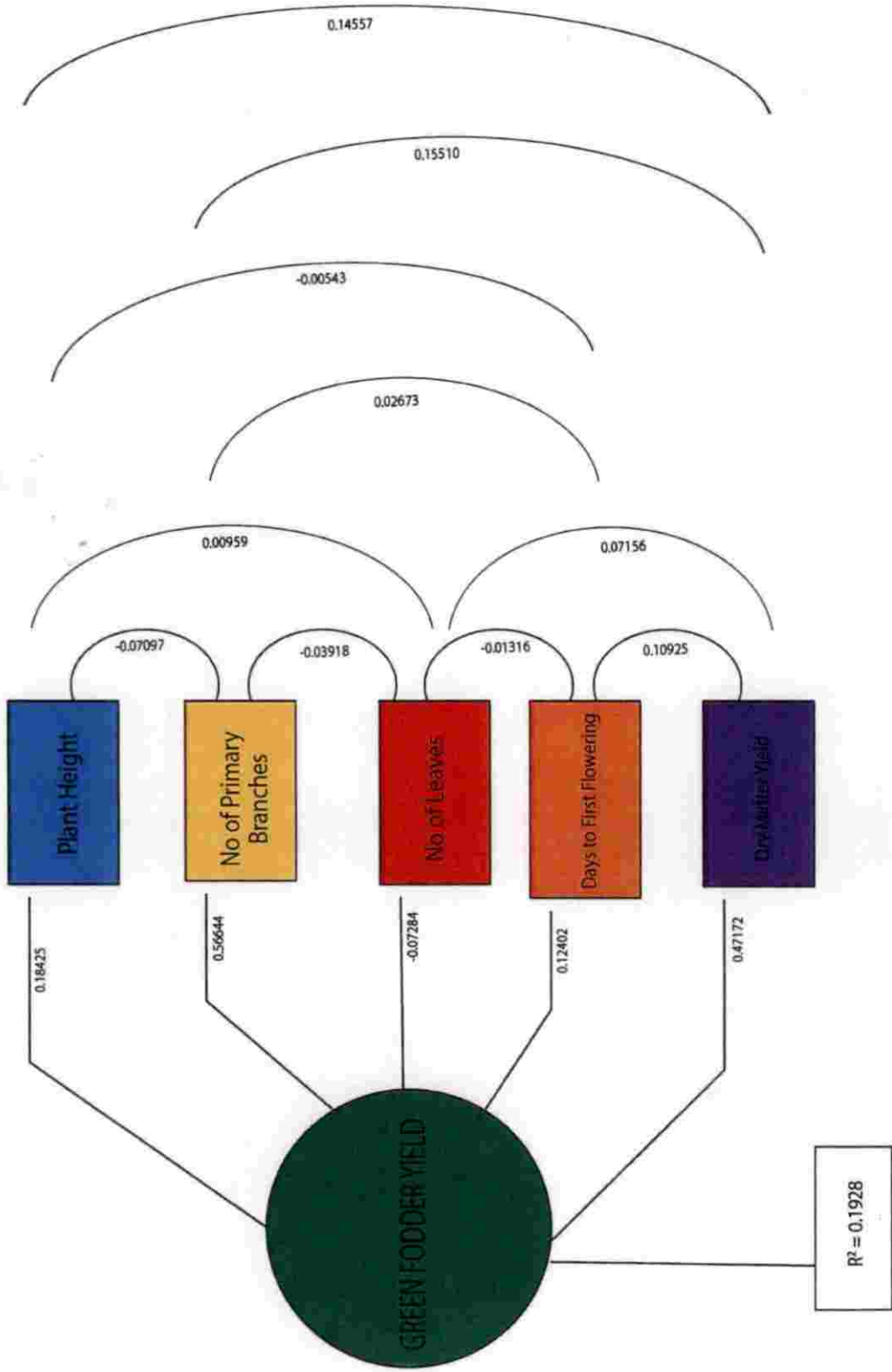
Table 10. Direct and indirect effects of six component characters on green fodder yield in fodder cowpea

Characters	X_1	X_2	X_3	X_4	X_5	Total genotypic correlation coefficient
X_1	**0.18425**	-0.07097	0.00959	-0.00543	0.14557	0.2630
X_2	-0.02309	**0.56644**	-0.03918	0.02673	0.15510	0.6860
X_3	-0.02425	0.30469	**-0.07284**	-0.01316	0.07156	0.2660
X_4	-0.00807	0.12207	0.00773	**0.12402**	0.10925	0.3550
X_5	0.05686	0.18625	-0.01105	0.02872	**0.47172**	0.7330

Residue $(R^2) = 0.1928$

Values on principal diagonal elements indicate direct effects

Values on off diagonal elements indicate indirect effects

X_1 = Plant height

X_2 = No. of primary branches

X_3 = No. of leaves plant^{-1}

X_4 = Days to first flowering

X_5 = Dry matter yield plant^{-1}

Table - 11. Grouping of genotypes into different clusters

Cluster number	Accessions in each cluster
I	CO – 8, EC – 394779, EC – 4216, IC – 9883, IC – 25105, IC- 97767, IC – 201095, IC - 202781, IC – 402101, IC – 394779
II	Vellayani - 1, MFC - 09 – 1, IC – 1071, IC – 202804, IC – 458485
III	MFC - 08 – 14, IC – 202777, IC – 402090, IC – 402154
IV	IC – 1061, IC – 253251, IC- 402162, IT – 38956-1
V	CO - 9
VI	EC – 458489
VII	KBC - 2
VIII	IC -39916
IX	IT – 37154999-38
X	Pant Lobe – 2
XI	KBC – 5

Table – 12. Average inter cluster and intra cluster distances

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	127.52										
II	239.10	101.49									
III	164.51	170.55	55.47								
IV	348.22	564.57	455.05	146.57							
V	430.68	408.82	345.12	923.74	0.00						
VI	351.13	208.64	255.93	574.73	754.32	0.00					
VII	188.91	518.31	246.44	399.71	664.83	513.24	0.00				
VIII	855.99	1367.65	781.10	1309.08	1057.18	1061.84	483.11	0.00			
IX	411.63	809.11	488.78	173.96	1050.25	782.37	268.69	920.94	0.00		
X	388.83	413.27	393.28	263.05	594.63	533.26	661.53	1559.98	459.41	0.00	
XI	563.02	809.27	573.44	167.47	1027.50	724.67	583.37	1480.33	160.10	283.89	0.00

FIG. 8 – CLUSTER DIAGRAM
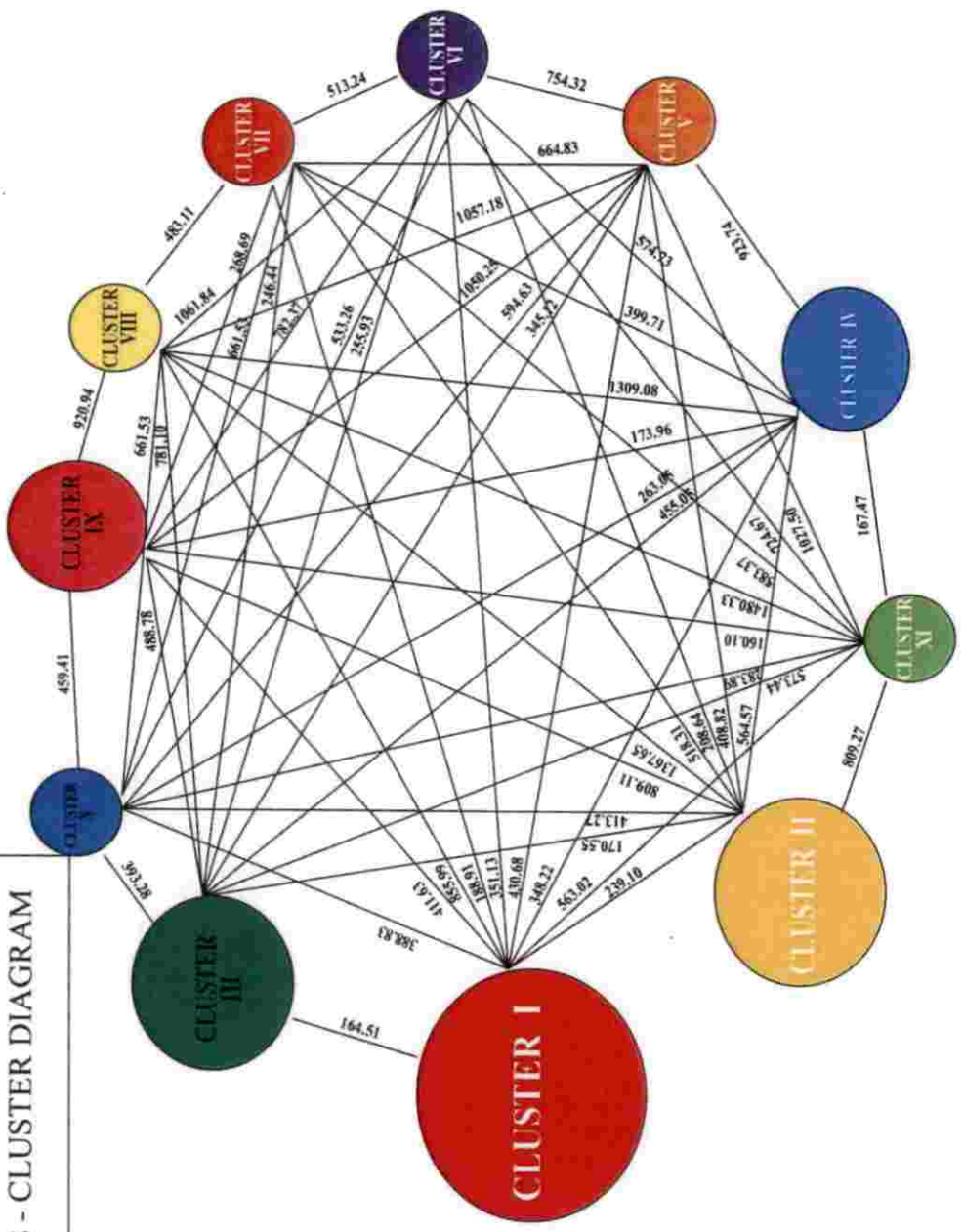
XI (1027.50), clusters V and IV (923.74), clusters VIII and IX (920.94), clusters I and VIII (855.99), clusters II and IX (809.27), clusters II and IX (809.11), clusters VI and IX (782.37), clusters III and VIII (781.10), clusters V and VI (754.32), clusters VI and XI (724.67), clusters V and VII (664.83) and clusters VII and X (661.53). Minimum inter cluster D^2 values were observed between clusters IX and XI (160.10), clusters I and III (164.51), clusters IV and XI (167.47), clusters II and III (170.55), clusters IV and IX (173.96), clusters I and VII (188.91), clusters II and VI (208.64), clusters I and II (239.10), clusters III and VII (246.44), clusters III and VI (255.93), clusters IV and X (263.05), clusters VII and IX (268.69), clusters X and XI (283.89), clusters III and V (345.12), clusters I and IV (348.22), clusters I and VI (351.13), clusters I and X (388.83), clusters III and X (393.28), clusters IV and VII (399.71), clusters II and V (408.82), clusters I and IX (411.63), clusters II and X (413.27), clusters III and IV (455.05), clusters IX and X (459.41), clusters VII and VIII (483.11), clusters III and IX (488.78), clusters VI and VII (513.24), clusters II and VII (518.31), clusters VI and X (533.26), clusters I and XI (563.02), clusters II and IV (564.57), clusters III and XI (573.44), clusters IV and VI (574.73), clusters VII and XI (583.37) and clusters V and X (594.63).

The cluster mean for the fourteen characters revealed considerable difference among all the clusters (Table 13). From the data, it was evident that cluster I had highest mean value for days to fifty per cent flowering (50.73). Cluster II had minimum value for number of primary branches plant^{-1} (1.51) and stem dry weight plant^{-1} (4.17g). Cluster IV has minimum value for days to fifty per cent flowering (46.75). Cluster V has maximum value for plant height (247.83cm), green fodder yield plant^{-1} (274.07g), dry matter yield plant^{-1} (26.38g), leaf fresh weight plant^{-1} (168.56g), stem fresh weight plant^{-1} (105.51g), stem dry weight plant $^{-1}$ (13.51g) and minimum for days to first flowering (40.58 days), leaf area index (18.63). Cluster VI had highest mean for leaf dry weight plant^{-1} (12.97g), crude fiber content (401.67mgg^{-1}) and minimum number of leaves plant^{-1} (13.50). Cluster IX

Table 13 - Mean value of different clusters for different characters along with per cent contribution

Characters	Clusters					% Contribution
	I	II	III	IV	V	
Plant height (cm)	178.64	157.65	182.23	161.06	**247.83**	-
No. of primary branches plant⁻¹	2.12	**1.51**	1.78	2.15	2.72	-
No. of leaves plant⁻¹	17.95	13.81	15.74	24.30	17.83	10.06
Days to first flowering	43.24	42.86	41.37	40.94	**40.58**	-
Days to 50% flowering	**50.73**	48.93	48.17	**46.75**	48.67	-
Leaf Area Index	25.12	19.83	24.55	31.87	**18.63**	12.10
Green fodder yield plant⁻¹ (g)	179.39	132.91	119.78	167.20	**274.07**	0.50
Dry matter yield plant⁻¹ (g)	15.49	10.98	10.44	17.77	**26.38**	10.06
Leaf fresh weight plant⁻¹ (g)	101.63	84.17	74.38	101.20	**168.56**	24.72
Stem fresh weight plant⁻¹ (g)	77.76	48.74	45.40	66.00	**105.51**	-
Leaf dry weight plant⁻¹ (g)	8.12	6.80	5.92	9.72	12.86	-
Stem dry weight plant⁻¹ (g),	7.37	**4.17**	4.55	7.14	**13.51**	16.48
Crude protein content (mgg⁻¹)	23.40	21.91	20.72	24.41	19.51	7.55
Crude fiber content (mgg⁻¹)	155.37	127.73	225.58	140.17	142.33	18.6

Table 13 - Mean value of different clusters for different characters along with per cent contribution conti.........

Characters	Clusters						% Contribution
	VI	VII	VIII	IX	X	XI	
Plant height (cm)	177.17	183.42	187.58	171.33	43	191.39	-
No. of primary branches	1.58	2.92	2.42	2.58	3.25	1.61	-
No. of leaves	13.50	20.94	19.39	24.08	22.53	27.11	10.06
Days to first flowering	42.80	43.07	43.73	44.30	42.40	41.07	-
Days to 50% flowering	48.67	50.33	50.33	49.33	48.33	47.67	-
Leaf Area Index	21.96	21.06	25.42	54.59	40.85	30.97	12.10
Green fodder yield (g)	161.55	184.05	248.23	183.94	179.41	110.54	0.50
Dry matter yield (g)	24.33	17.69	16.72	15.32	9.46	10.53	10.06
Leaf fresh weight (g)	89.57	97.61	151.65	101.16	113.19	71.78	24.72
Stem fresh weight (g)	71.99	86.44	96.58	82.78	66.22	38.76	-
Leaf dry weight (g)	12.97	9.35	10.81	7.60	7.50	5.74	-
Stem dry weight (g)	11.36	8.32	5.90	7.72	5.93	4.79	16.48
Crude protein content (mgg^{-1})	24.34	21.15	20.32	21.34	25.88	19.30	7.55
Crude fiber content (mgg^{-1})	401.67	244.00	195.00	213.67	95.00	182.00	18.6

had maximum mean value for days to first flowering (44.30) and leaf area index (54.59). Cluster X had minimum mean value for plant height (43.00cm), dry matter yield plant^{-1} (9.46g), crude fiber content (95.00mgg^{-1}) and maximum value for crude protein content (25.88 mgg^{-1}), number of primary branches plant^{-1} (3.25). Cluster XI had maximum mean value for number of leaves plant^{-1} (27.11) and minimum mean value for green fodder yield plant^{-1} (110.54g), leaf fresh weight plant^{-1} (71.78g), stem fresh weight plant^{-1} (38.76g), leaf dry weight plant^{-1} (5.74g), crude protein content plant^{-1} (19.30mgg^{-1}). The results had shown high variations for mean values for all fourteen characters.

Contribution of individual characters towards total divergence had been presented in table 13. The maximum contribution to divergence was shown by leaf fresh weight plant^{-1} (24.72 per cent) followed by crude fiber content (18.60 per cent), stem dry weight plant^{-1} (16.48 per cent), leaf area index (12.10per cent), dry matter yield plant^{-1} (10.06 per cent), number of leaves plant^{-1} (10.06 per cent), crude protein content (7.55 per cent) and green fodder yield plant^{-1} (0.50 per cent). Plant height, number of primary branches plant^{-1}, days to first flowering, days to fifty per cent flowering, stem fresh weight plant^{-1} and leaf dry weight plant^{-1} did not contribute to genetic divergence significantly.

