# Assessment of Genetic Variability in $M_3$ Generation of Cowpea (*Vigna unguiculata* L. Walp)

## Abstract

The experiment material comprised of 150 mutant lines including two checks *viz.,* RC-19 and RC-101 of cowpea to study genetic parameters for eleven characters. The estimates of PCV were found to be higher than estimates of GCV for all the eleven characters it showed that the apparent variation is not only due to genotypes but also due to the influence of environment. Higher GCV and PCV was observed for number of primary branches per plant and seed yield per plant. The estimates of heritability were observed higher for all the characters. Genetic advance as percentage of mean were higher observed for number of primary branches per plant, seed yield per plant, number of seeds per pod, number of pods per plant, pod length, harvest index and biological yield per plant.

**Keywords**: Cowpea, Genetic advance, GCV, Heritability and PCV

## Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most important food and forage legumes in the semi-arid tropics that include parts of Asia, Africa, Southern Europe, Southern United States and Central and South America (Simion, 2018). Cowpea has recently gained popularity among consumers and researchers worldwide due to its numerous health benefits including anti-diabetic, anti-cancer, anti-hyperlipidemic, anti-inflammatory and anti-hypertensive qualities (Jayathilake *et al.*, 2018). Cowpea grain is nutritionally similar to other pulses with a low-fat level and a high total protein content. Young leaves and succulent pods are utilized as vegetables in fresh form, while grain is used to produce a variety of snacks and main meal recipes. Cowpea is a nutrient dense food with a low energy density. Cowpea seed contains a good amount of protein (22-24%), carbohydrate (55-66%), iron (0.005%), calcium (0.08-0.11%) and essential amino acids (lysine 7.3-8.74 g/100g protein, leucine 6.45-8.5 g/100g protein, isoleucine 4.17-5.46 g/100g protein, threonine 3.89-5.12 g/100g protein, histidine 1.85-2 g/100g protein). Its starch is absorbed more slowly than cereal starch, which is better for human health (Jayathilake *et al*., 2018). Mutations brings heritable changes in genetic material, are the ultimate source of genetic variation among individuals. Mutation breeding offers enormous potential for enhancing genetic variation in qualitative and quantitative characteristics, as well as for broadening the genetic base. The effectiveness of mutant breeding is based on the creation of adequate genetic variation without much detrimental effects in plant type and its performance in terms of productivity and nutritional factors. It also depends on effective and need based selection, as well as closely monitoring changes at the plant level. Furthermore, creating genetic variation in this crop through gene recombination by hybridization is challenging and time consuming due to small, delicate floral structures that result in poor crossed seed setting in artificially hybridized buds (Bhosle, 2010).

## Materials and methods

The present investigation was carried out during *Kharif* 2022 at the Research Farm of Rajasthan Agriculture Research Institute Durgapura. This experiment material comprised of 150 mutant lines including two checks *viz.,* RC-19 and RC-101 of cowpea. The experimental materials of cowpea were sown in augmented block design with single row (4m) of each mutant line. The row to row and plant to plant distance was kept at 45 cm and 10 cm. All the recommended package of practices was be followed to raise a healthy crop. The analysis of variance for individual characters was carried out using the method given by Federer (1956). The observations were recorded for eleven characters viz, days to 50% flowering, number of primary branches per plant, numbers of pods per plant, pod length (cm), numbers of seeds per pod, days to maturity, plant height (cm), seed yield per plant (g), 100-seed weight (g), biological yield (g) and harvest index (%). The observations were recorded on five randomly selected plants from each line for all characters except days to 50% flowering and days to maturity which were recorded on plot basis. Genotypic coefficients of variance (GCV) and phenotypic coefficients of variance (PCV) were calculated by using the formula suggested by Burton (1952). Heritability in broad sense ($h^2$) was calculated according to the formula suggested by Burton and De Vane (1953). Genetic advance was worked out as per formula suggested by Johnson *et al.* (1955).

## Results and discussion

In variety RC-19, the analysis of variance revealed existence of significant difference in the $M_3$ generation for all the characters studied (Table 1). The mean squares due to entries and treatments were significant for all the characters studied whereas mean squares due to blocks were non-significant for all the characters except plant height. The mean squares due to checks were non-significant for all characters except number of primary branches per plant, pod length, days to maturity, plant height and 100-seed weight. Dividing the entries sum of squares into vivid components shows checks v/s treatments most of the characters were non-significant except number of pods per plant, pod length, number of seed per pod, days to maturity and plant height. Similar results were also observed by Ramakrishnan *et al.* (2018) and Reni *et al.* (2022).

