Biological Forum – An International Journal 15(11): 533-536(2023)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Analysis for Yield and other Important Characters Related to Yield in Cowpea (*Vigna unguiculata* (L.) Walp.)

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(Received: 12 September 2023; Revised: 15 October 2023; Accepted: 23 October 2023; Published: 15 November 2023)
(Published by Research Trend)

ABSTRACT: For the improvement of quantitative traits in cowpea, selection of parents, making cross combination and selecting better transgressive segregants require knowledge of various gene action that's why this study employed a six-parameter model to determine the significance of grain yield per plant and its constituent characteristics in two crosses, including both additive and dominant gene effects. The dominant gene action has a larger magnitude than the additive gene effect. In the cross NCK-13-11 × NCK-15-09, clusters per plant, pods per plant, seeds per pod, pod length, 100 seed weight, harvest index and protein content were found significantly impacted by additive × additive gene interaction among epistasis; similarly, plant height, clusters per plant, seeds per pod and 100 seed weight were found significantly impacted in the cross NCK-13-11 × GC-3. With the exception of plant height, branches per plant and harvest index in the cross NCK-13-11 × NCK-15-09 and reproductive phase duration, branches per plant, clusters per plant, pods per plant, pod length, grain yield per plant and harvest index in the cross NCK-13-11 × GC-3, dominance × dominance component contributed significantly in both the crosses. Non-allelic interactions, in addition to additive and dominant components, were important in determining the different cowpea characteristics. There was no evidence of complimentary gene interaction in any of the studied attributes. Cowpea's many characteristics were determined by non-allelic interactions in addition to additive and dominant components. It would be difficult for the breeder to produce possible segregants that are superior than the involved parents in this sort of situation by employing standard breeding approaches, such as making straightforward crosses and taking advantage of them through the direct pedigree approach. for improvement of cowpea, transgressive segregants can be produced by biparental mating system.

Keywords: Generation mean analysis, scaling tests, generations, gene actions.

INTRODUCTION

In many poor countries, cowpeas are a valuable crop due to their high protein content, adaptability to various soil types and intercropping systems, drought resilience, and capacity to increase soil fertility and reduce erosion. For farmers, a crucial source of revenue is the selling of the stems and leaves for use as animal fodder during the dry season.

A leguminous crop in the tribe *Phaseoleae*, subtribe *Phaseolinae*, order *Fabaceae*, subfamily *Faboideae* (*Papillionoideae*), genus Vigna is the cowpea [*Vigna unguiculata* L. Walp] (2n = 22). Grown mostly for vegetables and grains, and to a lesser extent as a fodder crop, it is found in tropical and subtropical parts of the world. It is unknown where exactly cowpeas came from. Africa and Asia, however, were mentioned as the crop's domestication sites. But because Southern Africa has the most genetic variety in crops and the most basic forms of wild animals, it is suggested that this region is the most likely place of domestication and genesis.

Understanding gene action in plant breeding facilitates the process of choosing parents, choosing a suitable breeding strategy for genetic enhancement of certain quantitative traits, and evaluating other genetic determinants. Additivity, dominance, and epistasis are the three categories into which gene activity falls in relation to genetic diversity. In self-pollinating crops such as cowpea, selection only affects additive genetic variation, meaning that genetic gain is required under selection. The inheritance of several quantitative traits in cowpea could involve non-additive variation as well, including as dominance and epistasis, in addition to additive variation.

MATERIALS AND METHODS

The experiment was carried out during *kharif*-2018 to *kharif*-2020 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari. In this experiment six generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of four crosses involving four diverse genotypes of cowpea were used to study the genetic analysis of quantitative traits in Compact Family Block Design (CFBD) with three replications. The crossing program was initiated during *kharif*-2018 to produce four F_1 hybrids among four selected genotypes, while backcrossing and selfing of F_1 was done in summer-2019 and *kharif*-2019 to obtain BC_1, BC_2 and F_2 generations of respective crosses.