4.1.5. Discriminant Function Analysis

Selection index was calculated for the genotypes based on the desired characters namely plant height, number of primary benches plant^{-1}, number of leaves plant^{-1}, days to first flowering, days to fifty per cent flowering, leaf are index, green fodder yield plant^{-1}, dry matter yield plant^{-1}, leaf fresh weight plant^{-1}, stem fresh weight plant^{-1}, leaf dry weight plant^{-1}, stem dry weight plant^{-1}, crude protein content and crude fiber content used in the present study and presented in Table 14. The maximum selection index value was obtained for IT-37154999-38 (860.8776) and least was for IC-202804 (177.1901). The genotypes were ranked for characters green fodder yield, crude protein content, crude fiber content and section index. The

Table - 14. Selection index and rank of 30 genotypes

Treatments	Genotype	Selection index	Rank
T_1	CO - 9	433.476	8
T_2	CO - 8	625.835	2
T_3	Aishwarya	192.102	29
T_4	MFC - 09 - 1	321.337	19
T_5	MFC - 08 - 14	326.563	18
T_6	EC - 394779	336.777	17
T_7	EC - 458489	616.807	3
T_8	EC - 4216	316.379	21
T_9	KBC - 2	288.465	23
T_{10}	IC - 1061	511.640	7
T_{11}	IC - 1071	316.797	20
T_{12}	IC - 9883	307.039	22
T_{13}	IC - 25105	220.905	27
T_{14}	IC – 25105	390.288	11
T_{15}	IC – 39916	406.693	10
T_{16}	IC- 97767	569.894	5
T_{17}	IC – 201095	377.741	12
T_{18}	IC – 202777	367.163	15
T_{19}	IC – 202781	282.971	24
T_{20}	IC – 202804	177.190	30
T_{21}	IC – 253251	374.803	13
T_{22}	IC – 402090	373.470	14
T_{23}	IC – 402101	410.474	9
T_{24}	IC- 402154	279.348	26
T_{25}	IC – 402162	352.305	16
T_{26}	IC – 458485	514.655	6
T_{27}	IT – 38956-1	610.103	4
T_{28}	IT – 37154999-38	860.878	1
T_{29}	Pant Lobe – 2	282.027	25
T_{30}	KBC – 5	201.306	28

Table 15–DNA yield and initial purity in fodder cowpea

Genotype	Accessions	DNA yield (ng/μl)	Purity
T_1	CO - 9	4140	1.5
T_2	CO – 8	6204	1.5
T_3	Vellayani-1	6225	1.8
T_4	MFC - 09 - 1	5466	1.6
T_5	MFC - 08 - 14	6897	1.7
T_6	EC - 394779	8544	1.8
T_7	EC - 458489	3423	1.4
T_8	EC - 4216	6102	1.6
T_9	KBC - 2	8292	1.5
T_{10}	IC - 1061	6816	1.7
T_{11}	IC - 1071	2622	1.4
T_{12}	IC - 9883	5589	1.7
T_{13}	IC - 25105	1575	1.9
T_{14}	IC – 39916	1287	2.0
T_{15}	IC- 97767	2676	2.1
T_{16}	IC – 201095	1777	1.8
T_{17}	IC – 202777	4317	2.1
T_{18}	IC – 202781	4476	2.0
T_{19}	IC – 202804	4026	1.9
T_{20}	IC – 253251	5217	2.1
T_{21}	IC – 402090	1203	1.6
T_{22}	IC – 402101	1899	2.0
T_{23}	IC- 402154	3735	1.8
T_{24}	IC – 402162	1215	2.1
T_{25}	IC – 458485	2469	1.6
T_{26}	IC – 394779	2820	1.8
T_{27}	IT – 38956-1	1003	2.1
T_{28}	IT – 37154999-38	1836	1.6
T_{29}	Pant Lobia – 2	7584	2.1
T_{30}	KBC – 5	6327	2.1

average of these four ranks were calculated and again ranked accordingly. Based on this rank and maximum inter cluster distance eight genotypes CO-8, MFC-09-1, IC-1061, IC-39916, IC-97767, IT-38956-1, IT-37154999-38 and Plant Lobia-2, were selected for further breeding programmers.

4.2 EXPERIMENT II

Molecular characterization was done in thirty genotypes of fodder cowpea accessions using four primers UBC-811, UBC-812, UBC-823 and UBC -834. The DNA was isolated from tender leave of the fodder cowpea genotypes.

4.2.1. Spectrophotometric Data

The quality of DNA isolated was checked using agarose gel (0.8 per cent) electrophoresis. The gels were visualized in a transilluminator and the image was captured under UV light using Gel documentation system (Plate 5). The assay of DNA samples revealed that the samples isolated were intact and native without any shearing. The purity of DNA samples calculated based on spectrophotometric data is given in Table 15. The yield ranged from 1003 to 8544 ng μl^{-1}. The initial purity of DNA ranged from 1.4 to 2.1 . The average purity was 1.8.

4.2.2. Molecular marker profile

The PCR reaction was done using four ISSR primers *viz.* UBC – 811, UBC-812, UBC-823 and UBC -834. The profile is given in Plates 6, 7, 8 and 9. The extend of polymorphism is given in table 16. Thirty two amplicons were produced by the four primers used. The average number of amplicons produced was eight amplicons per primer. Primer UBC-812 produced maximum number of amplicons (10). UBC-811 and UBC-834 produced 8 amplicons each. Primer UBC-823 produced six amplicons only. The amplification product's ranged in size approximately from 500 base pairs to 3000 base pairs. Number of amplicons per genotypes varied from zero to eight.

Table -16. Performance of four ISSR primers in the polymorphism of genomic DNA of thirty fodder cowpea genotypes.

Primer	Length of amplified loci (bp)	Total amplicons (No.)	Polymorphic amplicons (No.)	Polymorphism (%)
UBC-811	700-2750	8	8	100
UBC-812	500-2250	10	10	100
UBC-823	700-1500	6	6	100
UBC-834	650-3000	8	8	100

4.2.3. Dendrogram

Reproducible amplicons were scored for their presence (1) and absence (0) for all the thirty accessions studied. The scores (Table-17) were used to divide the thirty genotypes into different clusters and a dendrogram was drawn (Fig.9). Reproducible amplicons produced were scored for their presence (1) or absence (0) for all the genotypes studies (Plates-6, 7, 8 and 9).

The thirty genotypes were grouped into two clusters (I and II) with 0.34 per cent similarity. Cluster I and II had two sub clusters each Ia and Ib and IIa and IIb respectively.

4.3. EXPERIMENT III

Based on the statistical analysis in experiment I, eight parents were selected and crossed in diallel fashion without reciprocals. CO-8, MFC-09-1, IC-1061, IC-39916, IC-97767, IT-38956-1, IT-37154999-38 and Pant Lobia-2 (Plate – 10) were the eight parents with better yield, quality and divergence among the thirty genotypes screened. Hybridization was done as a field experiment (Plate 11).

Plate 5 – DNA sample electrophoresis image of 30 fodder cowpea accessions under transilluminator

Plate 6 – AMPLIFICATION PROFILES OF THE DNA OF 30 GENOTYPES OF FODDER COWPEA ACCESSIONS USING ISSR PRIMER UBC - 811
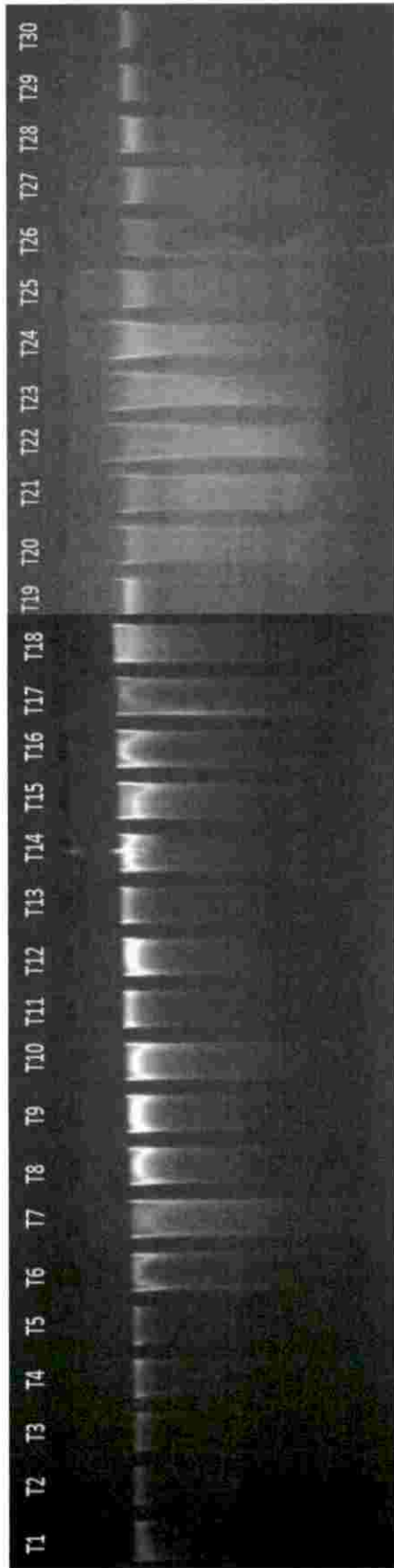

Plate 7 – AMPLIFICATION PROFILES OF THE DNA OF 30 GENOTYPES OF FODDER COWPEA ACCESSIONS USING ISSR PRIMER UBC - 812
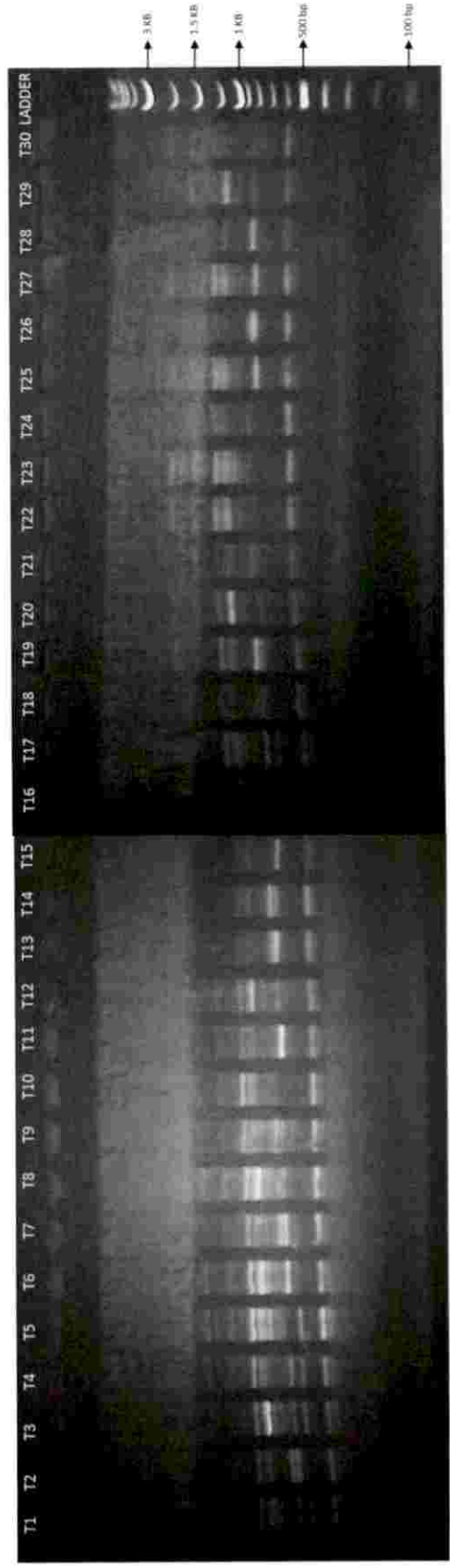
Plate 8 Amplification profiles of the DNA of 30 genotypes of fodder cowpea using the primer UBC – 823
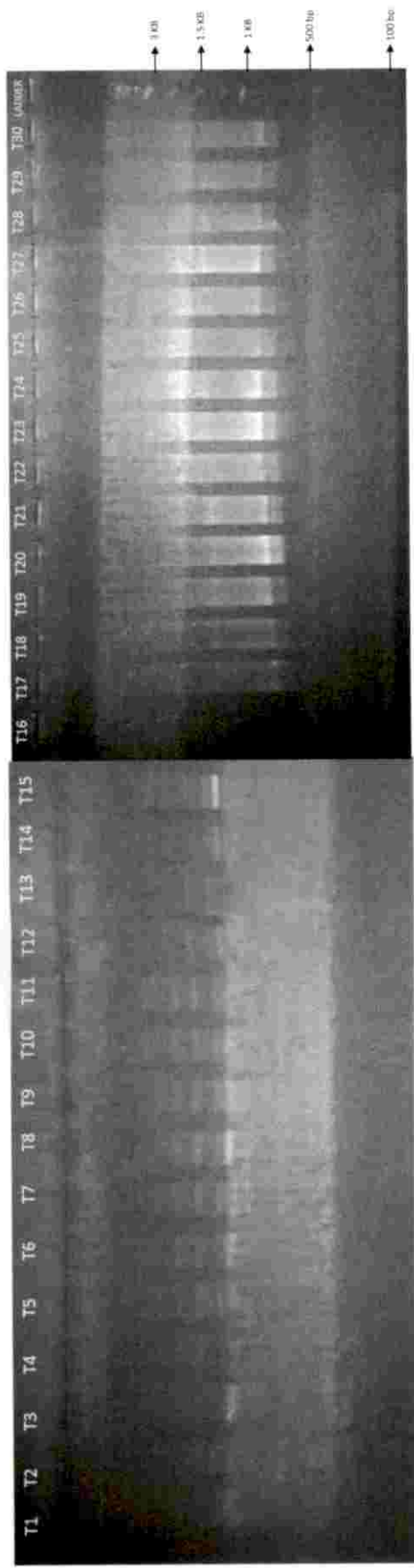
Plate 9 Amplification profiles of the DNA of 30 genotypes of fodder cowpea using the primer UBC - 834
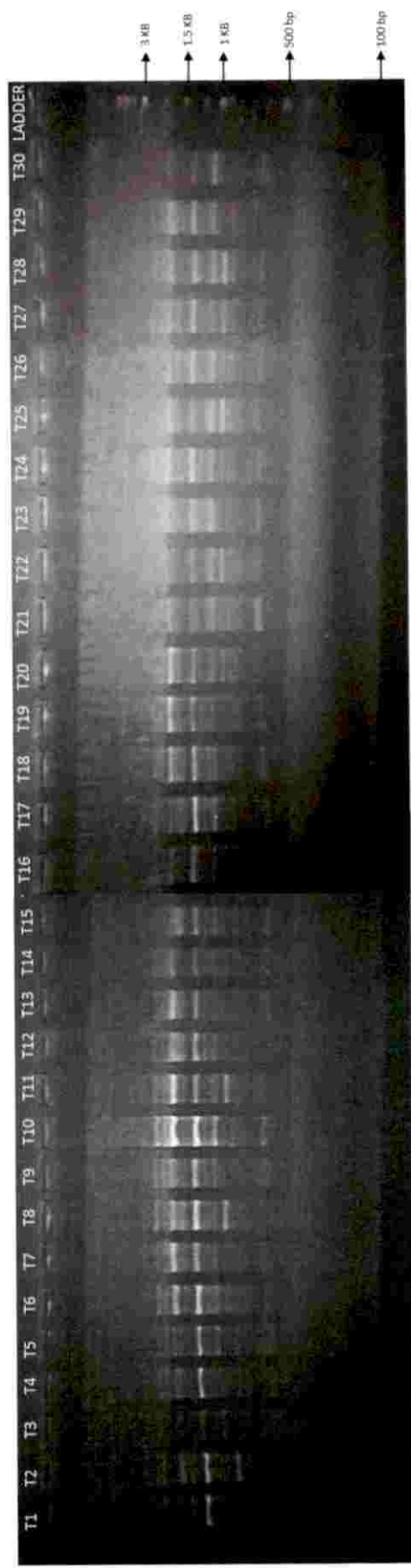
Table 17 – Scores for 32 bands for 30 genotypes of fodder cowpea accessions produced by four ISSR primers

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	1	1	0	1	1	1	1	1	1	1	0	1	1	0	1	1	0	1	1	1	0	1	1	1	1	1	1	1	0	1
2	1	0	0	0	1	1	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	1	0	0
3	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
4	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
6	1	1	0	1	1	1	1	1	1	0	1	1	1	0	1	1	1	0	1	1	0	1	1	1	1	1	1	0	1	1
7	1	1	0	1	0	0	1	1	0	0	0	0	1	0	1	0	0	0	1	1	0	1	0	0	1	1	0	1	0	0
8	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	0	1	0
9	0	0	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	1	0	0	0	1
10	0	1	1	1	1	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1
11	1	1	1	0	1	1	0	1	0	1	1	1	1	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	1
12	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
13	1	1	1	1	1	1	1	0	1	1	0	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1
14	0	1	0	0	0	1	1	1	1	1	0	0	1	0	1	1	1	0	0	1	0	0	1	1	0	0	1	1	0	0
15	1	1	1	1	0	0	0	0	1	0	1	1	1	0	0	0	0	0	1	1	1	1	0	1	1	1	1	0	0	1
16	0	0	1	1	1	0	1	1	1	0	0	0	0	0	1	0	1	0	0	0	1	1	1	0	0	0	1	0	0	1
17	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1
18	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0
20	0	0	0	0	1	1	1	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1	0	0	1	1	1	1	0	0
21	1	1	1	0	0	1	0	1	1	1	1	1	0	0	0	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	1	1	1	1	0	0	1	0	0	1	0	0	1	1
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	1	1	0	1	1	1	1	1	1	1	0	1	1	1	0	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
26	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1
27	1	1	0	0	0	1	0	0	0	0	0	1	0	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0
28	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1
30	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	1	1	0	1	0	0	0	0	1	1	0	0	1	0
31	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
32	0	0	1	1	1	0	1	0	0	0	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	0

