



# **Study of Genetic Variability of Cowpea (*Vigna unguiculata* L) Germplasm for Fodder Yield and It's Attributing 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**

The study investigated the phenotypic and genotypic coefficient of variation (PCV and GCV) and heritability estimates for various agronomic and nutritional traits in cowpea (*Vigna unguiculata*). The analysis aimed to identify traits with optimum variability and heritability, as well as to explore the potential presence of additive genetic variance in specific characteristics. The results revealed that the number of secondary branches, plant height, and leaf length exhibited high estimates of both PCV and GCV, indicating the presence of ample variability for these particular attributes within the population. Additionally, the heritability and genetic advance for the number of secondary branches, plant height, dry fodder yield, leaf length, number of primary branches, leaf width, fresh leaf weight (g), green fodder yield, and fresh stem weight (g) were found to be significant, indicating that these traits were predominantly governed by additive gene action. The findings of this study hold significant implications for future breeding programs and genetic improvement strategies. The

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identified high heritability and genetic advance for the aforementioned traits suggest that these characteristics can be effectively manipulated through selective breeding to develop improved and high-yielding plant varieties.

**Keywords:** Genetic variability; *Vigna unguiculata*; fodder yield; cowpea genotypes.

## 1. INTRODUCTION

“India possesses the largest livestock sector globally, with approximately 11.6 percent of the world's cattle herds and a leading position in milk production. According to the 20th Livestock Census in 2019, India is home to 57.3 percent of the global buffalo population and 14.7 percent of the global cattle population. Maintaining this status requires the production of high-quality, cost-effective feed” [1]. “During the 1990s, green fodder availability for cattle stood at about 60 percent. However, due to a surge in the animal population and depleting resources, this availability has now declined by 50 percent of the total requirement” [2]. Presently, the deficit in green fodder and dry fodder availability is 35.6 percent and 10.95 percent, respectively [3]. Looking ahead to the year 2050, the IGFRI Vision 2050 document estimates a projected demand of 1012 million tonnes of green fodder and 631 million tonnes of dry fodder. To meet this demand-supply gap, Dagar [4] highlights the need to increase net green forage supply by 1.69 percent annually. Over the past several decades, India has made significant efforts to enhance forage crops, leading to the development of various improved fodder crops. Despite their potential in the Indian forage context, certain crops, like fodder cowpea, remain underutilized.

Cowpea (*Vigna unguiculata* (L.) Walp) belongs to Fabaceae having chromosome number  $=2n=2x=22$ , is a widely embraced, early maturing, multi-seasonal, and versatile pulse crop extensively cultivated across tropical and subtropical regions in Africa, Asia, Nigeria, and America [5,6]. “In India, cowpea serves as a minor pulse crop grown in the arid and semi-arid regions of Rajasthan, Gujarat, Maharashtra, Karnataka, and Tamil Nadu, covering a total area of 407.93 lakh ha, with a production of 7925.25 lakh tonnes and a productivity of 19.47 tonnes/ha” [7]. “The crop is valuable for providing high-quality protein-rich food for human consumption, fodder for livestock, and nitrogen fixation, which enhances soil fertility” [8]. Its remarkable ability to adapt to hot, low-rainfall conditions and unpredictable weather patterns sets it apart. Additionally, its short growth

duration allows it to be easily incorporated into various cropping sequences.

One of the critical factors influencing the success of cowpea breeding programs is the presence of genetic variability among cowpea genotypes. Genetic variability refers to the range of genetic differences observed among individuals within a given species. In the context of cowpea, this variability is a treasure trove of diverse traits that can potentially be harnessed to develop improved varieties. The primary focus of exploring genetic variability among cowpea genotypes is to identify desirable traits related to increased fodder yield potential.

