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# Genetic Variability for Yield and Yield Component Traits in Advanced $F_2$ and $F_3$ Generations of Cowpea [*Vigna ungiculata* (L). Walp]

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**ABSTRACT**

*The present investigation aimed to study genetic variability generated from the IT-38956-1 x KBC-2 cross in $F_2$ and $F_3$ generation to make effective selections for improving productivity. The traits such as plant height, primary branches per plant, secondary braches per plant, pods per plant, pod length and seeds per plat exhibited the moderate values for variability parameters for $F_2$ generation. The higher heritability and genetic advance per mean were recorded in $F_2$ and $F_3$ generation for secondary braches per plant, pods per plant, pod length and seeds per pod, seed yield per plant recorded the moderate values that implicate additive gene action in inheritance of these traits thus phenotypic selection would be effective in yield improvement.*

***Key words:*** *Cowpea, additive gene action, genetic variability.*

## INTRODUCTION

Cowpea[*Vigna ungiculata* (L). Walp] belongs to the family leguminoceae, sub family papilinoceae having chromosome number 2n=22Cowpea is an annual herb with strong tap root system with different growth habit *i.e.*, erect, semi erect, trailing or climbing, bushy annual with glabourous stem. The trifoliate leaves arise alternatively and terminal leaflet is frequently longer and greater leaf area than that of a symmetrical lateral leaves. Flowers are racemose or indeterminate inflorescence at the distal ends of peduncles which are in leaf axil. The flower is typical with five sepals in gamo sepalous condition containing five petals in polypetalous condition. The flowers are born on short peduncle and corolla varies in colour from white to purple.

In India, cowpea is grown as a sole crop, inter crop, mixed crop and in agroforestry combinations. The area of cultivation of cowpea in India is 1.3 million hectares of area in Asian region. Cowpea is considered as a minor pulse crop in India and mainly cultivated in the states of Rajasthan, Gujrat, Karnataka, Tamil Nadu, Maharastra and few parts in other states and it is estimated to be cultivated in other states.

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In Karnataka, cowpea is grown in almost all the districts, with an area of 0.78 lakh hectares with a production of 0.22 lakh tones. The productivity is only 302 kg/ha during the year 2012-13 (Source: Directorate of Economics and Statistics, Govt of Karnataka)

Cowpea is a highly self-pollinated crop, tremendous genetic variability is available in the crop. In addition to selection, hybridization has been followed to get the recombinants with high seed yield coupled with the superior agronomic traits. The heterotic response over mid as well as better parents could be informative to identify true heterotic cross combinations. Heterosis for seed yield and other characters in grain legumes were first reported by Pal[14].

The choice of an appropriate selection/breeding method and its success for improvement of quantitative traits largely depends on the extent of genetic variability present in segregating material and gene action. Knowledge on genetic architecture of yield and related traits plays an important role in deciding breeding strategies and methodologies for crop improvement. In comparison to other economically important crops, relatively less effort has been made to understand the genetics of important quantitative traits in pigeonpea. Both additive and dominant/ non-additive effects have been reported to be important in determining yield, plant height, and protein content. Pleiotropic effects of gene, physiological changes, and highly sensitive nature of pigeonpea towards the environmental changes make it difficult to interpret the inheritance of yield and associated traits[4]. Information about nature and magnitude of gene action can be useful for breeding program[16]. Yield and its component characters that are quantitative in nature exhibit all the three types of gene action[17]. Knowledge of gene action, interaction effect and heritability involved in several quantitatively inherited traits helps in deciding appropriate breeding program. Thus, the present investigation aimed to study genetic variability generated from the IT-3895-1×KBC-2 cross in $F_3$ and $F_4$ generation to make effective selections for improving productivity.

## MATERIALS AND METHOD

The segregating material was developed by hybridization of IT-38956-1 x KBC-2 a total of 150 plants were selfed and advanced to $F_3$ generation. $F_2$ plants were sown during summer-2009 at Dry Land Agriculture Project, University of Agricultural Sciences, GKVK, Bnagalure. The experiment was laid out in Randomized Block Design with two replications. The sowing was done with 45 x 10 cm. $F_3$ plants were sown during rabi 2009 in progeny rows each progeny rows consisted of 15-20 individual plants. Data on various traits such as days to first flowering, days to maturity, plant height (cm), primary braches per plant, secondary braches per plant, pods per plant, seeds per pod, pod length(cm) , seed yield per plant(g) and seed yield per plant (g). Data recorded from both $F_2$ and $F_3$ generations were statistically analyzed (Panse and Sunhatme) computed genetic parameters viz., phenotypic and genotypic coefficient variation was calculated as per the formula suggested by Burton and DeVene[3]. Heritability (broad sense) was computed as suggested by Jhonson *et al*[9] and genetic advance as per of mean was estimated according to Jhonson *et al*[9].