X axis represents thirty genotypes T_1 to T_{30} as in table 2

Yaxis represents thirty two bands from four ISSR primers

Figure 9- Dendrogram for 30 genotypes of fodder cowpea accessions based on the ISSR analysis
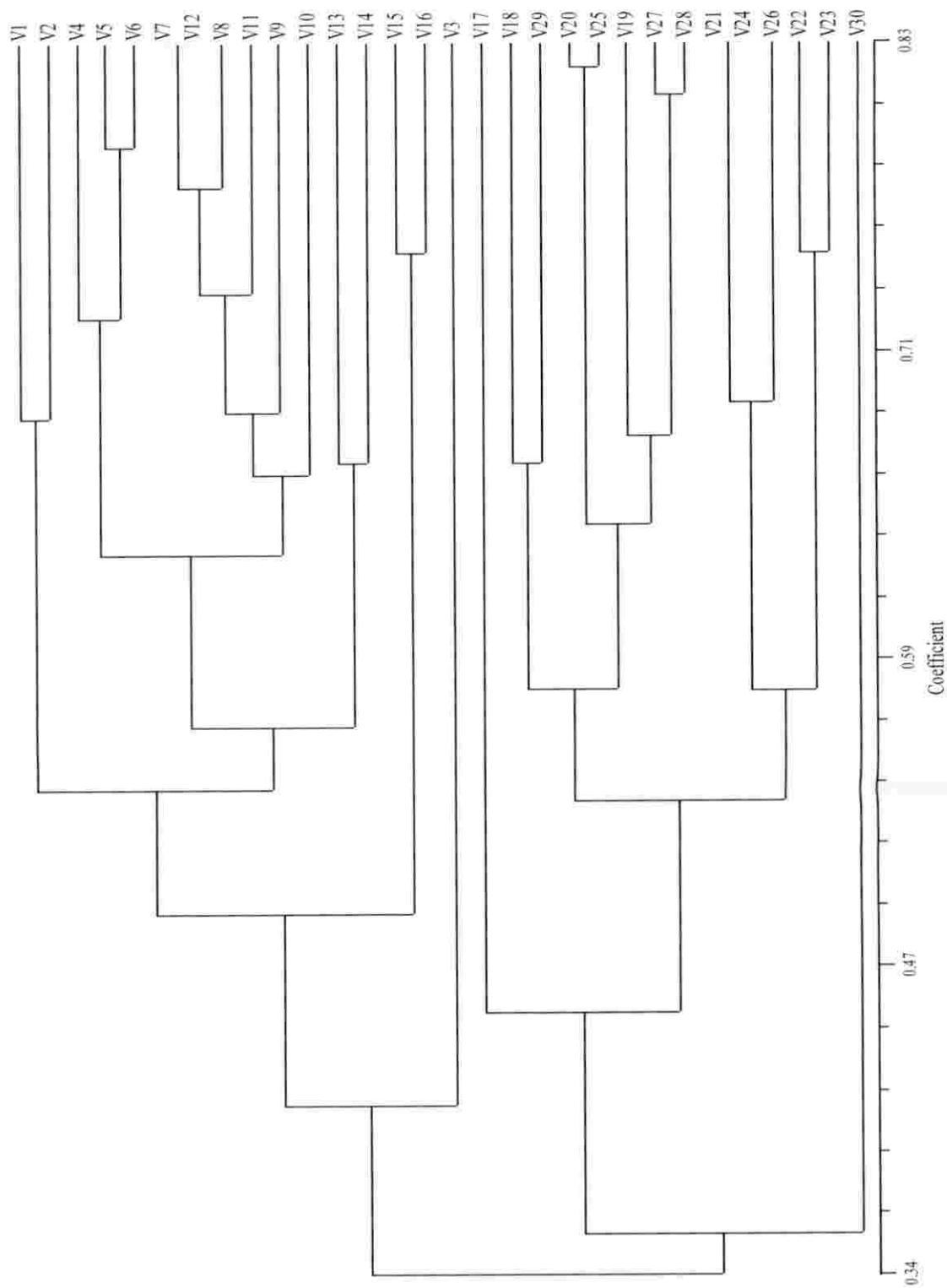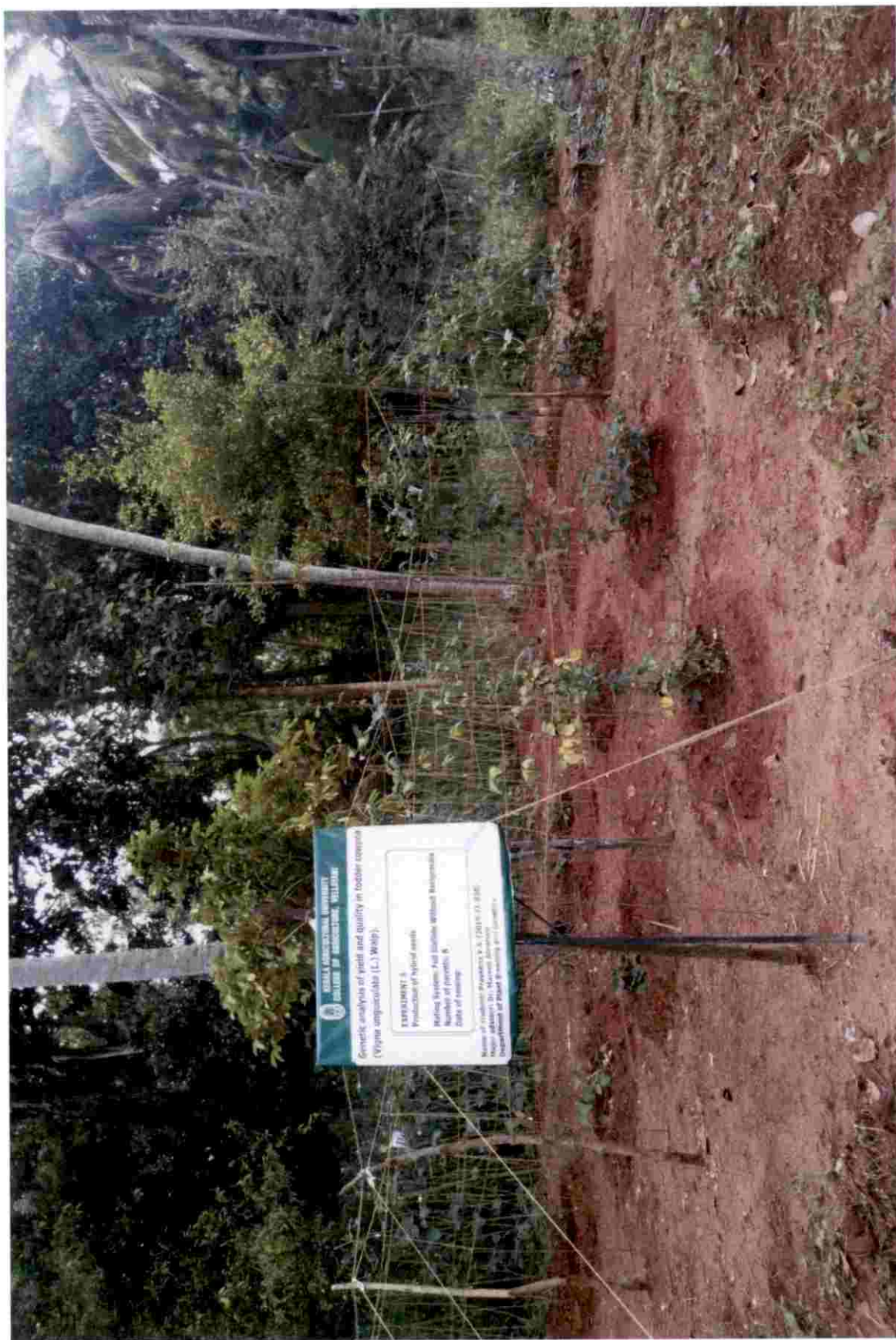
Fig. 11- Field view of hybridization block.

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Plate 10– Selected eight parents for hybridization

P₁- CO – 8

P₂ –MFC-09-1

P₃- IC – 1061

P₄ - IC-39916

Plate 10– Selected eight parents for hybridization continued…….

P₅ - IC-97767

P₆- IT – 38956-1

P₇ - IT – 37154999-38

P₈-Pant Lobia – 2

4.4. EXPERIMENT IV

The twenty eight hybrids obtained and eight parents were evaluated in a randomized block design with 3 replications in the field (Plate 12). Analysis of variance revealed significant difference between treatments for all the characters studied. The values are given in Table 18.

4.4.1. Mean Performance of Parents and Hybrids

The mean performance of the hybrids revealed wide range of variation among the hybrids. The mean values are presented in the table 19.

4.4.1.1. Plant Height at Harvest (cm)

Among hybrids, P_1 X P_7 (82.23 cm) had lowest plant height and P_4 X P_7 (208.47cm) had the highest plant height, P_5 X P_7 (196.43cm) and P_3 X P_6 (192.00cm) were on par with P_4 X P_7. Parents, P_1 (197.23cm), P_5 (192.57cm) and P_4 (185.33cm) were also on par with P_4X P_7. Among parents, P_8 and minimum plant height (130.30cm) and P_1 had maximum plant height (197.23cm).

4.4.1.2. Number of Primary Branches Plant-1

Number of primary branches plant^{-1} was highest for P_3 X P_8 (5.70) and lowest for P_2 X P_3 (1.00). Among parents only P_5 (5.13) was on par with P_3 X P_8. Hybrids, P_1 X P_8 (5.67), P_4 X P_8 (5.43), P_5 X P_7 (5.00), P_7 X P_8 (5.00), P_2 X P_7 (4.90) and P_4 X P_7 (4.87) were on par with P_3 X P_8.

4.4.1.3. Number of Leaves Plant-1

P_2 X P_3 (8.77) had minimum number of leaves plant^{-1} where as P_2 X P_8 (47.90) had highest followed by P_4 X P_8 (40.00). P_2 X P_8 and P_4 X P_8 were not on par with each other. P_2 (34.70) had maximum number of leaves and P_4 (17.00) had minimum number.

4.4.1.4. Days to First Flowering (days)

P_2 X P_8 (45.10 days) was the earliest to flower and P_6 X P_7 (59.00 days) flowered late. P_6 (41.53) was the earliest flowering parent and P_2 (47.90) was

Plate 12 – Field view of experiment IV

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Table 18 – Analysis of variance for various characters in experiment IV

Sl No.	Characters	Mean squares		
		Treatment	Replication	Error
1	Plant height at harvest (cm)	3252.31**	36.50	267.32
2	No. of primary branches plant^{-1}	5.24**	1.17	0.272
3	No. of leaves plant^{-1}	225.41**	15.38	11.38
4	Days to first flowering (days)	91.81**	5.51	0.97
5	Days to 50% flowering (days)	93.42**	21.77	4.06
6	Leaf area index	155.19**	11.75	72.73
7	Green fodder yield plant^{-1} (g)	131815.88**	7010.17	1668.61
8	Dry matter yield plant^{-1} (g)	11802.28**	702.50	160.30
9	Leaf fresh weight plant^{-1} (g)	32704.12**	751.70	304.47
10	Stem fresh weight plant^{-1} (g)	33475.24**	2890.67	722.38
11	Leaf dry weight plant^{-1} (g)	3053.58**	145.18	37.38
12	Stem dry weight plant^{-1} (g)	3091.90**	212.36	70.23
13	Crude protein content (mg g^{-1})	82599.14**	3.52	5.794
14	Crude fibre content (mg g^{-1})	3936.38**	0.00	1.27

*Significant at five percent level

**Significant at one percent level

Table – 19. Mean performance of eight parents and 28 crosses in experiment IV

Crosses	Plant height (cm)	No: of primary branches	No: of leaves plant^{-1}	Days to first flowering	Days to 50% flowering	Leaf Area Index	Green fodder yield plant^{-1}
1 X 1	197.23	2.67	19.23	44.67	54.33	52.70	250.33
1 X 2	157.13	3.77	9.30	55.30	66.33	20.00	138.00
1 X 3	152.90	2.43	14.10	51.67	61.33	27.34	121.67
1 X 4	135.47	2.90	32.87	47.13	62.67	64.19	371.67
1 X 5	125.43	2.77	19.87	54.90	69.00	51.32	403.67
1 X 6	138.57	2.33	28.90	56.87	72.00	68.04	577.67
1 X 7	82.23	2.90	26.67	54.87	65.67	55.08	747.00
1 X 8	75.33	1.87	20.23	57.20	66.67	50.63	389.67
2 X 2	174.53	1.67	34.70	47.90	55.67	77.48	139.67
2 X 3	84.20	1.00	8.77	55.00	68.67	17.77	188.00
2 X 4	146.57	4.13	15.33	47.67	59.00	32.28	266.67
2 X 5	126.47	3.43	14.43	57.67	71.00	26.56	199.00
2 X 6	175.57	4.00	29.90	58.87	69.00	70.52	729.00
2 X 7	148.10	4.90	27.90	54.67	67.33	75.80	592.00
2 X 8	129.90	3.87	47.90	45.10	59.33	101.14	664.00
3 X 3	158.57	1.43	19.43	43.23	51.33	30.90	165.33
3 X 4	146.13	2.33	20.67	47.23	60.00	37.97	172.33
3 X 5	125.33	1.90	15.57	51.43	62.00	33.28	195.67
3 X 6	192.00	3.80	18.57	46.23	59.67	39.99	278.33
3 X 7	150.00	3.20	30.43	46.43	60.67	76.18	335.67
3 X 8	122.70	5.70	36.00	46.33	52.33	68.87	293.00
4 X 4	185.33	2.43	17.00	42.33	52.33	21.94	228.67
4 X 5	174.97	2.00	22.00	52.90	62.00	47.77	467.67
4 X 6	142.67	4.20	22.23	56.00	64.33	47.26	535.33
4 X 7	208.47	4.87	26.00	56.13	66.33	59.81	337.00
4 X 8	163.70	5.43	40.00	56.47	62.33	87.67	488.33
5 X 5	192.57	5.13	20.10	45.43	63.33	53.79	220.67
5 X 6	172.13	4.33	21.57	58.57	63.67	69.11	749.00
5 X 7	196.43	5.00	33.37	46.70	54.67	88.92	636.33
5 X 8	114.90	5.67	30.87	56.00	63.00	70.79	614.00
6 X 6	174.63	4.80	17.67	41.53	56.67	36.77	223.33
6 X 7	143.47	4.77	24.57	59.00	69.00	70.07	635.00
6 X 8	107.53	4.77	35.57	56.23	68.67	105.68	581.67
7 X 7	132.43	4.00	19.90	44.87	61.67	30.80	178.00
7 X 8	124.77	5.00	29.10	57.13	70.00	53.57	732.67
8 X 8	130.30	4.77	20.57	46.77	62.00	48.15	161.33
SE	13.35	0.43	2.75	0.80	1.65	6.96	33.35
CD (5%)	26.63	0.85	5.50	1.60	3.28	13.89	66.54

Table – 19. Mean performance of parents and crosses in experiment IV continued……

Crosses	Dry matter yield plant^{-1} (g)	Leaf fresh weight plant^{-1} (g)	Stem fresh weight plant^{-1} (g)	Leaf dry weight plant^1 (g)	Stem dry weight plant^{-1} (g)	Crude protein content (mgg^{-1})	Crude fiber content (mgg^{-1})
1 X 1	44.88	140.67	109.67	24.11	20.77	231.33	130.33
1 X 2	39.14	84.67	53.33	22.51	16.63	394.00	110.00
1 X 3	27.85	72.33	49.33	14.25	13.60	261.33	143.67
1 X 4	93.70	211.33	160.33	46.24	47.47	247.33	145.00
1 X 5	97.44	225.67	177.67	44.47	52.97	369.33	120.33
1 X 6	151.85	310.00	267.67	70.49	81.37	254.67	103.33
1 X 7	219.95	385.33	361.67	101.32	118.63	361.33	138.33
1 X 8	94.30	212.67	177.00	46.00	48.30	425.33	108.67
2 X 2	27.80	90.33	49.33	17.43	10.37	254.00	116.33
2 X 3	41.05	107.67	80.33	19.75	21.30	234.67	135.00
2 X 4	63.59	147.00	119.67	29.59	34.00	243.33	141.67
2 X 5	53.76	120.00	79.00	30.23	23.53	256.33	124.33
2 X 6	194.62	389.67	339.33	89.08	105.53	222.67	113.00
2 X 7	178.84	303.33	288.67	88.77	90.07	498.33	111.67
2 X 8	116.67	349.00	315.00	65.00	51.67	296.67	105.33
3 X 3	30.60	98.33	67.00	17.73	12.87	243.33	100.33
3 X 4	39.72	106.00	66.33	21.55	18.17	263.00	132.33
3 X 5	43.42	117.67	78.00	22.75	20.67	238.33	125.33
3 X 6	99.89	153.67	124.33	49.95	49.93	476.33	148.00
3 X 7	72.77	183.33	152.33	32.54	40.23	355.67	122.00
3 X 8	92.09	157.67	135.33	44.35	47.73	282.33	88.33
4 X 4	40.50	144.33	84.33	23.97	16.53	222.67	175.33
4 X 5	107.29	249.67	218.00	45.39	61.90	359.67	187.67
4 X 6	149.33	285.67	249.67	70.97	78.37	357.67	114.00
4 X 7	106.91	175.00	152.67	57.21	49.70	321.00	134.33
4 X 8	140.30	261.67	226.67	69.17	71.13	264.33	125.67
5 X 5	42.01	122.67	96.67	22.13	19.88	244.67	169.67
5 X 6	273.17	391.67	357.33	143.07	130.10	272.67	144.00
5 X 7	176.71	334.33	302.00	112.38	64.33	895.67	100.00
5 X 8	133.45	324.33	289.67	72.92	60.53	976.00	78.33
6 X 6	41.07	147.33	75.33	27.73	13.33	264.67	131.00
6 X 7	170.94	338.00	297.00	100.24	70.70	312.00	251.67
6 X 8	124.27	302.67	279.00	52.57	71.70	197.67	70.67
7 X 7	32.53	101.67	76.33	18.83	13.70	214.67	206.33
7 X 8	147.49	379.00	353.67	73.92	73.57	285.00	80.33
8 X 8	31.60	101.67	59.67	20.70	10.90	262.00	90.00
SE	10.34	14.25	21.95	4.99	6.84	1.97	0.92
CD	20.62	28.42	43.78	9.96	13.65	3.92	1.84

the late flowering parent. Hybrids $P_3 X P_7$ (46.70), $P_3 X P_6$ (46.23), $P_3 X P_8$ (46.33), $P_3 X P_7$ (46.43) were on par with cross $P_2 X P_8$.