“Cowpea is equally important as nutritious fodder for livestock” [6]. “The nutritive value of cowpea grain, leaves, and haulms is very high. The crude protein content ranges from 22 to 30% in the grain and leaves on a dry weight basis” [9,10], and from 13 to 17% in the haulms with high digestibility and low fiber level [11]. “Some farmers sell cowpea fodder during the dry season when feed shortage is critical, and there have been suggestions that income from fodder sales makes a substantial contribution to the annual income in such cases” (ICRISAT 1991). In addition to the direct benefits of improved livestock production and health that result from feeding cowpea fodder, the quantity, and quality of manure from such better-fed animals will be improved and therefore, when returned to the land at the beginning of the growing season, contribute more towards the maintenance of soil fertility.

## 2. MATERIALS AND METHODS

The experimental material comprised 104 cowpea genotypes, including 100 genotypes and 4 check genotypes. These genotypes were tested using an augmented complete block design during the *Kharif-2022* with 5 blocks. This experiment was conducted at ARI Rajendranagar, Hyderabad, Telangana. The source of my experiment material is taken from NBPGR-New Delhi. The genotypes were planted in a single row with a spacing of 30 cm between the rows and 10 cm between the plants within a row.

## 2.1 Traits

**Days to 50 % flowering:** Number of days from planting of the genotypes to the date when at least 50% plants in each plot flowered, was noted down for the five plants and the numerical average of days for attainment of 50 percent flowering was recorded.

**Plant height (cm):** Each of the selected plant was measured and recorded at maturity. The height was considered from the base of fully grown plant to the tip of the main stem; an average was worked out and recorded in cm.

**Number of primary branches (per plant):** To be counted on the main stem at 50% flowering (average of five randomly selected representative plants).

**Number of secondary branches (per plant):** Number of branches arising from primary branches to be counted at 50% flowering (average of five randomly selected representative plants).

**Leaf length (cm):** To be measured on central leaflet of 5<sup>th</sup> fully grown leaf from base at 50% flowering (average of five randomly selected representative plants).

**Leaf width (cm):** To be measured on central leaflet of 5<sup>th</sup> fully grown leaf from base at widest point at 50% flowering (average of five randomly selected representative plants).

**Leaf weight per plant (g/plant):** Weight of green leaves, plucked from the main shoot and branches of a single plant to be recorded at 50% flowering (average of five randomly selected representative plants).

**Stem weight per plant (g/plant):** Green weight of bare main shoot and branches to be recorded from single plants at 50% flowering (average of five randomly selected representative plants).

**Leaf to stem ratio (green weight):** To be recorded as ratio of leaf and stem weight on green weight basis (average of five randomly selected representative plants).

**Green fodder yield per plant (g/plant):** To be recorded as weight of total foliage including stem at 50% flowering (average of five randomly selected representative plants).

**Dry fodder yield per plant (g/plant):** To be recorded as total dry weight of plant by drying in oven at 60°C till constant weight (average of five randomly selected representative plants).

**Dry matter content (%/plant):** The sample plants were collected and weighted fresh; later, they were dried using hot air oven and the final dry wt. was measured. After that the ratio was worked out and the value was recorded.

**Crude protein (%/plant):** Total nitrogen content of the leaf was determined by the Kjeldahl method (Kjeldahl, 1883).

“The total nitrogen content of the plant sample was estimated by micro Kjeldahl method (Kjeltec KES-06L model of Pelican make). From the representative sample of the dried plant material, 0.5 gram was taken in a 100 ml conical flask and 10 ml of concentrated sulphuric acid + 2-5 gram digestion mixture (K<sub>2</sub>SO<sub>4</sub> and CuSO<sub>4</sub> in the ratio of 9:1) was added and digested till the solution becomes clear. Then this was made up to 100 ml and from this, 10 ml aliquot was transferred to the distillation flask. 15-20 ml of 40 per cent sodium hydroxide was added to the distillation assembly to make the contents alkaline. The distillate was collected in 10 ml of two per cent boric acid solution containing 2-3 drops of mixed indicator. The distillation was continued for 10-15 minutes and the distillate collected after rinsing was titrated against 0.01 N sulphuric acid. The crude protein content in per cent was calculated by multiplying the total nitrogen by the factor 6.25” [12].

