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**Patil Snehal**  
M.Sc Scholar, Department of  
Agril. Botany, College of  
Agriculture, Dapoli,  
Maharashtra, India

**UB Pethe**  
Assistant Professor, Department  
of Agril. Botany, College of  
Agriculture, Dapoli,  
Maharashtra, India

**VV Dalvi**  
Professor (CAS) AICRP on  
Agroforestry, College of  
Forestry, Dapoli, Maharashtra,  
India

**SG Mahadik**  
Assistant Professor, Department  
of Agril. Botany, College of  
Agriculture, Dapoli,  
Maharashtra, India

**MS Joshi**  
Professor and HOD, Department  
of Plant Pathology, College of  
Agriculture, Dapoli,  
Maharashtra, India

**Corresponding Author:**  
**Patil Snehal**  
M.Sc Scholar, Department of  
Agril. Botany, College of  
Agriculture, Dapoli,  
Maharashtra, India

## Genetic variability, heritability and genetic advance studies for yield components in F<sub>3</sub> generation of cowpea (*Vigna unguiculata* L. Walp)

Patil Snehal, UB Pethe, VV Dalvi, SG Mahadik and MS Joshi

### Abstract

The present research entitled “Genetic variability and character association studies in F<sub>3</sub> generation of cowpea. (*Vigna unguiculata* (L.) Walp.)” was carried out for assessing the genetic variability, heritability, expected genetic advance for yield contributing traits in F<sub>3</sub> generation of 45 genotypes of cowpea. The results revealed that estimates of mean sum of squares due to genotypes was highly significant for all the characters studied. In general it was found that magnitude of phenotypic variances were higher than respective genotypic variances for all the characters. Plant height had highest estimate of phenotypic and genotypic variance. High estimates of heritability coupled with genetic advance as per cent of mean was observed for characters plant height at maturity, harvest index, seed yield per plant, number of pods per plant, number of branches per plant, and number of clusters per plants.

**Keywords:** cowpea, variability, PCV, GCV, heritability, genetic advance

### Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.), is the most important leguminous crop known to man. It belongs to family Leguminaceae (Mackie and Smith, 1935) [12], and subfamily Fabaceae with a chromosome number of 2n=22 (Darlington and Wylie, 1955) [9]. Its primary centre of origin is in Africa (Pasquet and Baudoin). Cowpea is grown commercially throughout India, for its seeds as pulses, green pods as vegetable and foliage as fodder for milch animals. Its cultivars grown for immature green pods are commonly referred as southern pea or black eye pea. India is largest cowpea producer in Asia. In India, it has been known since the Vedic times. The vegetable cowpea has been subdivided into five sub species; three cultivated, *unguiculata*, *sesquipedalis* and *cylindrica* and two wild, *dekindtiana* and *mensenensis* [1]. It is known by many vernacular names like Lobia (Hindi), Barbati (Bengali), Urohi (Assami), Sonta (Garhwali), Chavali (Marathi), Alasande (Kannada) and Manpayar (Malayalam). Among legumes, cowpea is one of the most important vegetable crops grown during rainy and summer seasons. Tender pods as well as green-shelled seeds are used as vegetable and as a pulse when dried. It is also suitable for green manuring, fodder cover and catch crop. It is well adapted to stress and has excellent nutritive qualities. Cowpea is a high protein vegetable. There are several diverse uses of cowpea due to which the varietal improvement in terms of plant type, pod type, maturity, pattern of use and growth is required to develop cultivars that can be suited to the diverse region of country. Therefore in cowpea, selection and evaluation programme has become more complex and no single variety can be recommended to full fill all the objectives (Barrett, 1987) [2].

Thus there is growing need to develop suitable varieties for a specific region and or use. However, the production factor is constrained by low and variable grain yield, grain quality, susceptibility to disease and pests and the less availability of improved cultivars. One of the major Genetic variability, heritability and genetic advance are pre-requisite for improvement of any crop for the selection of superior genotypes and improvement of any traits. Genetic variability is important to select traits, which are heritable and unless and until there is ample variability exist in the population, breeder has no scope for developing high yielding varieties suffers from alarmingly low yield, especially in south-east Asia. Moreover, estimates of heritability indicate the extent of transmissibility of a character in advance generations which helps in selection based improvement. The present study was, therefore aimed to study variability, heritability and genetic advance between yield and its contributing traits in cowpea.

