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# EVALUATION OF VARIABILITY PATTERN AMONG COWPEA ACCESSIONS

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**ABSTRACT**

The experiment was conducted to study the forage yield and its attributing traits in 46 accessions for seventeen agro-morphological traits. Analysis of variance revealed a significant amount of variability present in the studied materials. The genotypic and phenotypic co-efficient of variation recorded were high for green forage yield per plant, plant height and most of the traits, whereas the lowest phenotypic and genotypic coefficient of variation were obtained for the characters leaflet length. High heritability coupled with high genetic advance recorded respectively *viz*., for seed per pod, plant height and dry matter yield per plant.

***Key words*:** Cowpea, Forage yield, Germplasm, Variability parameters.

## Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.; Fabaceae) is an important legume and forage crop in the Indian economy as part of the traditional cropping systems and it is considered as a strategic crop because of its multiple uses as human food, animal feed, source of nitrogen for soil restoration and income for resource poor farmers as well as small scale processors. Fodder cowpea (*Vigna unguiculata* (L.) Walp) is reported better than other forage legumes in terms of both quantity and quality in semiarid areas. The average protein content of cowpea fodder is 21%, with 60% dry-matter digestibility. Due to its ability to restore soil fertility, improve soil physical properties and provide quality forage, it plays a vital role in the dairy farming sector in India. Genetic parameters *viz*., phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance provide an insight about the characteristics of different genotypes. A better and accurate breeding scheme can be devised when a breeder is known to all aspects of the traits under study. Finding a variety of lines appropriate for hybridization initiatives requires a methodical evaluation of the resources available in order to advance any breeding operation. The objective of the current study was to determine variability parameters of forage yield and its components while studying 46 Cowpea (*Vigna unguiculata* (L.) Walp) accessions, supplemented by parallel insights from diverse variability assessments in other crops (Sahu, 2021; Sahu *et al*., 2023; Mishra *et al*., 2025).

## Materials and Methods

Experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidalaya, Raipur, Chhattisgarh, India. Chhattisgarh is located between 17°14’N and 24°45’N latitudes and 79°16’E and 84°15' E longitudes. Raipur is the capital of the Chhattisgarh state and lies at 21°16’N latitude and 81°36' E longitude with an altitude of 289.60 meters above mean sea level. The experimental materials comprised 46 germplasm linesincluding 2 checks (UPC-5286, UPC-9202) grown in RBD statistical design with 2 replications and evaluated as per minimal descriptors – Indian grassland and Fodder Research Institute, Jhansi, India. Seventeen characters studied *viz*., day to 50% flowering (DFF), plant height (cm), leaf length (cm), leaf width (cm), stem width (cm), number of primary branches, number of secondary branches, number of nodes, internode length, day to maturity, pod length (cm), number of locules per pod, day of maturity, 100-seed weight (g), seed yield/ plant (g), seed per pod, seed yield per plot,

**Table 1:** Analysis of variance for Green forage yield and its attributing traits in Cowpea.

| MEAN SUM OF SQUARE | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Source of variation | DOF | DTF | PH | LL | LW | SG | NPB | NSB | NN | IL |
| Replication | 1 | 13.31 | 7.75 | 40.71 | 5.6 | 0.9 | 1.83 | 0.28 | 12.56 | 1.92 |
| Treatment | 45 | 128.18** | 4983.63 ** | 2.02 ** | 1.25 ** | 0.49 ** | 1.49 ** | 0.52 ** | 6.62 ** | 0.63 ** |
| Error | 45 | 33.13 | 507.96 | 0.58 | 0.44 | 0.1 | 0.7 | 0.44 | 2.85 | 0.24 |
| **MEAN SUM OF SQUARE** | | | | | | | | | | |
| Source of variation | DOF | DM | NSP | SYP | SW | CP | LSR | GYP | DMP | SYPP |
| Replication | 1 | 71.31 | 1.31 | 0.01 | 131.56 | 32.63 | 0.14 | 17.91 | 2.88 | 0.0083 |
| Treatment | 45 | 402.09 ** | 22.95 ** | 0.66 ** | 1206.55 ** | 14.67 ** | 0.05 ** | 182.01 ** | 19 ** | 18.63** |
| Error | 45 | 27.13 | 0.64 | 0.01 | 37.16 | 5.37 | 0.02 | 23.05 | 2.23 | 0.45 |