**Crude fiber (%/plant):** Crude fiber determination was done as per the method of described in AOAC (1995).

### Reagents:

- H<sub>2</sub>SO<sub>4</sub> (1.25 %)
- NaOH (1.25 %)

“Two gram defatted sample was weighed and transferred in a spout less 600ml beaker containing 200ml of 1.25 per cent H<sub>2</sub>SO<sub>4</sub> and boiled for 30 min. After 30 minutes, the beaker was removed and the solution was filtered through Whatman No. 54 filter paper and the residue washed with 100ml hot distilled water using Buchner funnel. The residue was then boiled in 1.25 per cent NaOH solution for exactly 30 min. after 30 min of boiling, the contents were filtered through Whatman No. 54 filter paper and washed with hot distilled water using Buchner funnel under gentle suction. The filter paper with the residue was dried in oven at 105°C for 3 to 4 hours or till constant weight. It was cooled in a desiccator and then weighed. The loss in weight represented the crude fiber content. It was calculated using the following formula” [12].

$$\text{Per cent crude fiber} = \frac{w^2-w^1}{\text{Weight of sample}} \times 100$$

“Mean and range was calculated as per the method proposed by Panse and Sukhtame [13], Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of Variability (GCV) was calculated using the procedure developed by Fisher et al. [14]. The PCV and GCV were categorized as low (less than 10%), moderate (10-20%), and high (more than 20%)” as per Sivasubramanian and Menon [15].

Heritability ( $h^2$ ) was worked out according to Lush et al. (1940) and the values were categorized as low (30 per cent), moderate (30-60 per cent) and high (> 60 per cent) as per Johnson et al. [16] and Genetic Advance as per cent over Mean (GAM) was estimated using the method suggested by Johnson et al. [16]. The range of genetic advance as per cent of the mean was classified as high (> 20%), moderate (10-20 %) and low (<10%) as given by Johnson et al. [16].

### 3. RESULTS AND DISCUSSION

#### 3.1 ANOVA

The analysis of variance (ANOVA) revealed that all the 104 genotypes varied significantly for all the 14 characters indicating that there exists considerable variation among the genotypes.

#### 3.2 Genetic Variability

The high estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for number of secondary branches (37.4) and (35.7), plant height (27.2) and (25.7) and leave length (22.2) and (20.1), indicating that sufficient variability is available for these characters (Table 1).

Selection based on these characters would result in obtaining desirable fodder cowpea genotypes. This result is in accordance with Malarvizhi et al. [17] and Vamshi et al. [12]. S. K. Jain et al. [18], Eswaran et al. [19], Sharma et al. [20], Thaware et al. [21].

(DFF-Days to 50 % flowering, PH- Plant height (cm), NPB-Number of primary branches, NSB-Number of secondary branches, LL-Leaf length (cm), LW-Leaf width (cm), FLW-Fresh leaf weight (g/plant), FSW-Fresh stem weight (g/plant), L/S-Leaf stem ratio, GFY-Green fodder yield (g/plant), DFY-Dry fodder yield (g/plant), DMC-Dry matter content (%/plant), CP-Crude protein (%), CF-Crude fiber (%), GCV-Genotypic coefficient of variation, PCV-Phenotypic coefficient of variation, hBS-Broad sense heritability, GAM-Genetic advance mean.).

The GCV for the characters viz., days to 50 per cent flowering (4.3), Crude protein (5.1) (%), Leaf stem ratio (5.3), Crude fiber (5.7) (%) and Dry matter content (8.0)(%) were found to be low indicating that there exists low variability for these characters. These results are in close association with the results of Eswaran et al. [19], S. K. Jain et al. [18], Sharma et al. [20], Thaware et al. [21], Malarvizhi et al., (2005) and Vamshi et al., [12].