## RESULTS AND DISCUSSION

The results of the variance component in this study indicated that the phenotypic coefficient of variation was higher that the genotypic coefficient of variation for all traits in both $F_2$ and $F_3$ generation coupled with negligible differences which indicated less environmental influence on all the traits were studied implied that the trait are mostly governed by genetic factors with little role of environment in the genetic expression of these characters. Thus the selection of these traits on of the basis of the phenotypic value may effective and was confirmed with the earlier studies of Jana *et al.*[8], Girish *et al.*[6], Kumar P *et al.*[11], Tigga K *et al*[19]. Kharde *et al*[10] and Inuwa *et al*[7].

The magnitude difference in GCV and PCV were recorded moderate in $F_2$ and $F_3$

generation for plant height, primary branches per plant, secondary braches per plant, pods per plant, pod length and seeds per plat exhibited the moderate values for variability parameters for $F_2$ generation. Similar results were observed by Kumar P *et al.*[11] and Tigga K *et al.*[19]. The magnitude of broad sense heritability ranged from 6.25 per cent for hundred seed weight (g) to 79.70 for days to first flowering in $F_2$ generation (Table-1) and 7.89 percent for hundred seed weight to 46.89 per cent in pod length (cm) in $F_3$ generation. Similarly the higher magnitude of heritability was observed in days to maturity (22.65 %) and other parameters were recorded the moderate values the character in $F_2$ generation and in $F_3$ generation higher magnitude of heritability was observed in seeds per pod (48.58 %), pods per plant (42.56 %), seed yield per plant (31.23 %), pod length (27.59 %) and secondary branches per plant (20.35 %) were observed. The broad sense heritability estimates in this study were generally moderate for all the traits in both generations. Moderate heritability suggested the major role of genetic constitution in the expression of the character and such traits are considered to be dependence for genetic up gradation of cowpea. The moderate heritability recorded in this study were in agreements the values reported from several other workers in cowpea[2,11,12,19]. Moderate heritability coupled with high genetic advance over mean in days to maturity in $F_2$ generation and secondary braches per plant, pods per plant, pod length and seeds per pod in $F_3$ generation. These findings are in agreement with the earlier reports of Yadav *et al.*[20], Eswaran *et al.*[5], Subbaiah *et al.*[18], and Bhadru *et al.*[1]. Heritability estimates along with genetic advance are more useful in predicting the resultant effect for the selection of the best individuals from a population. High broad sense heritability value coupled with genetic advance indicates the predominant additive gene action in the expression of these traits and thus they can be improved through individual plant selection[1,9,13,15].

In this study we found that moderate heritability coupled with high genetic advance over mean in days to maturity in $F_2$ generation and secondary braches per plant, pods per plant, pod length and seeds per pod in $F_3$ generation that implicate additive type of gene action in inheritance of these traits thus phenotypic selection would be effective in yield improvement.

**Table 1: Genetic variability estimates for ten quantitative traits $F_2$ generation in IT-38956-1 x KBC-2 cross in Cowpea**

