VARIABILITY ANALYSIS IN FODDER HORSE GRAM (*Macrotyloma uniflorum* (Lam.) Verdc.)

by

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(2017-11-051)

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DECLARATION

I, hereby declare that this thesis entitled **"Variability analysis in fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.)"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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CERTIFICATE

Certified that this thesis entitled **"Variability analysis in fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) "** is a record of research work done independently by **Ms. Christy George (2017-11-051)** 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 him.

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Per cent
CD	Critical Difference
cm	Centimetre
RBD	Randomised Block Design
DAS	Days After Sowing
^{0}C	Degree Celsius
et al.	And others
Fig.	Figure
g	Gram
g^{-1}	Per gram
Kg	Kilo gram
ha^{-1}	Per hectare
KAU	Kerala Agricultural University
t ha^{-1}	Tonne per hectare
kg ha^{-1}	Kilogram per hectare
Plant^{-1}	Per plant
Day^{-1}	Per day
via	Through
No.	Number
cv	Cultivar
Sl.	Serial

sp. or spp.	Species (Singular and Plural)
LAI	Leaf Area Index
viz.	Namely
i.e	that is
d.f	Degrees of freedom
S. E	Standard Error
kg ha^{-1} day^{-1}	Kilogram per hectare per day
PCV	Phenotypic Coefficient of Variation
GCV	Genotypic Coefficient of Variation
ANOVA	Analysis of Variance
&	and
GA	Genetic Advance
NBPGR	National Bureau of Plant Genetic Resources

INTRODUCTION

1. INTRODUCTION

Livestock production is the mainstay of Indian agriculture donating 4 per cent to national GDP and in addition is the source of employment and means of support for 70 per cent of the population in the rural areas. The contribution of livestock to agriculture sector has been steadily increasing. With an increase in the livestock population, there is an increase in the feed requirement. Presently there is a tremendous pressure of livestock on the available total feed and fodder, which has to be met from either increasing the productivity, utilizing untapped feed resources, increasing land area or through imports. Genetic resource improvement in crops was limited to cultivated crops over many decades. Hence, there arises the need for development of nutritious high yielding cultivars of fodder crops that are tolerant to biotic and abiotic stresses, with the help of conventional and biotechnological tools. Urbanization has led to an upsurge in demand of livestock products by bringing a noticeable shift in feeding habits of public towards milk, meat and eggs. There is no shortcut to sustain livestock husbandry, without focusing the issues related to the development of fodder and feed resources in the country. Presently, the country faces a shortage of 35.6 per cent green fodder, 10.95 per cent dry crop residues and 44 per cent concentrate feed ingredients. The requirements of green and dry fodder will reach to 1012 and 631 million tonnes by the year 2050 (IGFRI, 2015). At the current rate of growth in forage resources, there will be an 18.4 per cent deficit of green fodder and 13.2 per cent deficit in dry fodder by the year 2050. To meet out the deficit, green forage supply has to grow at 1.69 per cent annually (IGFRI, 2015). The only solution for connecting the gap between the demand and supply of green fodder lies in maximizing the fodder production over space and time. This can be done by identifying new forage resources and also by increasing the fodder production within the existing farming system. Cereals are widely used in the livestock nutrition as they have high dry matter production and are of low cost. But due to the poor protein content, their nutritive value is very low. Leguminous fodder crops are known for their quality, providing supplementary proteins,

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phosphorus, iron and certain water-soluble vitamins (Singh *et al.,* 2002, Pareek and Chandra, 2003). They are given to the livestock in addition to the bulk forages, usually in minute quantities. They can be used either to compensate for poor quality bulk forages or they can be used as substitutes for concentrates.

Horse gram (*Macrotyloma uniflorum*) is a short duration leguminous minor crop which can be grown as grain pulse and fodder. It is a drought tolerant crop which originated in the peninsular India (Bogdan, 1977). Horse gram provides high quality protein rich diet. The fodder is protein rich and widely used as a feed to milk producing animals and horses (Prakash *et al,* 2008). Horse gram also has high nitrogen fixation ability and improves soil fertility and soil conservation (Yadav, 2004). Horse gram is a self-fertilized cleistogamous short day plant with diploid chromosome number 2n = 20, 22, 24 (Cook *et al.,* 2005). Horse gram is a minor legume, which provides high quality inexpensive protein to diets based on cereal or starchy food. It is said to be the poor man's pulse and is eaten both as boiled and fried. Nutritionally horse gram contains about 23 per cent protein and richer in lysine content when compared to arhar and chickpea. Horse gram is a drought resistant crop that will be suitable for the changing climatic conditions. Though the crop has different desirable characteristics, being a minor leguminous crop very little scientific research has been carried out for the improvement of the crop. Owing to its medicinal importance and its capability to thrive under drought-like conditions, the US National Academy of Sciences has identified this legume as a potential food source for the future (National Academy of Sciences, 1979). Horse gram is used as an annual pulse and forage crop in India where it is grown as a dryland wet season crop in areas receiving less rainfall and in areas receiving high rainfall it is grown as a dry season crop. When grown as a fodder, horse gram yields around 5-12 t ha $^{-1}$ (Purseglove, 1974).

In Kerala, only 40 per cent of green and dry fodder requirement is roughly met from the available feed resources (NDDB, 2016). To narrow the demand supply gap in feed and fodder, genetic improvement of fodder crops with regard to high yield and quality is essential. Many fodder crops are under-utilized and their cultivation is reduced due to the fluctuant performance of diverse varieties. Being a promising fodder legume with ample advantages, horse gram demands genetic improvement in terms of productivity. Hence the present investigation of evaluating horse gram germplasm accessions was conducted to identify promising accessions for utilizing them in future crop improvement programmes. In this perspective, the present investigation was conducted to evaluate different fodder horse gram genotypes for yield, quality and multicut ability.

The main objective of this study was

- To identify genotypes of *Macrotyloma uniflorum* with high fodder yield, quality and multicut ability.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Horse gram (*Macrotyloma uniflorum)* is an under-utilized potential crop native to the Indian subcontinent. The plant has innumerable uses like vegetable, grain, fodder and also medicinal value. Being a member of Fabaceae family, it enriches the soil with nitrogen and thus improves the soil quality. It is a drought tolerant crop suitable for adverse soil conditions. The name *Macrotyloma* is derived from the Greek words *makros* meaning large, *tylos* meaning knob and *loma* meaning margin, in reference to the knobby statures on the pods (Blumenthal and Staples, 1993).

Initially horse gram was included in the genus *Dolichos* by Linnaeus. Verdcourt (1971) reorganized the different species under *Dolichos* and horse gram was assigned the genus *Macrotyloma.* The style, standard and pollen characteristics differentiate *Macrotyloma* from *Dolichos* (Verdcourt, 1971). Most of the wild species of the genus are restricted to Africa but some wild species have also been reported in Asia and Australia. *M. uniflorum* is the one cultivated species grown in the Indian subcontinent. The horse gram plant belongs to the kingdom Plantae, subkingdom *Tracheobionta*, division *Magnoliophyta* and class *Magnoliopsida*.

It is a diploid plant containing chromosome number 2n = 2x = 20. It is grown in India, Myanmar, Nepal, Mauritius and Sri Lanka for food purpose and primarily grown for fodder purpose in Australia and Africa (Asha *et al.,* 2006).

The US National Academy of Sciences has identified horse gram as a potential food source for the future, owing to its medicinal importance and capability to thrive in drought like conditions (National Academy of Sciences, 1979).

Though wild members of *M. uniflorum* exist in both Africa and India (Verdcourt, 1971), its centre of origin as cultivated plant is regarded as India (Purseglove, 1974; Vavilov, 1951; Zohary, 1970). Arora and Chandel (1972) have been more specific in arguing that the primary centre of origin and use of *M. uniflorum* var. *uniflorum* as a cultivated plant is southwestern India.

Selection of superior genotypes from a genetically diverse group is worked out with certain parameters such as variability, correlation, heritability, genetic advance, selection index and path analysis.

2.1 GROWTH, YIELD AND QUALITY ATTRIBUTES OF HORSE GRAM

2.1.1 Biometric Observations

In an evaluation and diversity study of horse gram germplasm found in Andhra Pradesh, a mean plant height of 97.7 cm was reported while the maximum plant height was recorded in IC426577 (131.6 cm) and the minimum plant height occurred in accession IC426550 (65.4 cm) (Neelam *et al.*, 2014). In a variability study conducted by Gumatad, (2014), among 100 genotypes of fodder cowpea, the mean plant height ranged from 27.5 cm to 50.33 cm.

In a study carried out with ricebean in Shillongani region of Assam, a maximum plant height of 77 cm (RBL-3) was recorded (Borah, 1994). In a study conducted in Sunabeda region of Orissa, a maximum plant height of 45.4 cm was recorded in ricebean (Mohapatra, 1998). Ricebean varieties collected and evaluated from the Nagaland region reported a maximum plant height of 32.23 cm (RBL-7) (Seyie *et al.*, 2006). In a study conducted with fodder field bean sown at different intervals, a maximum plant height of 134.5 cm was recorded (Yusufali *et al.*,2007). A maximum plant height of 148 cm (JRB-17) was observed for ricebean during the varietal trials conducted by AICRP on Forage Crops (2013). In fodder cowpea, Taipodia and Nabam (2013) recorded a maximum plant height of 153.8 cm. A maximum plant height of 135 cm was observed for for ricebean variety Bidhan-2 during a varietal evaluation study of AICRP on Forage Crops (2015).

In genetic analysis of fodder yield and its contributing traits in fodder cowpea, the number of branches per plant varied from maximum of 6.67 in MFC-09-6 to 3.50 in EC-458402. The genotypes PHG-9 and VLG-10 recorded an average number of 6.1 branches per plant (Gumatad, 2014). In horse gram, the number of primary branches ranged from 4.8 (IC426547) to 8.9 (IC426569) with a mean of 6.4. Among the controls, Palem-2 produced the maximum number of primary branches (4.0). (Neelam *et al.*, 2014).

In genetic analysis of fodder yield and its contributing traits in fodder cowpea, the number of leaves per plant varied from 55.00 (MFC-09-6) to 46.83 (MFC-09-17) (Gumatad, 2014).

A maximum leaf stem ratio of 2.11 was recorded in JC-1 fodder cowpea variety by Singh *et al.* (1979). In fodder ricebean a higher leaf stem ratio of 0.80 was noted in Bidhan-1 variety (AICRP on Forage Crops, 2003). The varietal evaluation trial directed by AICRP on Forage Crops (2013), revealed that a maximum leaf stem ratio of 0.80 was observed for fodder ricebean variety JRB-17. In genetic analysis of fodder yield and its contributing traits in fodder cowpea, leaf stem ratio ranging from 1.38 to 0.44 was reported by Gumatad (2014). Bidhan-2 ricebean variety recorded a leaf stem ratio of 0.87 (AICRP on Forage Crops, 2015). KBR-1 variety of ricebean recorded the highest leaf to stem ratio (0.81) and the varieties Bidhan-2 and Bidhan-1 had lower leaf stem ratio of 0.53 (Aswathi, 2016).

2.1.2 Physiological Characters

Dry matter production of 50.10 q ha $^{-1}$ was reported in the study entitled performance of different varieties of fodder cowpea in semi-arid region of Rajasthan (Singh *et al.*, 1979). Similar results of dry matter accumulation of 63.32 g plant $^{-1}$ was reported by Taipodia and Nabam (2013) in the study, impact of time of sowing, spacing and seed rate on potential seed production and fodder quality of cowpea. In genetic analysis of fodder yield and its contributing traits in fodder cowpea, dry matter production ranged from 69.5 g to 40.28 g (Gumatad, 2014).

Leaf stem ratio of 2.11 was recorded in JC-1 variety of fodder cowpea in a variability study by Singh *et al.* (1979). In fodder cowpea, leaf area index of 2.09 was recorded by Kurubetta (2006). In field bean a leaf area index of 7.20 was observed by Yusufali *et al.* (2007) and leaf area index of 2.19 was observed by Taipodia and Nabam (2013) in fodder cowpea. A leaf area index of 4.04 was recorded for fodder ricebean (Aswathi, 2016).

2.1.3. Yield Attributes

Fodder cowpea variety UPC-9020 recorded a maximum green fodder yield of 273.58 q ha $^{-1}$ (Singh *et al.,* 1979). Ricebean variety KRB-7 recorded a maximum green fodder yield of 259.8 q ha $^{-1}$ in field trials conducted by AICRP on Forage Crops (2006). In the study genetic analysis of fodder yield and its donating traits in fodder cowpea, the green fodder yield ranged from 235.11g to 157 g while the dry fodder yield ranged from 67.3 g to 42.46 g (Gumatad, 2014). In fodder ricebean KBR-1 recorded a high green fodder yield of 11.3 t ha $^{-1}$ (Aswathi, 2016).

2.1.4 Quality Parameters

Determination of crude protein in the feed is important as the feeds are classified according to the protein content. The proteins are mainly used for the production of lean meat and for replacing the physiological losses of protein from the body. The raw protein is required to supply the proteins in milk, wool and egg production in animals (Ranjhan, 1991).

When the protein content is high, the crude fibre content is usually low and in turn the digestibility of the fodder will be higher. Higher digestible fodder would give more digestible energy (Ranjhan, 1977). The crude protein content in fodder cowpea was 18.98 per cent in the variety MPKV-1 as reported by Singh *et al.* (1979). The crude protein content in KHRB-1 variety of rice bean was reported to be 14.30 per cent (Rudragouda and Angadi, 2002). The crude protein content was found to decrease as the harvest interval increased in napier grass (Mohammed *et al*., 1988). A decrease in crude protein content with increase in cutting intervals of *Pennisetum purpureum* was reported by Man and Wiktorsson (2003).

Crude protein percentage and crude protein yield reduced during the second cut in ratoon sorghum. The first cut was having more nutritive value in sorghum (Gill *et al.,* 1988). Similarly, Joon *et al.* (1993) also reported that the crude protein content and crude protein yield decreased during the subsequent cuts in fodder sorghum.

Crude fibre is that fraction of the total carbohydrates which is not digested after successive boiling with dilute acid and dilute alkali. Crude fibre consists of cellulose, hemicelluloses, pentosans and small fractions of lignin (Ranjhan, 1977). P-259 variety of fodder cowpea recorded a higher crude fibre content (19.63 %) (Hussain and Hussain, 1985). Crude fibre content was found to increase with the increasing cutting intervals in bajra napier hybrid (Pathan *et al.,* 2014).

A multicut fodder crop should be one that have high fodder yield along with supplying nutritious fodder regularly with a stable performance. The green fodder from a single cut crop is available only for short duration. A multicut crop will provide the green fodder required over a longer period. This eases the availability of green fodder and also reduces the cost required for land preparation and reseeding.

In grain sorghum, Duncan and Moss (1987) observed that the characters plant height, number of days to flowering and grain yield recorded lower values as compared to the base crop. In multicut sorghum, Gill *et al.* (1988) observed that the green fodder yield, dry fodder yield, crude protein content and crude protein yield were having higher values during the first cut. A reduction in the values were observed for these characters during the second cut. Main crop sorghum was having higher fodder yield when compared to the ratoon crop (Girija and Natarajaratnam, 1996). The successive

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cuts in fodder sorghum resulted in reduced green fodder yield and dry fodder yield (Joon *et al.,* 1993).

The Cumbu napier grass when studied for ratooning ability exhibited an unequal bimodal nature with respect to the characters plant height and number of tillers. The green fodder yield was also showing a decreasing trend as the number of cuts increased (Ramasamy *et al.,* 1993).

An increase in plant height, number of tillers and fodder yield in ratoon crop of sorghum was observed by Pal and Kaushik (1969). According to the studies of Rao and Damodaram (1971), plant height, leaf number and leaf length increased in the ratoon crop. The characters plant height, number of tillers and number of leaves had higher values during the second cut crop as compared to the first cut (Pathak and Sanghi, 1983).

2.2 GENETIC PARAETERS

2.2.1 Variability

The success of crop improvement programmes depends on the estimation and utilization of diversity present in a population. Coefficients of variation is the genetic parameter which gives an efficient estimation of the variability present in the population. The components of variation measures the genetic variability present in a population. The success of any crop improvement programme largely depends on the wide range of variability present in the population.

In horse gram, Ramakrishnan *et al.* (1979) observed high genotypic coefficient of variation for plant height. In a study conducted with 18 cultivars of cowpea significant difference was observed for characters like plant height, number of leaves, number of branches and dry matter production (Pal, 1988). Genetic variability study among 40 genotypes oh hedge Lucerne (Shanthi, 1995) revealed that maximum plant height was observed in the initial cutting. The genotypes showed a reduction in the plant height in the second cutting. Similarly, the green fodder yield was also observed to decrease in the second cut than in the initial cut. However, characters like number of branches, leaf stem ratio, crude protein and crude fibre was found to increase linearly in the second cut than in the first cut.