**Heritability and genetic advance:** Heritability is the proportion of observed variability which is due to heredity alone excluding the environmental influence. Lush [22] described it as the proportion of variability due to additive genetic effect. According to Burton [23], the heritability estimates serve as a useful guide in exercising selection and as described by Panse (1957), high heritability along with high genetic advance in a character suggest that the

**Table 1. Estimates of Mean, range, GCV, PCV, heritability and genetic advance as per cent of mean 15 different characters for 104 lines of cowpea taken into consideration**

Trait	Mean	Maximum	Minimum	GCV	PCV	hBS	GAM
DFF	53.7	58.4	50.4	4.3	4.4	94.5	8.6
PH	35.2	53.5	8.2	25.7	27.2	89.3	50.2
NPB	8.5	12.7	3.4	17.1	18.2	88.3	33.0
NSB	6.3	13.4	0.9	35.7	37.4	90.8	70.0
LL	8.8	14.7	4.8	20.1	22.2	81.8	37.4
LW	5.9	8.9	3.4	16.4	17	93.9	32.8
FLW	51.0	67.7	30.8	16.4	17	93.9	32.8
FSW	67.0	86.6	46.9	11.7	12	94.9	23.4
L/S	0.75	0.84	0.65	5.3	5.8	82.7	9.9
GFY	118.1	154.3	77.8	13.7	14.1	94.7	27.4
DFY	23.4	35.6	14.5	19.1	20	91.3	37.6
DMC	19.6	24.0	13.2	8	9.0	78.3	14.6
CP	16.4	19.0	14.0	5.1	6.9	54.4	7.7
CF	28.6	34.3	21.9	5.7	8.2	49.1	8.3

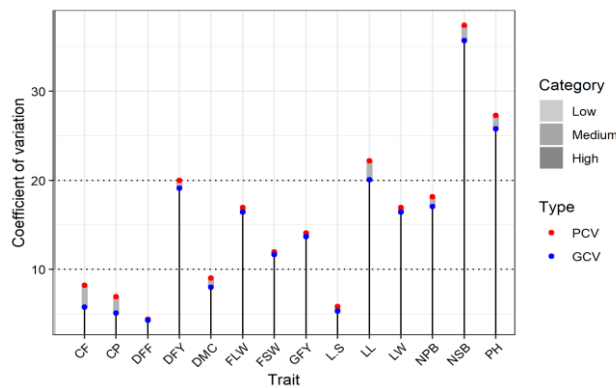
genotypic variation for a character is probably due to high additive genetic effects and the character is least influenced by environmental effect.

The high heritability values indicate that genetic factors strongly influence the observed variation in these traits. In other words, the differences in these traits among the individuals are primarily due to genetic control, with less influence from the environment. Breeding programs focused on improving these traits can be effective because the genetic basis of their variability is predominant.

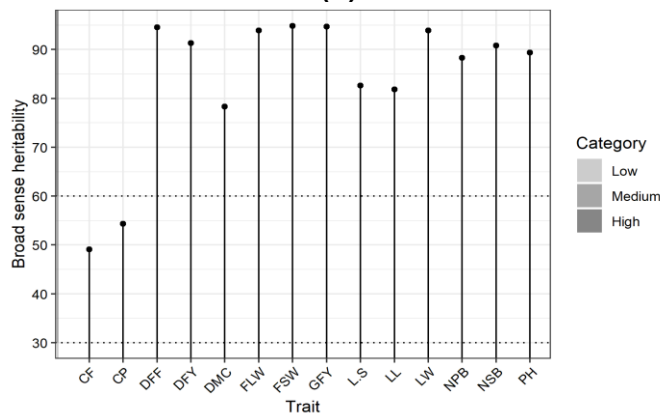
In the present study, high heritability values were observed for Fresh stem weight (94.9) (g), Green fodder yield (94.7) (g), Days to 50% flowering (94.5), Leaf width (93.9) (cm), Fresh leaf weight 93.9) (g), Dry fodder yield (91.3) (g), Number of secondary branches (90.0), Plant height (89.3)(cm), Number of primary branches (88.3), Leaf stem ratio (82.7), Leaf length (81.8) (cm) and Dry matter content (78.3) (%). Moderate heritability value was recorded for Crude protein (54.4) (%), Crude fiber (49.1) (%) selection for