## Materials and Methods

The present investigation entitled “Genetic variability and character association studies in F<sub>3</sub> generation in cowpea (*Vigna unguiculata* (L.) Walp)” was accomplished in *Rabi*, 2018-2019 in randomized block design. The experimental material comprises of forty-five genotypes of F<sub>3</sub> generation of cowpea obtained from Department of Agricultural Botany, College of Agriculture, Dapoli. The total 24 crosses were made by using L x T mating design with 8 lines and 3 testers and the F<sub>1</sub> were evaluated during *Rabi* 2016–2017 along with parents (by Dr. U. B. Pethe). Out of 24 crosses, 21 were selected as F<sub>2</sub> population and evaluated during *Rabi* 2017-18 along with parents (by Ms. Tate. P. T. M. Sc. Student). Seeds from 45 individual plants performing superior over others selected from F<sub>3</sub> families were sown in RBD with 2 replications. The seeds were dibbled at 20 cm distance between row to row and 15 cm distance between plant to plant. Each plot had 0.80 m x 2.1 m area with 4 rows for each population. Each row contain 15 plants thus there were 60 plants per F<sub>3</sub> population, constitute 120 plants per cross in two replications. The plot was selected on the basis of suitability of the land for cultivation of cowpea. The observations were recorded on ten randomly selected plants per cross for thirteen characters. *viz.* days to first flowering, days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, Number of clusters per plant, number of pods per cluster, pod length (cm), number of seeds per pod, plant height at maturity (cm), hundred seed weight (g), seed yield per plant (g), and harvest index (%). The mean of observation of the ten plants were used for statistical analysis. These observations were subjected to statistical analysis. The data were statistically analyzed for computation of genetic coefficients of variation and broad sense heritability was estimated as per the formula suggested by Burton<sup>[2]</sup>. The expected genetic advance was calculated by using formula as suggested by Johnson *et al.* Analysis of variance was performed using method described by Panse and Sukhatme (1967)<sup>[18]</sup>. Phenotypic coefficient of variance and genotypic coefficient of variability were calculated by the method explained by Singh and Chaudhary (1985)<sup>[22]</sup>. Heritability in broad sense and genetic advance were calculated by method given by (Burton and Devane, 1953)<sup>[3]</sup>.

## Results and Discussion

### Variability

In present investigation sum of squares due to genotypes were highly significant for all characters. This indicated that, F<sub>3</sub> segregating population of cowpea exhibits ample variation for all the characters. The maximum variation was observed for plant height (21.60 to 56.34 cm). Wide variability range was also reported by Khan *et al.* (2015)<sup>[10]</sup> and Subbiah *et al.* (2013)<sup>[23]</sup> for this character. The variation range for days to maturity (83.70 to 92.50), number of pods per plant (14.50 to 29.60) which showed wide range of variation. Similar results were obtained by Khan *et al.* (2015)<sup>[10]</sup>, Khanpara *et al.* (2015)<sup>[11]</sup> and Tigga *et al.* (2014)<sup>[28]</sup> for characters days to maturity and number of pods per plant. It is found that number of clusters per plant, numbers of pods per plant and number of pods per cluster directly contributes to seed yield per plant. Wide range of variation was observed for number of clusters per plant (5.6 to 9.6), number of pods per cluster (2.2 to 4.0), pod length (11.05 to 16.03) and 100 seed weight (10.70 to 16.90). This indicates that there is great scope for plant breeder to improve cowpea genotypes through

selection. Similar results were also reported by Subbiah *et al.* (2013)<sup>[23]</sup>, Manggoel *et al.* (2012)<sup>[14]</sup> and Nath *et al.* (2009)<sup>[16]</sup> in cowpea for these characters. Wide range of variation was observed for character seed yield per plant (16.50 to 36.00). Seed yield is the result of contribution of all other component characters. Similar results were recorded by Tigga *et al.* (2014)<sup>[28]</sup> and Bhadru and Navale (2012)<sup>[4]</sup>. The result obtained from analysed data showed that phenotypic variance was higher than genotypic variance for all the characters studied indicating influence of environmental factors in expression of character. The character plant height showed highest magnitude of phenotypic and genotypic variance followed by harvest index, seed yield per plant and number of pods per plant. Similar results in cowpea were also reported by Havaraddi *et al.* (2018)<sup>[7]</sup>, Sapara and Javia (2014)<sup>[21]</sup> and Manggoel *et al.* (2012)<sup>[14]</sup>.