** Significant at 1 % probability level, *Significant at 5 % probability level; DOF: Degree of freedom; DTF: Day to 50% flowering; PH: Plant height (cm); LL: Leaf length (cm); LW: Leaf width (cm); SG: Stem girth (cm); NPB: No. of primary branches; NSB: No. of secondary branches; NN: No. of nodes; IL: Internode length (cm); DM: Days to maturity; NSP: No. of seeds per pod; SYP: Seed yield per plot (kg); SW: 1000 seed weight; CP: Crude protein %; LSR: Leaf stem ratio; GYP: Green forage yield per plant (g); DMP: Dry matter yield per plant (g); SYPP: Seed yield per plant (g)

crude protein, leaf stem ratio, green forage yield per day (q/ha/day), dry matter yield (q/ha), dry matter yield per plant and green forage yield per plant.

## Results and Discussion

Analysis of variance was carried out for seventeen characters which indicated the existence of sufficient variability among the genotypes for the mentioned characters and sufficient scope for development of genotypes. The high phenotypic coefficient of variation and genotypic coefficient of variation were recorded for plant height followed by dry matter yield per plant, internode length and green forage yield per plant. Some characters only show high phenotypic coefficient of variation but not high genotypic coefficient of variation; these characters are stem girthness, number of primary branches, number of nodes. Whereas, the lowest phenotypic and genotypic coefficient of variation were obtained for the character leaflet length. The moderate phenotypic coefficient of variation and genotypic coefficient of variation were recorded for days to 50% flowering, leaflet width and most of the traits. Moderate

**Table 2:** Genetic variability parameters for green forage yield and its attributing traits in cowpea.

| | Chara-cters | Maxi-mum | Mini-mum | Grand mean | S.D. | SE | CV (%) | PCV (%) | GCV (%) | $H^2$(bs) % | GA | GA (as % of mean ) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | DTF | 76.5 | 45 | 62.533 | 8.01 | 5.757 | 9.206 | 14.36 | 11.02 | 58.9 | 10.9 | 17.430 |
| 2 | PH | 183.2 | 44.55 | 109.329 | 49.92 | 22.538 | 20.615 | 47.93 | 43.27 | 81.5 | 87.98 | 80.472 |
| 3 | LL | 9.95 | 5.45 | 8.304 | 1.01 | 0.762 | 9.179 | 13.75 | 10.24 | 55.5 | 1.3 | 15.654 |
| 4 | LW | 7.15 | 4.5 | 5.869 | 0.79 | 0.665 | 11.330 | 15.68 | 10.83 | 47.8 | 0.9 | 15.336 |
| 5 | SG | 3.3 | 1.25 | 2.214 | 0.5 | 0.326 | 14.746 | 24.8 | 19.93 | 64.6 | 0.73 | 32.970 |
| 6 | NPB | 6.5 | 2.5 | 4.663 | 0.86 | 0.839 | 17.989 | 22.46 | 13.45 | 35.9 | 0.77 | 16.512 |
| 7 | NSB | 3.7 | 2 | 2.823 | 0.51 | 0.210 | 7.454 | 18.97 | 17.45 | 84.6 | 0.93 | 32.946 |
| 8 | NN | 13.50 | 6 | 9.826 | 1.82 | 1.689 | 17.193 | 22.16 | 13.98 | 39.8 | 1.78 | 18.115 |
| 9 | IL | 3.5 | 1 | 1.992 | 0.57 | 0.492 | 24.693 | 33.33 | 22.38 | 45.1 | 0.62 | 31.111 |
| 10 | DM | 123 | 72.5 | 100.337 | 14.18 | 5.209 | 5.192 | 14.6 | 13.65 | 87.4 | 26.36 | 26.271 |
| 11 | SP | 19.5 | 6 | 12.120 | 3.39 | 0.805 | 6.645 | 28.35 | 27.56 | 94.5 | 6.69 | 55.199 |
| 12 | SY | 4.65 | 2.14 | 3.194 | 0.58 | 0.123 | 3.866 | 18.3 | 17.89 | 95.5 | 1.15 | 36.006 |
| 13 | SW | 153 | 61 | 99.891 | 24.56 | 6.103 | 6.096 | 24.96 | 24.21 | 94 | 48.3 | 48.352 |
| 14 | CP | 27.17 | 17.8 | 22.048 | 2.71 | 2.318 | 10.512 | 14.36 | 9.78 | 46.4 | 3.03 | 13.743 |
| 15 | LSR | 1.53 | 0.75 | 0.991 | 0.16 | 0.152 | 15.367 | 19.46 | 11.94 | 37.7 | 0.15 | 15.136 |
| 16 | GFY | 59.5 | 16 | 33.372 | 9.54 | 4.801 | 14.388 | 30.34 | 26.71 | 77.5 | 16.17 | 48.454 |
| 17 | DMY | 13.1 | 2.5 | 7.910 | 3.08 | 1.495 | 18.895 | 41.2 | 36.61 | 79 | 5.3 | 67.005 |
| 18 | SYP | 17.6 | 4.96 | 9.033 | 3.05 | 0.678 | 7.284 | 33.21 | 32.40 | 95.2 | 6.06 | 67.087 |