Ishrath (2016) conducted a study on cutting intervals and additives for quality silage production using hybrid Bajra Napier variety Suguna. The cutting interval 75 days recorded highest green fodder yield. The highest crude protein (10.56%) and the lowest crude fibre content (26.81%) were observed for 45 days cutting interval

Genetic variability study conducted by Sreekantaradhya *et al.* (1975), considering seven characters in 48 genotypes of horse gram suggested the presence of wide variability in the population studied. High heritability was shown by the character number of branches and plant height showed moderate heritability. In a study conducted with 15 horse gram genotypes, high genetic variation was observed for plant height (Suraiya *et al.*,1988). In a study conducted with 18 horse gram genotypes characters plant height and number of branches plant $^{-1}$ recorded maximum GCV.

Kumar and Mishra (1983) reported that for green fodder yield and dry matter yield environmental coefficient of variation was more than the genotypic variances. Genetic variability studies in 35 genotypes of cowpea revealed maximum genotypic coefficient of variation for characters such as plant height, dry matter yield and green forage yield (Sharma *et al.,* 1988). Roquib and Patnaik (1990) reported high phenotypic and genotypic variances for plant height and green fodder yield in fodder cowpea. High genotypic and phenotypic coefficient of variation was observed for plant height in cowpea (Siddique and Gupta, 1991). In a study conducted by Thaware *et al. (*1992) in 30 varieties of fodder cowpea, significant variation was reported for green fodder yield and nutrient composition.

In a variability study conducted by Backiyarni and Natarajan (1996), 34 genotypes of cowpea were studied for ten yield attributing characters and leaf area index recorded high PCV and GCV. Hazra *et al. (*1996) observed significant variation in number of primary branches per plant in fodder cowpea. Srinivasan and Das (1996) based on their correlation study in fodder yield in cowpea suggested that the desirable plant type would be one having tall stature, larger leaves and high protein content. Based on the variability studies in fodder cowpea by Manonmani *et al*. (2000) the green fodder yield had the highest PCV and GCV.

Variability studies conducted in 60 genotypes of fodder cowpea revealed that the genotypes varied significantly for all the characters studied. High heritability and genetic advance was recorded for characters number of branches per plant, number of leaves per plant, dry weight of leaves, dry weight of stem, dry matter yield and plant height. This indicates that these traits are controlled by additive genetic effects and serves as a better source population for developing high yielding varieties (Malarvizhi *et al.,* 2005).

High estimates of GCV and PCV were observed for leaf weight, number of leaves plant $^{-1}$, number of branches plant $^{-1}$, dry matter yield and green fodder yield suggesting that selection based on these characters would facilitate successful segregation of desirable types in cluster bean (Kapoor, 2014).

2.2.2 Heritability and Genetic advance

High estimates of heritability and genetic advance were observed in cowpea for plant height by Sohoo *et al.* (1971). Solanki *et al.* (1975) reported high heritability and high genetic advance for plant height, number of branches per plant, number of leaves per plant and dry matter production per plant in cluster bean. In a study conducted with 50 genotypes of cowpea high broad sense heritability was estimated for plant height and branches per plant (Angadi, 1976). In fodder cowpea high heritability was reported for number of branches plant $^{-1}$ and dry matter production reported low heritability by Manoharan, (1978). Broad sense heritability of 21.3 and 34.6 was reported for dry matter and green forage yield in fodder cowpea (Yadav and Krishna, 1985). In fodder cowpea, Thaware *et al.* (1992) reported high heritability and genetic advance for green fodder yield and number of leaves plant $^{-1}$.

In fodder cowpea high heritability was observed for characters plant height, green fodder yield, dry matter and crude protein content by Sharma and Singhania (1992). In a variability study conducted by Kumar *et al.* (1997) in ricebean, high heritability and high genetic advance for plant height was reported. High heritability coupled with high genetic advance was observed in fodder cowpea for the characters, plant height, number of leaves, number of branches, dry matter yield and green fodder yield by Borah and Fazlullahkhan, (2000).

Plant height and number of branches plant $^{-1}$ showed high heritability and high genetic advance in a variability study conducted by Kumar and Sangwan (2000) in fodder cowpea. Genetic studies conducted in forage cowpea by Manonmani *et al.* (2000) reported high genetic advance for green fodder yield. High heritability coupled with high genetic advance was observed for characters green fodder yield and plant height while dry fodder yield had high heritability in fodder cowpea (Santhoshkumar *et al.*,2002).

Evaluation of 14 cowpea genotypes showed that green fodder yield had high genotypic and phenotypic coefficient of variation. Heritability coupled with high genetic advance was observed for characters plant height, number of branches and green fodder yield (Lohithaswa, 2009). In a variability study conducted with 25 genotypes of fodder cowpea, Singh *et al.* (2010) reported that characters plant height, dry matter yield and green forage yield had high genotypic and phenotypic coefficient of variation, heritability and genetic advance.

Genetic variability study in cowpea conducted using 44 genotypes showed that the characters green fodder yield plant $^{-1}$, dry fodder yield plant $^{-1}$ and number of branches plant $^{-1}$ had high estimates of genotypic and phenotypic coefficient of variation (Nath and Tajane, 2014). High heritability along with high genetic advance

(GA) was recorded for characters number of leaves per plant, number of branches, dry matter yield and green fodder yield in guar which indicated that selection would be rewarding for these characters (Kapoor, 2014).

2.3 SELECTION INDEX

The plant breeder has to give due consideration to the characters which are of economic importance while selecting a desirable plant from a segregating population. Selection index is one such method of selecting plants for crop improvement. It was proposed by Smith (1936). Selection index with the use of discriminant function was proposed by Fisher (1936). Selection for yield would be made more efficient if the component traits that make up the yield and the relationship between these characters is studied. This formed the basis for formulation of selection index.

Wu (1966) studied discriminant function in eleven characters of nine varieties of soybean. From the study it was concluded that while height of the plant was the best character for discriminating two varieties, the number of branches was the worst character. Discriminant function studies in 40 varieties of field pea by Singh and Singh (1972), reported that selection based on a certain combination of traits would be more effective than that based on a single trait. Discriminant function based on characters such as pods plant $^{-1}$, primary branches and seeds pod $^{-1}$ was best for selection of high yielding lines in soybean (Malhotra, 1973). Singh *et al.* (1976) studied 36 strains of black gram and reported that the relative efficiency of selection was highest when discriminant function was based on number of primary branches, number of clusters and grain yield per plant when compared to direct selection for yield. Singh *et al.* (1977) studied 53 lines of green gram and reported that an index based on number of primary branches plant $^{-1}$, number of clusters plant $^{-1}$, number of pods plant $^{-1}$ and number of seeds pod $^{-1}$ would be most efficient for yield improvement.

Discriminant function analysis carried out by Suraiya (1980) in fifteen varieties of horse gram for the construction of selection indices for seed yield using six different combinations revealed that index based on yield with number of seeds pod $^{-1}$ and another based on yield with pod length were equal in effect and more advantageous. To identify superior genotypes of yard long bean Resmi (1998), constructed a selection index based on characters, vine length, primary branches, petiole length, length and breadth of leaflets, days to flowering, pod length, pod girth, pod weight, pods inflorescence $^{-1}$, pods kilogram $^{-1}$, pods plant $^{-1}$ and yield.

Five superior genotypes were selected from 50 genotypes of cowpea by Philip (2004), for hybridization programme using selection index. Selection index was constructed based on nine characters having significant positive correlation with yield in cowpea to identify superior genotypes (Lovely, 2005). Similar findings were reported by Madhukumar (2006) in cowpea. Ranking of genotypes based on selection index was done by Manju (2006), in cowpea using ten characters.

In cowpea the characters vine length, days to first flowering, pod length, pod girth, pod weight, pods plant $^{-1}$ and yield plant $^{-1}$ where used for construction of selection index to identify top ranking genotypes (Sivakumar, 2012). As per Shanko *et al.* (2014) the characters yield plant $^{-1}$ and pods plant $^{-1}$ could be used could be used as selection index for improving cowpea genotypes. Litty (2015) identified suitable top-ranking accessions for polyhouse cultivation based on selection index values.

2.4 PATH ANALYSIS

Path coefficient is a standardized partial regression coefficient. The technique of path coefficient to plant breeding was first applied by Dewey and Lu (1959). They found that it permits a critical examination of specific forces acting to produce a particular correlation. This technique was utilized in the analysis of components of seed production in crested wheat grass (*Agropyron cristatum*). The total correlation coefficient was partitioned into their direct and indirect effects and assigned the value of path coefficients contributing to yield which gives a clearer picture of the complex association which is of value in selection programmes.

Path analysis done by Chopra and Singh (1977) in fodder cowpea recorded that the characters, leaf number, plant height and branch number had direct contribution towards fodder yield. Fodder yield in cowpea was found to have positive correlation with plant height, number of branches and protein content (Tyagi *et al.,* 1978). Green forage yield was positively and significantly correlated with plant height in fodder cowpea (Sharma *et al.* (1988).

Path coefficient analysis in fodder cowpea by Jindal (1989) reported that all the characters viz., plant height, leaf number, green fodder yield, leaf weight, stem weight, number of branches and stem girth were positively and significantly correlated among themselves. Ushakumari and Chandrasekharan (1991) reported that green fodder yield had positive and significant genotypic correlation with plant height, dry weight of leaf and stem and dry matter production. Dry matter production had the maximum genetic advance as per cent of mean. As per the correlation and path analysis studies conducted by Vasanthi and Das (1996), the selection criteria for green fodder yield was dry weight of leaf and dry weight of stem.

Correlation studies in fodder cowpea revealed that plant height, number of branches plant $^{-1}$, and dry fodder yield were positively correlated with green fodder yield. Path analysis showed that dry fodder yield had the highest direct positive contribution towards green fodder yield and was followed by other characters like leaf stem ratio, number of branches plant $^{-1}$ and plant height (Santhoshkumar *et al.,* 2002).

Twenty-five genotypes of cowpea were evaluated to study the genetic variability, trait relationship and path analysis between green fodder yield and its component traits and adequate variability was observed among the genotypes. High phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as per cent of mean were reported for plant height, stem weight, leaf weight, biological yield, dry matter yield and green fodder productivity which indicates the predominance of additive gene effects in controlling these characters. Green fodder yield was significantly and positively correlated with green fodder productivity, dry matter yield, biological yield, leaf weight and stem weight. Path coefficient analysis revealed that the stem weight had maximum and positive direct effect on green fodder yield at phenotypic and genotypic level followed by leaf weight and dry matter yield. Biological yield and dry matter per cent had negative direct effect on green fodder yield (Singh *et al.,* 2010).

Correlation and path analysis in cowpea based on morphological and fodder yield related character showed that plant types with higher biomass plant $^{-1}$, dry weight plant $^{-1}$, number of secondary branches and leaves plant $^{-1}$ would be effective for improving fodder yield in cowpea (Sahai *et al.,* 2013).

Traits like plant height, number of leaves plant $^{-1}$ and dry matter yield had positive and significant correlation at genotypic as well as phenotypic level with green fodder yield and selection based on these traits will result in improving the green fodder yield green fodder yield in guar. Most of the yield contributing traits like plant height, number of leaves plant $^{-1}$ and dry matter yield showed direct effect in green fodder yield (Kapoor, 2014).

Correlation studies in 44 genotypes of fodder cowpea revealed that the characters dry matter yield plant $^{-1}$, plant height, leaf stem ratio and number of leaves plant $^{-1}$ had positive significant correlation with green fodder yield. Path analysis indicated that dry matter yield plant $^{-1}$ and leaf stem ratio had positive direct effect on green fodder yield (Nath and Tajane, 2014).

Genetic divergence studies in ricebean revealed that green fodder yield plant $^{-1}$ was positively and significantly correlated with green fodder yield day $^{-1}$, number of leaves plant $^{-1}$, number of branches plant $^{-1}$, crude protein yield plant $^{-1}$, dry matter yield plant $^{-1}$, leaf stem ratio and plant height. Path analysis revealed that crude protein yield plant $^{-1}$, dry matter yield plant $^{-1}$, day $^{-1}$ and plant height are important traits contributing toward fodder yield (Kujur *et al.,* 2017).

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The present investigation on "Variability analysis in fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.)" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram during 2017- 2019 to identify horse gram accessions having high fodder yield, quality and multicut ability.

The details of materials used and methodologies adopted in the present study are described below.

3.1 EXPERIMENTAL SITE

The present work was carried out in College of Agriculture, Vellayani, situated at 8°5' N latitude and 76°9'E longitude and at an altitude of 29 m above mean sea level. Predominant soil type of the experimental site was red loam of Vellayani series, texturally classified as sandy clay loam.

3.2 EXPERIMENTAL DESIGN

The experiment was laid out in Randomized Block Design (RBD) with thirty treatments and three replications. The spacing of 30 cm x 25 cm with a plot size of 2.1 m^2 was followed in the field experiment. The list of 30 fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) accessions used in the study are presented in table 1.

3.3 CULTURAL OPERATIONS

The land was prepared thoroughly by digging and levelling. The seeds collected were soaked overnight and sown at a spacing of 30 cm between rows and 25 cm between plants within a row.

Table 1. List of fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) accessions used in the study.

Sl. No.	Treatment name	Accession name
1	T1	IC- 120785
2	T2	IC- 139364
3	T3	IC-139432
4	T4	IC-71808
5	T5	IC-22767
6	T6	IC-561040
7	T7	IC-22791
8	T8	IC-321300
9	T9	IC-22776
10	T10	IC-22757
11	T11	IC-71809
12	T12	IC-19446
13	T13	IC-71747
14	T14	IC-23437
15	T15	IC-56138
16	T16	IC-19444
17	T17	IC-344193
18	T18	IC-22765
19	T19	IC-88990
20	T20	IC-22794
21	T21	IC-89011
22	T22	IC-16172
23	T23	IC-16977
24	T24	IC-89012

Table 1. Continued

25	T25	IC-32875
26	T26	IC-121640
27	T27	IC-123022
28	T28	IC-15729
29	T29	IC-22771
30	T30	IC-89016

3.4 RECORDING OF OBSERVATIONS

Five plants per treatment were randomly selected from each replication and was tagged for taking the observations of different characters. The mean values of five plants were considered for statistical analysis. The observations were taken on the following characters during the first cut *i.e.* at 50 per cent flowering stage and then 55 days after the first cut.

3.4.1 Growth Characters (Biometric observations)

3.4.1.1 Plant Height

The height of the plant was measured from the base of the plant to the tip of the branch at the time of each harvest using measuring scale and their mean values was expressed in centimeter.

3.4.1.2 Number of Branches Plant^{-1}

The total number of branches arising from the main stem was counted at each harvest.

3.4.1.3 Number of Leaves Plant^{-1}

The total number of leaves produced in a plant was counted at each harvest.

3.4.1.4. Leaf Stem Ratio

The sample plants were cut at the base. The leaves and the stem were separated, shade dried and later oven dried for 5 days at $70^0 \pm 5^0$C till constant weight was obtained. The dry weight of leaves and stem of individual plants were recorded. The ratio was computed by dividing leaf dry weight by the stem dry weight.

Plate 1. Field view of the experiment

3.4.2. Physiological Characters

3.4.2.1. Dry Matter Production

During the seed maturation stage five observational plants from each replication were uprooted. Shoot, leaves and roots were separated and dried to a constant weight at 70^0C in a hot air oven. The sum of these individual components gave total dry matter production.

3.4.2.2. Leaf Area Index

The leaf area was measured from the observational plants of each plot. Representative leaves were collected and the leaf area was measured using a graph paper. The total leaf area was worked out using the leaf area of selected leaves and number of leaves per plant. The leaf area index (LAI) was calculated using the formula according to Watson (1952).

$$\text{LAI}=\frac{\text{Leaf area of the plant (cm}^2\text{)}}{\text{Ground area occupied (cm}^2\text{)}}$$

3.4.3. Yield Attributes

3.4.3.1. Green Fodder Yield

The crop was harvested at the cutting intervals. The fresh weight of the plants in each plot was recorded. The total green fodder yield was calculated and expressed in t ha^{-1}.

3.4.3.2. Dry Fodder Yield

The crop samples collected from each harvest were first shade dried and later oven dried at $70^0 \pm 5^0$C till the samples attained a constant weight. The weight of these dry samples was taken and total dry fodder yield was calculated and expressed in t ha^{-1}.

3.4.3.3. Production Efficiency

The crop was harvested at the cutting intervals. The fresh weight of the plants in each plot was recorded and expressed in t ha^{-1}. The yield thus obtained was then divided by the number of days on which the cuts were taken to calculate the production efficiency. This was expressed in t ha^{-1} day^{-1}.

$$Production\ Efficieny = \frac{Green\ fodder\ yield\ (t\ /ha)}{Number\ of\ days\ taken\ for\ harvesting}$$

3.4.4. Quality Aspects

3.4.4.1. Crude Protein Content

The crude protein content was calculated by multiplying the nitrogen content of the plant by the factor 6.25 (Simpson *et al.*, 1965) and expressed in percentage (%).

$$CP(\%) = \%N \times 6.25$$

3.4.4.2. Crude Fibre Content

The crude fibre content was determined by AOAC method (AOAC, 1975) and expressed in percentage (%).

