



Evaluation of Genetic Variability in Fodder Cowpea for Enhancing Yield and its Contributing Traits

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Thirty fodder cowpea genotypes (*Vigna unguiculata* (L.) Walp) were analyzed for different genetic parameters for yield and its contributing traits using Randomized Block Design at Department of Genetics and Plant Breeding, College of Agriculture, Vellayani, Trivandrum. Significant differences among genotypes were observed for the eleven biometric traits studied. High phenotypic and genotypic coefficients of variation were observed for traits such as the number of primary branches, number of leaves per plant, dry matter yield, green fodder yield, leaf and stem dry weights and leaf

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area index. Traits like days to first flowering and days to 50% flowering exhibited high heritability with moderate genetic advance as a percentage of the mean, indicating that selection for these traits would be effective due to additive gene effects. Moderate heritability and high genetic advance as a percentage of the mean were observed for traits such as plant height, number of primary branches and leaves, dry matter yield, green fodder yield, leaf and stem dry weights, leaf area index and leaf-to-stem ratio, suggesting that additive gene action governs these traits to a great extent and offers a good potential for improvement through selection than traits with low heritability. Thus, the information on genetic variability, heritability and genetic advance as a percentage of the mean for yield-related traits provides a valuable foundation for improving traits and developing fodder cowpea genotypes with enhanced fodder yield potential.

Keywords: Fodder cowpea; genetic advance as percent mean (GAM); genotypic coefficient of variation (GCV); heritability; phenotypic coefficient of variation (PCV).

1. INTRODUCTION

Cowpea [*Vigna unguiculata*(L.) Walp. Fabaceae (2n=2x=22)] is one of the leading annual tropical leguminous fodder crops, valued for its high biomass yield, rich protein content, and fast growth. Though native to India, Tropical and Central Africa are regarded as secondary centers of origin. In India, cowpea is grown for food, vegetable and fodder. It is widely cultivated across tropical and subtropical regions, known for being an early-maturing, multi-season pulse crop [1]. Cowpea provides a low-cost source of quality protein, consumed both as a green vegetable and livestock fodder [2]. The green fodder of cowpea is protein-rich (18-21%) [3] and low fiber level improving the nutritional value of feed. Fodder-cum-grain cowpea varieties also help boost livestock nutrition by incorporating cowpea seeds into animal diets. Additionally, cowpea offers significant calories, vitamins, minerals and ample dietary protein and lysine [4]. In India cowpea is grown over 6.5 lakh hectares area with 3.0 lakh under fodder cowpea and productivity varies from 250 to 450 q/ha, depending upon the varieties and agro-climatic zones [3]. It is drought-tolerant crop and thrives under harsh climatic conditions, fitting well into various cropping systems due to its short growth period [5]. Therefore identifying stable fodder cowpea genotypes is essential for developing superior varieties to meet fodder demand [6]. According to the IGFRI Vision 2050, green fodder demand is projected to reach 1012 million tonnes by 2050, while dry fodder demand could rise to 631 million tones [7]. Dagar [8] reported that green forage supply needs to grow by 1.69% annually to close the demand-supply gap.

Fodder yield in cowpea is a complex trait, resulting from various contributing factors, as well as the genetic potential of the genotype and

environmental influences. Understanding the genetic parameters and components controlling yield is essential for improving forage production in cowpea. The best way to achieve higher yields is to utilize the genetic variability of available germplasm to identify high-yielding genotypes that perform well under various environmental conditions. This study analyzed 30 fodder cowpea accessions for variability parameters and genetic diversity to identify promising and diverse accessions for future breeding programs.