### Heritability and genetic advance

The magnitude of improvement over the base population by selection is determined by magnitude of genetic advance. The heritability and genetic advance are the important genetic parameters which helps in determining influence of environment in the expression of characters and the extent to which improvement is possible after selection.

The high estimates of broad sense heritability was observed for all characters under study. Estimates of heritability were highest for 100 seed weight (98.16%) followed by plant height at maturity (95.09%), number of pods per plant (90.14%), harvest index (89.50%), seed yield per plant (89.02%), days to initiation of flowering (87.76%), pod length (84.17%), days to 50% flowering (82.93%), number of clusters per plant (81.76%), number of branches per plant (80.76%), number of seeds per pod (76.36%), days to maturity (72.58%), and number of pods per cluster (61.44%). Similar results were reported by Vishwanatha and Yogesh (2017)<sup>[31]</sup>, Thorat and Gadewar (2013)<sup>[25]</sup> and Vavilpalli *et al.* (2013)<sup>[30]</sup> in cowpea for plant height and seed yield per plant. Rajput and Vineeta (2003)<sup>[20]</sup> recorded similar results for characters *viz.*, number of clusters per plant, plant height and number of pods per plant.

The magnitude of genetic advance determines expected progress over the base population under selection scheme. The characters under study showed wide range of genetic advance. It was ranged between 0.53 (number of pods per cluster) to 17.44 (plant height at maturity). The range for genetic advance as % of mean was observed between 3.83% (days to maturity) to 44.32% (plant height at maturity). It was 44.32 (plant height at maturity), 38.64% (harvest index), 35.73% (seed yield per plant), 30.85% (number of pods per plant), 23.20% (number of branches per plant), 19.04% (100 seed weight), 16.40% (number of pods per cluster), 14.91% (number of seeds per pod), 14.40% (pod length), 8.88 (days to initiation of flowering), 8.88% (days to 50 % flowering). Similar results were obtained by Thouseem *et al.* (2018)<sup>[27]</sup>, Idahosa *et al.* (2010)<sup>[8]</sup> and Suganthi and Murugan (2008)<sup>[26]</sup> in cowpea.

Estimates of heritability coupled with genetic advance is more important for plant breeder than heritability estimates alone for undertaking effective plant breeding programme. High heritability estimates along with moderate genetic advance were reported for plant height and harvest index. Whereas all other characters were showing high heritability but low genetic advance. These results revealed that, these traits are having additive gene action and less influence of

environmental factors on expression of traits so that, these characters can be selected for improving seed yield in further generation. Similar results were obtained by Das *et al.* (2018)<sup>[5]</sup> and Sharma *et al.* (2017)<sup>[13]</sup> for seed yield per plant.

High heritability with low genetic advance as percent of mean were reported for days to initiation of flowering, days to 50% flowering and days to maturity showing that the expression of traits are more likely to be influenced by environmental factors and controlled by nonadditive gene action. Similar results were also reported by Tigga *et al.* (2014)<sup>[28]</sup> and Thorat and Gadewar (2013)<sup>[25]</sup> for days to first flowering and Khanpara *et al.* (2015)<sup>[11]</sup> for days to 50% flowering.

## Conclusion

In present investigation, F<sub>3</sub> population showed wide range of

variation for all the characters under study in cowpea. The analysis of variance revealed that there is large amount of variation for all characters studied. The degree of variability is different for each character. The genotypes are thus highly suitable for genetical studies as their contribution to the genotypic sums of squares were highly significant for all the characters.

High heritability estimates along with moderate genetic advance were reported for plant height and harvest index. Whereas, all other characters were showing high heritability but low genetic advance. These results revealed that, these traits are having additive gene action and less influence of environmental factors on expression of traits so that, these characters can be selected for improving seed yield in further generation.