DTF = Day to 50% flowering; PH = Plant height (cm); LL = Leaf length (cm); LW = Leaf width (cm); ST= Stem girth (cm); NPB = Number of primary branches; NSB = Number of secondary branches; NN = Number of nodes; IL = Internode length (cm); DM = Days to maturity; SP = Seed per pod; SY = Seed yield per plot (kg); SW = 1000 Seed weight (g); CP = Crude protein; LSR = Leaf stem ratio; GFY = Green forage yield per plant (g); DMY= Dry matter yield per plant (g); SYP= Seed yield per plant (g)

genotypic coefficients of variation were recorded for stem girthness followed by number of primary branches and number of nodes while low genotypic coefficients of variation were recorded for crude protein %. Magnitude of GCV and PCV for majority of the traits were closer suggesting that genotype contribution is greater rather than phenotype. So, the selection can be very well on the phenotypic values. The GCV and PCV values indicated that a lot of variability exists among the genotypic and phenotypic level and better chances of improvement is possible by selection. These findings of GCV and PCV values are in close harmony with the result of Jain *et al.*, (2025) and Manggoel *et al.*, (2012) for 100-seed weight and grain yield, and echo the genetic architecture variability observed in relevant studies by Sahu *et al.* (2023) in oat (*Avena* sp. L.), Yadav and Sahu (2022) in tree bean (*Parkia timoriana*) and Upadhyay *et al.*, (2009) in dolichos bean (*Dolichos lablab* L.).

High broad sense heritability values indicated the predominance of additive gene action in the expression of these traits and can be improved through individual plant selection. High heritability estimates were recorded for seed yield per plot followed by number of seed per pod, 1000 seed weight, days to maturity, green forage yield and so many traits. Others characters such as stem thickness, days to 50% flowering and leaflet length indicated medium heritability. No characters were categorized as having low heritability. High heritability indicated that these characters were highly heritable and governed by additive gene effects. The phenotypic values could give a fairly good idea about their genetic material. The findings are in conformity to the findings of previous workers Bhadru and Navale (2012), Nwosu *et al.*, (2013), and Sahu *et al.*, (2008) in basil (*Ocimum* spp.).

High genetic advance as percentage of mean were recorded for plant height followed by seed yield per plant and dry matter yield per plant while the moderate genetic advance as percentage of mean were recorded for green forage yield per plant, followed by 1000 seed weight and seed yield per plot. Low genetic advance as percentage of mean were recorded for days to maturity, number of nodes and most of the traits. The findings are in conformity to the findings of previous workers Verma *et al.*, (2016) and Nair *et al.*, (2018).

## Conclusion

Significant amount of genetic variability was observed for most of the quantitative traits and the GCV and PCV values indicated that a lot of variability exists among the genotypes at genotypic and phenotypic level, and high genetic advance were recorded which indicated better chances of improvement is possible by selection. High estimates of heritability with high genetic advance as percentage of mean was recorded for plant height (cm), days to maturity, 1000 seed weight (g) indicating predominance of additive gene action and selection based on these traits may be effective and sufficient improvement in seed yield may be achieve through selection of these traits.

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