3.4.4.3. Crude Protein Yield (t ha^{-1})

Crude protein yield was calculated by multiplying the crude protein content with the yield of the respective genotype expressed in t ha^{-1}.

$$Crude\ protein\ yield\ = Crude\ protein\ \times Dry\ fodder\ yield$$

3.5 STATISTICAL ANALYSIS

The data recorded on different traits were subjected to the following statistical analysis.

1. Analysis of Variance
2. Heritability and Genetic Advance
3. Selection index
4. Path analysis

3.5.1 Analysis of Variance

3.5.1.1 *Analysis in Randomized Block Design (RBD)*

The Randomized Block Design (RBD) was adopted with three replications. As per the method outlined by Panse and Sukhatme (1985) the analysis of variance was carried out.

$$Y_{ij} = m + g_i + r_j + e_{ij}$$

Where, Y_{ij} = Phenotypic observation of i^{th} genotype in j^{th} replication

m = General mean

g_i = True effect of i^{th} genotype

r_j = True effect of j^{th} replication

e_{ij} = Random error associated with i^{th} genotype and j^{th} replication

For each character Analysis of Variance (ANOVA) was carried out as indicated below:

Source of variation	**d.f.**	**SS**	**MSS**	**F-ratio**
Replications	r-1	RSS	M_{sr}	M_{sr} / M_e
Genotypes	t-1	TSS	M_{st}	M_{st} / M_e
Error	(r-1) (t-1)	ESS	M_{se}	
Total	rt-1			

Where,

r = Number of replications

t = Number of treatments (genotypes)

M_{sr} = Mean sum of squares of replications

M_{st} = Mean sum of squares of treatments

M_{se} = Mean sum of squares of error

d.f = Degrees of freedom

The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' test (Fisher and Yates, 1967).

Standard Error Mean (SE(m)) = $(M_{se}/r)^{1/2}$

Where,

M_{se} = Error mean of squares

r = Number of replications

Critical Difference, C.D = S.E (d) x t

Where,

$S.E\ (d) = (2\ M_{se}/r)^{1/2}$

't' = t Table value at error degrees of freedom

$C.V = (S.D/\overline{X}) \times 100$

Where, S.D = Standard deviation of the population

$\overline{X}$ = Population mean

3.5.2 Estimation of Genetic Parameters

3.5.2 a. *Genetic Components of Variance*

Phenotypic and genotypic components of variance were estimated for each character by equating expected value of mean squares (MS) to the respective variance components (Jain, 1975).

Genotypic Variance (V_G) $V_G = \frac{Mst-Mse}{r}$

Environmental Variance (V_E) $V_E = Mse$

Phenotypic Variance (V_P) $V_P = V_{G+}\ V_E$

3.5.2 b. *Coefficient of Variation*

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

i. Genotypic Coefficient of Variation, GCV = $\frac{\sqrt{VG}}{X} \times 100$

ii. Phenotypic Coefficient of Variation, PCV = $\frac{\sqrt{VP}}{X} \times 100$

iii. Environmental coefficient of variation, ECV = $\frac{\sqrt{VE}}{X} \times 100$

Where, $\bar{X}$ = Grand mean

Sivasubrahmanian and Menon (1973) reported following categories for the range of variation.

High: > 20 percent

Medium: 10-20 percent

Low: < 10 percent

3.5.2.c. Broad Sense Heritability

Ratio of genotypic variance t the total observed variance in the population and character expressed in percentage.

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

Range of Heritability estimation (Johnson *et al.,* 1955)

High: > 60 percent

Medium: 30-60 percent

Low: < 30 percent

3.5.2.d Genetic Advance

The expected genetic gain or improvement in the next generation by selecting superior genotype under certain amount of selection pressure. Genetic Advance estimated by using Burton (1952) formula.

$GA = KH^2\sqrt{VP}$

Where K = selection differential

At 5% selection intensity K = 2.06

H^2 = Heritability

V_P = Phenotypic variance

3.5.2.e. Genetic Advance as Percent of Mean

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

GA = Genetic Advance

X = Grand Mean

Ranges of Genetic advance by Johnson *et al*., (1955).

High: > 20 percent

Medium: 10-20 percent

Low: < 10 percent

3.5.3. Estimation of Correlation

Degree and direction of association between two variables refers the correlation. Genotypic and phenotypic correlations were calculated by using Falconer (1960) formula.

Genotypic coefficient of correlation (r_g) = $r(X_i.X_j)_g = \frac{Cov((xi.xj)g}{\sqrt{v(xi)g.v(xj)g}}$

Phenotypic coefficient of correlation (r_p) = $r(X_i.X_j)_p = \frac{Cov((xi.xj)p}{\sqrt{v(xi)p.v(xj)p}}$

Error coefficient of correlation (r_e) = $r(X_i.X_j)_e = \frac{Cov((xi.xj)e}{\sqrt{v(xi)e.v(xj)e}}$

3.5.4. Selection Index

Selection index was first proposed by Smith (1936) based on the "discriminant function" of Fischer (1936). Hazel (1943) also developed a method of index selection based on the path coefficients. The aim of most breeding programmes is simultaneous improvement of several characters. It has been recognized that most rapid improvement in the economic value is expected from selection applied simultaneously to all the characters which determine the economic value of a plant, appropriate weights are assigned to each character according to their relative economic importance. The selection index was used to discriminate the genotypes based on different characters.

The selection index is described by the function,

$$I = b_1x_1+b_2x_2+\cdots+b_nx_n$$

and the merit of a plant is described by the function,

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

Where, $x_1,x_2\ldots\ldots x_n$ are the phenotypic values, $G_1,G_2\ldots..G_n$ are the genotypic values of the plants with respect to characters $x_1,x_2\ldots\ldots\ldots x_n$. H is the genetic worth of the plant.

It is assumed that the economic weight assigned to each character is equal to unity *i.e.,* $a_1,a_2,a_3\ldots\ldots\ldots a_n = 1$.

The regression coefficients (b_i) are determined such that the correlation between H and I is maximum. The procedure will reduce to an equation of the form, $b= P^{-1}Ga$ where, P is the phenotypic variance-covariance matrix and G is the genotypic variance-covariance matrix.

3.5.5 Path Coefficient Analysis

It is a standardized partial regression coefficient which separates the correlation coefficients into direct and indirect effects (Dewey and Lu, 1959).

$r_{1y} = P_{1y}\, r_{11}+P_{2y}r_{12}+P_{3y}r_{13}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots+P_{ny}r_{1n}$

$r_{2y} = P_{2y}\, r_{21}+P_{2y}r_{22}+P_{3y}r_{23}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots+P_{ny}r_{2n}$

$r_{ny} = P_{1y}\, r_{n1}+P_{2y}r_{n2}+P_{3y}r_{n3}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots+P_{ny}r_{nn}$

Where,

1,2………….n =independent variables

y = dependent variable

r_{1y}, r_{2y}………r_{ny} =coefficient of correlation between independent variables 1 to n on dependent variable y.

P_{1y}, P_{2y}…….P_{ny} =direct effect of character 1 to n on character y.

The above equation can be written in matrix form

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ \cdot \\ r_{ny} \end{bmatrix} \qquad \begin{bmatrix} 1 & r_{12} & r_{13} & \cdot & \cdot & r_{1n} \\ r_{21} & 1 & r_{23} & \cdot & \cdot & r_{2n} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ r_{n1} & r_{n2} & r_{n3} & \cdot & \cdot & 1 \end{bmatrix} \qquad \begin{bmatrix} P_{1y} \\ P_{2y} \\ \cdot \\ \cdot \\ \cdot \\ P_{ny} \end{bmatrix}$$

Then B=C^{-1}A where C^{-1}= $\begin{bmatrix} C_{11} & C_{12} & C_{13} & . & . & C_{1n} \\ C_{21} & C_{22} & C_{23} & . & . & C_{2n} \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ C_{n1} & C_{n2} & C_{n3} & . & . & C_{nn} \end{bmatrix}$

Direct effects:

$P_{1y} = \sum_{i=1}^{k} c_{1i}\, r_{iy}$

$P_{2y} = \sum_{i=1}^{k} c_{2i} r_{iy}$

$P_{ny} = \sum_{i=1}^{k} c_{ni} r_{iy}$

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

Where,$r^2 = (P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y} \dots\dots\dots\dots\dots\dots\dots\dots + P_{ny}r_{ny})$

P_{iy} = direct effect of X_i on y

r_{iy} = correlation coefficient of X_i on y

i = 1,2,3…..n

RESULTS

4. RESULTS

The present study was conducted to analyze variability in horse gram genotypes (*Macrotyloma uniflorum* Lam. Verdc.) in College of Agriculture, Vellayani with an objective to identify genotypes with good fodder yield, quality and multicut ability. The results obtained from the study are presented below under the following titles.

1. Analysis of variance
2. Mean performance
3. Selection index
4. Path analysis

4.1. ANALYSIS OF VARIANCE

Analysis of variance was done for the traits to test the significance of the differences among the genotypes and the ANOVA is presented in Table 2. It was observed that the ratio was significant for all the traits, even at 0.01 level, indicating that there were significant inherent differences among the genotypes for all the traits.

4.2. MEAN PERFORMANCE

The crop was cut at 50 per cent flowering stage. Then the plants were allowed to regrow and later the second cut was taken. Observations were recorded for all the characters. The mean performance of horse gram genotypes for different parameters of growth, yield, quality and physiological characters were recorded and presented below.

4.2.1 Biometric Observations

The mean performance of biometric characters of fodder horse gram genotypes recorded during the first cut are presented in the Table 3.

4.2.1.1 Plant Height

The plant height showed significant difference in all the genotypes. The genotype T6 recorded the maximum (144.67 cm) plant height. This was followed by

Table 2. Analysis of variance (mean square) for fodder horse gram accessions during the first cut

Source of variation	Replication	Genotype	Error	F calculated	F critical
Df	2	29	58		
Plant height	26.105	729.723	24.745	29.490	1.663
Number of branches plant^{-1}	0.081	1.245	0.102	12.207	1.663
Number of leaves plant^{-1}	20.537	645.936	3.976	162.442	1.663
Leaf stem ratio	0.146	0.013	0.005	2.486	1.663
Leaf area index	0.068	3.235	0.010	329.816	1.663
Green fodder yield	2.985	12.329	0.408	30.218	1.663
Dry fodder yield	0.590	0.224	0.012	18.907	1.663
Production efficiency	0.000	0.003	0.000	68.250	1.663
Crude protein content	0.003	18.360	0.117	156.591	1.663
Crude fibre content	0.021	17.542	0.080	219.261	1.663
Crude protein yield	0.029	0.022	0.001	32.100	1.663

Table 3. Mean performance of biometric characters for first cut of fodder horse gram accessions

Sl. No.	**Genotypes**	**Plant height (cm)**	**Number of branches per plant**	**Number of leaves per plant**	**Leaf stem ratio**	**Leaf area index**
1	T1	82.93	4.93	54.73	0.85	1.28
2	T2	89.53	5.80	59.07	0.99	2.10
3	T3	99.73	4.80	24.53	0.83	0.55
4	T4	91.27	4.47	50.00	0.95	1.21
5	T5	83.00	4.47	58.67	0.88	1.73
6	T6	144.67	6.60	73.67	0.95	4.30
7	T7	80.40	5.33	54.47	0.84	1.06
8	T8	102.87	6.00	57.67	0.99	1.72
9	T9	114.53	5.73	40.00	0.96	1.87
10	T10	90.13	6.07	52.67	0.95	1.87
11	T11	110.53	6.27	53.60	0.83	3.51
12	T12	100.93	5.20	50.40	0.95	3.74
13	T13	80.67	5.20	48.13	0.94	1.70
14	T14	85.33	5.73	40.20	0.89	1.47
15	T15	102.33	5.60	58.40	0.91	2.06
16	T16	107.07	6.07	49.20	0.77	1.72
17	T17	104.67	4.87	48.00	0.87	1.80
18	T18	119.07	5.80	79.53	0.92	2.27
19	T19	100.07	6.67	47.07	0.89	2.00
20	T20	99.13	5.80	63.40	0.99	4.82
21	T21	101.93	5.40	61.13	0.98	1.65
22	T22	100.40	5.67	44.87	1.04	2.15
23	T23	100.40	5.07	59.80	0.96	2.61
24	T24	82.80	6.40	38.27	1.00	1.05
25	T25	114.47	5.40	55.13	0.96	1.58
26	T26	123.53	6.87	91.13	0.97	4.06
27	T27	90.67	5.73	37.27	1.06	2.27
28	T28	103.80	6.27	36.60	1.00	1.10
29	T29	81.33	5.07	54.27	0.97	2.24
30	T30	130.80	6.53	89.13	0.96	3.38
Mean		100.63	5.66	54.37	0.93	2.16
S.E		2.872	0.184	1.151	0.042	0.057
C.D		8.151	0.522	3.267	0.120	0.162

genotype T30 (130.80 cm) and was on par with genotype T26 (123.53cm) in the first cut. The lowest measure of plant height was observed for genotype T7 (80.40 cm) which was on par with genotypes T 14 (85.33 cm), T 5 (83.00 cm) T1(82.93 cm), T 24 (82.80 cm), T 29 (81.33 cm) and T 13 (80.67 cm).

4.2.1.2 Number of Branches Plant^{-1}

Number of branches plant $^{-1}$ showed significant difference in all the genotypes studied. The mean observation values ranged from 6.87 branches in genotype T26 to an average number of 4.47 branches in genotypes T4 and T5. The highest number of branches plant $^{-1}$ seen in the genotype T26 (6.87), was found to be on par with genotypes T19 (6.67), T6 (6.60), T30 (6.53) and T 24 (6.40). The lowest number of branches plant $^{-1}$ observed for genotypes T4 and T5 (4.47) was on par with genotypes T1 (4.93), T17 (4.87) and T3 (4.80).

4.2.1.3 Number of Leaves Plant^{-1}

The number of leaves plant $^{-1}$ varied significantly between the genotypes. The maximum number of leaves was observed in the genotype T26 (91.13). This genotype was on par with genotype T30 (89.13). This was followed by genotype T18 (79.53) and genotype T6 (73.67). The lowest number of leaves was observed in the case of genotype T3 (24.533). This was preceded by genotype T28 (36.00) which was found to be on par with genotype T27(37.267) and T24 (38.267).

4.2.1.4. Leaf Stem Ratio

The leaf stem ratio was computed by dividing the dry weight of leaves by dry weight of stem. The ratio ranged from 1.06 to 0.77 with an average value of 0.93. The highest value for leaf stem ratio was observed for genotype T27 (1.06). The genotype T16 recorded the lowest leaf stem ratio 0.77.

4.2.2. Physiological characters

The mean performances of physiological characters of fodder horse gram genotypes during the first cut are given in Table 3.

4.2.2.1. Leaf Area Index

The values of leaf area index ranged from 4.82 to 0.55 with an average value of 2.16. The leaf area index was found to be maximum in genotype T20 (4.82) followed by genotypes T6 (4.30), T26 (4.06) and T12 (3.74). The lowest value was shown by genotype T3 (0.55).

4.2.3. Yield attributes

The mean performance of yield attributes of fodder horse gram genotypes for first cutting are given in table 4.

4.2.3.1. Green fodder yield

The highest value for green fodder was found in genotype T6 (14.97 t ha^{-1}) and was on par with genotype T18 (14.38 t ha^{-1}). The lowest value for green fodder yield was recorded for the genotype T3 with 6.79 t ha^{-1} and this was found to be on par with genotypes T28 (7.00 t ha^{-1}) and T27 (7.62 t ha^{-1}).

4.2.3.2. Dry fodder yield

The value for dry fodder yield expressed in t ha^{-1} was found to be maximum for genotype T6 (2.11 t ha^{-1}) and was on par with genotype T18 (1.98 t ha^{-1}) during the first cut. The lowest value was found for genotype T28 (1.00 t ha^{-1}). This was on par with genotypes T3 (1.09 t ha^{-1}), T27 (1.11 t ha^{-1}) and T13 (1.14 t ha^{-1}).

4.2.3.3. Production efficiency

Production efficiency was found to vary from 0.25 t ha^{-1} day^{-1} to 0.11 t ha^{-1} day^{-1}. The maximum value for production efficiency was shown by genotype T6 (0.25

Table 4. Mean performance of yield attributes for first cut of fodder horse gram accessions

Sl. No.	**Genotypes**	**Green fodder yield (t ha^{-1})**	**Dry fodder yield (t ha^{-1})**	**Production Efficiency (t ha^{-1} day^{-1})**
1	T1	8.60	1.27	0.14
2	T2	9.24	1.22	0.15
3	T3	6.79	1.09	0.11
4	T4	10.17	1.47	0.17
5	T5	10.67	1.55	0.18
6	T6	14.97	2.11	0.25
7	T7	12.54	1.81	0.21
8	T8	10.11	1.43	0.17
9	T9	9.60	1.35	0.16
10	T10	8.39	1.19	0.14
11	T11	10.12	1.50	0.17
12	T12	8.92	1.29	0.15
13	T13	7.88	1.14	0.13
14	T14	11.49	1.64	0.19
15	T15	9.22	1.39	0.15
16	T16	9.45	1.49	0.16
17	T17	9.30	1.40	0.15
18	T18	14.38	1.98	0.24
19	T19	12.36	1.77	0.21
20	T20	10.74	1.53	0.18
21	T21	11.09	1.52	0.18
22	T22	9.39	1.31	0.16
23	T23	11.02	1.55	0.18
24	T24	9.25	1.35	0.15
25	T25	10.92	1.56	0.18
26	T26	13.19	1.84	0.22
27	T27	7.62	1.11	0.13
28	T28	7.00	1.00	0.12
29	T29	10.81	1.50	0.18
30	T30	13.19	1.92	0.22
Mean		10.28	1.48	0.17
S.E		0.369	0.063	0.006
C.D		1.044	0.178	0.017

t ha $^{-1}$ day $^{-1}$) and genotype T18 (0.240 t ha $^{-1}$ day $^{-1}$) was found to be on par with T6. The lowest value was observed for genotype T3 (0.11 t ha $^{-1}$ day $^{-1}$) and the genotypes T28 (0.12 t ha $^{-1}$ day $^{-1}$) and T27 (0.13 t ha $^{-1}$ day $^{-1}$) were found to be on par with the genotype T3.