2. MATERIALS AND METHODS

The study comprised of 30 genotypes of fodder cowpea obtained from AICRP on Forage Crops and Utilization, which were evaluated for yield and related characters at College of Agriculture, Vellayani under Kerala Agricultural University during April to June of 2024. The genotypes were laid out in randomized block design each with three replications. Seeds soaked overnight in water were dibbled at a spacing of 30 × 15 cm into beds of 3m² area. Data was recorded on five randomly selected plants per replication by harvesting the plants at the time of days to 50 per cent flowering for 11 parameters viz., green fodder yield(g), plant height(cm), days to first flowering, number of primary branches per plant, days to 50% flowering, number of leaves per plant, days to maturity, dry matter yield per plant(g), leaf dry weight per plant(g), stem dry weight per plant(g), leaf to stem ratio, leaf area index (LAI). The statistical analysis for genetic parameters was carried out using GRAPES software of KAU [9]. The range of phenotypic and genotypic coefficient of variation data were estimated adopting the statistical methods suggested by Sivasubramanian and Menon [10] and for heritability and genetic advance by Johnson et al. [11].

3. RESULTS AND DISCUSSION

3.1 ANOVA

The analysis of variance revealed that all the 30 genotypes varied significantly for all the 11 characters indicating that there exists significant variation among the genotypes (Table 1).

3.2 Genetic Variability

The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were ranked as low (<10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Menon [10]. In the present study the estimates of PCV were higher than GCV indicating that these characters were influenced by the environment (Table 2) (Fig. 1). High PCV and GCV were observed for characters like number of primary branches per plant, number of leaves per plant, dry matter yield per plant, green fodder yield per plant, leaf dry weight per plant, stem dry weight per plant and LAI suggesting that selection based on these characters would be feasible for identification of desirable genotypes. These results are similar to the findings of Vamshi et al. [5] for green fodder yield, LAI and dry fodder yield; LAI, green fodder yield, stem dry weight, leaf dry weight Varanya et al. [12]; for green fodder yield and dry fodder yield Phogat et al. [3]; number of branches,

number of leaves, dry weight of leaves, dry weight of stem, dry matter yield and green fodder yield Malarvizhi et al. [13]. High PCV and moderate GCV was observed for plant height and leaf-to-stem ratio. Similar result was obtained by Phogat et al. [3] and Soni et al. [14] for leaf-to-stem ratio. Low PCV and GCV were observed for characters such as days to first flowering, days to 50% flowering and days to maturity indicating that there exists low variability for these characters. These results are in close association with the results of Surender et al. [15] for days to 50% flowering, Vamshi et al. [5] for days to 50% flowering and days to first flowering and Varanya et al. [12] for days to maturity.

3.3 Heritability and Genetic Advance

Heritability estimates for a quantitative trait are vital because environmental factors can alter the phenotypic expression of a genotype during its development. Heritability shows how selection for genotypes can be based on phenotypic variation and it indicates the extent to which phenotypes are determined by their underlying genotypes [14]. Broad sense heritability (h^2) is the ratio between genotypic variance to the total variance (phenotypic variance) in a population and heritability values were rated as low (<30%), moderate (30-60%) and high (>60%) as per Johnson et al. [11].

Table 1. Analysis of variance for 11 characters in fodder cowpea genotypes

Character	Mean sum of square			S.E.m	C.D@5%
	Replication	Genotype	Error		
Days to first flowering	3.68	20.31	1.23	0.64	1.81
Plant height(cm)	229.54	1828.93	450.34	12.25	34.68
Number of primary branches per plant	1.63	2.93	0.77	0.51	1.44
Number of leaves per plant	2.10	251.46	63.30	4.59	13.00
Days to 50% flowering	6.01	20.34	1.21	0.63	1.80
Days to maturity	8.41	20.14	1.09	0.60	1.71
Leaf dry weight per plant	0.23	19.83	6.19	1.44	4.07
Stem dry weight per plant	3.48	53.08	21.62	2.68	7.60
LAI	38.66	27.50	7.86	1.62	4.58
Leaf-to-stem ratio	0.01	0.05	0.01	0.07	0.20
Dry matter yield per plant	5.09	123.77	47.08	3.96	11.21
Green fodder yield per plant	9059.66	19991.65	8391.15	52.89	149.72

Table 2. Estimates of genetic variability parameters of various traits in fodder cowpea genotypes