**Table 1:** Analysis of variance for sixteen quantitative traits in cowpea

Sr. No	Characters	Mean sum of squares		
		Replications (1)	Genotypes (44)	Error (44)
1.	Days to Initiation of Flowering	0.27	14.97**	0.97
2.	Days to 50% Flowering	0.04	20.44**	1.90
3.	Days to Maturity	2.05	9.01**	1.43
4.	Number of branches/plant	0.00	1.40**	0.14
5.	Number of pods/plant	4.89	24.70**	1.28
6.	Number of clusters/plant	0.30	1.42**	0.14
7.	Number of pods/cluster	0.17	0.28	0.06
8.	Pod length (cm)	0.34	2.20**	0.18
9.	Number of Seed/pod	0.21	1.88**	0.25
10.	Plant height at Maturity (cm)	0.17	154.82**	3.89
11.	100 seed weight (g)	0.11	3.29**	0.03
12.	Seed yield/plant (g)	1.06	44.79**	2.60
13.	Harvest index (%)	0.52	69.33**	3.82

**Table 2:** Genetic parameters of variation for seed yield per plant and its component traits in cowpea genotypes

S. No.	Parameters Characters	Mean	Range		Coefficient of variation (%)		h <sup>2</sup> (b) (%)	Genetic advance as per cent of mean GAM (%)
			Min	Max	Genotypic GCV	Phenotypic PCV		
1.	Days to initiation of flowering	57.45	52.90	63.10	4.60	4.91	87.76	8.88
2.	Days to 50% flowering	64.27	59.50	71.50	4.73	5.20	82.93	8.88
3.	Days to maturity	89.08	83.70	92.50	2.18	2.56	72.58	3.83
4.	Number of branches per plant	6.31	4.50	8.50	12.53	13.94	80.76	23.20
5.	Number of pods per plant	21.69	14.50	29.60	15.77	16.61	90.14	30.85
6.	Number of clusters per plant	6.93	5.60	9.60	11.55	12.77	81.76	21.51
7.	Number of pods per cluster	3.23	2.20	4.00	10.15	12.95	61.44	16.40
8.	Pod length (cm)	13.17	11.05	16.03	7.62	8.30	84.17	14.40
9.	Number of seeds per plant	10.90	8.30	13.10	8.28	9.47	76.36	14.91
10.	Plant height at maturity (cm)	39.37	21.60	56.34	22.06	22.62	95.09	44.32
11.	Hundred seed weight (g)	13.69	10.70	16.90	9.33	9.42	98.16	19.04
12.	Seeds yield per plant (g)	24.98	16.50	36.00	18.38	19.48	89.02	35.73
13.	Harvest index (%)	28.85	19.40	42.35	19.83	20.96	89.50	38.64

## References

- Almeida WS, Fernandes FR, Maria E, Bertini. Correlation and path analysis in components of grain yield of cowpea genotypes. *Rev. Ciênc. Agron* 2014;45(4):726-736.
- Barrett RP. Integrating leaf and seed production strategies for cowpea (*Vigna unguiculata* (L.) Walp.). MS Thesis, Michigan State Univ., East Lansing 1987.
- Burton GW, De Vane EH. Estimation of heritability in tall fescue from replicated clonal material. *Agron. J* 1953;45:478-481.
- Bhadru D, Navale PA. Genetic variability parameters in F<sub>2</sub> and F<sub>3</sub> populations of cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Research* 2012;35(1):75-77.
- Das RR, Talukdar P, Kumar P, Neog SB. Relationship among different secondary traits and seed yield in cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Current Microbiology and Applied Sciences* 2018;7(2):1382-1396.
- Dinesh HB, Viswanatha KP, Lohithaswa HC, Pavan R, Poonam Singh. Variability, correlation and path analysis studies in F<sub>3</sub> generation of cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Current Microbiology and Applied Sciences* 2017;6(9):1420-1428.
- Havaraddi U, Deshpande SK. Genetic Variability Studies in Advanced Stabilised Lines of Cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Pure and Applied Bioscience* 2018;6(6):221-226.
- Idahosa DO, Alike JE, Omoregie AU. Genetic variability,