4.2.4. Quality parameters

The mean performance of fodder horse gram genotypes for quality aspects observed during the first cut are given in Table 5.

4.2.4.1. Crude protein content

Among the genotypes, the highest crude protein was recorded for the genotype T21 (25.52per cent). The genotype T26 (25.23per cent) was found to be on par with genotype T21. The lowest value of crude protein content was observed in genotype T20 (18.02 per cent) during the first cut.

4.2.4.2. Crude fibre content

The crude fibre content varied from 32.15 per cent to 24.40 per cent in the first cutting. The highest value for crude fibre content was observed for genotype T7 with 32.15 per cent. This was found to be on par with genotypes T28 (32.10per cent), T14 (31.77per cent) and T3 (31.76per cent). The lowest value for crude fibre was estimated for the genotype T1 (24.40per cent).

4.2.4.3. Crude protein yield

The crude protein yield values expressed in t ha $^{-1}$ was obtained by multiplying the crude protein content with the dry fodder yield. The value for crude protein yield was maximum for genotype T6 (0.53 t ha $^{-1}$) and was on par with genotype T18 (0.50 t ha $^{-1}$). The lowest value for crude protein yield was recorded for the genotype T3 (0.21 t ha $^{-1}$).

Table 5. Mean performance of quality characters for first cut of fodder horse gram accessions

S.No	Genotypes	Crude Protein Content (%)	Crude Fibre Content (%)	Crude Protein Yield (t ha^{-1})
	T1	20.396	24.40	0.259
2	T2	20.438	28.05	0.250
3	T3	19.542	31.76	0.213
4	T4	24.938	27.71	0.366
5	T5	23.979	25.40	0.372
6	T6	24.813	28.68	0.525
7	T7	21.563	32.15	0.391
8	T8	23.542	30.91	0.337
9	T9	20.354	26.81	0.274
10	T10	18.542	29.95	0.221
11	T11	18.917	31.38	0.284
12	T12	22.750	27.84	0.294
13	T13	21.833	30.60	0.249
14	T14	23.875	31.77	0.391
15	T15	18.917	28.43	0.263
16	T16	24.563	25.32	0.367
17	T17	18.083	26.72	0.252
18	T18	24.958	25.54	0.495
19	T19	23.229	24.90	0.412
20	T20	18.021	24.51	0.276
21	T21	25.521	26.73	0.388
22	T22	23.271	27.40	0.304
23	T23	18.583	27.65	0.288
24	T24	20.313	28.55	0.273
25	T25	24.292	30.58	0.381
26	T26	25.229	26.25	0.466
27	T27	20.979	30.17	0.232
28	T28	24.771	32.10	0.249
29	T29	20.979	26.35	0.314
30	T30	23.917	27.70	0.459
Mean		22.037	28.21	0.328
S.E		0.198	0.163	0.015
C.D		0.561	0.463	0.043

The plants were allowed to regrow after the first cut, and the observations were taken during the second cut. The Analysis of variance was carried out and all the genotypes were found to be significantly different for all the characters studied. The ANOVA table for the second cut is given in Table 6.

4.2.5. Biometric characters

The mean performance of biometric characters of fodder horse gram genotypes during the second cut are given in the Table 7.

4.2.5.1. Plant height

During the second cut the maximum plant height was showed by genotype T26 (69.67 cm) which was on par with genotypes T30 (67.47cm), T 19 (67.00 cm), T4 (66.47 cm), T2 (65.73 cm), T 22 (64.87 cm), T 5 (64.67 cm), T 18 (63.33) , T1 (62.73) and T15 (62.53). The plant height showed a decrease in values during the second cut. The lowest plant height was measured for genotype T27 (50.00 cm) during the second cut which was on par with genotypes T 20 (54.33 cm), T 24 (53.73 cm), T 8 (53.73 cm), T 23 (53.13 cm), T 28 (50.87 cm) and T 6 (50.20cm).

4.2.5.2. Number of branches plant $^{-1}$

During the second cut too the maximum number of branches was observed in the genotype T26 (9.33) which was on par with genotypes T15 (9.00), T16 (8.33), T1 (8.13), T11 (8.07), T17 (8.07), T23 (8.00), T2 (7.93), T14 (7.87) and T21 (7.87). The least number of branches plant $^{-1}$ observed during the second cut was for the genotype T24 (4.87) and T28 (4.87). This value was found to be on par with the genotypes T27 (6.33), T9 (6.13), T19(6.07) T22 (5.80) and T12 (5.67). An increase in the number of branches plant $^{-1}$ was observed during the second cut. In both the cases the maximum number of branches was shown by the genotype T26, in which there was an increase from the average value of 6.87 branches to 9.33 branches.

Table 6. Analysis of variance (mean square) for fodder horse gram accessions during the second cut

Source of variation	Replication	Genotype	Error	F calculated	F critical
Df	2	29	58		
Plant height	3.107	87.539	24.831	3.525	1.663
Number of branches plant^{-1}	1.277	3.678	0.880	4.181	1.663
Number of leaves plant^{-1}	10.430	861.142	18.076	47.639	1.663
Leaf to stem ratio	0.032	0.033	0.010	3.391	1.663
Leaf area index	0.006	0.652	0.011	59.230	1.663
Dry matter production	379559.435	1,226,550.46	39,205.785	31.285	1.663
Green fodder yield	0.040	11.928	0.025	479.622	1.663
Dry fodder yield	0.017	0.628	0.024	26.518	1.663
Production efficiency	0.000	0.004	0.000	479.270	1.663
Crude protein	0.0025	17.192	0.047	369.718	1.663
Crude fibre	0.365	17.626	0.241	73.058	1.663
Crude protein yield	0.001	0.036	0.001	31.805	1.663

Table 7. Mean performance of biometric characters for second cut of fodder horse gram accessions

Sl. No.	**Genotypes**	**Plant height (cm)**	**Number of branches per plant**	**Number of leaves per plant**	**Leaf stem ratio**	**Leaf area index**
1	T1	62.73	8.13	52.47	0.83	1.14
2	T2	65.73	7.93	57.33	0.78	1.93
3	T3	55.07	5.93	25.47	0.70	0.52
4	T4	66.47	7.00	51.27	0.87	1.13
5	T5	64.67	6.60	62.00	0.70	1.62
6	T6	50.20	6.60	64.80	0.94	1.34
7	T7	57.00	6.47	55.40	0.67	0.94
8	T8	53.73	7.67	58.00	0.85	1.60
9	T9	56.53	6.13	40.67	0.81	1.33
10	T10	58.33	6.72	56.47	0.78	0.79
11	T11	58.13	8.07	55.13	0.81	1.44
12	T12	56.87	5.67	51.73	0.84	1.48
13	T13	58.20	6.47	48.20	0.87	1.06
14	T14	60.73	7.87	40.80	0.66	1.28
15	T15	62.53	9.00	58.93	0.77	1.38
16	T16	57.67	8.33	50.53	0.93	1.59
17	T17	57.07	8.07	46.93	0.84	1.16
18	T18	63.33	7.47	80.87	0.79	1.79
19	T19	67.00	6.07	47.80	0.70	1.24
20	T20	54.33	6.87	63.07	0.74	2.06
21	T21	60.87	7.87	61.27	0.76	0.95

Table 7. Continued

22	T22	64.87	5.80	43.07	0.66	1.29
23	T23	53.13	8.00	47.07	0.83	1.47
24	T24	53.73	4.87	38.07	0.77	0.79
25	T25	57.07	6.80	38.27	0.69	0.69
26	T26	69.67	9.33	121.27	0.81	2.83
27	T27	50.00	6.33	49.53	1.07	1.22
28	T28	50.87	4.87	41.40	0.62	0.64
29	T29	59.67	7.40	72.60	0.83	1.51
30	T30	67.47	7.33	68.87	1.04	1.24
Mean		59.45	7.08	54.98	0.80	1.31
S.E		2.877	0.541	2.455	0.057	0.061
C.D		8.145	1.533	6.950	0.161	0.172

4.2.5.3. Number of leaves plant $^{-1}$

During the second cut also the maximum number of leaves was observed for the genotype T26 (121.267). This was then followed by genotype T18 (80.867). The least number of leaves was observed for genotype T3 (25.467). This was preceded by the genotypes T24(38.067), T25 (38.267), T9 (40.667), T28 (41.400) and T22 (43.067).

4.2.5.4. Leaf stem ratio

During the second cut leaf stem ratio ranged from 1.07 to 0.62 with an average value of 0.93. The highest value for leaf stem ratio was observed for genotype T27 (1.07). The genotype T28 recorded the lowest leaf stem ratio 0.62.

4.2.6. Physiological characters

The mean performance of physiological characters of fodder horse gram accessions are given in Table 7.

4.2.6.1. Dry matter production

The maximum value for dry matter production was found in the genotype T26 (4690.93). This was followed by genotype T18 (4016.36), T19 (3861.00) and T15 (3719.81). The lowest dry matter production was found for the genotype T27 (1998.13) and was found to be on par with genotypes T8 (2301.16), T10 (2289.69), T2 (2191.11), T1 (2161.33), T13 (2150.41) and T28 (2149.91).

4.2.6.2. Leaf area index

During the second cut the maximum leaf area index was observed in genotype T26 (2.83) followed by genotype T20 (2.06) which was on par with genotype T2 (1.93). The lowest value for leaf area index was observed for the genotype T3 (0.52). The next lower observations were recorded for the genotypes T28 (0.64), T25 (0.69) and T24 (0.79).

4.2.7. Yield Attributes

The mean performance of yield attributes of horse gram genotypes for second cutting are given in Table 8.

4.2.7.1. Green Fodder Yield

During the second cut the maximum value for green fodder was obtained in the genotype T26 (9.69 t ha^{-1}). This was followed by genotype T19 (8.44 t ha^{-1}). The least value for green fodder yield was observed in genotype T8 (2.15 t ha^{-1}) and was on par with genotypes T6 (2.17 t ha^{-1}) and T1 (2.30 t ha^{-1}). The genotype T26 recorded a total green fodder yield of 22.87 t ha^{-1} from both the cuttings. The values for total green fodder yield is presented in Table 9.

4.2.7.2. Dry Fodder Yield

In the second cut the highest value for dry fodder yield was observed for genotype T26 (2.45 t ha^{-1}) followed by T15 (2.02 t ha^{-1}) and T19 (1.79 t ha^{-1}). The lowest value was observed for genotype T6 (0.51 t ha^{-1}) and was on par with genotypes T1 (0.55 t ha^{-1}), T8 (0.56 t ha^{-1}), T27 (0.59 t ha^{-1}), T2 (0.66 t ha^{-1}), T13 (0.68 t ha^{-1}), T9 (0.69 t ha^{-1}) and T17 (0.72 t ha^{-1}). The maximum value for total dry fodder yield was observed for genotype T26 (4.29 t ha^{-1}). The values for total dry fodder yield is presented in Table 9.

4.2.7.3. Production Efficiency

The production efficiency during the second cut was found to be maximum in genotype T26 (0.18 t ha^{-1} day^{-1}), followed by T19 (0.15 t ha^{-1} day^{-1}). The lowest value for production efficiency was observed for genotype T8 (0.04 t ha^{-1} day^{-1}) and T6 (0.04 t ha^{-1} day^{-1}).

Table 8. Mean performance of yield attributes for second cut of fodder horse gram accessions

Sl. No.	**Genotypes**	**Green fodder yield ($t\ ha^{-1}$)**	**Dry fodder yield ($t\ ha^{-1}$)**	**Production Efficiency ($t\ ha^{-1}\ day^{-1}$)**
1	T1	2.30	0.55	0.042
2	T2	2.47	0.65	0.045
3	T3	3.63	1.03	0.066
4	T4	3.66	0.91	0.067
5	T5	4.62	1.29	0.084
6	T6	2.17	0.51	0.039
7	T7	5.35	1.25	0.097
8	T8	2.15	0.56	0.039
9	T9	2.65	0.69	0.048
10	T10	3.16	0.80	0.058
11	T11	3.52	0.87	0.064
12	T12	5.23	1.31	0.095
13	T13	2.76	0.68	0.050
14	T14	7.20	1.50	0.131
15	T15	7.70	2.01	0.140
16	T16	3.77	0.92	0.069
17	T17	2.86	0.72	0.052
18	T18	5.33	1.39	0.097
19	T19	8.44	1.79	0.154
20	T20	2.90	0.79	0.053
21	T21	4.05	0.98	0.074

Table 8. Continued

22	T22	7.64	1.65	0.139
23	T23	3.96	1.01	0.072
24	T24	4.27	1.09	0.078
25	T25	5.10	1.06	0.093
26	T26	9.69	2.44	0.176
27	T27	2.49	0.59	0.045
28	T28	3.13	0.86	0.057
29	T29	4.66	1.19	0.085
30	T30	5.23	1.23	0.095
Mean		4.40	1.08	0.080
SE		0.091	0.089	0.002
C.D		0.258	0.252	0.005

Table 9. Mean performance of yield attributes of fodder horse gram accessions

Sl. No.	Genotypes	Total Green Fodder yield (t ha $^{-1}$)	Total Dry Fodder Yield (t ha $^{-1}$)	Dry matter production (kg ha $^{-1}$)
1	T1	10.898	1.822	2161.33
2	T2	11.707	1.878	2191.11
3	T3	10.418	2.114	2421.23
4	T4	13.831	2.378	2682.81
5	T5	15.289	2.842	3147.73
6	T6	17.138	2.622	2919.64
7	T7	17.893	3.066	3384.89
8	T8	12.258	1.989	2301.16
9	T9	12.249	2.036	2339.19
10	T10	11.556	1.989	2289.69
11	T11	13.644	2.366	2665.24
12	T12	14.151	2.602	3097.38
13	T13	10.640	1.823	2150.41
14	T14	18.693	3.142	3470.76
15	T15	16.916	3.405	3719.81
16	T16	13.218	2.412	2720.47
17	T17	12.160	2.112	2457.18
18	T18	19.716	3.371	4016.36
19	T19	20.809	3.557	3861.00
20	T20	13.636	2.321	2659.02
21	T21	15.147	2.496	2805.96

Table 9. Continued

22	T22	17.031	2.951	3291.47
23	T23	14.987	2.556	2897.16
24	T24	13.520	2.441	2750.72
25	T25	16.018	2.628	2963.91
26	T26	22.880	4.289	4690.93
27	T27	10.107	1.692	1998.13
28	T28	10.133	1.868	2149.91
29	T29	15.467	2.685	2984.27
30	T30	18.418	3.147	3452.13
Mean		14.684	2.553	2888.03
S.E		0.405	0.114	114.318
C.D		1.145	0.324	323.686

4.2.8. Quality Parameters

The mean performance of fodder horse gram genotypes for quality aspects are given in Table 10.

4.2.8.1. Crude Protein Content

During the second cut the highest value for crude protein content was observed for the genotype T4 (24.87 per cent). Genotype T21 (24.58 per cent) was on par with genotype T4. The lowest value for crude protein content was observed for genotype T20 (17.50 per cent).

4.2.8.2. Crude Fibre Content

During the second cutting the maximum value was observed in genotype T7 (32.21per cent). This was on par with the genotypes T14 (32.99 per cent), T28 (32.83 per cent) and T25 (32.45 per cent). The lowest values were observed in genotype T21 (24.73 per cent).

4.2.8.3. Crude Protein Yield

During the second cutting the genotype T26 showed maximum crude protein yield of 0.59 t ha $^{-1}$. The lowest value of crude protein yield was found to be for the genotype T1 (0.11 t ha $^{-1}$).

4.3. GENETIC PARAMETERS

Genotypic and Phenotypic coefficient of variation, Heritability and Genetic advance were calculated. The results are given in the Table 11.

