

Genetic variability Studies in F₂ and F₃ Segregating Generations for Biometrical Traits in Cowpea (*Vigna unguiculata* L. Walp)

Sunil R.*, Jiji Joseph, Santhosh Kumar A.V. and Biju S.
Research Farm, Department of Plant Breeding and Genetics,
College of Agriculture, Kerala Agricultural University, Thrissur (Kerala), India.

(Corresponding author: Sunil R.*)

(Received: 15 July 2023; Revised: 17 August 2023; Accepted: 18 September 2023; Published: 15 October 2023)

(Published by Research Trend)

ABSTRACT: Pulses play a vital and diverse role in agricultural systems and the food habit of people around the world. They are ideal crops for reducing poverty, enhancing human health and nutrition, and improving the ecosystems' resilience. Among legumes, Cowpea is the traditional and most important one and the potential source of protein for the majority of Kerala's population. They also provide most of the essential amino acids. Combination breeding aims to breed crop with desired objectives. Developing cowpea genotypes with high yield combined with high protein content is challenging. The present study aimed to identify potential segregates with high yield and high protein from inter-varietal crosses of cowpea. The evaluation was carried out in Department of Plant Breeding and Genetics, Kerala Agricultural University during 2016-2017. In this research, two crosses of F₁ generation were advanced to F₂ and F₃ segregating generations for genetic variability studies isolate good segregates with high seed yield coupled with protein content. Between the two crosses studied, Anaswara × PKB 4 registered superior performance in both F₂ and F₃ generations for seed yield and its related attributes such as plant height, pod weight and number of seeds per pod. Anaswara × PKB 6 exhibited better performance for seed protein content in the segregating generations. The F₂ and F₃ generations of Anaswara × PKB 6 and Anaswara × PKB 4 showed moderate PCV, GCV coupled with high heritability and high genetic advance as percentage of mean for seed yield and seed protein content indicating possibility of genetic improvement in succeeding generations of the crop. Segregants with high yield and high protein content were identified and forwarded to next generations. This helps in developing a novel cowpea genotypes with high yield and high protein quality.

Keywords: Cowpea, Segregating generations, PCV, GCV, Heritability, Genetic advance.

INTRODUCTION

Pulses are considered as super natural foods for poor community due to its cheapest source of protein and other nutrients (Maphosa and Jideani 2017). The protein content of pulses range from 20 to 25 per cent by weight, which is twice of wheat protein and trice of rice protein (Gowda *et al.*, 2013; Ramamurthi *et al.*, 2012). The reliable data on area and production of cowpea in India is not available due to its limited cultivation and low status in country. Improvement in the cowpea production largely helps to raise the nutritional status of the country. Generally, in pulses, advancement in seed yield and quality is of greatest importance to the nation. Among the pulses, Cowpea (*Vigna unguiculata* L. Walp) is most widely cultivated in Kerala and seen in traditional cuisines. The negative correlation between seed yield and protein content is a major hindrance in development of high yield and protein rich cowpea lines. Information on genetic variability and trait relationship are necessary to improve yield potential in any effective breeding programme (Govindaraj *et al.*, 2015). The varietal development programme of cowpea should have sound

objectives, considering the basic needs of the farmer and the consumer. In a breeding programme, direct estimation of seed yield in segregating generations is quite difficult (Slinkard *et al.*, 2000). The present investigation was planned to quantify the extent of genetic variability available for seed yield, protein content and yield associated traits in the segregating populations of cowpea and to know the genetic gain that can be made by selection. The study also identifies desirable segregates with high seed yield coupled with protein content.

MATERIALS AND METHODS

The present investigation was carried out at the Research Farm of Postgraduate Studies, Department of Plant Breeding and Genetics, Kerala Agricultural University, Thrissur during two successive cowpea seasons of 2016 and 2017. The experimental materials used in the study were F₂ and F₃ generations of the two interspecific crosses of cowpea, i.e. H10 (Anaswara × PKB 6) and H11 (Anaswara × PKB 4). The features of parental genotypes are displayed in Table 1. Pedigree selection method was used for quantitative traits

includes plant height (cm), number of branches per plant, days to first flowering, days to maturity, number of pods per plant, pod length (cm), single pod weight (g), number of seeds per pod, hundred seed weight (g), seed yield per plant (g) and seed protein content (%). In both generations, all agricultural practices were maintained at optimum levels for attaining maximum homogeneity. Data was recorded on above mentioned traits on individual plants from each family and genetic parameters were estimated using mean and variance as suggested by Kurer (2007).