- heritability and expected genetic advance as indices for yield and yield components selection in cowpea (*Vigna unguiculata* (L.) Walp.). *Academia Arena* 2010;2(5):22-26.
9. Johnson HW, Robinson HF, Comstock RF. Estimation of genetic environmental variability in soybean. *Agronomy Journal* 1955;47:314-318.
  10. Khan H, Viswanatha KP, Sowmya HC. Study of genetic variability parameters in cowpea (*Vigna unguiculata* (L.) Walp.) germplasm lines. *The Bioscan* 2015;10(2):747-750.
  11. Khanpara SV, Jivani LL, Vachhani JH, Kachhadia VH. Genetic variability, heritability and genetic advance studies in Vegetable Cowpea (*Vigna unguiculata* (L.) Walp.). *Electronic Journal of Plant Breeding* 2015;7(2):408-413.
  12. Mackie WW, Smith FL. Evidence of field hybridization in beans. *Journal American Society Agronomy* 1935;27:903-908.
  13. Mahesh Sharma, Sharma PP, Hemlata Sharma, Deva ram meghawal. Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] Germplasm lines. *Journal of pharmacognosy and Phytochemistry* 2017;6(4):1384-1387.
  14. Manggoel W, Uguru MI, Ndam ON, Dasbak MA. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp.] assessments. *Journal of Plant Breeding and Crop Science* 2012;4(5):80-86.
  15. Mishra M. Genetic Variability, Correlation and Path analysis for yield and its components in Cowpea [*Vigna unguiculata* (L.) Walp]. M.Sc. (Ag.) thesis submitted to Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur 2013.
  16. Nath V, Lal H, Rai M, Rai N, Ram D. Hierarchical clustering and character association studies in cowpea (*Vigna unguiculata* (L.) Walp.). *Indian Journal of Plant Genetic Resources* 2009;22(1):22-25.
  17. Nwosu DJ, Olatunbosun BD, Adetiloye IS. Genetic variability, heritability and genetic advance in cowpea genotypes in two agroecological environments, *Greener Journal of Biological Science* 2013;3(5):202-207.
  18. Panse VG, Sukhatme PV. *Statistical method for agricultural workers*, 4<sup>th</sup> Edn., ICAR, New Delhi 1985.
  19. Pasquet RS, Baudoin JP. Cowpea. In: Charrier AM, Jacquot S, Hamon and D. Nicolas (eds), *Tropical Plant Breeding*. Science publishers, Enfield 2001, 177-198.
  20. Rajput SS. Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in cowpea. M. Sc.(Ag.) thesis submitted to Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur 2016.
  21. Sapara GK, Javia RM. Correlation and path analysis in vegetable cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of plant sciences* 2014;9(1):134-141.
  22. Singh PK, Chaudhary BD. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani publishers. New Delhi, India 1985.
  23. Subbiah A, Prabhu M, Rajangam J, Jagadeesan R, Anbu S. Genetic analysis of vegetable cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Research* 2013;36(1):1-9.
  24. Sunita. Genetic variability, correlation and path coefficient analysis in diverse genotypes of cowpea (*Vigna unguiculata* (L.) Walp.). M.Sc. (Agri) Thesis submitted to BHU, Varanasi 2016.
  25. Thorat Archana, Gadewar RD. Variability and correlation studies in cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal for Environmental Rehabilitation and Conservation* 2013;4(1):44-49.
  26. Suganthi S, Murugan S. Association analysis in cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Research* 2008;31(2):130-132.
  27. Thouseem N, Thomas B, Elizabeth N. Genetic parameters in seed yield components of cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Current Microbiology and Applied Sciences* 2018;7(2):2268-2274.
  28. Tigga K, Kumar DR, Solanki A, Pandey RL. Genetic Variability in Cowpea (*Vigna unguiculata* (L.) Walp.). At Chhattisgarh Plains. *Trends in Biosciences* 2014;7(2):1-8.
  29. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica* 1949;13:1-54.
  30. Vavilpalli S, Celina VA, Duggi S, Padakipati S, Magdum S. Genetic variability and heritability studies in bush cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Genomics and Genetics* 2013;4(4):27-31.
  31. Viswanatha KP, Yogesh LN. Genetic variation and morphological diversity in cowpea (*Vigna unguiculata* (L.) Walp.). *Archives of Agriculture and Environmental Science* 2017;2(3):176-180.