4.3.1. Coefficient of Variation

4.3.1.1. Phenotypic Coefficient of Variation

The Phenotypic Coefficient of Variation (PCV) ranged from 8.61 per cent for crude fibre content to 48.15 per cent for leaf area index. High PCV was observed for

Table 10. Mean performance of quality characters for second cut of fodder horse gram accessions

Sl. No.	**Genotypes**	**Crude Protein Content (%)**	**Crude Fibre content (%)**	**Crude Protein Yield (t ha^{-1})**
1	T1	20.27	26.323	0.112
2	T2	20.25	30.263	0.132
3	T3	18.71	32.077	0.192
4	T4	24.90	29.043	0.227
5	T5	22.65	27.620	0.293
6	T6	23.54	29.217	0.119
7	T7	20.27	33.210	0.254
8	T8	22.40	31.503	0.125
9	T9	20.28	29.703	0.140
10	T10	18.04	31.673	0.143
11	T11	18.09	32.293	0.157
12	T12	23.92	28.133	0.313
13	T13	21.69	32.260	0.148
14	T14	22.96	32.987	0.345
15	T15	17.96	29.020	0.362
16	T16	24.13	26.937	0.222
17	T17	17.98	27.957	0.129
18	T18	24.17	25.787	0.336
19	T19	22.34	24.733	0.399
20	T20	17.50	25.990	0.138
21	T21	24.58	27.660	0.240
22	T22	22.04	29.037	0.363

Table 10. Continued

23	T23	17.92	28.933	0.181
24	T24	19.67	31.113	0.215
25	T25	23.56	32.447	0.251
26	T26	24.29	27.637	0.594
27	T27	20.92	31.077	0.122
28	T28	23.40	32.830	0.202
29	T29	20.08	27.873	0.239
30	T30	23.40	27.373	0.287
Mean		21.40	29.424	0.233
S.E		0.124	0.283	0.019
C.D		0.353	0.804	0.055

leaf area index (48.15 per cent), number of leaves plant $^{-1}$ (27.16 per cent), crude protein yield (26.75 per cent), dry fodder yield (24.76 per cent), green fodder yield (23.09 per cent), production efficiency (23.09 per cent) and dry matter production (22.84 per cent). Plant height (16.02 per cent) and number of branches plant $^{-1}$ (12.28 per cent) showed moderate phenotypic coefficient of variation. Low PCV was recorded for the character leaf stem ratio (9.60 per cent) and crude fibre content (8.61per cent).

4.3.1.2. Genotypic Coefficient of Variation

The value of Genotypic Coefficient of Variation (GCV) ranged from 47.93 per cent for leaf area index to 5.53 per cent for leaf stem ratio. The characters like leaf area index (47.93 per cent), crude protein yield (25.5 per cent), number of leaves plant $^{-1}$ (26.91per cent) dry fodder yield (23.51.per cent), green fodder yield (22.60 per cent), production efficiency (22.60 per cent) showed high genotypic coefficient of variation. Moderate genotypic coefficient of variation was observed for the characters like, plant height (15.23 per cent) and number of branches plant $^{-1}$ (10.91per cent). The character crude fibre content (8.55 per cent) and leaf stem ratio (5.53 per cent) recorded low genotypic coefficient of variation.

4.3.2. Heritability

High heritability was observed for leaf area index (99.10 per cent) followed by crude fibre content (98.64 per cent), number of leaves (98.18 per cent), crude protein content (98.11 per cent), green fodder yield (95.73 per cent), production efficiency (95.73 per cent), crude protein yield (91.20 per cent), dry matter production (90.99 per cent), plant height (90.47 per cent), dry fodder yield (90.16 per cent) and number of branches plant $^{-1}$ (78.88 per cent). Low heritability was recorded for leaf to stem ratio (33.13 per cent).

Table 11. Estimates of variability parameters for various characters of fodder horse gram

S. no	**Characters**	**PCV%**	**GCV%**	**Heritability %**	**Genetic advance as percentage of mean**
1	Plant height	16.015	15.233	90.473	29.848
2	Number of branches per plant	12.281	10.907	78.883	19.956
3	Number of leaves per plant	27.156	26.907	98.176	54.920
4	Leaf stem ratio	9.601	5.526	33.132	6.553
5	Leaf area index	48.146	47.928	99.096	98.284
6	Dry matter yield	22.837	21.783	90.986	42.803
7	Green fodder yield	23.093	22.595	95.730	45.540
8	Dry fodder yield	24.757	23.508	90.162	45.982
9	Production efficiency	20.360	19.389	90.688	38.037
10	Crude protein content	11.298	11.190	98.108	22.833
11	Crude fibre content	8.552	8.611	98.644	17.497
12	Crude protein yield	26.753	25.549	91.202	50.263

4.3.3. Genetic Advance (as Percentage of Mean)

The highest value of genetic advance recorded was 98.28 per cent (leaf area index) followed by number of leaves plant $^{-1}$ (54.92 per cent), crude protein yield (50.26 per cent), dry fodder yield (45.98 per cent), green fodder yield (45.54 per cent), production efficiency (45.54 per cent), dry matter production (42.80 per cent), plant height (29.85 per cent) and crude protein yield (22.83 per cent). Moderate genetic advance was observed for number of branches plant $^{-1}$ (19.96 per cent) and crude fibre content (17.50 per cent). Low genetic advance was observed for leaf to stem ratio (6.55 per cent).

4.4 SELECTION INDEX

Selection Index was calculated with an aim to discriminate desirable genotypes from a group of genotypes. For calculating the index, the biometrical characters such as plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$ and leaf area index were selected.

The index value for each genotype was determined and they were ranked. The values obtained for the treatments based on the selection index are given in Table 12.

Maximum value of selection index was recorded for genotype T26 (238.349) followed by genotype T30 (236.175) and genotype T6 (232.533).

4.5 CORRELATION COEFFICIENT ANALYSIS

Genotypic, phenotypic and environmental correlation coefficients were worked out as the correlation between different characters. The results are presented here.

Table 12. Selection index for 30 fodder horse gram genotypes

Sl. No.	List of genotypes	Selection index	Ranking of genotype
1	T26	238.349	1
2	T30	236.175	2
3	T6	232.533	3
4	T18	214.919	4
5	T25	180.597	5
6	T20	179.426	6
7	T11	177.670	7
8	T15	175.646	8
9	T21	175.246	9
10	T23	173.533	10
11	T8	170.463	11
12	T19	167.765	12
13	T16	166.545	13
14	T12	165.634	14
15	T9	162.285	15
16	T22	160.632	16
17	T17	160.554	17
18	T2	160.309	18
19	T5	155.583	19
20	T10	154.174	20
21	T7	152.001	21
22	T29	151.599	22
23	T4	151.403	23

Table 12. Continued

24	T28	146.972	24
25	T1	146.831	25
26	T14	143.811	26
27	T13	139.022	27
28	T27	137.634	28
29	T24	134.501	29
30	T3	128.520	30

4.5.1 Genotypic Correlation Coefficient

The genotypic correlation coefficients are given in Table 13.

The interrelationship of plant height was positive with the characters number of leaves plant $^{-1}$ (0.559), number of branches plant $^{-1}$ (0.558), leaf area index (0.564), green fodder yield (0.389), crude protein content (0.340) and dry fodder yield (0.333). Non-significant correlation was found to be with plant height and leaf stem ratio (0.050).

The number of branches plant $^{-1}$ showed positive significant correlation with plant height (0.558), leaf area index (0.440), green fodder yield (0.391), number of leaves plant $^{-1}$ (0.351), dry fodder yield (0.347), leaf stem ratio (0.293) and crude protein yield (0.217). Number of branches plant $^{-1}$ had non-significant correlation with crude fibre content (0.059).

The number of leaves plant $^{-1}$ had positive correlation with leaf area index (0.626), green fodder yield (0.616), dry fodder yield (0.563), plant height (0.559), number of branches plant $^{-1}$ (0.351) and crude protein content (0.316). Number of leaves plant $^{-1}$ had non-significant correlation with leaf stem ratio (0.135). The number of leaves plant $^{-1}$ was found to be negatively correlated with crude fibre content (0.392).

Leaf to stem ratio was found to be positively correlated with leaf area index (0.300) and number of branches plant $^{-1}$ (0.293). Leaf stem ratio had non-significant correlation with number of leaves plant $^{-1}$ (0.135), crude protein content (0.128), plant height (0.050), crude fibre content (0.040). Leaf to stem ratio showed negative non-significant correlation with dry fodder yield (-0.140) and green fodder yield (-0.081).

Leaf area index showed positive correlation with number of leaves plant $^{-1}$ (0.626), plant height (0.564), number of branches plant $^{-1}$ (0.440), green fodder yield (0.352), dry fodder yield (0.308) and leaf stem ratio (0.300). Leaf area index showed

Table 13. Genotypic correlation coefficients among the characters of fodder horse gram

	X 1	**X 2**	**X 3**	**X 4**	**X 5**	**X 6**	**X 7**	**X 8**	**X 9**
X 1	1								
X 2	0.558^{**}	1							
X 3	0.559^{**}	0.351^{**}	1						
X 4	0.050^{NS}	0.293^{**}	0.135^{NS}	1					
X 5	0.564^{**}	0.440^{**}	0.626^{**}	0.300^{**}	1				
X 6	0.340^{**}	0.217^{*}	0.316^{**}	0.128^{NS}	-0.031^{NS}	1			
X 7	-0.108^{NS}	0.059^{NS}	-0.392^{**}	0.040^{NS}	-0.311^{**}	-0.050^{NS}	1		
X 8	0.389^{**}	0.391^{**}	0.616^{**}	-0.081^{NS}	0.352^{**}	0.448^{**}	-0.270^{*}	1	
X 9	0.333^{**}	0.347^{**}	0.563^{**}	-0.140^{NS}	0.308^{**}	0.387^{**}	-0.269^{*}	0.976^{**}	1

X1 – Plant height
X2 - Number of branches plant $^{-1}$
X3 – Number of leaves plant $^{-1}$
X4 – Leaf stem ratio
X5 – Leaf stem ratio
X6- Crude protein content
X7- Crude fibre content
X8 Green fodder yield
X9- Dry fodder yield

negative non-significant correlation with crude protein content (-0.031). Leaf area index showed negative correlation with crude fibre content (-0.311).

Crude protein content had positive correlation with green fodder yield (0.448), dry fodder yield (0.387), plant height (0.340), number of leaves plant $^{-1}$ (0.316) and number of branches plant $^{-1}$ (0.217). crude protein showed negative non-significant correlation with leaf area index (- 0.031) and crude fibre content (-0.050).

Crude fibre showed negative correlation with dry fodder yield (-0.269), green fodder yield (-0.270), leaf area index (-0.311) and number of leaves plant $^{-1}$ (-0.392). Crude fibre non-significant correlation with number of branches plant $^{-1}$ (0.059) and leaf stem ratio (0.040). crude protein had negative non-significant correlation with plant height (-0.108) and crude protein content (-0.050).

Green fodder yield showed positive significant correlation with dry fodder yield (0.976), number of leaves plant $^{-1}$ (0.616), crude protein content (0.448), number of branches plant $^{-1}$ (0.391), plant height (0.389) and leaf area index (0.352). Green fodder yield showed negative correlation with crude fibre content (-0.270). Green fodder yield showed negative non-significant correlation with leaf stem ratio (-0.081).

Positive significant correlation was shown by dry fodder yield and green fodder yield (0.976), number of leaves plant $^{-1}$ (0.563), crude protein content (0.387), number of branches plant $^{-1}$ (0.347), plant height (0.333) and leaf area index (0.308). Dry fodder yield showed negative correlation with crude fibre content (-0.269). Dry fodder yield showed negative non-significant correlation with leaf area index (-0.140).

4.5.2 Phenotypic Correlation Coefficient

Phenotypic correlation coefficient is given in Table 14.

Plant height showed positive significant correlation with leaf area index (0.540), number of leaves plant $^{-1}$ (0.536), number of branches plant $^{-1}$ (0.484), green fodder yield (0.370), crude protein content (0.318) ad crude fibre content (0.304). Plant

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Table 14. Phenotypic correlation coefficients among the characters of fodder horse gram

	X 1	**X 2**	**X 3**	**X 4**	**X 5**	**X 6**	**X 7**	**X 8**	**X 9**
X 1	1								
X 2	0.484^{**}	1							
X 3	0.536^{**}	0.316^{**}	1						
X 4	0.058^{NS}	0.115^{NS}	0.056^{NS}	1					
X 5	0.540^{**}	0.395^{**}	0.628^{**}	0.163^{NS}	1				
X 6	0.318^{**}	0.183^{NS}	0.304^{**}	0.088^{NS}	-0.034^{NS}	1			
X 7	-0.098^{NS}	0.047^{NS}	-0.385^{**}	0.026^{NS}	-0.307^{**}	-0.051^{NS}	1		
X 8	0.370^{**}	0.336^{**}	0.597^{**}	-0.038^{NS}	0.344^{**}	0.440^{**}	-0.257^{*}	1	
X 9	0.304^{**}	0.278^{**}	0.525^{**}	-0.104^{NS}	0.288^{**}	0.368^{**}	-0.244^{*}	0.944^{**}	1

X1 – Plant height
X2 - Number of branches plant $^{-1}$
X3 – Number of leaves plant $^{-1}$
X4 – Leaf stem ratio

X5 – Leaf stem ratio
X6- Crude protein content
X7- Crude fibre content
X8 Green fodder yield
X9- Dry fodder yield

height showed negative non-significant correlation with crude fibre content (-0.098) and non-significant correlation with leaf to stem ratio (0.058).

Number of branches plant $^{-1}$ showed positive significant correlation with plant height (0.484), leaf area index (0.395), green fodder yield (0.336), number of leaves plant $^{-1}$ (0.316) and dry fodder yield (0.278). Number of branches plant $^{-1}$ showed non-significant correlation with crude protein content (0.183), leaf to stem ratio (0.115) and crude fibre content (0.047).

Number of leaves plant $^{-1}$ showed positive significant correlation with leaf area index (0.628), green fodder yield (0.597), plant height (0.536), dry fodder yield (0.525), number of branches plant $^{-1}$ (0.316) and crude protein content (0.304). Number of leaves plant $^{-1}$ showed negative significant correlation with crude fibre content (-0.385). it had non-significant correlation with leaf stem ratio (0.056).

Leaf to stem ratio had non-significant correlation with all the characters. It showed non-significant correlation with leaf area index (0.163), number of branches plant $^{-1}$ (0.115), crude protein content (0.088), plant height (0.058), number of leaves plant $^{-1}$ (0.056) and crude fibre content (0.026). It showed negative non-significant correlation with dry fodder yield (-0.104) and green fodder yield (-0.038).

Leaf area index showed positive significant correlation with number of leaves plant $^{-1}$ (0.628), plant height (0.540), Number of branches plant $^{-1}$ (0.395), green fodder yield (0.344), dry fodder yield (0.288) and leaf stem ratio (0.163). Leaf area index showed negative correlation with crude fibre content (-0.307). Leaf area index showed negative non-significant correlation with crude protein content (-0.034).

Crude protein content showed positive correlation with green fodder yield (0.440), dry fodder yield (0.368), plant height (0.318), number of leaves plant $^{-1}$ (0.304), number of branches plant $^{-1}$ (0.183) and leaf stem ratio (0.088). it showed negative non-significant correlation with leaf area index (-0.034) and crude fibre content (-0.051).

Crude fibre content showed negative significant correlation with number of leaves (-0.385), leaf area index (-0.307), green fodder yield (-0.257) and dry fodder yield (-0.244). it showed non-significant correlation with number of branches plant $^{-1}$ (0.047) and leaf to stem ratio (0.026). It exhibited negative non-significant correlation with crude protein content (-0.051) and plant height (-0.098).

Green fodder yield showed positive significant correlation with dry fodder yield (0.944), number of leaves plant $^{-1}$ (0.597), crude protein content (0.440), plant height (0.370) and leaf area index (0.344). green fodder yield showed negative correlation with crude fibre content (-0.257). Green fodder yield showed negative non-significant correlation leaf to stem ratio (-0.038).

Dry fodder yield showed positive significant correlation with green fodder yield (0.944), number of leaves plant $^{-1}$ (0.525), crude protein content (0.368), plant height (0.304), leaf area index (0.288) and number of branches plant $^{-1}$ (0.278). crude fibre content and dry fodder yield showed negative significant correlation (-0.244). It had negative non-significant correlation with leaf to stem ratio (-0.104).

4.6. PATH COEFFICIENT ANALYSIS

Path coefficient analysis is used to estimate the direct and indirect effects of component characters on yield. The path correlation coefficients representing the direct and indirect effects are given in Table 15.

Plant height showed negative direct effect on green fodder yield (-0.006). Plant height showed positive indirect effect through dry fodder yield (0.297), number of leaves plant $^{-1}$ (0.036), crude protein content (0.027), number of branches plant $^{-1}$ (0.017) and leaf area index (0.017). the indirect effect through crude fibre content was negative (-0.0008). Plant height showed a positive correlation with green fodder yield (0.389).