RESULTS AND DISCUSSION

Genetic Variability in F₂ and F₃ Generations of Cowpea Crosses: Genetic variability is prerequisite of any breeding programme. Selection of individual plants in F₂ and F₃ generations are very effective in fixing the desirable trait combinations (Selvi *et al.*, 2022). Quantitative characters of cowpea were recorded and the data was analyzed for genetic variability parameters in segregating generations of cowpea crosses (Table 1 & 2). The quantitative traits studied display a wide range of variation in F₂ and F₃ generations of cowpea crosses. In segregating generations of cross H10 (Anaswara × PKB 6) and Cross H11 (Anaswara × PKB 4) the range of variation was greatest for plant height followed by seed yield per plant. The smallest range of variation was found for single pod weight followed by number of branches per plant. The variability exhibited in quantitative traits studied is quite appreciable. In segregating generations (F₂ and F₃) of cross H10 and cross H11, high mean values were observed for plant height followed by days to maturity and seed yield per plant. In cross H10, the mean values were lowest for single pod weight followed by number of branches per plant and number of seeds per pod, whereas, in cross H11 number of branches per plant had lowest mean values followed by single pod weight and number of seeds per plant. In F₃ generation of the crosses (H10 and H 11), the lowest mean values were exhibited by number of branches per plant followed by single pod weight and number of seeds per plant. Similar findings were reported Kurer *et al.* (2010).

In F₂ generation of cross H10 (Anaswara × PKB 6), phenotypic coefficient of variation (PCV) was observed high in plant height (20.99%), number of branches per plant (23.34%) and number of pods per plant (20.99%) along with moderate genotypic coefficient of variation (GCV). The other quantitative traits studied registered moderate PCV and GCV values. In cross H11 (Anaswara × PKB 4), high PCV and GCV values were observed for seed yield per plant. Days to maturity displayed low PCV and GCV values. Moderate PCV and low GCV was observed for days to 50% flowering. Remaining traits presented moderate PCV and GCV values. Meenatchi *et al.* (2019) reported high PCV and GCV values for traits such as number of branches per plant, number of pods per plant and single plant yield in F₂ generation of cowpea crosses. In F₃ generation of cross H10, number of branches per plant displayed high PCV value with moderate GCV. The PCV and GCV

values were low for days to 50% flowering, days to maturity and hundred seed weight. Moderate PCV and low GCV were registered for pod length, number of seeds per pod and seed protein content. In cross H11, number of pods per plant, pod length and seed protein content displayed moderate PCV and low GCV values. Traits such as days to 50% flowering, days to maturity and hundred seed weight registered low PCV and GCV values. Subbiah *et al.* (2012) reported low PCV and GCV values for plant height and days to flowering in the F₃ generation of cowpea crosses. The scope of improvement for such traits is less. In common, PCV was higher than GCV in all the quantitative characters, which specifies that the characters be influenced by growing environment.

All the characters studied in segregating generations (F₂ & F₃) of cowpea crosses (H10 & H11) registered high heritability (>60%) expect number of branches per plant (59.62%) of cross H10 and pod length (58.80%) of cross H11 in F₃ generation. In F₂ and F₃ generations of cross H10, the highest heritability was observed for hundred seed weight followed by days to 50% flowering. In F₂ generation of cross H11, highest heritability was presented by days to 50% flowering followed by number of pods per plant, whereas, in F₃ generation days to 50% of flowering showed highest heritability followed by seed yield per plant. Mariyammal *et al.* (2019) reported that the heritability of the yield and yield associated traits are high in F₂ generation of mung bean crosses except for plant height, which registered moderate heritability in a cross. A study on quantitative characters in segregating generation of cowpea by Salimath *et al.* (2010) reported that quantitative characters are highly heritable in early generations. Selection will be effective based on such characters. It is also reported that number of pods per plant display moderate heritability in F₃ generation, which coincides with the present study. In general, high heritability of characters recorded indicates the predominance of additive gene action for expression of the characters and selection of these characters in the segregating generations of cowpea would be effective likely to express in the succeeding generations. Genotype improvement is likely possible if some of these characters are considered as selection criteria in further breeding process. A similar finding was reported by Tyagi *et al.* (2000).