Character	Mean	PCV (%)	GCV (%)	H2 (%)	GAM (5%)
Days to first flowering	37.21	7.40	6.78	83.80	12.78
Plant height (cm)	129.50	23.29	16.55	50.50	24.23
Number of primary branches per plant	3.63	33.60	23.34	48.30	33.40
Number of leaves per plant	32.27	34.79	24.54	49.80	35.67
Days to 50% flowering	45.41	6.06	5.56	84.10	10.50
Days to maturity	75.58	3.61	3.33	85.40	6.34
Leaf dry weight per plant (g)	9.97	32.88	21.39	42.30	28.67
Stem dry weight per plant (g)	14.91	38.00	21.72	32.70	25.57
LAI	8.66	43.83	29.55	45.50	41.05
Leaf-to-stem ratio	0.70	22.74	15.08	44.00	20.61
Dry matter yield per plant (g)	24.88	34.26	20.32	35.20	24.84
Green fodder yield per plant (g)	251.05	44.10	24.77	31.50	28.66

The PCV and GCV alone cannot reveal the extent of heritable variation. Thus, understanding heritability and genetic advance in quantitative traits is important for carrying out an effective selection process [11]

In the study heritability was high for days to first flowering (83.80%), days to 50% flowering (84.10%) and days to maturity (85.40%) indicating that the variability for these traits is under genetic control and therefore heritable. The results are in accordance with the earlier findings of Phogat et al. [3] and Surender et al. [15] for days to 50% flowering; Sahu [16] for days of 50% flowering and days to maturity. However, it contradicts the observations where moderate heritability was registered for days to first flowering and days to 50% flowering (Vamshi et al. [5], Olayiwola and Soremi [17]). Moderate heritability was observed for all other characters viz., plant height (50.50%), number of primary branches per plant (48.30%), number of leaves per plant (49.80%), dry matter yield per plant (35.20%), green fodder yield per plant (31.50%), leaf dry weight per plant (42.30%), stem dry weight per plant (32.70%), LAI (45.50%), leaf to stem ratio (44.00%) indicating moderate genetic control, implying direct selection for these traits may not be very successful. This observation contradicts the findings of Vamshi et al. [5] who reported plant height, green fodder yield, LAI, dry fodder yield, number of leaves per plant and number of primary branches possess high heritability and Phogat et al. [3] for dry fodder yield, green fodder yield, number of branches, plant height and leaf to stem ratio.

Genetic advance represents the advancement in the mean of selected population over the base population. It can also be expressed as a percentage of the mean, known as genetic advance as a percent of mean (GAM). Traits with

high genetic advance are more likely to respond well to selection, as this suggests a dominance of additive gene effects. The estimation of GAM was classified as high (>20), moderate (10-20) and low (<10) proposed by Johnson et al. [11].

High GAM were obtained for traits like plant height(24.23), number of primary branches (33.40), number of leaves per plant(35.67), dry matter yield per plant (24.84), green fodder yield per plant (28.66), leaf dry weight per plant (28.67), stem dry weight per plant (25.57), LAI (41.05) and leaf to stem ratio (20.61). This indicate that these traits may have high additive genetic variance and under additive gene effects. As these traits are controlled by additive gene action, it suggests there is greater potential for improving these characters in fodder cowpea through selection. This is in agreement with the findings of Rathod et al. [18] for number of leaves per plant, plant height, green forage yield, dry matter yield, leaf to stem ratio and LAI; Siddapur et al. [19] for number of leaves per plant, LAI, green fodder yield, stem dry weight, leaf dry weight, plant height; Surender et al. [15] for plant height, dry fodder yield ,leaf number of primary branches, green fodder yield; Vamshi et al. [5] for green fodder yield, LAI, plant height, dry fodder yield, the number of leaves per plant and number of primary branches; Varanya et al. [12] for number of leaves per plant, LAI, green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, plant height. Phogat et al.[3] for green fodder yield, dry fodder yield, leaf to stem ratio, plant height and the number of branches per plant.