The genetic variability parameters are presented in table 2. The estimates of PCV were found to be higher than estimates of GCV for all the eleven characters it showed that the apparent variation is not only due to genotypes but also due to the influence of environment. Higher GCV and PCV was observed for number of primary branches per plant and seed yield per plant. Medium GCV and PCV was observed for number of seeds per pod followed by pod length, number of pods per plant, harvest index and biological yield per plant whereas, plant height, 100-seed weight, days to 50% flowering and days to maturity had low genotypic coefficient of variation phenotypic coefficient of variation. Similar results were also observed by Wani *et al.* (2012), Padavai (2015) and Goyal *et al.* (2021).

The estimates of heritability were observed higher for all the characters *viz.*, seed yield per plant, number of seeds per pod, number of pods per plant, pod length, days to maturity, biological yield per plant, plant height, days to 50% flowering, 100-seed weight, number of primary branches per plant and harvest index. Similar results were also observed by Wani *et al.* (2012), Padavai (2015) and Mahamune (2018).

Genetic advance as percentage of mean were higher observed for number of primary branches per plant followed by seed yield per plant, number of seeds per pod, number of pods per plant, pod length, harvest index and biological yield per plant. Medium genetic advance as percentage of mean was observed for plant height and 100-seed weight whereas, days to 50% flowering and days to maturity had low genetic advance as percentage of mean. Similar results were also observed by Azad (2012), Kashid (2016) and Goyal *et al.* (2021).

## Conclusion

The results of the present investigation indicate, the presence of adequate genetic variability within among the genotypes. Therefore, induced genetic variability can be successfully utilized to develop new cultivars of cowpea.

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**Table 1: Analysis of variance for different character in variety RC-19 of cowpea in $M_3$ generation**

| Source of variation | Blocks (eliminating treatments) | Entries (checks + treatment) | Checks | Treatments (ignoring blocks) | C vs T | Error |
|---|---|---|---|---|---|---|
| **d. f.** | **9** | **151** | **1** | **149** | **1** | **9** |
| **Days to 50 % flowering** | 0.09 | 4.74** | 3.20 | 4.76** | 3.52 | 0.97 |
| **No. of primary branches/ plant** | 0.01 | 0.45** | 1.80** | 0.44** | 0.28 | 0.09 |
| **No. of pods/ plant** | 0.06 | 1.68** | 0.02 | 1.64** | 9.68** | 0.13 |
| **Pod length (cm)** | 0.06 | 2.47** | 1.21** | 2.45** | 7.38** | 0.20 |
| **No. of seeds/pod** | 0.03 | 1.71** | 0.45 | 1.57** | 23.91** | 0.11 |
| **Days to maturity** | 1.42 | 9.52** | 72.20** | 7.56** | 237.25** | 0.98 |
| **Plant height (cm)** | 4.71** | 10.12** | 380.90** | 7.11** | 88.40** | 1.41 |
| **Seed yield/ plant (g)** | 0.43 | 3.43** | 0.23 | 3.46** | 1.00 | 0.20 |
| **100-seed weight (g)** | 0.10 | 0.35** | 0.64** | 0.35** | 0.20 | 0.10 |
| **Biological yield (g)** | 2.07 | 15.07** | 8.37 | 15.21** | 1.86 | 2.41 |
| **Harvest index (%)** | 14.53 | 41.65** | 1.87 | 42.17** | 5.25 | 10.64 |

** Significant at 1% level of significance

**Table 2: Genetic variability parameters for yield and its component characters in variety RC-19 of cowpea in $M_3$ generation**

| Characters | Mean | Range | | GCV | PCV | Heritability (bs) (%) | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|
| | | Min. | Max. | | | | |
| **Days to 50 % flowering** | 38.85 | 33.90 | 46.90 | 5.01 | 5.62 | 79.46 | 9.21 |
| **No. of primary branches/plant** | 2.49 | 0.76 | 4.96 | 23.8 | 26.78 | 78.9 | 43.6 |
| **No. of pods/ plant** | 6.93 | 3.07 | 9.67 | 17.74 | 18.46 | 92.4 | 35.19 |
| **Pod length(cm)** | 8.43 | 2.93 | 11.93 | 17.77 | 18.53 | 91.99 | 35.17 |
| **No. of seeds/pod** | 6.49 | 2.85 | 9.45 | 18.56 | 19.26 | 92.84 | 36.9 |
| **Days to maturity** | 64.43 | 59.60 | 74.60 | 3.98 | 4.26 | 87.07 | 7.66 |
| **Plant height (cm)** | 24.89 | 20.60 | 35.13 | 9.57 | 10.69 | 80.09 | 17.67 |
| **Seed yield/ plant (g)** | 8.61 | 4.47 | 13.87 | 20.98 | 21.63 | 94.14 | 42.03 |
| **100-seed weight (g)** | 7.83 | 5.94 | 9.83 | 6.76 | 7.61 | 78.96 | 12.39 |
| **Biological yield (g)** | 25.63 | 14.47 | 36.30 | 13.96 | 15.22 | 84.15 | 26.42 |
| **Harvest index (%)** | 33.80 | 18.48 | 58.39 | 16.61 | 19.21 | 74.75 | 29.63 |