In F₂ generation of cross H10, high heritability with high genetic advance as percentage of mean (GAM%) was recorded for plant height, number of branches per plant, days to maturity, number of pods per plant, pod length, single pod weight, number of seeds per pod, hundred seed weight and seed yield per plant. Days to 50% flowering and seed protein content displayed high heritability with moderate GAM%. In cross H11, plant height, number of branches per plant, number of pods per plant, single pod weight, number of seeds per pod, hundred seed weight and seed yield per plant registered high heritability coupled with high GAM%. In the findings of Nair *et al.* (2018), F₂ generation of cowpea crosses registered high GAM % for plant height, pod

length, number of pods per plant, pod and seed yield per plant. In F₃ generation of cross H10, high heritability with high GAM% were observed for plant height, number of pods per plant, single pod weight and seed yield per plant. Days to 50% flowering, days to maturity, pod length, number of seeds per pod, hundred seed weight and seed protein content presented high heritability coupled with moderate GAM%. Medium heritability with high GAM% was found in number of branches per plant. In cross H11, high heritability with high GAM% were recorded for plant height, number of branches per plant, number of seeds per pod and seed yield per plant. High heritability with moderate GAM%

was observed for days to 50% flowering, days to maturity, number of pods per plants, single pod weight, hundred seed weight and seed protein content. Pod length showed medium heritability with medium GAM%. Traits registered with high heritability coupled with high genetic advance represent the additive gene action and phenotypic selection would be effective for such characters in the segregating generations of cowpea. Gowda *et al.* (1991) reported similar findings. Further improvement through breeding procedures can be made for traits having medium heritability and high genetic advance.

Table 1: Characteristic features of parental genotypes.

Genotypes	Released by	Salient features
Anaswara	Kerala Agricultural University, Thrissur	Semi trailing, medium long pods, dual purpose variety
PKB 6	University of Agricultural Sciences, GKVK, Bangalore	Bushy to semi spreading type, dual purpose, high yield and seed protein content
PKB 4		Spreading type, vegetable cowpea, high seed protein

Table 2: Genetic variability parameters for quantitative traits in F₂ and F₃ generations of cowpea cross H10 (Anaswara × PKB 6).

Traits/Crosses	Generations	Range	Mean	PCV (%)	GCV (%)	h ² (%)	GA	GAM (%)
Plant height (cm)	F ₂	198.50-298.80	245.65	20.99	18.51	77.77	82.60	33.63
	F ₃	195.20-279.80	227.87	18.80	16.60	77.97	68.80	30.19
No. of branches per plant	F ₂	5.00-8.00	6.97	23.34	18.47	62.62	2.10	30.11
	F ₃	5.00-7.00	5.78	20.80	16.06	59.62	1.48	25.54
Days to 50% flowering	F ₂	44.00-67.00	57.92	10.54	10.01	90.20	11.34	19.58
	F ₃	49.00-72.00	59.50	9.14	8.16	79.71	8.93	15.01
Days to maturity	F ₂	106.00-151.00	138.82	12.21	11.13	83.08	29.01	20.90
	F ₃	112.00-149.00	135.23	9.87	8.54	74.87	20.58	15.22
No. of pods per plant	F ₂	43.00-56.00	48.66	20.48	18.84	84.63	17.37	35.70
	F ₃	38.00-54.00	43.30	15.22	13.52	78.91	10.71	24.74
Pod length (cm)	F ₂	20.40-31.80	27.22	16.16	13.44	69.17	6.27	23.03
	F ₃	19.50-29.80	26.60	11.93	9.61	64.89	4.24	15.95
Single pod weight (g)	F ₂	5.60-6.40	6.10	14.53	12.90	78.82	1.44	23.59
	F ₃	5.01-6.60	5.90	14.16	12.06	72.54	1.25	21.16
No. of seeds per pod	F ₂	10.00-18.00	15.39	18.03	15.06	69.77	3.99	25.91
	F ₃	9.00-20.00	14.85	11.37	9.23	65.90	2.29	15.44
Hundred seed weight (g)	F ₂	19.50-23.90	21.60	18.28	17.55	92.17	7.50	34.71
	F ₃	16.57-25.97	21.53	9.34	8.85	89.78	3.72	17.27
Seed yield per plant (g)	F ₂	95.50-145.60	124.57	19.22	15.39	64.12	31.62	25.39
	F ₃	120.19-142.84	125.96	18.83	15.07	64.05	31.30	24.85
Seed protein content (%)	F ₂	24.60-31.20	27.27	12.87	10.87	71.33	5.16	18.91
	F ₃	22.60-29.50	27.10	11.14	9.29	69.54	4.32	15.96