Moderate GAM was obtained for days to first flowering (12.78), and days to 50% flowering (20.61), while low GAM was noted for days to maturity (6.34) indicating that these characters are accompanied by non-additive gene action and may possess low selection value. These results were in line with earlier findings of Vamshi et al. [5] and Phogat et al. [3] for days to maturity.

Broad sense heritability estimate does not serve as a true indicator of genetic potentiality of genotypes. Johnson et al. [11] suggested that using both estimates of heritability and genetic advance together provides a more valuable approach for predicting the effectiveness of selection compared to using heritability alone. The Fig. 2 represents heritability and GAM for selected biometric characters under study.

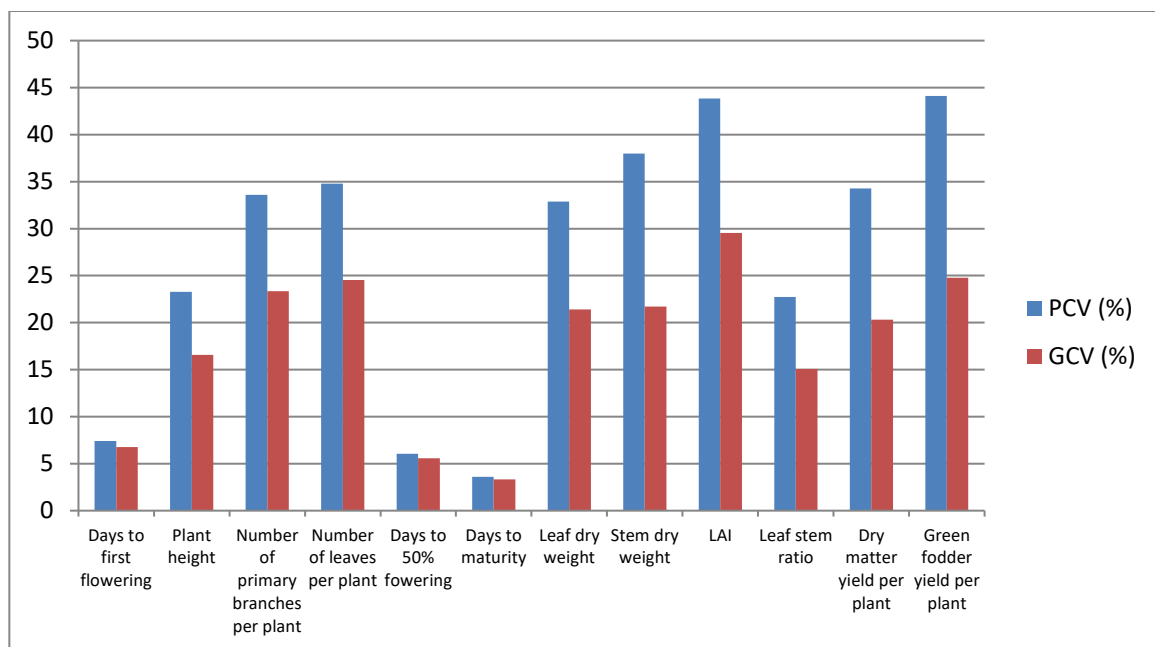


Fig. 1. PCV & GCV for selected biometric characters

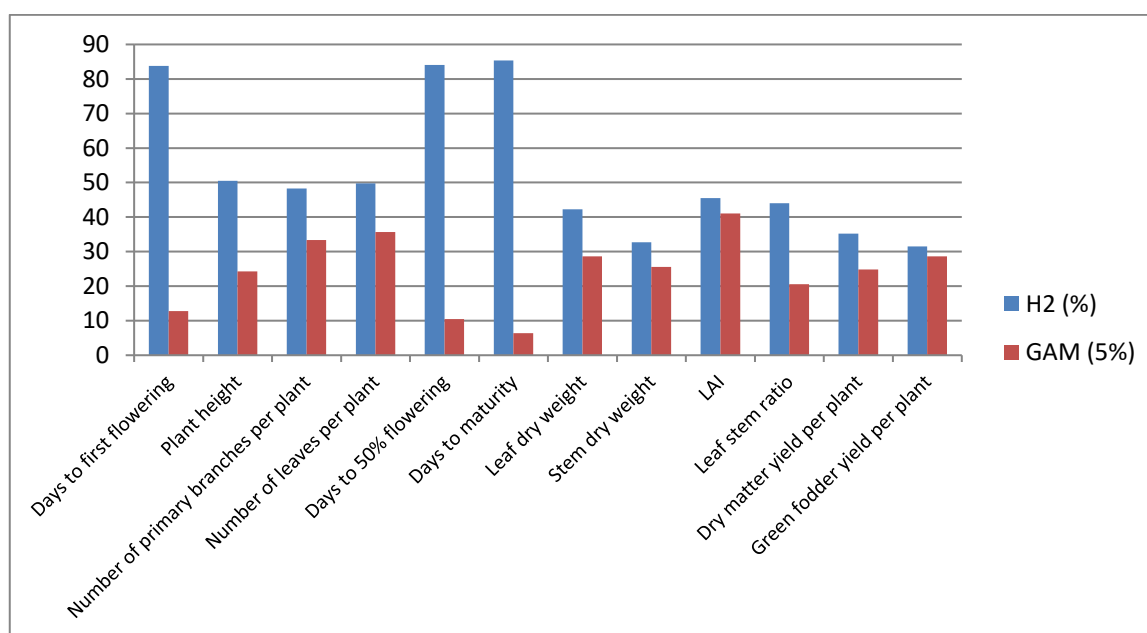


Fig. 2. Heritability & GAM for selected biometric characters

In this study, high heritability along with moderate GAM were obtained for characters like days to first flowering and days to 50% flowering where selection is effective due to additive gene effects. Moderate heritability and high GAM for plant height, number of primary branches per plant, number of leaves per plant, dry matter yield per plant, green fodder yield per plant, leaf dry weight per plant, stem dry weight per plant, LAI, leaf to stem ratio. It reveals the character is governed by additive gene action and moderate heritability is due to the influence of environmental effects, therefore selection will be effective for such traits. High heritability with low genetic advance was found for days to maturity where selection may not be rewarding because of non-additive gene action and favorable influence of environment. This was contrary to the results of Siddapur et al. [19] and Varanya et al. [12] where high heritability and the genetic advance was