| Sl No. | Character | Range | | Mean | PCV (%) | GCV (%) | $h^2$ (%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| | | Min | Max | | | | | |
| 1 | Days to first flowering | 31.00 | 50.00 | 33.68 | 10.28 | 2.86 | 79.70 | 11.66 |
| 2 | Days to maturity | 70.00 | 98.00 | 84.39 | 7.12 | 1.81 | 64.30 | 22.65 |
| 3 | Plant height(cm) | 10.20 | 42.70 | 27.73 | 23.13 | 3.75 | 36.30 | 1.25 |
| 4 | Primary branches per plant | 2.00 | 9.00 | 5.23 | 25.54 | 14.14 | 16.13 | 3.06 |
| 5 | Secondary branches per plant | 4.00 | 16.00 | 10.17 | 13.71 | 5.52 | 16.23 | 4.58 |
| 6 | Pods per plant | 9.00 | 20.00 | 14.65 | 13.64 | 7.09 | 11.27 | 7.6 |
| 7 | Pod length(cm) | 9.10 | 26.00 | 16.69 | 18.44 | 9 | 23.00 | 16.69 |
| 8 | Seeds per pod | 6.00 | 20.00 | 13.30 | 19.78 | 12.85 | 42.20 | 13.3 |
| 9 | Seed yield per plant(g) | 9.17 | 30.35 | 18.74 | 22.81 | 7.91 | 12.05 | 18.74 |
| 10 | Hundred seed weight(g) | 9.12 | 13.34 | 11.11 | 7.24 | 1.72 | 6.25 | 11.11 |

**Table 2: Genetic variability estimates for ten quantitative traits $F_3$ generation in IT-38956-1 x KBC-2 cross in Cowpea**

| Sl No. | Character | Range | | Mean | PCV (%) | GCV (%) | $h^2$ (%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| | | Min | Max | | | | | |
| 1 | Days to first flowering | 40.0 | 52.0 | 45.72 | 45.79 | 5.08 | 22.9 | 16.39 |
| 2 | Days to maturity | 78.0 | 86.0 | 82.32 | 81.59 | 2.3 | 20.27 | 2.96 |
| 3 | Plant height(cm) | 15.20 | 30.60 | 22.85 | 22.85 | 14.11 | 26.43 | 7.39 |
| 4 | Primary branches per plant | 4.0 | 7.0 | 5.5 | 5.54 | 15.67 | 20.01 | 5.94 |
| 5 | Secondary branches per plant | 8.0 | 15.0 | 11.97 | 11.97 | 24.43 | 30.01 | 20.35 |
| 6 | Pods per plant | 12.0 | 16.0 | 14.25 | 1.98 | 27.14 | 36.78 | 42.56 |
| 7 | Pod length(cm) | 12.10 | 18.90 | 15.28 | 15.28 | 37.85 | 46.89 | 27.59 |
| 8 | Seeds per pod | 8.0 | 18.0 | 15.92 | 12.92 | 37.67 | 33.57 | 48.58 |
| 9 | Seed yield per plant(g) | 12.15 | 26.35 | 19.80 | 19.82 | 14.56 | 14.11 | 31.23 |
| 10 | Hundred seed weight(g) | 10.12 | 13.35 | 11.75 | 11.75 | 6.96 | 7.89 | 3.57 |

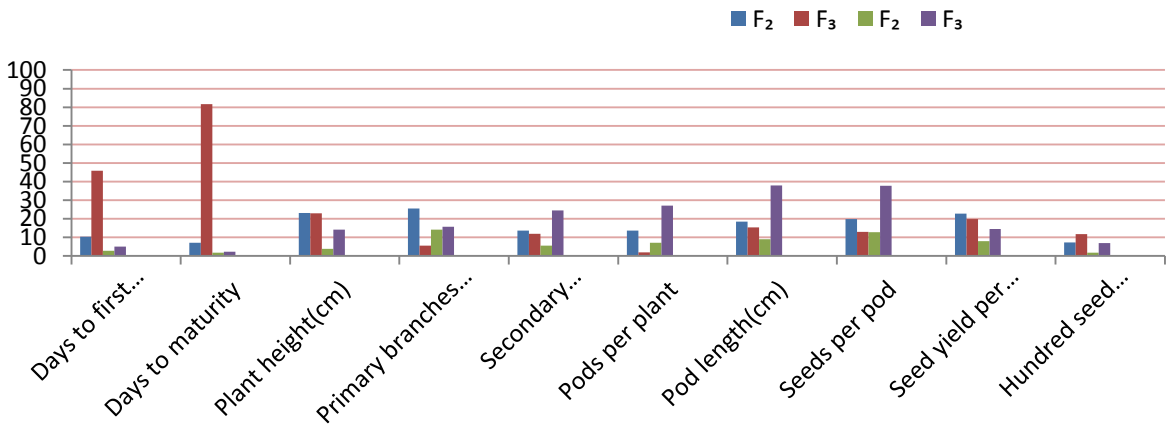


**Fig. 1: Phenotypic and genotypic coefficient of variance for 12 quantitative traits of IT-38965-1 × KBC-2 in $F_2$ and $F_3$ generation**

