

Original Research Article

**STUDY OF GENETIC VARIABILITY FOR FODDER YIELD AND
YIELD ATTRIBUTES IN GERMPLASM OF COWPEA (*VIGNA
UNGUICULATA* (L.) WALP).**

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 sufficient variability and high 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 identified high heritability and genetic advance for the

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aforementioned traits suggest that these characteristics can be effectively manipulated through selective breeding to develop improved and high-yielding plant varieties.

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, as emphasized by Kumari *et al.* in 2017. 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, as noted by Agrawal *et al.* in 2008. Presently, the deficit in green fodder and dry fodder availability is 35.6 percent and 10.95 percent, respectively, as reported by Singh *et al.* in 2022. 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 (2017) 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., Fabaceae ($2n=2x=22$)] 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 (Ehlers and Hall, 1997; Singh *et al.*, 1997). 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 (Kumar *et al.*, 2020). The crop is valuable for providing high-quality protein-rich food for human consumption, fodder for livestock, and nitrogen fixation, which enhances soil fertility (Murdock *et al.*, 2008). 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.

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 season of 2022. The genotypes were planted in a single row with spacing of 30cm between the rows and 10cm between the plants within a row. The experiment was organized into 5 blocks.

Comment [ak2]: Mention the experimental site where experiment was performed

Mean and range was calculated as per the method proposed by Panse and Sukhtame (1967), Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of Variability (GCV) was calculated using the procedure developed by Fisher *et al.* (1932). The PCV and GCV were categorized as low (less than 10%), moderate (10-20%), and high (more than 20%) as per Sivasubramanian and Menon (1973). 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.* (1955) and Genetic Advance as per cent over Mean (GAM) was estimated using the method suggested by Johnson *et al.* (1955). The range of genetic advance as per cent of the mean was classified as high (> 20%), moderate (10-20 %) and low (<10%) Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed that all the 104 genotypes varied significantly for all the 14 characters indicating that there exists considerable variation among the genotypes. The PCV and GCV values were categorized according to Sivasubramanian and Menon (1973).

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Genetic variability:

The high estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for number of secondary branches, plant height and leaf length, 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.*, (2005) and Vamshi *et al.*, 2022.

Table 1. Magnitude of variability, heritability and genetic advance as per cent of mean different characters in the advanced lines of forage cowpea studied during kharif, 2022.

| 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 |

Comment [ak4]: Include value of CV in the table

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, Crude protein (%), Leaf stem ratio, Crude fiber (%) and Dry matter content (%) were found to be low indicating

that there exists low variability for these characters. These results are in close association with the results of Malarvizhi *et al.*, (2005) and Vamshi *et al.*, 2022.

Heritability and genetic advance: Heritability is the proportion of observed variability which is due to heredity alone excluding the environmental influence. Lush (1940) described it as the proportion of variability due to additive genetic effect. According to Burton (1952), 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 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 (g), Green fodder yield, Days to 50 % flowering, Leaf width (cm), Fresh leaf weight (g), Dry fodder yield, Number of secondary branches, Plant height (cm), Number of primary branches, Leaf stem ratio, Leaf length (cm) and Dry matter content (%). Moderate heritability value was recorded for Crude protein (%), Crude fiber (%) 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 (Olayiwola and Soremi, 2014).

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 was observed to be high for 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, While low GAM was observed for Leaf stem ratio, Days to 50 % flowering, Crude fiber (%) and Crude protein (%). 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.*, (2005) and Vamshi *et al.*, 2022.

Johnson *et al.*, (1955) 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, plant height, Dry fodder yield, leaf length, number of primary branches, leaf width, Fresh leaf weight (g), green fodder yield, Fresh stem weight (g) indicating that these traits were controlled by additive gene action.

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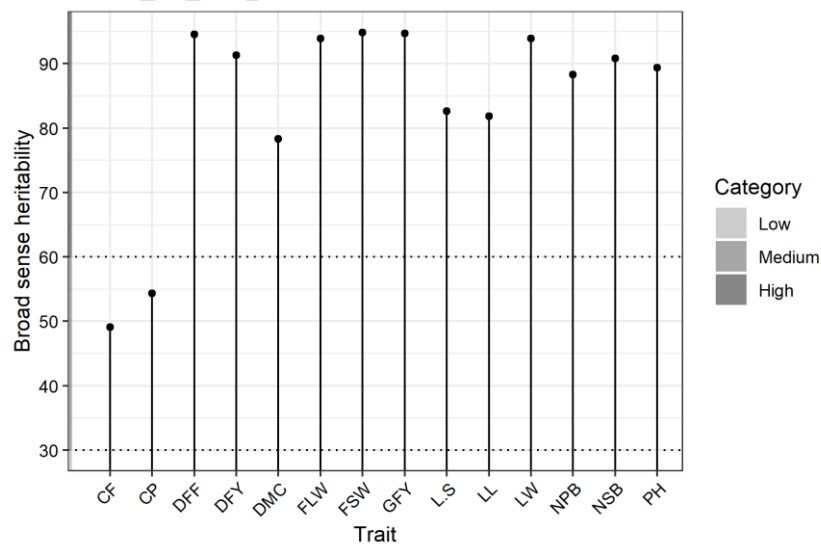
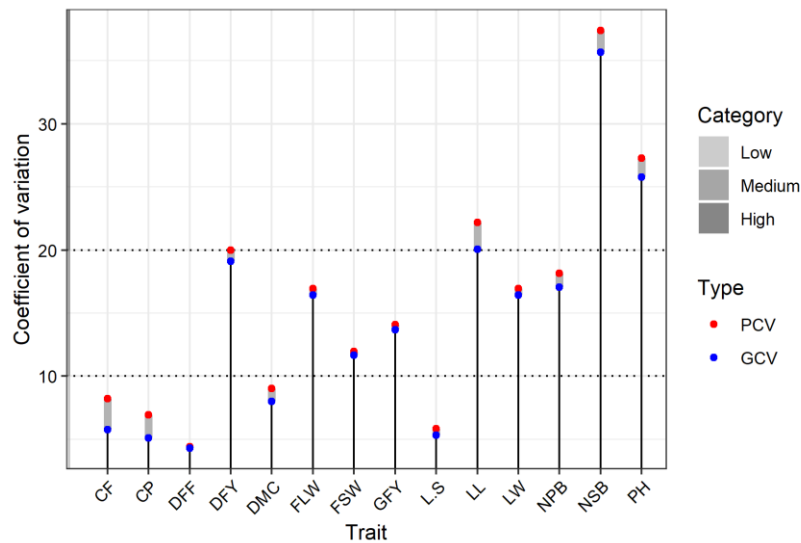


Figure 1. Graphical representation of GCV, PCV, heritability and genetic advance as per cent mean for the traits understudy.

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.

Moreover, the high heritability and genetic advance observed for traits such as 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) suggest that these traits are predominantly governed by additive gene action. This signifies that the potential for improvement through selective breeding is significant, as these traits are heritable and can be passed on to the next generations.

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