4.4.1.5. Days to Fifty Per Cent Flowering (days)

$P_1 X P_6$ (72.00 days) had maximum days to fifty per cent flowering and $P_3 X P_8$ (52.33 days) had minimum.

4.4.1.6. Leaf Area Index (LAI)

$P_1 X P_2$ (20.00) had lowest leaf area index and $P_6 X P_8$ (105.68) had highest leaf area index. $P_6 X P_8$ was on par with $P_2 X P_8$ (101.14) only. Among the parents, P_4 (77.48) had maximum LAI and P_2 (21.94) had minimum leaf area index.

4.4.1.7. Green Fodder Yield Plant^{-1} (g)

$P_1 X P_3$ had least green fodder yield plant^{-1} (121.67g) and $P_5 X P_6$ had maximum for green fodder yield plant^{-1} (749.00g). $P_1 X P_7$ (747.00g), $P_2 X P_6$ (729.00g) and $P_7 X P_8$ (732.67g) were on par with $P_5 X P_6$.

4.4.1.8. Dry Matter Yield Plant^{-1} (g)

$P_1 X P_3$ (27.85g) had least dry matter yield plant^{-1} and $P_5 X P_6$ had maximum dry matter yield plant^{-1} (273.17g). No other hybrids were on par with $P_5 X P_6$. Among the parents highest dry matter yield was seen in P_1 (44.88g) and least in P_2 (27.80g).

4.4.1.9. Leaf Fresh Weight Plant^{-1} (g)

$P_5 X P_6$ (391.67g) had the highest leaf fresh weight and $P_1 X P_3$ (72.33g), the lowest. Hybrids $P_2 X P_6$ (389.67g), $P_1 X P_7$ (385.33g) and $P_7 X P_8$ (379.00g) were on par with $P_5 X P_6$. P_6 (147.33g) had highest leaf fresh weight and P_2 (90.33g) had least value among parents.

4.4.1.10. Stem Fresh Weight Plant^{-1}(g)

$P_1 X P_3$ (49.33g) had the lowest stem fresh weight among hybrids and P_2 (49.33g) had lowest value among parents. $P_1 X P_7$ (361.67g) had the highest stem dry weight among hybrids and it was on par with $P_5 X P_6$ (357.33g), $P_7 X P_8$ (353.67g) and $P_2 X P_6$ (339.33g).

4.4.1.11. Leaf Dry Weight Plant^{-1} (g)

P_5 X P_6 (143.07g) had highest leaf dry weight and P_1 X P_3 (14.25g) had lowest leaf dry weight.

4.4.1.12. Stem Dry Weight Plant^{-1}(g)

P_5 X P_6 (130.10g) is having the maximum stem dry weight and this was on par with P_1 X P_7 (118.63g).

4.4.1.13. Crude Protein Content (mg g^{-1})

P_5 X P_8 (976.00mg g^{-1}) had maximum crude protein content and P_6 X P_8 (197.67mgg^{-1}) minimum.

4.4.1.14. Crude Fibre Content (mg g^{-1})

P_6 X P_7 (251.67mgg^{-1}) had maximum crude fibre content and P_6 X P_8 (70.67mgg^{-1}) the minimum crude fiber content.

4.4.2 Combining Ability Analysis

Analysis of variance for combining ability revealed significant general combining ability (*gca*) and specific combining ability (*sca*) for all the characters (Table-20).

4.4.2.1. Combining Ability Effects

General combining ability of parents and specific combining abilities of hybrids are presented in table -21 and table -22 respectively.

4.4.2.1.1. Plant Height at Harvest (cm)

Significant positive *gca* effect was seen in parents P_4, P_5 and P_6. Parents P_1, P_3 and P_8 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by ten hybrids. Significant *sca* effects in negative direction were shown by twelve hybrids. *gca* variance was greater than *sca* variance.

Table 20. Mean squares of gca and sca for individual characters in experiment IV

Sl No.	Characters	Mean Squares			$\sigma^2 A$	$\sigma^2 D$	$\sigma^2 A/\sigma^2 D$
		gca (df = 7)	sca (df = 28)	Error (df = 70)			
1	Plant height at harvest (cm)	4344.98**	2979.14**	267.32	809.17	31.82	25.43
2	No. of primary branches/plant	14.31**	2.97**	0.27	2.27	2.70	0.84
3	No. of leaves/plant	290.64**	209.10**	11.38	16.31	197.72	0.08
4	Days to first flowering (days)	64.84**	98.56**	0.97	-6.75	97.59	-0.07
5	Days to 50% flowering (days)	106.01**	90.27**	40.6	3.15	86.21	0.04
6	Leaf area index	2130.13**	1413.96**	72.73	143.23	1341.23	0.107
7	Green fodder yield/ plant (kg)	220544.34**	109633.76**	1668.61	22182.12	107965.20	0.21
8	Dry matter yield/plant (kg)	17317.28**	10423.55**	160.30	1378.75	10263.25	0.14
9	Leaf fresh weight/plant (g)	56453.19**	26766.86**	304.47	5937.27	26462.39	0.22
10	Stem fresh weight/plant (g)	53931.39**	28361.20**	722.38	5114.04	27638.82	0.19
11	Leaf dry weight/plant (g)	5017.36**	2562.62**	37.38	490.95	2525.24	0.19
12	Stem dry weight/plant (g)	3798.66**	2915.21**	70.23	176.69	2844.98	0.06
13	Crude protein content (mg g^{-1})	73720.78**	84818.73**	5.79	-2219.59	84812.94	-0.03
14	Crude fibre content (mg g^{-1})	8058.31**	2905.89**	1.27	1030.48	2904.62	0.35

*Significant at five percent level

**Significant at one percent level

Table 21 – General combining ability effects of parents in experiment IV

Characters	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8	SE (gi)	SE (gi-gi)	CD (5%)
Plant height at harvest	-6.563**	-1.017	-3.677**	16.147**	9.363**	9.403**	-0.883	-22.773**	4.836	7.312	9.649
No. of primary branches plant^{-1}	-0.824	-0.411	-0.931	-0.181	0.282	0.526	0.609	0.929	0.154	0.233	0.308
No. of leaves plant^{-1}	-2.742*	0.512	-3.485**	-0.472	-1.995*	-0.118	2.002*	6.298**	0.998	1.509	1.991
Days to first flowering	0.566	0.846	-3.081*	-1.341	0.743	1.322	0.306	0.639	0.291	0.440	0.581
Days to 50% flowering	0.883	0.850	-3.617**	-2.217*	0.850	1.617	1.350	0.283	0.596	0.901	1.189
Leaf area index	-5.055**	0.650	-12.934**	-7.172**	0.279	5.168**	4.850**	14.213**	2.523	3.814	5.033
Green fodder yield plant^{-1}	-25.183**	-44.583**	-158.650**	-40.550**	20.483**	103.0823**	86.983**	58.417**	12.083	18.268	24.106
Dry matter yield plant^{-1}	-7.138**	-14.211**	-40.739**	-10.353**	8.389**	36.083**	25.330**	2.639*	3.745	5.662	7.472
Leaf fresh weight plant^{-1}	-12.317**	-22.450**	-81.150**	-18.150**	10.217**	55.950**	39.517**	28.383**	5.162	7.803	10.297
Stem fresh weight plant^{-1}	-12.600**	-21.833**	-77.233**	-23.033**	10.267**	47.267**	46.833**	30.333**	7.950	12.020	15.861
Leaf dry weight plant^{-1}	-5.884**	-7.253**	-21.171**	-6.429**	6.314**	17.951**	15.171**	1.300	1.809	2.734	3.608
Stem dry weight plant^{-1}	-1.254	-6.958**	-19.568**	-3.925**	2.075*	18.132**	10.159**	1.339	2.479	3.748	4.945
Crude protein content	-18.900**	-31.100**	36.667**	-46.333**	89.233**	-34.200**	49.333**	28.633**	0.712	1.076	1.420
Crude fibre content	-2.558*	-8.192**	-6.025**	17.575**	6.375**	5.108**	19.542**	-31.825**	0.333	0.504	0.665

*Significant at five percent level   **Significant at one percent level

Table 22 – Specific combining ability effects of hybrids in experiment IV

Crosses	PH	NPB	NL	DFF	DFPF
$P_1 \times P_2$	17.250**	1.386	-12.672**	2.599*	1.989*
$P_1 \times P_3$	15.677**	0.573	-3.875**	2.892*	1.456
$P_1 \times P_4$	-21.580**	0.289	11.878**	-3.381*	1.389
$P_1 \times P_5$	-24.830**	-0.307	0.401	2.302*	4.656**
$P_1 \times P_6$	-11.736**	-0.984	7.558**	3.689**	6.889**
$P_1 \times P_7$	-57.783**	-0.501	3.205*	2.705*	0.822
$P_1 \times P_8$	-42.793**	-1.854	-7.525**	4.705**	2.889*
$P_2 \times P_3$	-58.570**	-1.274	-12.462**	5.945**	8.822**
$P_2 \times P_4$	-16.026**	1.109	-8.909**	-3.128*	-2.244*
$P_2 \times P_5$	-29.343**	-0.054	-8.285**	4.789**	6.689**
$P_2 \times P_6$	19.717**	0.269	5.305**	5.409**	3.922**
$P_2 \times P_7$	2.537*	1.086	1.185	2.225*	2.522*
$P_2 \times P_8$	6.227**	-0.267	16.888**	-7.675**	-4.411**
$P_3 \times P_4$	-13.800**	-0.171	0.421	0.365	3.222*
$P_3 \times P_5$	-27.816**	-1.067	-3.155*	2.482*	2.156*
$P_3 \times P_6$	38.810**	0.589	-2.032*	-3.298*	-0.944
$P_3 \times P_7$	7.097**	-0.094	7.715**	-2.081*	0.322
$P_3 \times P_8$	1.687	2.086*	8.985**	-2.515*	-6.944**
$P_4 \times P_5$	1.994	-1.717	0.265	2.209*	0.756
$P_4 \times P_6$	-30.346**	0.239	-1.379	4.729**	2.322*
$P_4 \times P_7$	45.740**	0.823	0.268	5.879**	4.589**
$P_4 \times P_8$	22.864**	1.069	9.971**	5.879**	1.656
$P_5 \times P_6$	5.904**	-0.091	-0.522	5.212**	-1.411
$P_5 \times P_7$	40.490**	0.493	9.158**	-5.638**	-10.144**
$P_5 \times P_8$	-19.153**	0.839	2.361*	3.329*	-0.744
$P_6 \times P_7$	-12.516**	0.016	-1.519	6.082**	3.422*
$P_6 \times P_8$	-26.560**	-0.304	5.185**	2.982*	4.156**
$P_7 \times P_8$	0.960	-0.154	-3.402*	4.899**	5.756**
SE (Sij)	6.448	0.205	1.330	0.388	0.794
CD (Sij-Sik) (5%)	43.761	1.396	9.029	2.636	5.393
CD (Sij-Skl) (5%)	41.259	1.316	8.513	2.485	5.085

*Significant at five percent level   **Significant at one percent level   PH-plant height,

NPB-no: of primary branches, NL-no: of leaves, DFF-days to first flowering,

DFPF- days to fifty pre cent flowering $i \neq j \neq k \neq l$

Table 22 – Specific combining ability effects of hybrids in experiment IV continued....

Crosses	LAI	GFY	DMY	LFW
$P_1 X P_2$	-30.321**	-181.326**	-37.883**	-92.400**
$P_1 X P_3$	-9.396**	-83.593**	-22.648**	-46.033**
$P_1 X P_4$	21.691**	48.307**	12.820**	29.967**
$P_1 X P_5$	1.367	19.274**	-2.189*	15.933**
$P_1 X P_6$	13.198**	110.674**	24.533**	54.533**
$P_1 X P_7$	0.556	296.107**	103.383**	146.300**
$P_1 X P_8$	-13.257**	-32.659**	0.421	-15.233**
$P_2 X P_3$	-24.672**	2.141*	-2.375*	-0.567
$P_2 X P_4$	-15.928**	-37.293**	-10.221**	-24.233**
$P_2 X P_5$	-29.092**	-165.993**	-38.793**	-79.600**
$P_2 X P_6$	9.973**	281.407**	74.369**	144.333**
$P_2 X P_7$	15.577**	160.507**	69.346**	74.433**
$P_2 X P_8$	31.554**	261.074**	29.864**	131.233**
$P_3 X P_4$	3.347*	-17.559**	-7.563**	-6.533**
$P_3 X P_5$	-8.794**	-55.259**	-22.605**	-23.233**
$P_3 X P_6$	-6.970**	-55.193**	6.167**	-32.967**
$P_3 X P_7$	29.538**	18.241**	-10.193**	13.133**
$P_3 X P_8$	12.869**	4.141**	31.812**	-1.400
$P_4 X P_5$	-0.067	98.641**	10.876**	45.767**
$P_4 X P_6$	-5.466**	83.707**	25.228**	36.033**
$P_4 X P_7$	7.409**	-98.526**	-6.442**	-58.200**
$P_4 X P_8$	25.906**	81.374**	49.640**	39.600**
$P_5 X P_6$	8.940**	236.341**	130.323**	113.667**
$P_5 X P_7$	29.061**	139.774**	44.616**	72.767**
$P_5 X P_8$	1.575	146.007**	24.048**	73.900**
$P_6 X P_7$	5.329**	55.841**	11.152**	30.700**
$P_6 X P_8$	31.573**	31.074**	-12.823**	6.500**
$P_7 X P_8$	-20.223**	198.174**	21.143**	99.267**
SE (Sij)	3.364	0.444	6.628	9.135
CD (Sij-Sik) (5%)	22.826	109.334	33.888	46.704
CD (Sij-Skl) (5%)	21.521	103.081	31.950	44.033

*Significant at five percent level   **Significant at one percent level   LAI – leaf area index,

GFY – green fodder yield, DMY – dry matter yield, LFW – leaf fresh weight. $i \neq j \neq k \neq l$

Table 22 – Specific combining ability effects of hybrids in experiment IV continued..........

Crosses	SFW	LDW	SDW	CPC	CFC
P_1 X P_2	-89.159**	-14.612**	-23.270**	114.556**	-7.648**
P_1 X P_3	-37.759**	-8.954**	-13.694**	-12.544**	23.852**
P_1 X P_4	19.041**	8.290**	4.530**	-16.878**	1.585
P_1 X P_5	3.074*	-6.219**	4.030**	-30.444**	-11.881**
P_1 X P_6	56.074**	8.160**	16.373**	-21.678**	-27.615**
P_1 X P_7	150.507**	41.770**	61.613**	1.456	-7.048**
P_1 X P_8	-17.659**	0.322	0.100	86.156**	14.652**
P_2 X P_3	2.474*	-2.085*	-0.290	-27.011**	20.819**
P_2 X P_4	-12.393**	-6.987**	-3.234*	-8.678**	3.885**
P_2 X P_5	-86.359**	-19.093**	-19.700**	-131.245**	-2.248*
P_2 X P_6	136.974**	28.126**	46.243**	-41.478**	-12.315**
P_2 X P_7	86.741**	30.596**	38.750**	150.656**	-28.081**
P_2 X P_8	129.574**	20.694**	9.170**	-30.311**	16.952**
P_3 X P_4	-10.326**	-1.106	-6.457**	16.556**	-7.615**
P_3 X P_5	-31.959**	-12.648**	-9.956**	-143.678**	-3.415*
P_3 X P_6	-22.626**	2.914*	3.253*	217.756**	20.519**
P_3 X P_7	5.807**	-11.719**	1.526	13.556**	-19.915**
P_3 X P_8	5.307**	13.966**	17.846**	-39.078**	-2.215*
P_4 X P_5	53.841**	-4.757**	15.634**	-12.678**	35.319**
P_4 X P_6	48.507**	9.185**	16.043**	108.756**	-37.081**
P_4 X P_7	-48.059**	-1.792	-4.650**	-11.444**	-31.181**
P_4 X P_8	42.441**	24.037**	25.603**	-47.411**	11.519**
P_5 X P_6	122.874**	68.546**	61.777**	-111.811**	4.119**
P_5 X P_7	67.974**	40.633**	3.984**	427.656**	-54.315**
P_5 X P_8	72.141**	15.044**	9.004**	528.689**	-24.615**
P_6 X P_7	25.974**	16.859**	-5.707**	-32.578**	98.619**
P_6 X P_8	24.474**	-16.936**	4.113**	-126.211**	-31.015**
P_7 X P_8	99.574**	7.190**	13.953**	-122.411**	-35.781**
SE (Sij)	14.071	3.201	4.387	1.260	0.589
CD (Sij-Sik) (5%)	71.939	16.364	22.431	6.442	3.016
CD (Sij-Skl) (5%)	67.824	15.428	21.148	6.074	2.844

*Significant at five percent level   **Significant at one percent level   SFW- stem fresh weight,

LDW – leaf dry weight, SFW – stem fresh weight, CPC – crude protein content, CFC- crude fiber content

$i \neq j \neq k \neq l$

4.4.2.1.2. Number of Primary Branches Plant[1]

No significant *gca* effect was in parents. P_3 X P_8 (2.086) alone showed significant *sca* effect towards positive direction. *gca* variance was greater than *sca* variance.