recorded for number of leaves per plant, LAI, green fodder yield, stem dry weight, leaf dry weight and plant height; Rathod et al. [18] for number of leaves per plant, plant height, green forage yield, dry matter yield, leaf-to-stem ratio and LAI; Vamshi et al. [5] for plant height, number of primary branches, green fodder yield and dry matter yield; Phogat et al. [3] for green fodder yield, followed by dry fodder yield, leaf-to-stem ratio, plant height, days to 50% flowering and number of branches per plant; High heritability with low genetic advance was observed for days to 50% flowering as per Malarvizhi et al. [13]. Vamshi et al. [5] reported moderate heritability and low genetic advance for days to first flowering and a low heritability and genetic advance for days to 50% flowering.

4. CONCLUSION

The current study concluded that the selected genotypes exhibited a wide range of variability, as indicated by the ANOVA results, which revealed significant genotypic differences across all traits. It was found that the PCV values were higher than the GCV values, highlighting the environmental influence on these traits. High heritability in some characters indicates the traits are less influenced by environment. The study found high heritability with moderate GAM for traits such as days to first flowering and days to 50% flowering. Moderate heritability and high GAM were observed for plant height, number of primary branches per plant, number of leaves per plant, dry matter yield per plant, green fodder yield per plant, leaf dry weight per plant, stem weight per plant, LAI and leaf-to-stem ratio,

suggesting that selection would be effective due to additive gene effects. These findings suggest significant potential for improvement through selection, as many of these traits are heritable and can be passed on to future generations.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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