## REFERENCES


1. Bhadru, D. and Navale., 2012, Genetic variability parameters in $F_2$ and $F_3$ populations of cowpea [*Vigna unguiculata* L.Walp.]. *Legume Res*., **35(1):** 75-77 (2012).
2. Bhawna, P. and Y.V. Singh., 2015, Heterosis for yield and yield contributing characters in cowpea genotypes, *Legume Res.*, **38 (5):** 570-574 (2015).
3. Burton G.W., and De Vane E.H., 1953, Estimating heritability in talli Feschue (*Festuca arundinances*) from replicated clones material, *Agron. J.*, **45:** 478-481.
4. Byth D.E., Wallis E.S., and Saxena K.B., 1981, Adaptation and breeding strategies (1981).
5. Eswaran, R.S., Kumar, T. and Venkatesan., M., Genetic Variability studies in Cowpea[*Vigna unguiculata (L.)* Walp]. *Legume Res.*, **30** (1)**:** 13-16 (2007).

6. Girish, G., Viswanath, K. P., Manjunath, A. and Yogeesh, L. N., Genetic variability, heritability and genetic advance analysis in cowpea [*Vigna unguiculata* L. Walp.]. *Envi. Eco.*, **24 (4):** 1172-1174 (2006).
7. Inuwa, A. H., Ajeigbe, H. A., Muhammed, S. G and Mustapha, Y., In: Proceedings of the 46th annual conference of the agricultural society of Nigeria, 5th – 9th November 2012, Kano, Nigeria (2012).
8. Jana, S., Som, M. G. and Das, N. D., Studies in cowpea, *Haryana J. Hort. Sci*.**12 (3-4):** 224-226 (1983).
9. Johnson H.F., Robinson H.F., and Comstock R.E., 1955, Genotypic and Phenotypic correlation in soyabean and their implication in selection, *Agron.J.*, **47:** 477-483 (1955).
10. Kharde, R. P., Kale, V. S. and Bhogave, A. F., Genetic variability studies in cowpea, 2014, *Bioinfolet*, **11(1A):** 113-118 (2014).
11. Kumar, P. K., Kumar, N. R., Muneeswari, T., Nagajothi., Lamror, R. and Kumari, U. R,Morphological and genetic variation studies in cowpea genotypes [*Vigna unguiculata* (L.) Walp] (2013).
12. Kumar, R., Sangawan, R. S., and Singh, S., Genetic variability and heterosis in [*Vigna unguiculata* (L.) Walp*]*. *Indian J. Pl. Genet. Resour*. **22(1):** 74-75 (2009).
13. Makeen K.A., Garad J., Arif J., Singh K.A., Genetic variability and correlation studies in yield and yield component in mugbean (Vigna radiate (L.) wilezek), *J. Agron.*, **6:** 216-218 (2007).
14. Pal and B. P., Studies in hybrid vigour. *Indian J. Genet.*, **5:** 106-108 (1945).
15. Panse V.G., and Sukhatme P.V., Statistical methods for agricultural workers, ICAR, pigeonpea, Proceedings of ICRISAT/ICAR international workshop on pigeonpea., 15-19 December., **1** 450-465 (1985).
16. Satish Kumar D., Koteswara Roa Y., Rama Kumar P.V., and Srinivas Roa V., Genetic (2006).
17. Saxena K.B., Singh L., Gupta M.D., Variation for natural out-crossing in pigeonpea (2008).
18. Subbiah, A., Prabhu, M., Rajangam, J., JAGADEESAN, R. AND ANBU, S., Genetic analysis of vegetable cowpea [*VignaUnguiculata* (L.) Walp.]. *Legume Res*., **36(1):** 1-6 (2013).
19. Tigga, K., K. D. Rakesh, Akash, S. and Pandey, R. L., 2014, Genetic variability in cowpea [*Vigna unguiculata* (L.) *Walp]*. *Trend. Biosci***., 7(2):** 98-100 (2014).
20. Yadav, K. S., Yadav, H. S. and Naik, M. L., Gene action governing the inheritance of pod yield in cowpea. *Legume Res*., **27(1):** 66-69 (2004).