4.4.2.1.3. Number of Leaves Plant[1]

Significant positive *gca* effect was seen in parents P_7 and P_8. Parents P_1, P_3 and P_5 exhibited significant negative *gca* effect.

Significant *sca* effects in positive direction were shown by twelve hybrids. Significant *sca* effects in negative direction were shown by seven hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.4. Days to First Flowering (days)

Parent, P_3 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by twenty hybrids. Significant *sca* effects in negative direction were shown by seven hybrids. *sca* variance was greater than *gca* varaiance.

4.4.2.1.5. Days to Fifty Per Cent Flowering (days)

Parents P_3 and P_4 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by fifteen hybrids. Significant *sca* effects in negative direction were shown by four hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.6. Leaf Area Index (LAI)

Significant positive *gca* effect was seen in parents P_6, P_7 and P_8. Parents P_1, P_3 and P_4 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by fourteen hybrids. Significant *sca* effects in negative direction were shown by ten hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.7. Green Fodder Yield Plant^{-1}(g)

Significant positive *gca* effect was seen in parents P_5, P_6, P_7 and P_8. Parents P_1, P_2, P_3 and P_4 exhibited significant negative *gca* effect.

Significant *sca* effects in positive direction were shown by nineteen hybrids. Significant *sca* effects in negative direction were shown by nine hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.8. Dry Matter Yield Plant^{-1}(g)

Significant positive *gca* effect was seen in parents P_5, P_6, P_7 and P_8. Parents P_1, P_2, P_3 and P_4 exhibited significant negative *gca* effect.

Significant *sca* effects in positive direction were shown by sixteen hybrids. Significant *sca* effects in negative direction were shown by eleven hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.9. Leaf Fresh Weight Plant^{-1}(g)

Significant positive *gca* effect was seen in parents P_5, P_6, P_7 and P_8. Parents P_1, P_2, P_3 and P_4 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by seventeen hybrids. Significant *sca* effects in negative direction were shown by nine hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.10. Stem Fresh Weight Plant^{-1}(g)

Significant positive *gca* effect was seen in parents P_5, P_6, P_7 and P_8. Parents P_1, P_2, P_3 and P_4 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by nineteen hybrids. Significant *sca* effects in negative direction were shown by nine hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.11. Leaf Dry Weight Plant^{-1}

Significant positive *gca* effect was seen in parents P_5, P_6, and P_7. Parents P_1, P_2, P_3 and P_4 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by fifteen hybrids. Significant *sca* effects in

negative direction were shown by ten hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.12. Stem Dry Weight Plant^{-1}(g)

Significant positive *gca* effect was seen in parents P_5, P_6, and P_7. Parents P_2, P_3 and P_4 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by sixteen hybrids. Significant *sca* effects in negative direction were shown by eight hybrids. *gca* variance was greater than *sca* variance.

4.4.2.1.13. Crude Protein Content (mg g^{-1})

Significant positive *gca* effect was seen in parents P_3, P_5, P_7 and P_8. Parents P_1, P_2, P_4 and P_6 exhibited significant negative *gca* effect. Significant *sca* effects in positive direction were shown by nine hybrids. Significant *sca* effects in negative direction were shown by eighteen hybrids. *sca* variance was greater than *gca* variance.

4.4.2.1.14 . Crude Fibre Content (mg g^{-1})

Significant positive *gca* effect was seen in parents P_4, P_5, P_6 and P_7. Parents P_1, P_2, P_3 and P_8 exhibited significant negative *gca* effect.

Significant *sca* effects in positive direction were shown by ten hybrids. Significant *sca* effects in negative direction were shown by seventeen hybrids. *gca* variance was greater than *sca* variance.

4.4.3. Genetic Components of Variance

Additive variances (σ^2 A), dominance variance (σ^2 D) and their ratios for all the fourteen characters are given in Table-23. The ratio of additive to dominance variance was less than unity for thirteen characters and more than unity for plant height (25.426). This shows high influence of dominance variance.

Table – 23. Genetic components of variance for different characters in experiment IV

Sl No.	Characters	$\sigma^2 A$	$\sigma^2 D$	$\sigma^2 A/ \sigma^2 D$
1	Plant height at harvest (cm)	809.1674	31.824	25.426
2	No. of primary branches/plant	2.2676	2.695	0.841
3	No. of leaves/plant	16.309	197.717	0.082
4	Days to first flowering (days)	-6.7454	97.593	-0.069
5	Days to 50% flowering (days)	3.1478	86.211	0.036
6	Leaf area index	143.2344	1341.225	0.106
7	Green fodder yield/ plant (kg)	22182.12	107965.2	0.205
8	Dry matter yield/plant (kg)	1378.745	10263.25	0.134
9	Leaf fresh weight/plant (g)	5937.267	26462.39	0.224
10	Stem fresh weight/plant (g)	5114.037	27638.82	0.185
11	Leaf dry weight/plant (g)	490.948	2525.238	0.194
12	Stem dry weight/plant (g)	176.69	2844.982	0.062
13	Crude protein content (mg g^{-1})	-2219.59	84812.94	-0.026
14	Crude fibre content (mg g^{-1})	1030.484	2904.624	0.355

4.4.4. Heterosis

Relative heterosis (RH) and heterobeltiosis (HB) were estimated for twenty eight hybrids with respect to fourteen characters under study and the results are furnished in Table -24 to 28.

4.4.4.1. Plant Height at Harvest (cm)

Among the twenty eight hybrids P_3 X P_6 (15.246 per cent), P_3 X P_7 (3.094 per cent), P_4 X P_7 (31.209 per cent), P_4 X P_8 (3.728 per cent) and P_5 X P_7 (20.883 per cent) showed significant positive heterosis over mid parent value. P_3 X P_6 (9.945 per cent), P_4 X P_7 (12.482 per cent) and P_5 X P_7 (2.008 per cent) showed significant positive heterosis over better parent.

4.4.4.2. Number of Primary Branches Plant^{-1}

Significant positive heterobeltiosis was expressed by the hybrids P_1X P_2 (41.250 per cent), P_1 X P_4 (8.750 per cent), P_2 X P_4 (70.096 per cent), P_2 X P_7 (22.500 per cent), P_3 X P_8 (19.497 per cent), P_4 X P_7 (21.667 per cent), P_4 X P_8 (13.906 per cent), P_5 X P_8 (10.461 per cent), P_7 X P_8 (4.822 per cent).

4.4.4.3. Number of Leaves Plant^{-1}

P_2 X P_6 hybrid showed significant positive relative heterosis. Eighteen hybrids showed significant positive heterobeltiosis for number of leaves plant^{-1}.

4.4.4.4. Days to First Flowering

P_2 X P_8 showed significant negative relative heterosis (-4.718 per cent) and significant negative heterobeltiosis (-5.846 per cent).

4.4.4.5. Days to Fifty Per Cent Flowering (days)

P_3 X P_8 and P_5 X P_7 showed significant negative relative heterosis and heterobeltiosis. P_2 X P_8 (-4.301 per cent), P_3 X P_5 (-2.105 per cent) and P_4 X P_5 (-2.105 per cent) showed significant negative heterobeltiosis.

Table 24- Heterosis (%) for plant height at harvest, number of primary branches plant[-1] and number of leaves plant[-1] in experiment IV

Crosses	Plant height at harvest		No. of primary branches plant[-1]		No. of leaves plant[-1]	
	RH	HB	RH	HB	RH	HB
1 X 2	-15.466**	-20.331**	73.846**	41.250**	-65.511**	-73.200**
1 X 3	-14.054**	-22.478**	18.796**	-8.750**	-27.063**	-27.444**
1 X 4	-29.180**	-31.317**	13.800**	8.750**	81.433**	70.914**
1 X 5	-35.642**	-36.404**	-29.030**	-46.069**	1.026	-1.161
1 X 6	-25.475**	-29.745**	-37.500**	-51.389**	56.654**	50.286**
1 X 7	-50.111**	-58.307**	-13.000**	-27.500**	36.298**	34.003**
1 X 8	-54.000**	-61.805**	-49.798**	-60.867**	1.684	-1.621
2 X 3	-49.445**	-51.757**	-35.414**	-40.000**	-67.611**	-74.736**
2 X 4	-18.543**	-20.916**	101.790**	70.096**	-40.683**	-55.812**
2 X 5	-31.100**	-34.326**	1.030	-33.073**	-47.324**	-58.405**
2 X 6	0.563	0.535	23.711**	-16.667**	14.195**	-13.833**
2 X 7	-3.506**	-15.145**	72.941**	22.500**	2.198*	-19.597**
2 X 8	-14.773**	-25.573**	20.145**	-18.938**	73.341**	38.040**
3 X 4	-15.013**	-21.150**	20.898**	-3.978**	13.460**	6.365**
3 X 5	-28.612**	-34.914**	-42.073**	-62.963**	-21.241**	-22.554**
3 X 6	15.246**	9.945**	21.990**	-20.833**	0.099	-4.443**
3 X 7	3.094*	-5.403**	17.864**	-20.000**	54.759**	52.931**
3 X 8	-15.047**	-22.619**	83.871**	19.497**	80.015**	75.041**
4 X 5	-7.401**	-9.140**	-47.090**	-61.014**	18.598**	9.453**
4 X 6	-20.733**	-23.022**	16.183**	-12.500**	28.269**	25.849**
4 X 7	31.209**	12.482**	51.374**	21.667**	40.921**	30.653**
4 X 8	3.728**	-11.673**	50.926**	13.906**	112.955**	94.490**
5 X 6	-6.245**	-10.611**	-12.722**	-15.530**	14.210**	7.297**
5 X 7	20.883**	2.008*	9.529**	-2.534*	66.833**	66.003**
5 X 8	-28.825**	-40.332**	14.478**	10.461**	51.803**	50.081**
6 X 7	-6.556**	-17.847**	8.333**	-0.694	30.778**	23.451**
6 X 8	-29.470**	-38.422**	-0.383	-0.694	86.034**	72.934**
7 X 8	-5.023**	-5.787**	14.025**	4.822**	43.821**	41.489**
CD (5%)	23.064	26.633	0.736	0.850	4.759	5.495

*Significant at five percent level   **Significant at one percent level

Table 25- Heterosis (%) for days to first flowering, days to 50% flowering and Leaf area index in experiment IV

Crosses	Days to first flowering		Days to 50% flowering		Leaf area index	
	RH	HB	RH	HB	RH	HB
1 X 2	19.477**	15.449**	20.610**	19.162**	-69.273**	-74.187**
1 X 3	17.553**	15.663**	16.096**	12.890**	-34.591**	-48.121**
1 X 4	8.348**	5.515**	17.504**	15.345**	72.007**	21.803**
1 X 5	21.860**	20.836**	17.284**	8.947**	-3.622**	-4.598**
1 X 6	31.936**	27.304**	29.736**	27.059**	52.083**	29.102**
1 X 7	22.557**	22.288**	13.226**	6.486**	31.915**	4.510**
1 X 8	25.114**	22.309**	14.616**	7.527**	0.397	-3.934**
2 X 3	20.702**	14.823**	28.349**	23.346**	-67.207**	-77.065**
2 X 4	5.652**	-0.487	9.256**	5.982**	-35.068**	-58.342**
2 X 5	23.571**	20.390**	19.324**	12.105**	-59.529**	-65.716**
2 X 6	31.644**	22.895**	22.845**	21.765**	23.439**	-8.987**
2 X 7	17.858**	14.127**	14.769**	9.189**	40.009**	-2.164*
2 X 8	-4.718**	-5.846**	0.847	-4.301**	61.014**	30.541**
3 X 4	10.406**	9.261**	15.759**	14.650**	43.722**	22.883**
3 X 5	16.019**	13.206**	8.143**	-2.105*	-21.412**	-38.136**
3 X 6	9.088**	6.947**	10.497**	5.294**	18.191**	8.747**
3 X 7	5.415**	3.492**	7.378**	-1.621	146.937**	146.564**
3 X 8	2.967*	-0.927	-7.644**	-15.591**	74.253**	43.029**
4 X 5	20.551**	16.434**	7.208**	-2.105*	26.155**	-11.198**
4 X 6	33.551**	32.294**	18.046**	13.529**	60.983**	28.508**
4 X 7	28.751**	25.111**	16.37**	7.568**	126.823**	94.178**
4 X 8	26.754**	20.741**	9.041**	0.538	150.174**	82.071**
5 X 6	34.693**	28.916**	6.114**	0.532	52.630**	28.487**
5 X 7	3.437*	2.796*	-12.531**	-13.680**	110.222**	65.303**
5 X 8	21.400**	19.743**	0.535	-0.521	38.888**	31.611**
6 X 7	36.580**	31.501**	16.616**	11.892**	107.389**	90.555**
6 X 8	27.374**	20.242**	15.727**	10.753**	148.874**	119.466**
7 X 8	24.700**	22.167**	13.207**	12.903**	35.686**	11.242**
CD (5%)	1.3900	1.604	2.842	3.282	12.031	13.892

*Significant at five percent level   **Significant at one percent level

Table 23- Heterosis (%) for days to first flowering, days to 50% flowering and Leaf area index in experiment IV

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Table 25- Heterosis (%) for days to first flowering, days to 50% flowering and Leaf area index in experiment IV

Crosses	Days to first flowering		Days to 50% flowering		Leaf area index	
	RH	HB	RH	HB	RH	HB
1 X 2	19.477**	15.449**	20.610**	19.162**	-69.273**	-74.187**
1 X 3	17.553**	15.663**	16.096**	12.890**	-34.591**	-48.121**
1 X 4	8.348**	5.515**	17.504**	15.345**	72.007**	21.803**
1 X 5	21.860**	20.836**	17.284**	8.947**	-3.622**	-4.598**
1 X 6	31.936**	27.304**	29.736**	27.059**	52.083**	29.102**
1 X 7	22.557**	22.288**	13.226**	6.486**	31.915**	4.510**
1 X 8	25.114**	22.309**	14.616**	7.527**	0.397	-3.934**
2 X 3	20.702**	14.823**	28.349**	23.346**	-67.207**	-77.065**
2 X 4	5.652**	-0.487	9.256**	5.982**	-35.068**	-58.342**
2 X 5	23.571**	20.390**	19.324**	12.105**	-59.529**	-65.716**
2 X 6	31.644**	22.895**	22.845**	21.765**	23.439**	-8.987**
2 X 7	17.858**	14.127**	14.769**	9.189**	40.009**	-2.164*
2 X 8	-4.718**	-5.846**	0.847	-4.301**	61.014**	30.541**
3 X 4	10.406**	9.261**	15.759**	14.650**	43.722**	22.883**
3 X 5	16.019**	13.206**	8.143**	-2.105*	-21.412**	-38.136**
3 X 6	9.088**	6.947**	10.497**	5.294**	18.191**	8.747**
3 X 7	5.415**	3.492**	7.378**	-1.621	146.937**	146.564**
3 X 8	2.967*	-0.927	-7.644**	-15.591**	74.253**	43.029**
4 X 5	20.551**	16.434**	7.208**	-2.105*	26.155**	-11.198**
4 X 6	33.551**	32.294**	18.046**	13.529**	60.983**	28.508**
4 X 7	28.751**	25.111**	16.37**	7.568**	126.823**	94.178**
4 X 8	26.754**	20.741**	9.041**	0.538	150.174**	82.071**
5 X 6	34.693**	28.916**	6.114**	0.532	52.630**	28.487**
5 X 7	3.437*	2.796*	-12.531**	-13.680**	110.222**	65.303**
5 X 8	21.400**	19.743**	0.535	-0.521	38.888**	31.611**
6 X 7	36.580**	31.501**	16.616**	11.892**	107.389**	90.555**
6 X 8	27.374**	20.242**	15.727**	10.753**	148.874**	119.466**
7 X 8	24.700**	22.167**	13.207**	12.903**	35.686**	11.242**
CD (5%)	1.3900	1.604	2.842	3.282	12.031	13.892

*Significant at five percent level   **Significant at one percent level

Table 26- Heterosis (%) for Green fodder yield/ plant, Dry matter yield/plant and Leaf fresh weight/plant in experiment IV