Table 15. Direct and indirect effects of yield and component characters on green fodder yield

	X1	X2	X3	X4	X5	X6	X7
X1	**-0.00604**	0.01722	0.03642	0.01751	0.02702	-0.00080	0.29744
X2	-0.00337	**0.03087**	0.02285	0.01365	0.01727	0.00044	0.30930
X3	-0.00338	0.01083	**0.06514**	0.01943	0.02513	-0.00292	0.50206
X4	-0.00340	0.01357	0.04075	**0.03105**	-0.00245	-0.00232	0.27496
X5	-0.00205	0.00671	0.02060	-0.00096	**0.07946**	-0.00037	0.34504
X6	0.00065	0.00183	-0.02553	-0.00966	-0.00397	**0.00745**	-0.24029
X7	-0.00201	0.01070	0.03666	0.00957	0.03073	-0.00201	**0.89205**

X1 – Plant height
X2 - Number of branches plant $^{-1}$
X3 – Number of leaves plant $^{-1}$
X4 – Leaf area Index

X5 – Crude protein content
X6- Crude fibre content
X7- Dry fodder yield

Residual are 0.03519

The direct effect of number of branches plant $^{-1}$ on green fodder yield was positive (0.031). Indirect effect through dry fodder yield (0.309), number of leaves plant $^{-1}$ (0.022), crude protein content (0017), leaf area index (0.013) and crude fibre content (0.0004) was positive. Plant height showed a negative indirect effect with green fodder yield (-0.003). Number of branches plant $^{-1}$ had a positive genotypic correlation of 0.391.

Number of leaves plant $^{-1}$ showed a positive direct effect on green fodder yield (0.065). The indirect effects through dry fodder yield (0.502), crude protein content (0.025), leaf area index (0.019), number of branches plant $^{-1}$ (0.010) were positive. The indirect effect through plant height (-0.003) and crude fibre content (-0.002) were negative. Number of leaves plant $^{-1}$ had a positive genotypic correlation of 0.616 with green fodder yield.

Leaf area index had positive direct effect on green fodder yield (0.031). The indirect effects through dry fodder yield (0.274), number of eaves plant $^{-1}$ (0.040) and number of branches plant $^{-1}$ (0.013) were positive. The indirect effects through plant height (-0.003), crude protein content (-0.002) and crude fibre content (-0,002) were negative. Leaf area index had a positive correlation of 0.352 with green fodder yield.

Crude protein content showed a positive direct effect on green fodder yield (0.079). The indirect effect of crude protein content through dry fodder yield (0.345), number of leaves plant $^{-1}$ (0.020) and number of branches plant $^{-1}$ (0.006) were positive. The indirect effects through plant height (-0.002), leaf area index (-0.0009) and crude fibre content (-0.0003) was negative. The crude protein content had a positive correlation of 0.448 with the green fodder yield.

Crude fibre content showed a positive direct effect of 0.007 on green fodder yield. The indirect effects through characters like number of branches plant $^{-1}$ (0.0018) and plant height (0.0006) on green fodder yield was positive. The indirect effects through dry fodder yield (-0.240), number of leaves plant $^{-1}$ (0.025), leaf area index (-

0.0096), crude protein content (-0.0039) on green fodder yield was negative. The crude fibre content had a negative correlation of -0.270 with green fodder yield.

Dry fodder yield had a positive direct effect of 0.892 on green fodder yield. The indirect effect of dry fodder yield through number of leaves plant $^{-1}$ (0.036), crude protein content (0.030), number of branches plant $^{-1}$ (0.010) and leaf area index (0.009) on green fodder yield was positive. The dry fodder yield had negative indirect effects through plant height (-0.002) and crude fibre content (-0.002) on green fodder yield. Dry fodder yield had a high positive genotypic correlation of 0.976 with green fodder yield.

The residual effect obtained was 0.0351.

DISCUSSION

5. DISCUSSION

Livestock sector is the backbone of Indian economy. Forages are the mainstay of livestock. The economics of the milk production largely depends on the quality of fodder fed to the animals. Legumes are the most important forage plants that improve the feed available for livestock. The soil fertility and productivity of the succeeding crops are also enhanced by the cultivation of legumes. In terms of productivity, the pulses are very low in yield, so that breeding programmes are to be aimed at improving their productivity. The pre-requisite for any breeding programme is to collect the basic data regarding the variability present in the germplasm. Success of any breeding programme largely depend on the extent of genetic variability present in the population. Yield being a complex character controlled by polygenes, selection based on the phenotypic expression alone would not be effective. So, to make an effective selection for higher yield, it is necessary to determine the relative contribution of each character towards yield.

In the present investigation, conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, thirty diverse horse gram genotypes were evaluated for fodder yield, quality and multicut ability. The crop was initially cut at 50 per cent flowering stage. The plants were then allowed to regrow to check the multicut ability. The promising genotypes identified in the study could be utilized for further crop improvement programs for developing suitable multicut fodder horse gram varieties.

5.1 VARIABILITY ANALYSIS

A wide range of observations were reported for different genotypes in terms of biometric characters which indicated the extend of variability present in the germplasm. In the present study, twelve characters were studied for thirty genotypes, in which all characters had considerable variation among the genotypes. From the analysis of variance, the genotypes showed significant differences for all the characters studied, which revealed the presence of genetic variability among the genotypes. Significant differences among the genotypes gave greater opportunity for selecting suitable genotypes with high mean value for all the characters of interest.

Analysis of variance revealed significant differences among the 30 genotypes of fodder horse gram for all the characters studied *viz.,* plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf stem ratio, leaf area index, dry matter production, green fodder yield, dry fodder yield, production efficiency, crude protein content, crude fibre content, crude protein yield. The existence of variability in several characters in horse gram are reported by Neelam *et al.* (2014). Similar findings were reported for yield and yield related characters by Sharma and Singhanja (1992), and Mary and Gopalan (2006) in fodder cowpea.

5.1.1 Mean Performance

The mean values for the twelve characters in the 30 fodder horse gram genotypes recorded during the first and second cut were worked out separately. The different varieties recorded varying mean values for all the characters studied (Fig.1 & 2).

Plant height varied from 144. 67 cm to 80.40 cm during the first cut. The genotype T6 (IC-139432) was having the maximum plant height. The apparent variation in plant height in different varieties might be due to their different growth behavior or due to their genetic constitution. The inherent genetic material is the factor which decides the biometric characters. This varies in each genotype. Suraiya (1980) recorded a maximum plant height of 118 cm in horse gram. Borah (1994), recorded a plant height of 77 cm in fodder ricebean. Similarly, Neelam *et al.* (2014) observed a range of 90 to 130 cm for plant height in horse gram. During the second cut the plant height showed a general trend of decrease in height. The maximum value for plant height was observed for genotype T26 (IC-121640). Afzal *et al.* (2013) also reported a decrease in plant height in multicut sorghum in the subsequent cuts after the first cut.

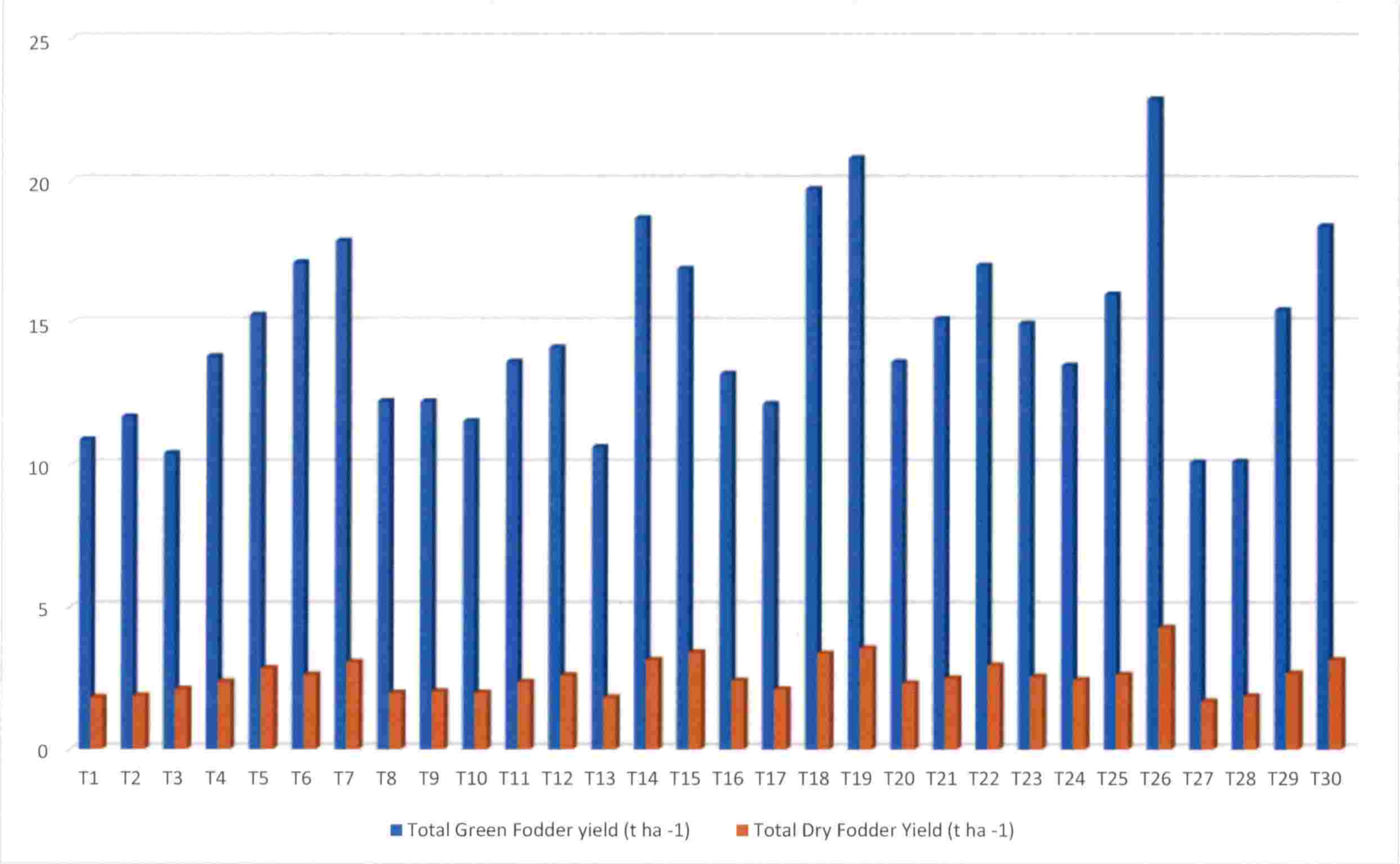

Fig. 1. Comparative mean yield performance of 30 genotypes of fodder horse gram

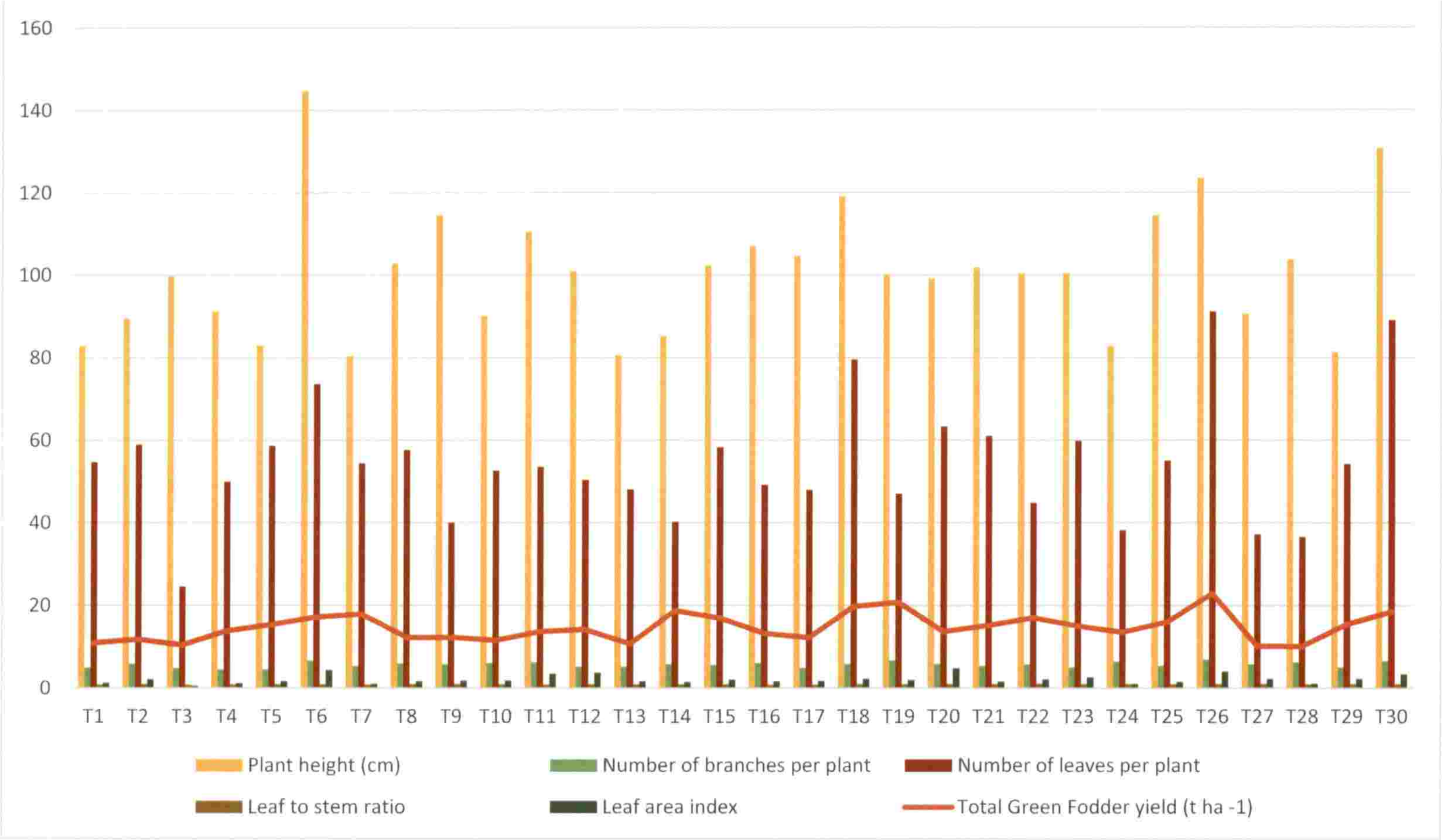

Fig 2. Comparative mean performance of genotypes of fodder horse gram genotypes based on yield and biometrical characters

The maximum number of branches plant $^{-1}$ during the first cut of the crop was 6.87 reported in the genotype T26 (IC-121640). The number of branches increased during the regrowth of the crop. The second cut the genotype T26 (IC-121640) had the highest number of branches. The branch number increased from a mean value of 6.87 to 9.33. Neelam *et al*, (2014) observed a range for number of primary branches in horse gram ranging from 4.8 to 8.9. This might be due to the activation of dormant buds after the first cut.

Number of leaves plant $^{-1}$ during the first cut was maximum for genotype T26 (IC-121640). The number of leaves had wide variation among the 30 fodder horse gram genotypes. During the second cut the maximum number of leaves was observed for genotype T26 (IC-121640). Prakash *et al.* (2010) observed the number of leaves to vary from 46 to 55 in fodder cowpea.

Leaf stem ratio was computed by dividing the dry weight of leaves by dry weight of stem. The ratio ranged from 1.06 to 0.77 with an average value of 0.93. During the second cut also, similar range was observed for leaf stem ratio. Similar results were observed by Prakash *et al*., (2010) in leaf stem ratio ranging from 1.38 to 0.55 in fodder cowpea. Aswathi, (2016) observed that leaf stem ratio of fodder ricebean reduced with advance of crop age. Genetic difference among the genotypes might result in differential rate of profuse growth of the genotypes.

Leaf area relates to accumulation and partitioning of photosynthates to the economic parts of the plant and has an important role in the final biomass of the crop. The highest value for leaf area index observed during the first cut was 4.82. During the second cut there was decrease in the values for leaf area index. The regrown plants had leaves with smaller size which may be the cause for decrease in leaf area index. This reduction in leaf area index may have resulted in decrease in yield during the second cut. Leaf area gives a measure of photosynthetic efficiency. The variability observed in the leaf area index between the genotypes may be due to the genetical variations among the genotypes. Dogra (2006) also reported similar results in leaf area index of horse gram genotypes that it varies between 1.98 to 3.41. Kurubetta, (2006) observed leaf area index in cowpea to be 2.09.

Dry matter production had a value ranging from 4690 kg ha $^{-1}$ to 1998 kg ha $^{-1}$. Plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index leaf stem ratio are the major factors that influenced the dry matter production. Maximum dry matter accumulation was given by genotype T26 (IC-121640). The genetic potential of the variety and its contributing characters would have resulted in varying dry matter production for the genotypes. Singh *et al.* (1979) reported dry matter production of 50.10 q ha $^{-1}$ in fodder cowpea. Aswathi (2016), reported dry matter production of 3355.9 kg ha $^{-1}$ in fodder ricebean. Rudragouda and Angadi (2002) also reported similar findings in ricebean.

Green fodder yield during the first cut was recorded to be 14. 97 t ha $^{-1}$ by genotype T6 (IC-139432) while during the second cut the genotype T26 (IC-121640) recorded a green fodder yield of 9.69 t ha $^{-1}$. The plants after the first cut showed different rate of growth. The superior genotype in first cut, the genotype T6 (IC-139432) was having poor regrowth ability. Thus, it had lesser green fodder yield compared to the first cut. While considering the total green fodder the genotype T26 (IC-121640), was superior during the second cut and was one among the superior genotypes during the first cut. The high yield for genotype T26 (IC-121640) may be due to the superior performance of characters like number of leaves, number of branches and maximum plant height observed for the genotype.