PCV – Phenotypic coefficient of variation; GCV - Genotypic coefficient of variation; h² – Heritability; GA – Genetic advance; GAM – Genetic advance as percentage of mean

Table 3: Genetic variability parameters for quantitative traits in F₂ and F₃ generations of cowpea cross H11 (Anaswara × PKB 4).

Traits/Crosses	Generations	Range	Mean	PCV (%)	GCV (%)	h ²	GA	GAM (%)
Plant height (cm)	F ₂	210.60-302.50	263.16	18.62	15.57	69.92	70.58	26.82
	F ₃	215.20-307.50	239.56	15.08	12.60	69.81	51.95	21.69
No. of branches per plant	F ₂	5.00-8.00	6.50	19.13	15.29	63.88	1.64	25.17
	F ₃	5.00-8.00	6.23	18.04	14.12	61.26	1.42	22.77
Days to 50% flowering	F ₂	48.00-71.00	63.71	10.46	9.83	88.32	12.12	19.03
	F ₃	50.00-75.00	63.18	7.96	7.07	78.89	8.17	12.94
Days to maturity	F ₂	112.00-155.00	143.64	8.76	7.59	75.07	19.46	13.55
	F ₃	119.00-152.00	139.83	8.53	7.17	70.65	17.36	12.42
No. of pods per plant	F ₂	42.00-53.00	47.90	17.49	15.84	82.02	14.16	29.55
	F ₃	40.00-51.00	42.93	10.87	9.17	71.17	6.84	15.94
Pod length (cm)	F ₂	18.00-30.30	24.48	13.56	10.90	64.62	4.42	18.05
	F ₃	15.50-28.60	23.52	10.72	8.22	58.80	3.05	12.98
Single pod weight (g)	F ₂	5.50-6.97	6.60	15.58	13.21	71.89	1.52	23.07
	F ₃	4.80-6.95	6.20	13.77	10.98	63.58	1.12	18.04
No. of seeds per pod	F ₂	15.00-23.00	18.13	15.87	13.86	76.27	4.52	24.94
	F ₃	11.00-22.00	15.88	15.03	12.83	72.87	3.58	22.56
Hundred seed weight (g)	F ₂	18.13-25.36	20.95	18.60	16.76	81.19	6.52	31.11
	F ₃	15.61-25.65	21.44	8.76	7.53	73.89	2.86	13.33
Seed yield per plant (g)	F ₂	128.75-151.88	133.39	25.08	21.22	71.59	49.33	36.99
	F ₃	123.15-149.70	137.32	19.58	17.37	78.70	43.59	31.74
Seed protein content (%)	F ₂	18.00-30.10	26.95	12.16	10.19	70.22	4.74	17.59
	F ₃	20.10-28.90	26.16	10.96	9.02	67.73	4.00	15.29

PCV – Phenotypic coefficient of variation; GCV - Genotypic coefficient of variation; h² – Heritability; GA – Genetic advance; GAM – Genetic advance as percentage of mean

CONCLUSIONS

Breeding of pulses for high yield and nutritionally stable is an alarming need to meet out the outbreak of Indian population. The results of present study revealed that high range of variability for quantitative traits exist in the early segregating generations, providing a better scope for improving the traits of breeder's interest. The PCV and GCV values were high to medium for most of the traits indicate that selection will be effective in early segregating generations to better extent. High heritability values for quantitative traits indicate inheritance of the genes in early segregating generations. Traits with high heritability coupled with high genetic advance over mean reveals additive gene action and effective for phenotypic selection. Thus, the investigation provides understanding of the genetic basis of inheritance of quantitative trait in early segregating generations of cowpea, which may be useful in future breeding programmes.