Crosses	Green fodder yield/ plant		Dry matter yield/plant		Leaf fresh weight/plant	
	RH	HB	RH	HB	RH	HB
1 X 2	-29.230**	-44.872**	7.714**	-12.782**	-26.696**	-39.811**
1 X 3	-41.459**	-51.397**	-26.205**	-37.945**	-39.470**	-48.579**
1 X 4	55.185**	48.470**	119.497**	108.786**	48.302**	46.420**
1 X 5	71.409**	61.253**	124.267**	117.104**	71.390**	60.422**
1 X 6	143.914**	130.762**	253.366**	238.354**	115.275**	110.407**
1 X 7	248.796**	198.406**	468.248**	390.084**	218.014**	173.927**
1 X 8	89.313**	55.661**	146.591**	110.108**	75.513**	51.181**
2 X 3	23.277**	13.709**	40.582**	34.150**	14.136**	9.491**
2 X 4	44.795**	16.618**	86.207**	57.012**	25.285**	1.847
2 X 5	10.452**	-9.818**	54.010**	27.959**	12.677**	-2.173*
2 X 6	301.649**	226.417**	465.198**	373.904**	227.914**	164.479**
2 X 7	272.713**	232.584**	492.839**	449.713**	215.977**	198.360**
2 X 8	341.191**	311.570**	292.817**	269.198**	263.548**	243.278**
3 X 4	-12.520**	-24.635**	11.729**	-1.925	-12.636**	-26.558**
3 X 5	1.382	-11.329**	19.592**	3.348*	6.487**	-4.076**
3 X 6	43.225**	24.626**	178.753**	143.230**	25.103**	4.298**
3 X 7	95.535**	88.576**	130.538**	123.688**	83.336**	80.327**
3 X 8	79.389**	77.221**	196.098**	191.413**	57.669**	55.081**
4 X 5	108.158**	104.516**	160.046**	155.363**	87.018**	72.983**
4 X 6	136.871**	134.107**	266.162**	263.636**	95.887**	93.891**
4 X 7	65.736**	47.373**	192.770**	163.975**	42.278**	21.249**
4 X 8	150.425**	113.553**	289.181**	246.419**	112.740**	81.297**
5 X 6	237.387**	235.373**	556.895**	548.809**	190.123**	165.837**
5 X 7	219.230**	188.368**	373.520**	319.705**	198.068**	172.554**
5 X 8	221.465**	178.247**	262.127**	216.958**	189.153**	164.402**
6 X 7	216.445**	184.328**	364.510**	316.249**	171.485**	129.411**
6 X 8	202.426**	160.448**	242.036**	202.613**	143.105**	105.429**
7 X 8	331.827**	311.610**	359.940**	353.344**	272.786**	272.786**
CD (5%)	57.624	66.539	17.86054	20.624	24.615	28.423

*Significant at five percent level   **Significant at one percent level

Table 27- Heterosis (%) for Stem fresh weight/plant, Leaf dry weight/plant and Stem dry weight/plant in experiment IV

Crosses	Stem fresh weight/plant		Leaf dry weight/plant		Stem dry weight/plant	
	RH	HB	RH	HB	RH	HB
1 X 2	-32.915**	-51.369**	8.368**	-6.636**	6.840**	-19.916**
1 X 3	-44.152**	-55.016**	-31.888**	-40.895**	-19.135**	-34.520**
1 X 4	65.289**	46.196**	92.345**	91.773**	154.490**	128.534**
1 X 5	72.210**	62.001**	92.330**	84.446**	160.598**	155.015**
1 X 6	189.364**	144.065**	171.921**	154.158**	377.177**	291.750**
1 X 7	288.881**	229.777**	371.862**	320.226**	588.328**	471.176**
1 X 8	109.051**	61.393**	105.296**	90.778**	205.020**	132.546**
2 X 3	38.112**	19.900**	12.332**	11.372**	83.330**	65.544**
2 X 4	79.056**	41.897**	42.958**	23.463**	152.756**	105.645**
2 X 5	8.221**	-18.275**	52.801**	36.566**	55.592**	18.376**
2 X 6	444.399**	350.442**	294.494**	221.213**	790.451**	691.500**
2 X 7	359.428**	278.165**	389.603**	371.362**	648.372**	557.420**
2 X 8	477.999**	427.933**	240.938**	214.009**	385.817**	374.006**
3 X 4	-12.334**	-21.343**	3.381*	-10.069**	23.568**	9.879**
3 X 5	-4.684**	-19.310**	14.156**	2.801**	26.208**	3.957**
3 X 6	74.707**	65.044**	119.752**	80.120**	281.122**	274.500**
3 X 7	112.558**	99.563**	77.992**	72.778**	202.847**	193.674**
3 X 8	113.684**	101.990**	130.826**	114.267**	301.626**	270.888**
4 X 5	140.888**	125.517**	96.891**	89.347**	240.016**	211.368**
4 X 6	212.741**	196.059**	174.514**	155.889**	424.835**	374.087**
4 X 7	90.045**	81.034**	167.315**	138.673**	228.812**	200.665**
4 X 8	214.822**	168.785**	209.678**	188.555**	418.653**	330.328**
5 X 6	315.495**	269.642**	473.810**	415.877**	683.420**	554.426**
5 X 7	249.126**	212.403**	448.624**	407.725**	283.164**	223.608**
5 X 8	270.567**	199.644**	240.466**	229.442**	293.329**	204.493**
6 X 7	291.657**	289.083**	330.522**	261.442**	423.122**	416.058**
6 X 8	313.343**	270.370**	117.095**	89.567**	491.828**	437.884**
7 X 8	420.098**	363.339**	273.962**	257.101**	498.103**	436.983**
CD (5%)	37.914	43.780	8.624	9.959	11.822	13.651

*Significant at five percent level   **Significant at one percent level

Table 28- Heterosis (%) for Crude protein content and Crude fibre content in experiment IV

Crosses	Crude protein content		Crude fibre content	
	RH	HB	RH	HB
1 X 2	62.363**	55.118**	-10.809**	-15.598**
1 X 3	10.113**	7.397**	24.568**	10.233**
1 X 4	8.958**	6.917**	-5.124**	-17.300**
1 X 5	55.183**	50.953**	-19.776**	-29.076**
1 X 6	2.688*	-3.778**	-20.917**	-21.119**
1 X 7	62.034**	56.198**	-17.821**	-32.956**
1 X 8	72.433**	62.340**	-1.360	-16.621**
2 X 3	-5.630**	-7.611**	24.617**	16.049**
2 X 4	2.097*	-4.199**	-2.856*	-19.201**
2 X 5	2.807*	0.918	-13.052**	-26.719**
2 X 6	-14.138**	-15.869**	-8.624**	-13.740**
2 X 7	112.660**	96.194**	-30.784**	-45.880**
2 X 8	14.987**	13.231**	2.101*	-9.452**
3 X 4	12.876**	8.083**	-3.989**	-24.524**
3 X 5	-2.321*	-2.588*	-7.159**	-26.129**
3 X 6	87.534**	79.974**	27.955**	12.977**
3 X 7	55.314**	46.166**	-20.433**	-40.872**
3 X 8	11.742**	7.760**	-7.178**	-11.957**
4 X 5	53.921**	47.002**	8.793**	7.036**
4 X 6	46.784**	35.138**	-25.570**	-34.979**
4 X 7	46.797**	44.159**	-29.606**	-34.895**
4 X 8	9.077**	0.890	-5.275**	-28.325**
5 X 6	7.067**	3.022*	-4.213**	-15.129**
5 X 7	289.985**	266.075**	-46.809**	-51.534**
5 X 8	285.262**	272.519**	-39.667**	-53.831**
6 X 7	30.180**	17.883**	49.209**	21.970**
6 X 8	-24.936**	-25.315**	-36.048**	-46.056**
7 X 8	17.605**	8.778**	-45.781**	-61.065**
CD (5%)	3.396	3.921	1.590	1.836

*Significant at five percent level   **Significant at one percent level

4.4.4.6. Leaf Area Index (LAI)

Twenty hybrids, out of twenty eight showed significant positive relative heterosis. Seventeen hybrids expressed significant positive heterobeltiosis.

4.4.4.7. Green Fodder Yield Plant^{-1}(g)

Significant positive relative heterosis was obtained in twenty five hybrids. Significant positive heterobeltiosis was reported for twenty two hybrids.

4.4.4.8. Dry Matter Yield Plant^{-1}(g)

Twenty seven hybrids showed significant positive relative heterosis of twenty eight hybrids evaluated, twenty five hybrids showed significant positive heterobeltiosis.

4.4.4.9 .Leaf Fresh Weight Plant^{-1}(g)

Twenty five hybrids showed significant positive relative heterosis. Twenty two hybrids showed significant positive heterobeltiosis.

4.4.4.10 .Stem fresh Weight Plant^{-1}(g)

Significant positive relative heterosis was seen in twenty four hybrids. Twenty three hybrids expressed significant positive heterobeltiosis.

4.4.4.11. Leaf Dry Weight Plant^{-1}(g)

Twenty six hybrids showed significant positive relative heterosis and twenty five hybrids reported significant positive heterobeltiosis.

4.4.4.12. Stem Dry Weight Plant^{-1}(g)

Twenty seven hybrids showed significant positive relative heterosis and twenty six hybrids exhibited significant positive heterobeltiosis.

4.4.4.13. Crude Protein Content (mg g^{-1})

Twenty five hybrids expressed significant positive relative heterosis. Twenty hybrids showed significant positive heterobeltiosis.

4.4.4.14. Crude Fibre Content (mg g^{-1})

Significant negative relative heterosis was shown by twenty one hybrids, and twenty three hybrids expressed significant negative heterobeltiosis.

4.5. EXPERIMENT V

The twenty eight hybrids in experiment IV were analyzed and the best four hybrids namely $P_1 X P_7$, $P_2 X P_7$, $P_5 X P_7$, and $P_5 X P_8$ were selected based on their green fodder yield, dry matter yield, protein content and crude fibre content. The selected families were evaluated by raising F_2 families in compact family block design in the field without replications. The twelve characters studied in the experiment were plant height at harvest, number of primary branches, number of leaves plant^{-1}, days to first flowering, days to fifty percent flowering, leaf area index, green fodder yield plant^{-1}, dry matter yield plant^{-1}, leaf fresh weight plant^{-1}, stem fresh weight plant^{-1}, leaf dry weight plant^{-1} and stem dry weight plant^{-1}. Mean and variance were calculated and presented in table 29.

4.5.1. Plant Height

Plant height at harvest ranged from 210.80cm to 101.19cm. Family 1 ($P_1 X P_7$) had maximum plant height (210.795cm), followed by Family 4 ($P_5 X P_8$), Family 3 ($P_5 X P_7$) and Family 2 ($P_2 X P_7$). Families 1, 3 and 4 were on par with each other.

4.5.2. Number of Primary Branches Plant^{-1}

Number of primary branches plant^{-1} ranged from 1.10 to 6.75. Primary branches were maximum for Family 4 (6.75) and minimum for Family 2 (1.46). Family 4 was on par with Family 1 (6.135). Family 1 (6.135) was on par with family 3 (5.810).

4.5.3. Number of Leaves Plant^{-1}

Mean for number of leaves plant^{-1} among the families ranged from 21.63 - 70.93. Number of leaves plant^{-1} was maximum for family 1 (70.93) and minimum for Family 2 (21.63). Family 4 (56.755) and family 3 (55.060) followed Family 1 but not on par with it. Family 4 and Family 3 were on par with each other.

Plate 13 – F₂ seeds

P₁ X P₇

P₂ X P₇

P₅ X P₇

P₅ X P₈

Plate 14 – Field view of experiment V

Plate 15 – Pods of F$_2$ plants

Family -1   Family -2   Family -3   Family -4

Table 29 – Mean square values of twelve characters in four families of fodder cowpea in experiment V

Sources	Replication	Families	Error	Progenies in				Pooled error
				Family 1	Family 2	Family 3	Family 4	
df	3	3	9	4	4	4	4	48
Plant height at harvest	204.850	46868.650**	1201.361	15430.020**	710.047	2220.031	1692.578	1201.361
No. of primary branches plant[-1]	1.037	112.519**	0.555	0.391	0.338	0.283	0.095	0.53
No. of leaves plant[-1]	374.771	6931.396**	122.290	30.865	23.296	25.926	112.476	53.651
Days to first flowering	68.760	125.2521	35.187	16.511**	14.038	0.1348	10.729	8.320
Days to 50% flowering	88.501	79.334	58.633	3.375	24.675	7.325	3.300	5.360
Leaf area index	29.347	1473.368**	18.150	5.691	13.476	32.938	9.531	28.614
Green fodder yield plant[-1]	20565.200	717268.700**	14037.740	7177.500	990.250	4081.500	9995.375	6342.672
Dry matter yield plant[-1]	470.671	22979.270**	565.799	244.422	57.780	88.027	305.022**	213.643
Leaf fresh weight plant[-1]	11222.130	612585.300**	8417.066**	4593.125	356.500	2000.313	6397.188**	3751.240
Stem fresh weight plant[-1]	1536.167	15746.870**	790.244	287.133	158.406	367.273	428.6719**	368.800
Leaf dry weight plant[-1]	451.550	17046.130**	137.653	594.988	20.780	43.141	195.311**	311.447
Stem dry weight plant[-1]	53.981	465.361**	12.788	37.294	9.242	9.434	12.197**	24.980

4.5.4. Days to first Flowering

Days to first flowering was longest for Family 3 (50.855 days) followed by Family 2 (47.685 days), Family 1 (45.645 days) and family 4 (45.480 days).

4.5.5. Days to Fifty Per cent Flowering

Days to fifty per cent flowering was longest for Family 3 (55.10 days) followed by Family 2 (52.70 days), family 1 (51.00 days) and family 4 (50.80days).

4.5.6. Leaf Area Index

Leaf area index was highest for Family 3(47.065) followed by Family 4(38.490), family 1 (35.110) and family 2 (26.315)

4.5.7. Green Fodder Yield Plant[-1]

Green fodder yield was maximum for family 1 (753.014g) followed by Family 3 (427.927g), Family 4 (419.763g) and Family 2 (316.551g). Family 1 was not on par with any other family. Family 3 and Family 4 were on par with each other.

4.5.8. Dry Matter Yield Plant[-1]

Dry matter yield plant[-1] was highest for Family 1(140.474g) followed by Family 3 (80.421g), Family 4 (79.883g) and Family 2 (63.364g). Family 3 and Family 4 were on par with each other.

4.5.9. Leaf Fresh Weight Plant[-1]

Leaf fresh weight plant[-1] was highest for Family 1 (602.411g), followed by Family 4 (335.809g), Family 3 (299.549g) and family 2 (189.932g).

4.5.10. Stem fresh Weight Plant[-1]

Stem fresh weight plant[-1] was highest for Family 1 (150.600g), followed by Family 3 (128.373g), Family 2 (126.616g) and Family 4 (83.497g).

4.5.11. Leaf Dry Weight plant[-1]

Leaf dry weight plant[-1] was highest for Family 1 (106.931g), followed by Family 4 (63.900g), Family 3 (56.290g) and Family 2 (38.015g).

4.5.12. Stem Dry Weight Plant[-1]

Stem dry weight plant[-1] was highest for family 1 (26.728g), followed by family 2 (25.342g), family 3 (24.028g) and family 4 (15.974g).

DISCUSSION

5. Discussion

Agriculture and animal husbandry in India are interwoven, as mixed farming and livestock rearing forms an integral part of rural living. As per 19th Livestock census, 2012 (GoI.2014) India's livestock sector is one of the largest in the world with a holding of 11.6 per cent of world livestock population.

One of the major challenges of animal husbandry sector is shortage of feed and fodder, which needs to be addressed (GoI.2016). The major reasons for shortage of feed and fodder are; increasing pressure on land for growing food grains, oil seeds and pulses. Though the availability of feed and fodder has improved in the last decade, still a lot needs to be done to bridge the gap between the demand and availability of fodder in the country, particularly during the lean periods and crisis situations.

Kerala has a large livestock population of 27.35 lakh (Livestock census,2012).the land devoted for fodder cultivation is less than 1 per cent of the cultivable area, which produces 94.5 lakh m.t. of fodder compared to the required quantity of 232 lakh mt(FIB,2011). Protein is required for growth,tissue repair and milk production among other desirable characters. Considering the land availability, cropping systems and climatic factors of Kerala, fodder cowpea is the best option.

Cowpea (*vigna unguiculata* L.Walp) is a self-pollinating annual herbaceous legume belonging to the family Fabaceae which originated in West Africa. As a fodder crop, it's short duration and multicut nature (KAU, 2011) makes it attractive to farmers. Not much systematic research work appears to have been conducted on cowpea for its utility as fodder crop in Kerala.

The study of genetic diversity is important for the selection of suitably diverse parents to obtain heterotic hybrids as well as for germplasm characterization. Molecular characterization of germplasm is important, especially in the changing scenario with regard to plant Biodiversity Act (2002). The use of molecular markers provides a much more reliable approach to distinguish cowpea genotypes (Doumbia,

2012). Inter Simple Sequence Repeat marks are considered as more discriminating (Qian *et al.*,2001). Diallel analysis is an effective means of understanding the genetic nature of quantitatively inherited traits and their inheritance (Ayo-Vaughan *et al.*, 2011).It has been used in cowpea to provide important information on general combining ability (*gca*) and specific combining ability (*sca*), determine genetic variance, estimate heritability and maternal effects (Hazra *et al.,* 1994).

Therefore, in the present study evaluation of different fodder cowpea accessions were done to assess the variability in the available population to identify the good performers for forage yield and quality. Based on the morphological and through hybridization to develop superior cross combinations. The salient features of the study are discussed below.

5.1.EXPERIMENT I - EVALUATION OF FODDER COWPEA ACCESSIONS

The primary forces of selection in nature in the base populations favour certain characteristics in reproduction (Allard, 1960). The efficiency of these primary forces depends on the extent of genetic variability present in the base population (Singh and Narayanan, 1993). Based on this finding, 30 genotypes of fodder cowpea accessions including released varieties were evaluated for yield and quality parameters.

5.1.1. Mean and variability components

Significant variation was observed for all the 14 characters studied which implied that selection would be desirable in the germplasm evaluated for the characters under consideration. The range of mean values observed refers to the phenotypic and genotypic variability present in the base population. Similar results were observed by Paniker (2000), Anbuselvam *et al.* (2000), Vidya (2000), Ajith (2001), Jyothi (2001), Misra *et al.*(2003), Philip (2004), Malarvizhi *et al.*(2005), Abe *et al.*(2015) and Sunil *et al.*(2017).