Dry fodder yield was calculated by oven drying the samples taken for green fodder yield. During the first cut the highest value was observed for genotype T6 (IC-139432), the genotype which was having highest green fodder yield. Similarly, during the second cut the genotype T26 (IC-121640) which was having high green fodder yield had high dry fodder yield. Similar results were obtained while considering the total dry fodder yield. As in the case of green fodder yield, dry fodder yield might also be widely influenced by the characters that contribute yield, such as plant height, number of branches, number of leaves, leaf stem ratio and leaf area index.

Production efficiency was found to be highest for the genotype having highest green fodder yield. Genotype T6 (IC-139432) was having maximum production efficiency during the first cut and genotype T26 (IC-121640) was having maximum production efficiency during the second cut.

Crude protein content was significantly influenced by genotypes. Crude protein content ranged from 25.52 per cent to 18.02 per cent in the present study in the genotypes of fodder horse gram. During the second cut crude protein content value ranged from 24.58 per cent to 17.50 per cent. Crude protein is one of the important parameters which determines the quality of green fodder. Genotypes which had the genetic potential of profuse vegetative growth and dry matter accumulation will ultimately leads to higher nutrient uptake especially nitrogen, an essential component of protein will result in more crude protein content in that variety (Iqbal, 1998). In ricebean the crude protein content was found to decrease in the regrown crop. Chauhan (1980) observed that during multiple cuts the crude protein content decreases in berseem and clusterbean. Borah (1994) reported protein content in horse gram seeds ranged from 15.83 per cent to 22.67 per cent. In fodder ricebean, Aswathi, (2016) reported a crude protein content of 15.64 per cent.

The values for crude fibre content ranged from 32.15 per cent to 24.40 per cent during the first cut. In the second cut the crude fibre content ranged from 33.210 per cent to 26.323 per cent. An increase in crude fibre content was observed during the succeeding cut. Among the quality parameters, crude fibre content is the most important parameter that influences the digestibility of the fodder. Those fodder crops, that contain a low amount of crude fibre content is more palatable to the animals and also contain digestible nutrients. Chauhan (1980) from his study in nutritive value of berseem and clusterbean observed that during multiple cuts the crude fibre content increases.

The crude protein yield of the varieties of horse gram genotypes varied significantly among the genotypes. The crude protein yield was calculated based on dry fodder yield and crude protein content. The genotype T6 (IC-139432) having high fodder yield during the first cut and genotype T26 (IC-121640), superior during the second cut were having high values for crude protein yield in the respective cuts. This occurred because crude protein content is the direct product of dry fodder yield and crude protein content. In the studies by Rudragouda and Angadi (2002) and Aswathi (2016) also showed that the crude protein yield varied according to the variation in dry fodder yield and crude protein content in ricebean.

5.1.2 Coefficient of variation

An estimate of magnitude of variability present in a population is of great importance as it provides the basis for effective selection. The observed variation in a population is the total variation arising due to genotypic and environmental effects. Only the genotypic component of total variability contributes to gain under selection. So, it's necessary to have the knowledge about the nature and magnitude of genetic variations which governs the inheritance of the quantitative characters such as yield and yield attributing characters. The phenotypic and genotypic coefficients of variations measure the variability that is present in a population. The PCV measures the extend of total variation present in a population and is the sum total of GCV and environmental effects. The GCV provides the genetic variability present in the population and is a valid base for comparison. The GCV and PCV are better indices for the comparison of quantitative traits with different units of measurement.

In the present study high values of PCV and GCV was observed for the character leaf area index, number of leaves plant $^{-1}$, crude protein yield, dry fodder yield, green fodder yield, production efficiency and dry matter production. Similar to

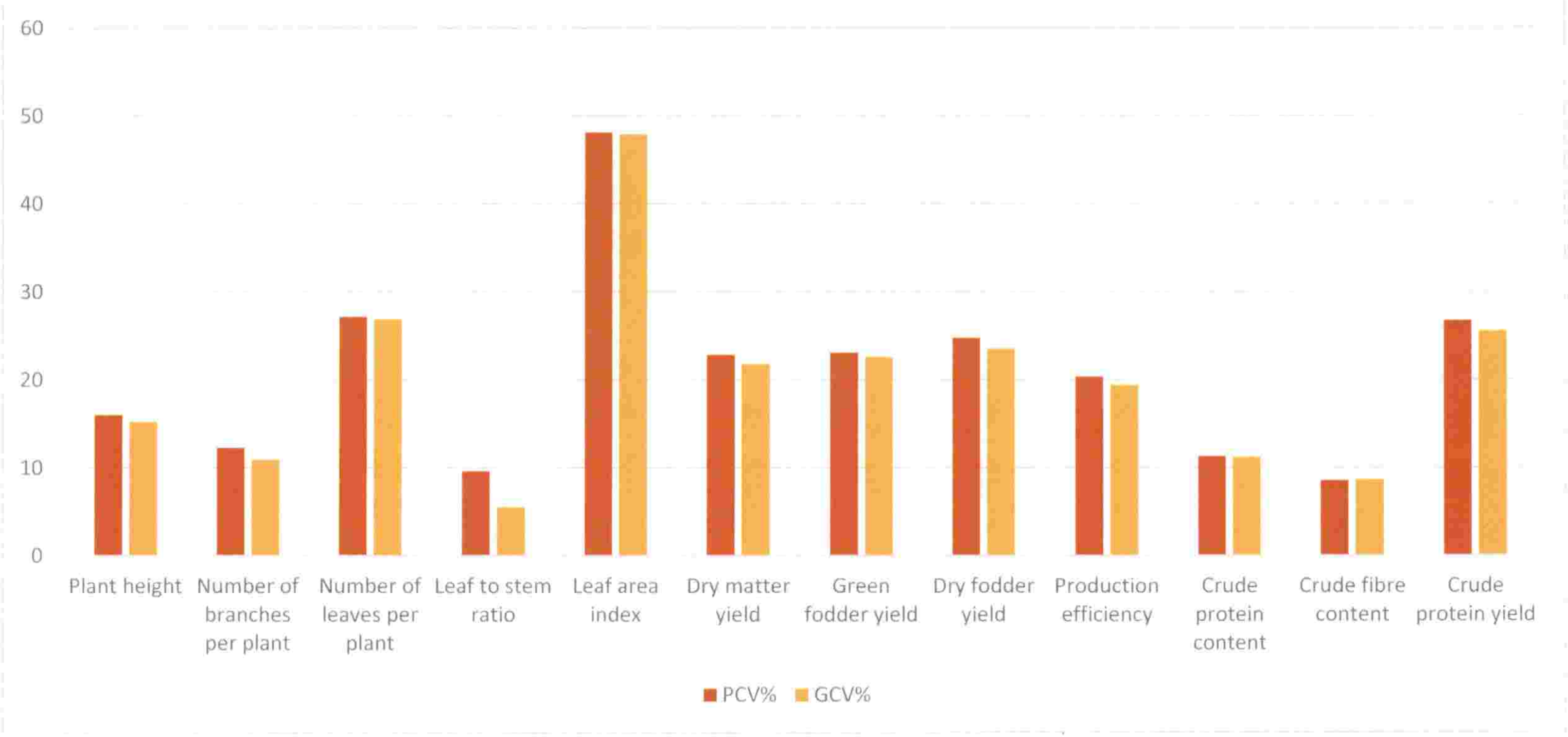

Fig. 3. GCV and PCV for the characters of fodder horse gram genotypes

this, Borah and Fazlullahkhan (2000) reported the high GCV and PCV for plant height, green fodder yield plant $^{-1}$, number of main branches plant $^{-1}$ in fodder cowpea. Similar reports of high GCV for leaf area index, were obtained by Thorat and Gadewar (2013) in a study conducted in cowpea. Nath and Tajane (2014) also reported high GCV and PCV for green fodder yield plant $^{-1}$ in cowpea.

In the present study plant height and number of branches plant $^{-1}$ showed moderate PCV and GCV. Similar reports were given by Aravindhan and Das (1995), Backiyarni and Natarajan (1996), Srinivasan and Das (1996), Ponmariammal and Das (1996) in fodder cowpea. Kumar *et al.* (2017) reported the same in rice bean. Low PCV and GCV were recorded for the characters leaf stem ratio and crude fibre content. Low values for GCV and PCV was observed for leaf stem ratio by Kumar *et al.,* (2017). PCV and GCV values are similar indicating that influence of environment on the character is less (Fig.3).

5.1.3 Heritability and Genetic advance

The variability present in a population can be subdivided to heritable and non-heritable components. The heritability values provide the information on the degree of inheritance of characters from the parents to the progeny. Heritability values >60 per cent indicates that the phenotype of the trait strongly reflects the genotype. For the success of any breeding programme, knowledge of heritability is essential as it is a measure in separating genotypes by selection. Characters having high heritability can be improved directly through selection as these characters will be less affected by the environment. The estimates of heritability together with genetic advance are helpful in predicting the selection potential in a population.

In the present study high heritability coupled with high genetic advance was observed for leaf area index, number of leaves plant $^{-1}$, crude protein yield, green fodder yield, dry fodder yield, production efficiency, dry matter production, plant height and crude protein yield. This indicates that these characters were governed by additive gene action and direct selection for these characters can be effective. High heritability and moderate genetic advance were observed for characters number of branches plant $^{-1}$ and crude fibre content. The characters with high heritability and moderate genetic advance could be due to additive and non-additive interactions. Low heritability and low genetic advance was observed for leaf stem ratio.

In fodder cowpea, Borah and Fazlullahkhan, (2000) reported high heritability for plant height, green fodder yield plant $^{-1}$, number of main branches plant $^{-1}$. Santhoshkumar *et al.* (2002), observed high heritability coupled with high genetic advance for green fodder yield, plant height and dry fodder yield in cowpea. Similarly, Kumar *et al.* (2017), observed high heritability coupled with high genetic advance for crude protein content. High heritability accompanied with high genetic advance was observed for green forage yield plant $^{-1}$, dry matter yield plant $^{-1}$, plant height and branches plant $^{-1}$ in cowpea (Nath and Tajane, 2014). These characters had high heritability coupled with high genetic advance due to the predominance of additive gene effect controlling these characters (Fig.4).

5.1.4 Selection index

Selection of genotypes based on suitable index is highly efficient in any breeding programme. The selection index gives information on the proportionate weightage to be given to a yield component. Efficiency of selection can be increased by formulating selection index using the important characters that contribute to yield. Selection based on suitable index was more efficient than individual selection based on individual characters (Hazel, 1943).

The characters, plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index and green fodder yield were used for the construction of the selection index. The selection values ranged from 238.349 to 128.520. The top-ranking superior genotypes were genotype T26 (IC-121640), T30 (IC-89016), T6 (IC-561040)

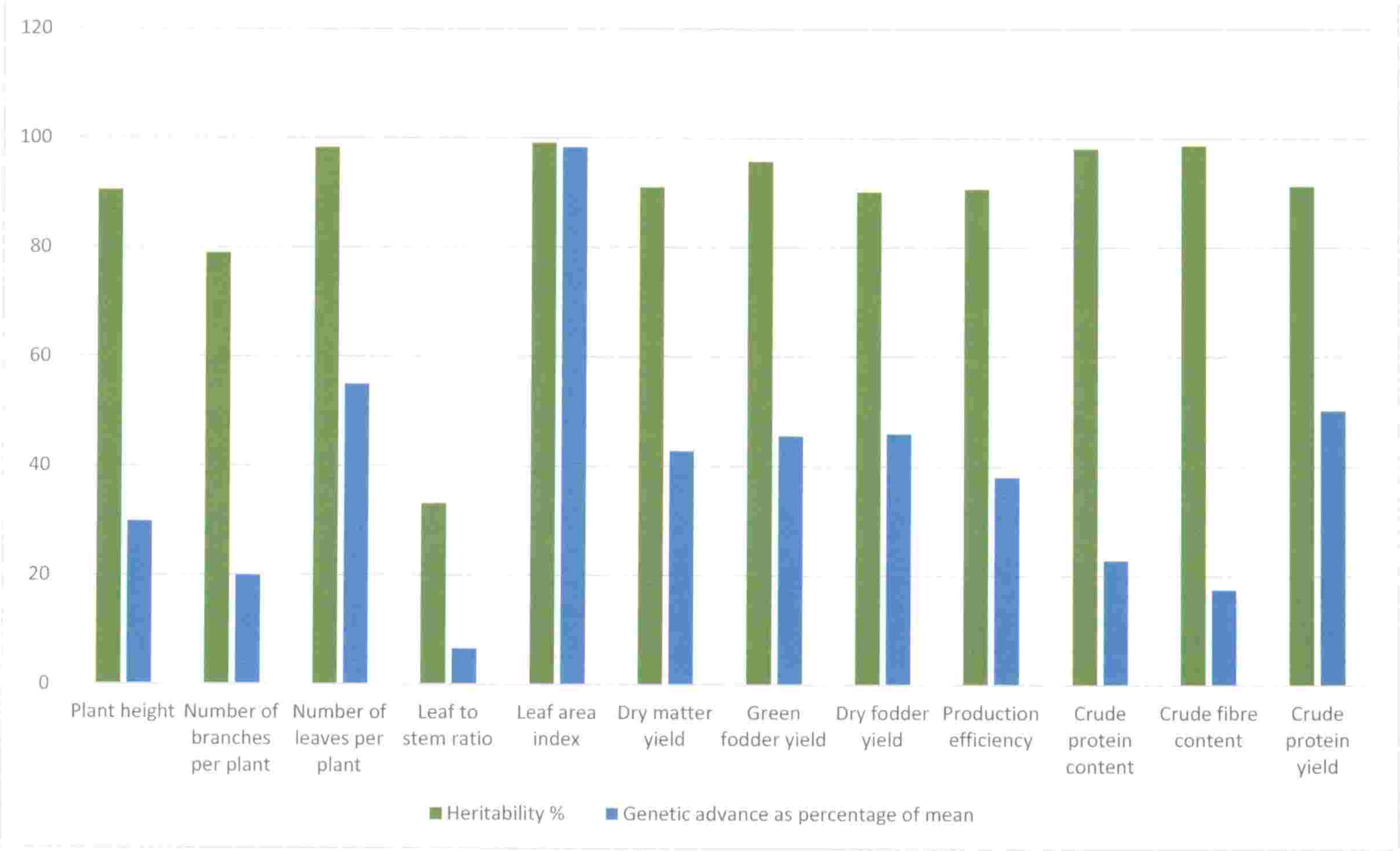

Fig.4. Heritability and Genetic advance for the characters of fodder horse gram genotypes

and T18 (IC-22765). Promising genotypes identified on the basis of the selection index formulated can be used for further crop improvement programs.

The selection index is constructed to identify superior genotypes from a group of genotypes. In the procedure of formulating selection index, the component characters are combined into a score or index. Selection is carried on the basis of the score, as if the score were a single character, it would result in the most rapid possible improvement of economic value. According to Suraiya (1980), for making considerable improvement of seed yield in horse gram, the characters seed pod $^{-1}$ and length of pod are to be given importance. Selection indices were used for identification of superior cowpea accessions by Resmi (1998), Manju (2006), Jithesh (2009) Sivakumar (2012) and Litty (2015). Selection indices were constructed in fodder sorghum for simultaneous selection for fodder and grain purpose by Biswas *et al.* (2001). Kour *et al.* (2018) constructed selection index in forage sorghum using six biometrical characters which includes, plant height, number of tillers, number of leaves plant $^{-1}$ and green fodder yield which are included in the present study.

5.1.5 Correlation studies

There are many characters that influences the yield in positive and negative direction. Correlation studies provide information regarding the nature and magnitude of relationship between the characters. When selection is carried out for a trait of interest in a population it is associated with the improvement of other traits associated with the trait of interest. The phenotypic and genotypic correlation coefficients of the component characters provide a better understanding of the characters, nature and magnitude of contribution towards yield which ultimately helps in the selection of high yielding genotypes.

In the present study, green fodder yield showed positive significant correlation with dry fodder yield, number of leaves plant $^{-1}$, crude protein content, number of branches plant $^{-1}$, plant height and leaf area index. Due to positive correlation, improvement in any one of these characters will simultaneously result in improvement of all other correlated characters. Green fodder yield showed negative correlation with crude fibre content.

Significant positive correlation of fodder yield with number of branches plant $^{-1}$, leaf area index, dry matter yield and crude protein content was reported by Aravindhan and Das (1995) in fodder cowpea. Kumar *et al.* (2017) studied twenty elite cowpea genotypes in two environments and observed positive significant correlation with green fodder yield and number of branches plant $^{-1}$. In the study it was observed that crude protein content had negative significant correlation with plant height and number of branches plant $^{-1}$ in the second environment. However, in the first environment negative correlation between crude protein content and number of branches plant $^{-1}$ was reported.