these characters may not be fruitful. “Heritability is a mixture of fixable (additive) and non-fixable (dominant and epistatic) variances; hence it should not be employed exclusively in determining the genetic potentials” [24].

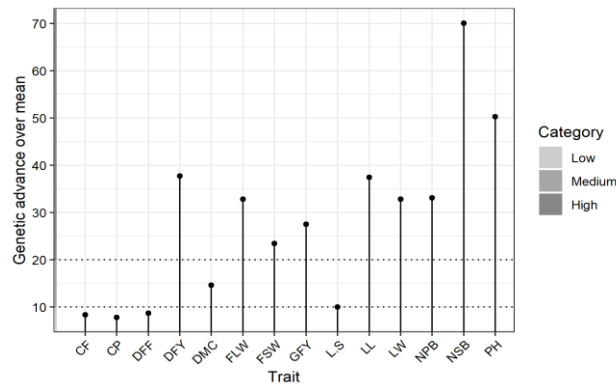
Genetic advance is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population. In the present study, GAM (Genetic advance as per cent of mean) was observed to be high for Number of secondary branches (70.0), plant height (50.2) (cm), Dry fodder yield (37.6) (g), leaf length (37.4) (cm), number of primary branches (33.0), leaf width (32.8) (cm), Fresh leaf weight (32.8) (g), green fodder yield (27.4) (g) and Fresh stem weight (23.4) (g), While low GAM (Genetic advance as per cent of mean) was observed for Leaf stem ratio (9.9), Days to 50% flowering (8.6), Crude fiber (8.3) (%) and Crude protein (7.7) (%). The high GAM indicated that those characters may have high additive genetic variance which is due to additive gene effects. These results were similar to the findings of Malarvizhi et al. [17] and Vamshi et al. [12].



(A)



(B)



(C)

**Fig. 1. Graphical representation of GCV, PCV (A), heritability (B) and genetic advance as per cent mean (C) for the traits understudy**

Johnson et al. [16] proposed that using estimates of heritability and genetic advance together to anticipate the value of selection is more valuable than using heritability alone. In the present study, the heritability and genetic advance was high for the characters Number of secondary branches (90.8) and (70.0), plant height (89.3) and (50.2), Dry fodder yield (91.3) and (37.6), leaf length (81.8) and (37.4), number of primary branches (88.3) and (33.0), leaf width (93.9) and (32.8), Fresh leaf weight (g) (93.9) and (32.8), green fodder yield (91.3) and (27.4), Fresh stem weight (g) (94.9) and (23.4) indicating that these traits were controlled by additive gene action. These results were similar to the findings of Suganthi and Murugan (2008), Bertini et al. [25], Dinesh et al. [26], Patel et al. [27], [28].

#### 4. CONCLUSION

In conclusion, the study revealed significant levels of phenotypic and genotypic coefficient of variation for various plant characteristics, highlighting the presence of ample variability for these traits. Particularly, number of secondary branches, plant height, and leaf length demonstrated the highest estimates of PCV and GCV, indicating considerable genetic diversity within the population for these attributes.

In addition, traits like the number of secondary branches, plant height, dry fodder yield, leaf length, number of primary branches, leaf width, fresh leaf weight (g), green fodder yield, and fresh stem weight (g) have high heritabilities and genetic progress, suggesting that these traits are primarily controlled by additive gene action. This indicates that there is tremendous room for improvement through selective breeding because these qualities are heritable and transferable to subsequent generations.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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