FUTURE SCOPE

Increase in yield per unit area and seed protein content in cowpea is essential to obtain maximum profitability and to meet out protein demands, respectively. However, combining these traits in a single genotype is difficult, as they are negatively correlated. The current study aids in understanding the inheritance nature of the yield related traits and protein content in segregating generations, which in turn helps to select better segregants for the next generations. Focusing on the high protein lines with stable yield in F₂ and F₃ generations is advisable. Therefore, a new genotype with high yield coupled with high protein content can be evolved in future.

Acknowledgment. The author gratefully acknowledges Kerala Agricultural University for providing financial assistance in terms of research fund during the period of study.

Conflict of Interest. None.

REFERENCES

- Govindaraj, M., Vetriventhan, M. and Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics Research International*, 1, 1-14.
- Gowda, C. L., Samineni, S., Gaur, P. M. and Saxena, K. B. (2013). Enhancing the productivity of pulses in India. *ICRISAT*, 145-159.
- Gowda, T.H., Hiremath, S.R. and Salimath, P.M. (1991). Estimation of genetic parameters in intervarietal crosses of cowpea (*Vigna unguiculata*) and their implication in selection. *Legume research*, 14, 15-19.
- Kurer, S. (2007). Genetic variability studies in F₂ and F₃ generations of cowpea (*Vigna unguiculata* (L.) Walp). M. Sc. (Ag) thesis, University of Agricultural Sciences, Dharwad, 54-57.
- Kurer, S., Gangaprasad, S., Uma, M. S., Shanthakumar, G. and Salimath, P. M. (2010). Genetic variability studies in F₂ and F₃ generations of cowpea (*Vigna unguiculata* (L.) Walp). *Electronic Journal of Plant Breeding*, 1, 1344-1346.
- Maphosa, Y. and Jideani, V. A. (2017). The role of legumes in human nutrition. *Functional Food Improve Health Through Adequate Food*, 1, 13.
- Mariyammal, I., Pandiyan, M., Vanniarajan, C., Kennedy, J. S. and Senthil, N. (2019). Genetic variability in segregating generations of greengram (*Vigna radiata* L. Wilczek) for quantitative traits. *Electronic Journal of Plant Breeding*, 10, 293-296.
- Meenatchi, T., Thangaraj, K., Gnanamalar, R. P. and Pushpam, K. (2019). Genetic variability and

- heritability study on yield and its component traits in segregating population of cowpea (*Vigna unguiculata* L. Walp). *Electronic Journal of Plant Breeding*, 10, 736-741.
- Nair, K. R., Desai, S. S., Sawardekar, S. V. and Burondkar, M. M. (2018). Study of genetic variability parameters in F₂ generation of interspecific hybrids in cowpea. *International Journal of Pure and Applied Bioscience*, 6, 954-958.
- Ramamurthi, K., Geethalakshmi, R. and Sahadevan, S. (2012). Pulses: The poor man's protein. *Market survey*, 23-25.
- Salimath, P. M., Biradar, S., Linganagowda and Uma, M. S. (2010). Variability parameters in F₂ and F₃ populations of cowpea involving determinate, semideterminate and indeterminate types. *Karnataka Journal of Agricultural Science*, 20, 255-256.
- Selvi, V. M., Nirmalakumari, A., Anandakumar, C. R. and Amudha, R. (2022). Evaluation of genetic potential between F₂ and F₃ generations of cowpea (*Vigna unguiculata* L. Walp.) using parent progeny regression analysis. *Biological Forum – An International Journal*, 14(1), 1146-1153.
- Slinkard, A. E., Solh, M. B. and Vandenberg, A. (2000). Breeding for yield: the direct approach. In *Linking Research and Marketing Opportunities for Pulses in the 21st century*, Springer, Dordrecht, 183-190.
- Subbiah, A., Prabhu, M., Rajangam, J., Jagadeesan, R. and Anbu, S. (2013). Genetic analysis of vegetable cowpea (*Vigna unguiculata* (L.) Walp). *Legume research*, 35, 1-9.
- Tyagi, P. C., Kumar, N. and Agarwal, M. C. (2000). Genetic variability and association of component characters for seed yield in cowpea (*Vigna unguiculata* L.). *Legume research*, 23, 92-96.

How to cite this article: Sunil R., Jiji Joseph, Santhosh Kumar A.V. and Biju S. (2023). Genetic variability Studies in F₂ and F₃ Segregating Generations for Biometrical Traits in Cowpea (*Vigna unguiculata* L. walp). *Biological Forum – An International Journal*, 15(10): 234-238.