5.1.6 Path analysis

Path analysis confirms whether the correlation of component characters with the dependent character is due to their direct effector due to their indirect effect through other characters. The correlation studies provide the nature and magnitude of influence of yield and yield related characters. The relative importance of each character on yield is more clearly depicted with path analysis. Thus, the rate of improvement can be accelerated if differential emphasis is laid on the characters during selection. The difference in the emphasis would be based on the degree of direct and indirect influence of various characters on the economic character of interest. Path coefficient analysis splits the correlation coefficient into direct and indirect effects of the component characters on the yield based on which crop improvement can be carried out more effectively.

If the correlation between yield and any of its component characters is due to the direct effect, this reveals that there exists a true relationship between them. Selection on such characters can improve the yield. If the correlation is due to indirect effect of the character through another character, the character through which the indirect effect is expressed is selected.

In the present investigation, path coefficient analysis was used to separate the genotypic correlation coefficients of green fodder yield with plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index, crude protein content, crude fibre content and dry fodder yield. The characters dry fodder yield, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index, crude protein content, crude fibre content showed direct positive effects on green fodder yield. The characters, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index, crude protein content and dry fodder yield had positive genotypic correlation and direct effect on green fodder yield. This suggests that these characters can be selected directly for crop improvement program (Fig.5).

The character crude fibre content was having negative genotypic correlation with green fodder yield, but has got positive direct effect on green fodder yield. This suggests that restricted simultaneous selection should be applied for the selection of this character. The restrictions are to be imposed to nullify the undesirable indirect effects expressed through other characters, so that the direct effect of these character can be used.

The character plant height has negative direct effect on green fodder yield. Plant height has indirect positive effects on green fodder yield through characters dry fodder yield, number of leaves plant $^{-1}$, crude protein content, number of branches plant $^{-1}$ and leaf area index. It had positive significant correlation with green fodder yield. Though the character has positive correlation with green fodder yield, the direct negative effect indicates that the indirect effects are the cause for the correlation. The indirect effects are to be considered for selection in this case. A case of increase in plant height alone cannot have a direct effect on increase in green fodder yield. Along with increase in the plant height, simultaneously there should be increase for other yield attributing

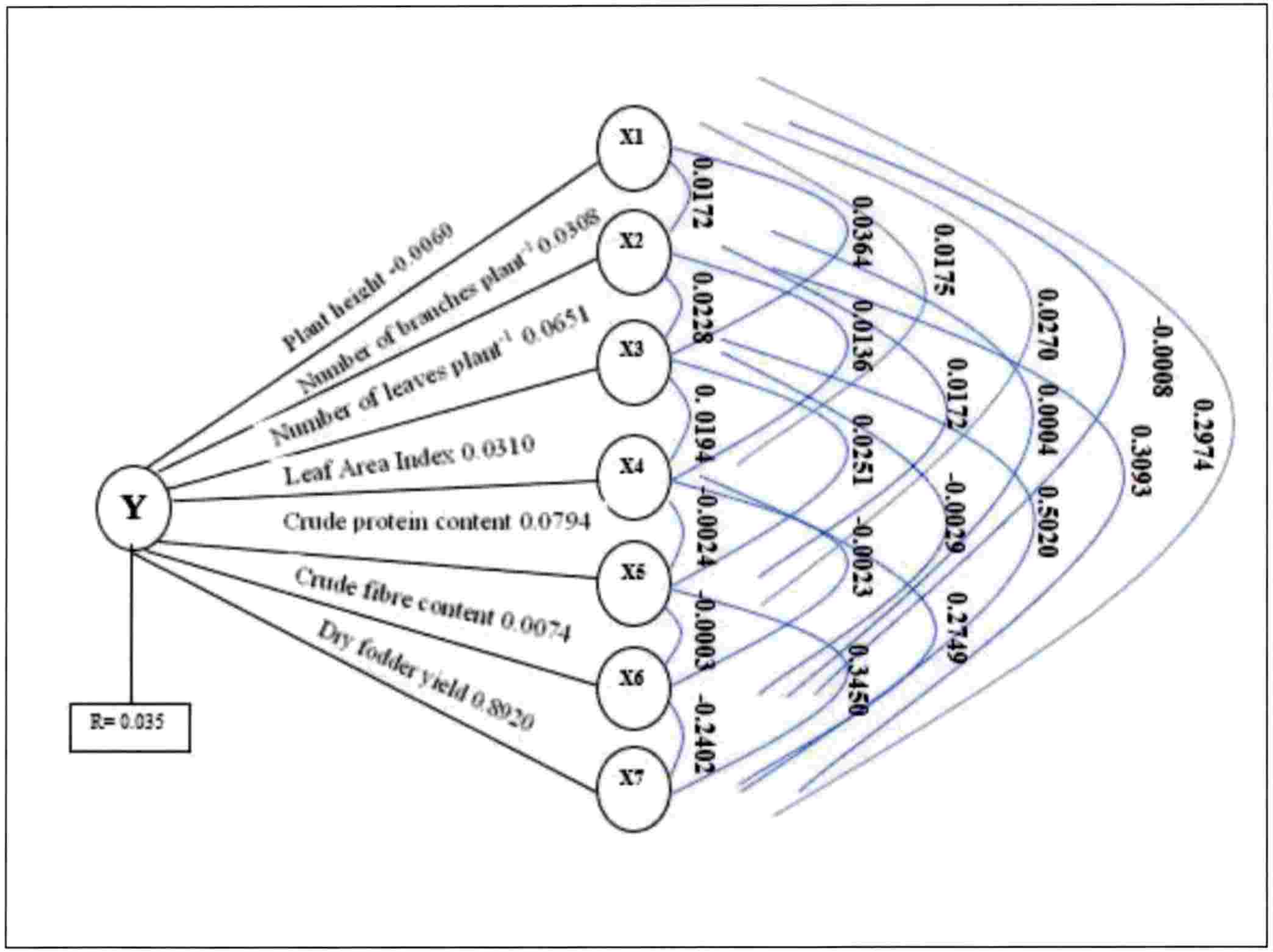

Fig. 5. Path diagram showing direct and indirect effect of different characters on fodder horse gram

characters such as number of branches plant $^{-1}$, number of leaves plant $^{-1}$, and leaf area index.

Results of path analysis by Aravindhan and Das (1995), also showed that dry matter and leaf area index are the main components of green fodder yield which is line with the present study. Santhoshkumar *et al.* (2002) also reported that dry fodder yield had highest direct positive effect on green fodder yield and was followed by number of branches plant $^{-1}$ and plant height. Similar observations were also made by Nath and Tajane (2014) in fodder cowpea where they observed direct positive effect of green fodder yield on dry fodder yield in path analysis.

The residual effect of 0.031 indicates that the characters selected in the present study contributes 96.49 percent to the yield. The lower residual effect indicated that the characters chosen for path analysis were adequate and appropriate. The cause and effect system is well explained by the characters under the study.

a. IC-561040

b. IC-121640

Plate 2. Superior fodder horse gram genotypes identified in the study

c. IC-89016

d. IC-22765

Plate 2 (Continued). Superior fodder horse gram genotypes identified in the study

SUMMARY

6. SUMMARY

The present study on variability analysis in fodder horse gram accessions (*Macrotyloma uniflorum* (Lam.) Verdc.) was conducted at the department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during 2017-19 with an objective identify genotypes with high fodder yield, quality and multicut ability.

The present investigation was conducted with thirty genotypes of fodder horse gram accessions collected from NBPGR. The field experiment was laid in Randomized Block Design (RBD) with three replications during 2018-19. The seeds were soaked overnight for germination. The germinated seeds were dibbled in the field in a spacing of 30 x 25 cm, in a plot size of 2.1 m^2. A total of 28 plants were maintained in each plot and each genotype was considered as each treatment. The genotypes were evaluated for biometric characters which includes plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$ and leaf stem ratio. Quality characters included in the study are crude protein content, crude fibre content and crude protein yield. The physiological characters studied are leaf area index and dry matter production. The yield attributes such as green fodder yield, dry fodder yield and production efficiency were also recorded. The crop was cut at 50 per cent flowering stage. These plants were then allowed to regrow to check their multicut ability. The regeneration ability of the genotypes varied significantly. Statistical analysis *viz* estimates of mean for all different varieties, analysis of variance of the characters, genotypic and phenotypic coefficients of variation, heritability, genetic advance, selection index and path coefficient analysis were also carried out. Analysis of variance showed presence of significant variation in the germplasm for all the characters evaluated.

The mean performance of the characters studied of the 30 fodder horse gram accessions revealed that the genotype T26 (IC-121640) was superior in terms of green fodder yield (22.88 t ha $^{-1}$), number of branches plant $^{-1}$ (6.87), number of leaves plant $^{-1}$ (91.13), dry matter production (4,690.93 kg ha $^{-1}$), dry fodder yield (4.29 t ha $^{-1}$) and

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production efficiency (0.22 t ha $^{-1}$ day $^{-1}$). It was having relatively high protein content (25.23 per cent) and a low fibre content (26.25 per cent). The genotype was found suitable for multicut purpose, as this performed better during both cuts. During the field experiment no incidence of pest attack was noticed. The plants were affected by web blight. The necessary measurements were taken timely.

The variations present in a population is measured by GCV and PCV. The PCV measures the extend of total variation present in a population and is the sum total of GCV and environmental effects. The GCV provides the genetic variability present in the population and is a valid base for comparison. The character leaf area index recorded highest PCV (48.146 per cent) and GCV (47.928 per cent). High PCV and GCV were observed for the characters leaf area index, number of leaves plant $^{-1}$, crude protein yield, dry fodder yield, green fodder yield, production efficiency and dry matter production. The characters plant height and number of branches plant $^{-1}$ showed moderate PCV and GCV. Low PCV and GCV were recorded for leaf stem ratio and crude fibre content. The low values of PCV and GCV indicates lower variability, which limits the scope for improvement of these traits through selection. The PCV and GCV serves as better indices for comparison of quantitative characters that may be expressed in different units.

Heritability provides the information on the degree of inheritance of characters from parents to progeny. High heritability coupled with high genetic advance was observed for the characters leaf area index, number of leaves plant $^{-1}$, crude protein content, green fodder yield, production efficiency, crude protein yield, dry matter production, plant height and dry fodder yield. High heritability coupled with high genetic advance indicates additive gene action which suggests that genetic improvement of these characters can be achieved through selection. The characters number of branches plant $^{-1}$ and crude fibre content had high heritability and moderate genetic advance. The character leaf stem ratio recorded low heritability and low genetic advance.

Selection of genotypes based on suitable index is highly efficient in breeding programs. In the present study, selection index was calculated based on the green fodder yield, plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$ and leaf area index. The genotypes were ranked based on the scores obtained by them. The selection index values ranged from 238.349 to 128.520. The top-ranking genotypes were genotype T26 (IC-121640), T30 (IC-89016), T6 (IC-561040) and T18 (IC-22765).

The yield being a quantitative character is influenced by different component characters in both positive and negative direction. Correlation studies provide information regarding the nature and magnitude of relationship between the characters. When selection is carried out for a trait of interest in a population will simultaneously result in the improvement of other trait that is associated with the trait of interest. The phenotypic and genotypic correlation coefficients of the component characters provide a better understanding of the characters nature and magnitude of contribution towards yield which helps in the selection and improvement of high yielding genotypes.

In the present study, green fodder yield showed positive significant correlation with dry fodder yield, number of leaves plant $^{-1}$, crude protein content, number of branches plant $^{-1}$, plant height and leaf area index. Due to positive correlation, improvement in any one of these characters will simultaneously result in improvement of all other correlated characters. Green fodder yield showed negative correlation with crude fibre content.

Path coefficient analysis splits the genotypic correlation coefficient into direct and indirect effects of the component character on the yield. the knowledge about this can help in the crop improvement. The green fodder yield was significantly and positively correlated with plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index, crude protein content and dry fodder yield at both phenotypic and genotypic levels. Crude fibre content was observed to be negatively correlated with the green fodder yield at both phenotypic and genotypic levels.

Path analysis revealed that the characters number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index and dry fodder yield had positive direct effect on green fodder yield. Plant height had negative direct effect on green fodder yield, in spite of having a positive significant correlation with green fodder yield. Plant height had positive indirect expressed through other characters like number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index, crude protein content and dry fodder yield.

The results from the study shows that genotype T6 (IC-561040) performed superior in terms of yield and yield attributing character plant height during the first cut. The genotype T26 (IC-121640) was found to be suitable for multicut purpose. A multicut fodder crop should be one that have high fodder yield along with supplying nutritious fodder regularly with a stable performance. The genotype T26 (IC-121640) performed better during both the cuts. It was superior for yield attributing biometric characters such as number of branches plant $^{-1}$, number of leaves plant $^{-1}$and leaf area index. It was also observed that the genotype T26 (IC-121640) had considerably high protein content and low fibre content. From the selection index, genotype T26 was found to be superior, followed by genotypes T30 (IC-89016), T18 (IC-22765) and T6 (IC-561040). Thus, the genotype T26 (IC-121640) was found to be superior in terms yield, quality and multicut ability.

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Variability analysis in fodder horse gram
(*Macrotyloma uniflorum* (Lam.) Verdc.)

by

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ABSTRACT

The present study entitled "Variability analysis in fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.)" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2017-2019, with an objective to identify superior genotypes of horse gram for fodder yield, quality and multicut purpose.

The study was conducted with thirty genotypes of fodder horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.), which were collected from NBPGR. These genotypes were evaluated for yield, quality and multicut ability. The field experiment was laid out in Randomized Block Design (RBD) with thirty treatments and three replications during September 2018- January 2019. The crop was cut at 50 per cent flowering stage and was allowed to regrow to check the multicut ability. The observations were taken during the harvest and the recorded data was subjected to statistical analysis. Analysis of variance was conducted for all the characters studied and it was found that the genotypes were significantly different for all the characters, namely plant height (cm), number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf to stem ratio, leaf area index, dry matter production, green fodder yield, dry fodder yield, production efficiency, crude protein content, crude fibre content and crude protein yield. The significant difference shows scope for selection of desirable genetic material for further improvement. The genotype T26 (IC-121640) recorded maximum total green fodder yield (22.88 t ha $^{-1}$) and dry fodder yield (4.29 t ha^{-1}). A minimum green fodder yield of 10.11 t ha^{-1} was recorded for the genotype T27(IC-123022).

The genotype T6 (IC-561040) recorded the maximum green fodder yield (14.97 t ha $^{-1}$) and dry fodder yield (2.11 t ha $^{-1}$) in the first cut. The genotype T6 (IC-561040) performed better for characters such as plant height (144 cm), crude protein yield (0.525 t ha $^{-1}$) and production efficiency (0.25). The genotype T26 (IC-121640) performed superior for characters such as number of branches plant $^{-1}$ (6.87) and number of leaves plant $^{-1}$ (91.13). The genotype T21 (IC-89011) had

highest crude protein content (25.52%) and low value for crude fibre content was estimated for genotype T1 (24.40%). Observations from the regrown plants revealed that the regeneration ability of genotypes varied widely. During the second cut, the highest green fodder yield was recorded for genotype T26 (IC-121640) (9.69 t ha $^{-1}$) along with the highest dry fodder yield (2.44 t ha $^{-1}$). The genotype T26 (IC-121640) recorded the maximum total green fodder yield (22.88 t ha $^{-1}$) and dry fodder yield (4.29 t ha^{-1}). Incidence of web blight was noticed and necessary measurements were taken.

The components of variation namely, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were analysed. High PCV and GCV was observed for characters leaf area index, crude protein yield and number of leaves per plant. The character leaf area index exhibited the highest GCV (48.146%) and PCV (47.928%). Selection can be carried out for these characters which will result in the improvement of the genotypes. High heritability coupled with high genetic advance was observed for the characters *viz.* leaf area index, number of leaves, crude protein content, green fodder yield, crude protein yield, dry matter yield, production efficiency, plant height and dry fodder yield. These characters if selected, would improve over generations.

The green fodder yield was found to be significantly and positively correlated with dry fodder yield, number of leaves plant $^{-1}$, crude protein content, number of branches plant $^{-1}$, plant height and leaf area index. Green fodder yield showed negative correlation with crude fibre content. Path analysis partitions the correlation coefficients into the measures of direct and indirect effects of the characters studied. Path analysis revealed that the characters *viz.* dry fodder yield, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index, crude protein content and crude fibre content had direct positive effect on green fodder yield. The character plant height had negative direct effect on green fodder yield.

The selection index was calculated based on the characters plant height, number of branches plant $^{-1}$, number of leaves plant $^{-1}$, leaf area index and green fodder yield. From the selection index calculated, genotype T26 (IC-121640) ranked first and was followed by genotype T30 (IC-89016) and T6 (IC-561040).

The study revealed that there was wide variability present among the genotypes for all the characters studied. The genotype T26 (IC-121640) which was superior in green fodder yield, dry fodder yield and the yield attributing characters like number of branches plant^{-1} and number of leaves plant $^{-1}$ was found suitable for multicut purpose. The top-ranking genotypes such as T26 (IC-121640), T30 (IC-89016) and T6 (IC-561040) can be forwarded to further trials for variety development.