High genotypic and phenotypic coefficient of variation was observed for number of primary branches plant^{-1}, number of leaves plant^{-1}, leaf are index,

green fodder yield plant^{-1}, dry matter yield plant^{-1}, leaf fresh weight plant^{-1}, stem fresh weight plant^{-1}, leaf dry weight plant^{-1}, stem dry weight plant^{-1} and crude fibre content. Similar results were reported by Borah and Falullakhkhan (2000), Manonmani *et al.* (2000), Kumar and Sangwan (2000), Malarvizhi *et al.* (2005) and Sunil *et al.* (2017).

High heritability and genetic advance for crude fibre content, crude protein content, leaf area index, leaf dry weight plant^{-1}, dry matter yield plant^{-1}, stem dry weight plant^{-1}, number of leaves plant^{-1}, stem fresh weight plant^{-1}, leaf fresh weight plant^{-1} and green fodder yield shows that these characters are less influenced by environment in their expression. Therefore, they may be used for selection of superior by Borah and Falullahkhan (200), Manonmani *et al.* (2000), Kumar and Sangwan (2000), Malarvizhi *et al.* (2005) and Sunil *et al.* (2017). Medium heritability and high genetic advance was recorded for number of primary branches and plant height which indicates that improvement can be made through simple selection. Similar result was reported by Kumar and Sangwan (2000). Days to first flowering and days to fifty per cent flowering had medium to high heritability were as genetic advance was low. None of the characters exhibited low heritability.

5.1.2. Correlation between different characters

Significance of correlation between characters in a breeding program is essential for selection of appropriate character combinations and genotypes for further improvement. Since yield is a complex character, estimation of its direct and indirect association with other characters is inevitable for a rational improvement of the yield.

Green fodder yield had significant positive phenotypic and genotypic correlation with leaf fresh weight plant^{-1}, followed by stem fresh weight plant^{-1}, stem dry weight plant^{-1}, dry matter yield plant^{-1}, leaf dry matter plant^{-1}, number of primary branches plant^{-1} and number of leaves plant^{-1}. Green fodder yield exhibited no significant phenotypic correlation with plant height, days to first flowering, leaf area

index, days to fifty per cent flowering, crude protein content and crude fibre content where as it had significant genotypic correlation with number of primary branches plant[-1], leaf dry weight plant[-1], days to fifty per cent flowering, days to first flowering, number of leaves plant[-1] and plant height.

Dry matter yield had highly significant positive genotypic and phenotypic correlation with leaf dry weight plant[-1], followed by stem dry weight plant[-1], leaf fresh weight plant[-1], green fodder yield, stem fresh weight plant[-1] and number of primary branches plant[-1]. Dry matter yield had no significant phenotypic and genotypic correlation with crude protein content, days to first flowering, number of leaves plant[-1] and crude fibre content.

Similar results were obtained by Chopra and Singh (1977), Jindal (1989), Ushakumari and Chandrasekharan (1991), Aaravindhan and Das (1995), Chopra and Singh (1977), Tyagi et al.(1978), Roquib and Patniak (1988), Sharma and Gupta (1994), Vasanthi and Das (1996a), Manonmani et al. (2000), Santosh kumar et al.(2002), Radhika (2003) and Sunil et al. (2017).

Sharma et al. (1988) reported that green forage yield was positively and significantly correlated with days to first flowering and plant height. This was in contradiction to present study.

5.1.3. Cluster analysis

The thirty fodder cowpea genotypes were grouped into eleven clusters. The cluster mean for the fourteen characters revealed considerable difference among all the clusters. Maximum contribution to divergence was shown by leaf fresh weight plant[-1] followed by crude fibre content, stem dry weight plant[-1].leaf area index, dry matter yield plant[-1] number of leaves per plant[-1] plant, crude protein content and green fodder yield plant[-1].Plant height, number of primary branches plant[-1], days to first flowering, days to fifty per cent flowering, stem fresh weight plant[-1] and leaf dry weight plant[-1] did not contribute to genetic divergence significantly. Plant height, number of primary branches plant[-1], days to first

flowering, days to fifty per cent flowering, stem fresh weight plant^{-1} and leaf dry weight plant^{-1} did not contribute to genetic divergence. The above findings are broadly in agreement with previous workers (Lodhi *et al.*, 1990; Roquib and Patnaik, 1990; Sharma and Singhania, 1992; Sharawy and El-Fiky, 2002; Radhika, 2003; Omokanye *et al.*, 2003; Malarvizhi *et al.*, 2005; Sheela and Gopalan, 2006; Adeyanyu, 2009; Thaware *et al.*, 1991; Nagalakshmi *et al.*, 2010; Noubissie *et al.*, 2011)

The present study exhibited a high level of genetic diversity among thirty fodder cowpea genotypes which were grouped into eleven clusters based on D^2 statistics. The estimates of intra and inter-cluster D^2 values for eleven clusters revealed that the genotypes of the same cluster have little genetic divergence. The above findings are broadly in agreement with previous workers (Lodhi *et al.*, 1990; Roquib and Patnaik, 1990; Sharma and Singhania, 1992; Sharawy and El-Fiky, 2002; Radhika, 2003; Omokanye *et al.*, 2003; Malavizhi *et al.*, 2005; Sheela and Gopalan, 2006; Adeyanyu, 2009; Thaware *et al.*, 1991; Nagalakshmi *et al.*, 2010; Noubissie *et al.*, 2011).

The present study exhibited a high level of genetic diversity among thirty fodder cowpea genotypes which were grouped into eleven clusters based on D^2 statistics. The estimates of intra and inter-cluster D^2 values for eleven clusters revealed that the genotypes of the same cluster have little genetic divergence from each other with respect to aggregate effects of 14 characters under study. More genetic diversity was observed between the genotypes of different clusters. Since high or optimum genetic divergence is required between the parents for hybridization for obtaining high frequency of desirable recombinants, the chances of obtaining good sergeants in the segregating generations is possible from the evaluated genotypes. It would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster D^2 values. The crossing

between the genotypes which show high mean values coupled with relatively large inter cluster D^2 values would result in high heterotic expression.

There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity (Nagalekshmi *et al.*, 2010 and Asoontha and Mareen, 2017). The contribution mainly depends upon the genotypes included in the study and the environment influences over the character.

5.1.4. Discrimination function analysis

Selection index was highest for IT-37154999-38 and least for IC-202804. Selection index calculated for the genotypes based on the desired characters were used in the present study for selection of parents for hybridization programme for yield and quality improvement. The genotypes were ranked for characters green fodder yield, crude protein content, crude fibre content and selection index. The average of the four ranks were calculated and again ranked accordingly. Based on this rank and maximum inter cluster distance eight genotypes CO-8, MFC-09-1, IC-1061, IC-39916, IC-97767, IT-38956-1, IT-37154999-38 and Pant Lobia-2 were selected for further hybridization programmes.

5.2. EXPERRIMENT 2 - MOLECULAR CHARACTERIZATION

Molecular characterization revealed two characters (I and II) with 0.34 per cent similarity. Cluster I and Cluster II had two sub clusters each Ia and Ib and IIa and IIb respectively. The statistical cluster diagram from D^2 value and dendrogram from molecular characterization were not similar. But the eight parents selected had considerable difference in dendrogram except for parents IT-38956-1 and IT-37154999-38.

5.3. EXPERIKMENT 4- COMBINING ABILITY, GENE ACTION AND HETEROSIS

Combining ability analysis gives information related to selection of parents in terms of performance of their hybrids. It is tool to find out nature and magnitude of various types of gene action involved in the expression of quantitative

characters. Diallel analysis is one of the techniques used to find the genetic makeup. It measures the *GCA* and *SCA* variance for a character indicates the predominance of additive gene action and if *SCA* variance is greater, then non-additive gene action plays an important role in that trait. Simple selection is enough for a character controlled by additive gene action as it can be fixed. Predominance breeding may be rewarding or selection has to be postponed to later generation. *gca* variance was greater than *sca* variance, for all characters except for days to first flowering and crude protein content, indicating predominance of additive gene action for most characters. Days to first flowering and crude protein content had non-additive gene action.

Kheradnam and Nikhejad (1971), Kumar *et al.*(1978), Luthra *et al.*(1979), Zaveri *et al.* (1980), Jain *et al.* (1981), Jain (1982), Imrie and Bray (1983), Patil and Patil (1987), Mishra *et al.* (1987), Suaporn (1992), Tiwari *et al.* (1993), Naidu and Satyanarayana (1993 b), Madhusudan *et al.* (1995), Sawant (1995), Ponmaraiammal and Das (1997), chaudhary *et al.* (1998), Chaudhary *et al.* (1998), sobha *et al.* (1998), Dokashi and Mohamed (2002), Chauhan *et al.* (2003), Manivannan and Sekar (2005), Patil and Navale (2006), Pal *et al.* (2007), Adeyanju *et al.* (2012), Idahosa and Alika (2013) also reported similar results.

Patil and Bhapkar (1986), Prataung (1993), Mehta and Zaveri (1997) and Ayo-Vaughan *et al.* (2011) reported additive gene action for days to first flowering. This was in contradiction with the present study. Birada *et al.* (1993) also reported significant *sca* effect in protein content. Zaveri *et al.* (1983), Bhushana *et al.* (2000) and Anitha *et al.* (2017) reported predominance of non - additive gene action in cowpea.

Presence of heterosis also shows the ability of the parents to combine well in a hybridization programme. Superior expression of F_1 may be due to fixable (additive) type of gene action and non-additive type of gene action. Thus combining ability and heterosis helps in identifying desirable cross combinations.

Twenty eight hybrids from eight parents were evaluated for combining ability in diallel mating design without reciprocals. Relative heterosis and heterobeltiosis were calculated for different traits. The results are discussed below.

5.3.1. Plant Height

Gca variance was greater than *sca* variance, indicating predominance of additive gene action. P_4, P_5 and P_6 were good general combiners among eight parents. Twelve of the hybrids were good specific combiners for longer plant height with maximum magnitude for crosses P_4 X P_7, P_5 X P_7, and P_3 X P_6. Thirteen of the hybrids were good specific combiners for lesser plant height with maximum magnitude for crosses P_2 X P_3, P_1 X P_7 and P_1 X P_8. Most of the hybrids exhibited negative relative heterosis and heterobeltiosis except P_4 X P_7, P_5 X P_7 and P_3 X P_6. Hoffmann (1926), Sawant *et al.* (1994), Bhore *et al.* (1997), Patel *et al* (2009), Kajale *et al*, (2013) and Anitha *et al.*(2016) reported high positive hererotic effect for plant height. Damarany (1994) reported medium heterotic effect.

5.3.2. Number of Primary Branches Plant^{-1}

gca variance was greater than *sca* variance, indicating predominance of additive gene action. None of the parents were good general combiners. Only P_3 X P_8 had good specific combining ability. Crosses P_2 X P_4 and P_1 X P_2 had higher relative heterosis and heterobeltiosis for this character. Significant positive heterosis for number of branches plant^{-1} was reported by Hiralal *et al.*, (2007) and Anitha *et al.*, (2016).

5.3.3. Number of Leaves Plant^{-1}

Gca variance was greater than *sca* variance, indicating predominance of additive gene action. P_7 and P_8 were good general combiners. Twelve of the hybrids were good specific combiners for higher number of leaves plant^{-1} with maximum magnitude for crosses P_2 X P_8, P_1 X P_7 and P_2 X P_3. Seven of the hybrids were good specific combiners for lower number of leaves plant $^{-1}$ with maximum

magnitude for crosses $P_2 \times P_4$, $P_2 \times P_5$ and $P_1 \times P_8$. $P_3 \times P_8$ and $P_6 \times P_8$ had maximum relative heterosis and crosses, $P_3 \times P_8$, $P_4 \times P_8$ and $P_6 \times P_8$ had maximum superiority over their respective better parent. Most recently, significant positive heterosis for number of leaves plant^{-1} was reported by Anitha *et al.* (2016) in cowpea and Jain and Patel (2014) in fodder sorghum, as in the present study.

5.3.4. Days to First Flowering

Sca variance was greater than *gca* variance, indicating predominance of non-additive gene action. Twenty of the hybrids were good specific combiners for longer days to first flowering with maximum magnitude for crosses $P_4 \times P_7$ and $P_4 \times P_8$. Seven of the hybrids were good specific combiners for lesser days to first flowering with maximum magnitude for crosses $P_2 \times P_8$ and $P_5 \times P_7$. Relative heterosis was maximum for $P_1 \times P_6$, $P_2 \times P_6$, $P_4 \times P_6$, $P_5 \times P_6$ and $P_6 \times P_7$. Heterobeltiosis was higher for $P_4 \times P_6$ and $P_6 \times P_7$.

5.3.5. Days to Fifty Per Cent Flowering

gca variance was greater than *sca* variance, indicating predominance of additive gene action. Fifteen of the hybrids were good specific combiners for longer days to fifty per cent flowering with maximum magnitude for crosses $P_1 \times P_6$, $P_2 \times P_5$ and $P_2 \times P_3$. Early flowering is a desirable feature of a genotype. Therefore, negative heterosis for days to fifty per cent flowering was considered desirable by Anitha *et al.* (2016). Four of the hybrids were good specific combiners for lower days to fifty per cent flowering with maximum magnitude for crosses $P_3 \times P_8$, and $P_5 \times P_7$. Relative heterosis was also maximum for $P_3 \times P_8$, and $P_5 \times P_7$. Heterobeltiosis was highest for $P_3 \times P_8$ and $P_5 \times P_7$. So these crosses could be used for this character. Similar results were also reported in fodder cowpea by Hira lal *et al.* (2007), Prakash *et al.* (2010) and Anitha *et al.* (2016).

5.3.6. Leaf Area Index

gca variance was greater than sca variance, indicating predominance of additive gene action. P_6, P_7 and P_8 were good general combiners. Fourteen of the hybrids were good specific combiners for higher leaf area index with maximum magnitude for crosses. P_2 X P_8, P_6 X P_8, P_3 X P_7. Ten of the hybrids were good specific combiners for lower leaf index with maximum magnitude for crosses P_3 X P_8 and P_2 X P_5. Relative heterosis was maximum for P_3 X P_7, P_4 X P_8, P_4 X P_7 and P_6 X P_8. Heterobeltiosis was highest for P_3 X P_7 and P_6 X P_8.

5.3.7. Green Fodder Yield Plant^{-1}

gca variance was greater than sca variance, indicating predominance of additive gene action. P_5, P_6, P_7 and P_8 were good general combiners. Nineteen of the hybrids were good specific combiners for higher green fodder yield plant^{-1} with maximum magnitude for crosses P_1 X P_7, P_2 X P_6, P_2 X P_8 and P_5 X P_6. Nine of the hybrids were good specific combiners for lower green fodder yield plant^{-1} with maximum magnitude for crosses P_3 X P_8 and P_2 X P_5. The crosses P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_8 and P_7 X P_8 had maximum superiority than mid parent value. Hybrids P_1 X P_6, P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum heterosis over better parent. Positive heterosis for green fodder yield was earlier reported by Lodhi et al. (1990) and recently by Anitha et al. (2016) in fodder cowpea.

5.3.8. Dry Matter Yield Plant^{-1}

gca variance was greater than sca variance, including predominance of additive gene action. P_5, P_6, P_7 and P_8 were good general combiners. Sixteen of the hybrids were good specific combiners for higher dry matter yield plant^{-1} with maximum magnitude for crosses P_1 X P_7 and P_5 X P_6. Eleven of the hybrids were good specific combiners for lower dry matter yield plant^{-1} with maximum magnitude for crosses P_1 X P_2 and P_2 X P_5. The crosses, P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum superiority than mid

parent value. Hybrids P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum heterosis over better parent. Recently Anitha *et al.* (2016) reported positive significant heterosis for dry mater yield in fodder cowpea.

5.3.9. Leaf Fresh Weight Plant^{-1}

gca variance was greater than *sca* variance, indicating predominance of additive gene action. P_5, P_6, P_7 and P_8 were good general combiners. Seventeen of the hybrids were good specific combiners for higher leaf fresh weight plant^{-1} with maximum magnitude for crosses P_1 X P_7, P_2 X P_6 and P_2 X P_8. Nine of the hybrids were good specific combiners for lower leaf fresh weight plant^{-1} with maximum magnitude for crosses P_1 X P_2 and P_2 X P_5. The crosses P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_8 and P_7 X P_8 had maximum superiority than mid parent value. Hybrids P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum heterosis over better parent.

5.3.10. Stem Fresh Weight Plant $^{-1}$

gca variance was greater than *sca* variance, indicating predominance of additive gene action. P_5, P_6, P_7 and P_8 were good general combiners. Nineteen of the hybrids were good specific combiners for higher stem fresh weight plant^{-1} with maximum magnitude for crosses P_1 X P_2 and P_2 X P_5. Nine of the hybrids were good specific combiners for lower stem fresh weight plant^{-1} with maximum magnitude for crosses P_1 X P_2 and P_2 X P_5. The crosses P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum superiority than mid parent value. Hybrids P_1 X P_6, P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum heterosis over better parent.

5.3.11. Leaf Dry Weight Plant[-1]

gca variance was greater than sca variance, indicating predominance of additive gene action. P_5, P_6 and P_7 were good general combiners. Fourteen of the hybrids were good specific combiners for higher leaf dry weight plant[-1] with maximum magnitude for crosses P_1 X P_7 and P_5 X P_7. Nine of the hybrids were good specific combiners for lower leaf dry weight yield plant[-1] with maximum magnitude for crosses P_6 X P_8 and P_2 X P_5. The crosses P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum superiority than mid parent value. Hybrids P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum heterosis over better parent.

5.3.12. Stem Dry Weight Plant[-1]

gca variance was greater than sca variance, indicating predominance of additive gene action. P_5, P_6, and P_7 were good general combiners. Seventeen of the hybrids were good specific combiners for higher stem dry weight plant[-1] with maximum magnitude for crosses P_2 X P_6 and P_5 X P_6. Eight of the hybrids were good specific combiners for lower stem dry weight yield plant[-1] with maximum magnitude for crosses P_6 X P_8 and P_2 X P_5. The crosses, P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum superiority than mid parent value. Hybrids P_1 X P_7, P_2 X P_6, P_2 X P_7, P_2 X P_8, P_4 X P_6, P_4 X P_8, P_5 X P_6, P_5 X P_7, P_5 X P_8, P_6 X P_7, P_6 X P_8 and P_7 X P_8 had maximum heterosis over better parent.

5.3.13. Crude protein content

sca variance was greater than gca variance, indicating predominance of non-additive gene action. P_3, P_5, P_7 and P_8 were good general combiners. Eight of the hybrids were good specific combiners for lower crude protein content with maximum magnitude for crosses P_3 X P_6, P_3 X P_7 and P_5 X P_8. Eight of the hybrids were good specific combiners for lower crude protein content

with maximum magnitude for crosses $P_2 \times P_5$ and $P_3 \times P_5$. Crosses $P_2 \times P_7$, $P_5 \times P_7$ and $P_5 \times P_8$ had maximum relative heterosis and heterobeltiosis among the crosses. Similar results were observed by Aravindhan and Das (1996) and Anitha *et al.* (2016) in cowpea for crude protein content.

5.3.14. Crude Fibre Content

gca variance was greater than *sca* variance, indicating predominance of additive gene action. P_4, P_5, P_6 and P_7 were good general combiners. Ten of the hybrids were good specific combiners for higher crude fiber content with maximum magnitude for crosses $P_6 \times P_7$ and $P_4 \times P_5$. Seventeen of the hybrids were good specific combiners for lower crude fibre content with maximum magnitude for crosses $P_5 \times P_7$, $P_7 \times P_8$, $P_6 \times P_8$, $P_4 \times P_7$ and $P_4 \times P_7$. The crosses $P_2 \times P_7$, $P_4 \times P_7$, $P_6 \times P_8$, $P_7 \times P_8$, $P_5 \times P_7$ and $P_5 \times P_8$ had minimum heterobeltiosis and relative heterosis. Significant negative standard heterosis for crude fibre content were earlier reported by Anitha *et al.* (2016) in fodder cowpea.

5.4 EXPERIMENT 5 – F_2 POPULATION STUDIES

Genetic variability for yield and yield related traits in the initial population is necessary for identification of superior genotypes. Identification of superior F_2 ($P_5 \times P_7$) progenies is useful in further improvement programmes.

Maximum and minimum plant heights were obtained by family 1 ($P_1 \times P_7$) and family 2 respectively. Number of primary branches was maximum in family 4 and minimum in family 2. Number of leaves plant-1 was maximum in family 1 and minimum I n family 2. Family 3 ($P_5 \times P_7$) was late to flower and family 4 ($P_5 \times P_8$) flowered early for days to flowering and days to fifty per cent flowering. Leaf area index was maximum for family 3 and minimum family 2. Family 1 had maximum value for green fodder yield, dry matter yield, leaf fresh weight, stem fresh weight, leaf dry weight and stem dry weight. Family 2 had minimum green fodder yield, dry matter yield, leaf dry weight plant^{-1} and leaf fresh

weight. Family 4 had minimum value for stem fresh weight plant^{-1} and stem dry weight plant^{-1}.

In various cop improvement programs across the world many researchers have reported improvement of characters and difference in and among the progenies of different cross combinations F_2 population of pulses, but no work related to the compact family block design in cowpea was found.

SUMMARY

6. SUMMARY

In India agriculture and animal husbandry are interwoven. Livestock sector provides employment to fifty two per cent of the work force. Milk production alone involves more than thirty million small producers. As per 19th Livestock census, 2012 (GOI, 2014) India's livestock sector is one of the largest in the world with a holding of 11.6 percent of world livestock population. Kerala has a large livestock population of 27.35 lakh (Livestock Census, 2012). One of the major challenges of animal husbandry is shortage of nutritive feed and fodder. Legumes provide potential to enhance for its quality grass. Protein is required for growth, tissue repair and milk production among other desirable characters. Hench the cultivation of fodder legumes is very important. Considering the land availability, cropping systems and climatic factors of Kerala, fodder cowpea is the best option. Not much systematic research work appears to have been conducted on cowpea for its utility as fodder crop in Kerala.

The present study entitled "Genetic analysis of yield and quality in fodder cowpea (*Vigna unguiculata* (L.) (Walp)" was undertaken with the objectives for genetic analysis of fodder yield and quality in fodder cowpea accessions and evaluation of F_2 progenies to identify superior recombinants. Five experiments were conducted at instructional Farm, COA, Vellayani during 2016-2019 Kharif and rabi seasons. The observations analyzed were plant height, number of primary branches plant $^{-1}$, number of leaves plant $^{-1}$, days to first flowering, days to fifty per cent flowering, leaf area index, green fodder yield plant $^{-1}$, dry matter yield plant $^{-1}$, leaf fresh weight plant $^{-1}$, crude protein content and crude fibre content.

In experiment I, thirty accessions (T_1 and T_{30}) of fodder cowpea collected from different agro climatic zones of India and AICRP Centers were evaluated in RBD design with three replications. The ANOVA also revealed significant difference among the genotypes for all characters studied. The

components of variation, Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were estimated. Number of primary branches plant $^{-1}$, number of leaves plant^{-1}, leaf area index, green fodder yield plant $^{-1}$, dry matter yield plant $^{-1}$, leaf fresh weight plant $^{-1}$, stem fresh weight plant $^{-1}$, leaf dry weight plant $^{-1}$, stem dry weight plant $^{-1}$ and crude fibre plant $^{-1}$ had high GCV and PCV. This indicates that phenotypic selection for these characters would improve the genotype of the selected material which in turn would give rise to better off springs through hybridization. Characters *viz.* plant height and crude protein content had medium GCV and PCV. Days to first flowering and days to Fifty percent flowering had low GCV and PCV, indicating higher influence of environment on the expression of these characters. High heritability and genetic advance was observed for number of leaves plant^{-1}, leaf area index, green fodder yield, dry matter yield plant^{-1}, leaf fresh weight plant^{-1}, crude protein content and crude fibre content. These characters, if selected for, would improve over generations. Medium heritability and high genetic advance was observed for plant height and number of primary branches. Medium heritability and low genetic advance was exhibited by days to first flowering. Days to Fifty percent flowering exhibited high heritability and low genetic advance.

Correlation studies with phenotypic correlation coefficient, genotypic correlation coefficient and environmental correlation coefficient was done. Crude protein content and crude fibre content had no phenotypic correlation with any other characters. Crude fibre content had genotypic correlation only with plant height. Crude protein content had significant genotypic correlation with plant height, days to Fifty percent flowering and stem dry weight plant.

Path analysis was done with green fodder yield as dependent variable. Different character combinations were used as component characters. Of all the characters, a combination with minimum residual effect was selected for analysis. Five characters *viz.* plant height, days to first flowering, number of primary branches,

number of leaves plant $^{-1}$ and dry matter yield plant $^{-1}$ showed high and positive direct effect on green fodder yield plant $^{-1}$. Number of leaves plant $^{-1}$had an indirect effect through number of primary branches. The residual effect obtained was 19.28 per cent. We can infer that 80.72 per cent of the variation in yield was contributed by the characters selected for analysis.

Cluster analysis revealed eleven clusters. Cluster I was the biggest, with ten genotypes, followed by cluster II (Five genotypes), cluster III (Four genotypes) and cluster IV (Four genotypes). All the remaining clusters had single accession. Cluster VIII and cluster X had maximum inter cluster distance, and minimum distance was seen between cluster XI and cluster IX. Divergence was also calculated and only eight characters out of the fourteen characters studied, contributed to divergence. They were green fodder yield plant $^{-1}$, crude protein content, number leaves plant $^{-1}$, leave area index, stem dry weight plant $^{-1}$, crude fibre content and leaf fresh weight plant $^{-1}$.

Discriminant function analysis was done with all the characters and selection indices were calculated. The highest selection was obtained by IT-37154999-38 and lowest by IC-253251. From the above analyses eight divergent parents from distinct clusters with better quality or yield were selected for further hybridization programme. The eight parents were CO-8, MFC-09-1, IC-1061, IC-39916, IC-97767, IT-38956-1, IT-37154999-38 and Pant Lobia – 2 (P_1, P_2......P_8 respectively).

Experiment II was molecular characterization of the thirty genotypes for the conformation of genetic diversity. DNA isolation was done with NucleoSpin Plant II Kit. DNA samples isolated were intact and without shearing. Purity ranged from 1.4 to 2.1 and average purity was 1.8. PCR was done using ISSR primers *viz.* UBC-811, UBC-812, UBC-823 and UBC-834. PCR products produced thirty two amplicons from four primers. Average number of amplicons was eight amplicons

per primer. Primer UBC-812 produced ten amplicons. UBC-811 and UBC-834 produced eight amplicons each. UBC-823 produced six amplicons. Amplification products size ranged from 600 to 2750 base pairs. Number of amplicons per genotype varied from zero to eight. The amplicons were scored and a dendrogram was prepared using NTSYS (Version 2.2). Two main clusters (I and II) with 0.34 per cent similarity was observed minimum similarity between sub-cluster was 0.83 per cent. Two main clusters, Cluster I and Cluster II, had two sub clusters each Ia & Ib and IIa & IIb respectively. It-38956-1 and IT-37154999-38 had minimum variation. The eight parents selected from experiment I exhibited considerable variation in molecular analysis also.

In experiment III, the eight parents were raised in diallel mating system for crossing. Twenty eight hybrids were made by crossing eight parents in all possible cross combinations without reciprocals. The hybrids were collected and raised in RBD with three replications (Experiment IV) to find out the general and specific combining ability and gene action involved in the expression of different characters.

In experiment IV, mean data showed vide range of variability and highly significant differences between hybrids were observed in ANOVA. Green fodder yield plant $^{-1}$ was highest in P_5 X P_6 followed by P_1 X P_7, P_2 X P_6, P_7 X P_8, P_2 X P_8, P_5 X P_7 and P_5 X P_8. Crude protein content was highest in P_5X P_8 followed by P_5 X P_7 and P_2 X P_7. Crude fibre content was lowest in P_6 X P_8 followed by P_5 X P_8. The *gca* and *sca* variances were highly significant were and *gca* variance was greater than *sca* variance for all characters. Predominant effect of additive gene action was observed. This means, selection is effective in this population. P_5, P_6, P_7 and P_8 were good general combiners for green fodder yield. P_3, P_5, P_7 and P_8 were good general combiners for protein content. P_1, P_2, P_3 and P_8 were good general combiners for crude fibre content. Based on superiority for yield and quality from several hybrids,

P_1X P_7, P_2 X P_7, P_5 X P_7 and P_5 X P_8 were selected for further raising of F_2 generation. The selected genotypes had significant positive relative heterosis and heterobeltiosis for green fodder yield, dry matter yield and crude protein content. They also had significantly negative relative heterosis and heterobeltiosis for crude fibre content. Seeds from the above four hybrids were collected to raise the F_2 generation in experiment V.

The analysis of variance in experiment V, showed differences for all the characters. All characters except days to first flowering and days to fifty per cent flowering showed significant differences among the families. Family 1 (P_1X P_7) was the best yielder for green fodder yield, dry matter yield, leaf fresh weight, stem fresh weight, leaf dry weight and stem dry weight. This was followed by family 3 (P_5 X P_7) and family 4 (P_5 X P_8).

The research confirmed the variability present in the germplasm for the fourteen characters studied. Cluster analysis elucidated that 61 per cent of divergence in the population was mainly due to leaf fresh weight, crude fibre content and stem dry weight. Greater GCA variance for plant height, number of primary branches plant^{-1}, number of leaves plant^{-1}, days to fifty per cent flowering, leaf area index, green fodder yield plant^{-1}, dry matter yield plant^{-1}, leaf fresh weight plant^{-1}, stem fresh weight plant^{-1}, leaf dry weight plant^{-1}, stem dry weight plant^{-1}and crude fibre content indicated predominance of additive gene action.

IC-97767, IT-38956-1, IT-37154999-38 and Pant Lobia-2 were good general combiners for yield. IC-1061, IC-97767, IT-37154999-38 and Pant Lobia-2 were good general combiners for crude fibre content. P_1X P_7, P_2XP_7, P_5X P_7 and P_5X P_8 were superior hybrids with high yield and quality parameters. CO-8 X IT-37154999-38 (P_1X P_7) produced the best progenies for the desired green fodder yield, leaf fresh weight, leaf dry weight, stem dry weight and dry fodder yield.

Superior F_2 progenies identified in $P_1 \times P_7$, $P_2 \times P_7$, $P_5 \times P_7 \times P_8$ families could be carry forward to F_6 and superior varieties could be identified.

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GENETIC ANALYSIS OF YIELD AND QUALITY IN

FODDER COWPEA

(*Vigna unguiculata* (L.) Walp)

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ABSTRACT

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ABSTRACT

In the present study, "genetic analysis of yield and quality in fodder cowpea (*Vigna unguiculata* (L.) Walp)", evaluation of different fodder cowpea accessions were done to assess the variability in the available population to identify the good performers for forage yield and quality. Based on the morphological and molecular characterization superior parents were selected for crop improvement through hybridization to develop superior cross combinations. The salient features of the study are discussed below.

Significant variation was observed for all the fourteen characters studied. the range of mean values observed refers to the phenotypic and genotypic variability present in the base population. High genotypic and phenotypic coefficient of variation was observed for number of primary branches plant^{-1}, number of leaves plant^{-1}, leaf area index, green fodder yield plant^{-1}, dry matter yield plant^{-1}, leaf fresh weight plant^{-1}, stem fresh weight plant^{-1}, leaf dry weight plant^{-1}, stem dry weight plant^{-1} and crude fiber content. High heritability and genetic advance for crude fiber content, crude protein content, leaf area index, leaf dry weight plant^{-1}, dry matter yield plant^{-1}, stem dry weight plant^{-1}, number of leaves plant^{-1}, stem dry weight plant^{-1}, number of leaves plant^{-1}, stem fresh weight plant^{-1}, leaf fresh weight plant^{-1} and green fodder yield plant^{-1}.

Green fodder yield and dry matter yield had significant positive phenotypic and genotypic correlation with leaf fresh weight plant^{-1}, followed by stem fresh weight plant^{-1}, stem dry weight plant^{-1}, dry matter yield plant^{-1}, leaf dry matter plant^{-1}, number of primary branches plant^{-1} and number of leaves plant^{-1}.

The thirty fodder cowpea genotypes were grouped into eleven clusters. Maximum contribution to divergence was shown by leaf fresh weight plant^{-1} followed by crude fibre content, stem dry weight plant^{-1}, leaf area index, dry matter yield plant^{-1}, number of leaves plant^{-1}, crude protein content and green fodder yield plant^{-1}.

Selection index was highest for IT-37154999-38 and least for IC-202804. The genotypes were ranked for characters green fodder yield, crude protein content, crude fibre content and selection index. Based on this and maximum inter cluster distance eight genotypes CO-8, MFC-09-1, IC-1061, IC-39916, IC-97767, IC-38956-1, IT-37154999-38 and Pant Lobia-2 were selected for further hybridization programmes.

Molecular characterization revealed two clusters (I and II) with 0.34 per cent similarity. The statistical cluster diagram from D^2 value and dendrogram from molecular characterization were not similar. But the eight parents selected had considerable difference in dendrogram with minimum difference between parents IT-38956-1 and IT-37154999-38.

Diallel analysis is one of the techniques used to find the genetic makeup. *Gca* variance was greater than *sca* variance, for all characters except for days to first flowering and crude protein content, indicating predominance of additive gene action for most of the characters. Days to first flowering and crude protein content had non-additive gene action.

Presence of heterosis also shows the ability of the parents to combine well in a hybridization programme. Superior expression of F_1 may be due to fixable (additive) type of gene action and non-additive type of gene action. Thus combining ability and heterosis helps in identifying desirable cross combinations.

Twenty eight hybrids from eight parent were evaluated for combining ability in diallel mating design without reciprocals. Relative heterosis and heterobeltiosis were calculated for different traits.

Gca variance was greater than *sca* variance, indicating predominance of additive gene action. P_4, P_5 and P_6 were good general combiners among eight parents for plant height. *Gca* variance was greater than *sca* variance, indicating predominance of additive gene action in green fodder yield and dry matter yield. P_5, P_6, P_7 and P_8 were good general combiners for green fodder yield, dry matter yield, leaf fresh weight, stem fresh weight, crude protein content and crude fibre content. Nineteen of the hybrids were good specific combiners for

green fodder yield. Seventeen hybrids were good specific combiners for lower crude fibre content.

$P_1 \times P_7$, $P_2 \times P_7$, $P_5 \times P_7$ and $P_5 \times P_8$ were selected based on high green fodder yield, dry matter yield, high protein content and low fibre content for raising F_2 population. F_2 families of these four hybrids exhibited differences among the progenies for different characters studied. Progenies of hybrid $P_1 \times P_7$ was identified as the best superior cross combinant useful for further improvement for superior variety development.