Details of experimental material

Eight rows of F_2 and two rows each of P_1, P_2, F_1, BC_1, BC_2, and F_2 are shown in each plot. The suitability of the additive-dominance model in each cross for non-allelic interaction was assessed using the individual scaling tests (A, B, C, and D) described by Hayman and Mather (1955). Furthermore, Cavalli's Joint scaling test approach (1952) was used to calculate the chi-square value for each cross with ten characters. Higher-order interaction or linkage was absent if the character's Chi-square value was not significant. In the context of non-allelic interactions, different gene effects were computed using Hayman's six-parameter model (1958). The significance of any one of these scales is taken to indicate the presence of non-allelic interaction.

1. D provides a test for ‘i’ (additive × additive) type of interaction.
2. C provides a test for ‘l’ (dominance × dominance) type of gene interaction.
3. ‘j’ (additive × dominance) type of interaction has no effect on C and D but it affects A and B. The test A and B provide evidence of 'i', 'j' and 'l' type of gene interactions.

Cross	Generation	Details
I	**NCK-13-11(♀) × NCK-15-09(♂)**	
	P_1	NCK-13-11
	P_2	NCK-15-09
	F_1	(NCK-13-11 × NCK-15-09)
	F_2	(NCK-13-11× NCK-15-09) selfed
	BC_1	(NCK-13-11× NCK-15-09) × NCK-13-11
	BC_2	(NCK-13-11 × NCK-15-09) × NCK-15-09
II	**NCK-13-11(♀) × GC-3(♂)**	
	P_1	NCK-13-11
	P_2	GC-3
	F_1	(NCK-13-11 × GC-3)
	F_2	(NCK-13-11× GC-3) selfed
	BC_1	(NCK-13-11 × GC-3) × NCK-13-11
	BC_2	(NCK-13-11 × GC-3) × GC-3

RESULT AND DISCUSSION

For each of the two crosses, an individual character analysis of variance was performed; the findings are shown in Table 1. Two crosses demonstrated a noteworthy average variation for the majority of the traits analyzed.

Variation among the generations mean was highly significant for days to flowering (NCK-13-11 × NCK-15-09, NCK-13-11×GC-3), days to maturity (NCK-13-11×GC-3), reproductive phase duration (NCK-13-11× NCK-15-09), plant height (NCK-13-11 × NCK-15-09, NCK-13-11×GC-3), clusters per plant (NCK-13-11 × NCK-15-09, NCK-13-11 × GC-3), pods per plant (NCK-13-11 × GC-3), seeds per pod (NCK-13-11 × NCK-15-09, NCK-13-11 × GC-3), pod length (NCK-13-11 × NCK-15-09), 100 seed weight (NCK-13-11 × NCK-15-09, NCK-13-11 × GC-3), grain yield per plant (NCK-13-11 × NCK-15-09) and protein content (NCK-13-11 × NCK-15-09, NCK-13-11 × GC-3). Moreover, significant difference was recorded among the generations for days to maturity (NCK-13-11 × NCK-15-09), reproductive phase duration (NCK-13-11 × GC-3), branches per plant (NCK-13-11 × NCK-15-09, NCK-13-11 × GC-3), pods per plant (NCK-13-11 × NCK-15-09), pod length (NCK-13-11 × GC-3) and harvest index (NCK-13-11 × NCK-15-09, NCK-13-11 × GC-3). Non-significant difference was observed between generations in cross II (NCK-13-11 ×GC-3) for grain yield per plant. Therefore, further analysis was not carried out for grain yield per plant in cross II.

Table 2 displays the cross-wise and character findings. Significance of (m) parameters for the majority of the characters examined in the two crosses with the majority of approaches indicating that sufficient variability existed among the generations included in the study and that different generations of a respective cross differed significantly from one another; therefore, this component has not been explained separately. Any of the scaling tests (A, B, C, and D) that were significant for grain production per plant and its component features suggested that there was a significant level of epistasis and that the additive-dominance model was inadequate. Therefore, a six-parameter model was used to estimate the genetic components of the two crossings, with the exception of the length of the reproductive phase in both crosses and the number of branches per plant in cross II, in order to evaluate different non-allelic gene effects.

Table 1: Analysis of variance for six generations in two crosses.

Sources	d.f.	Mean sum of squares						
		Days to flowering	Days to maturity	Reproductive phase duration	Plant height (cm)	Branches per plant	Clusters per plant	Pods per plant
Cross I (NCK-13-11 × NCK-15-09)								
Replications	2	0.23	0.92	1.10	22.41	0.04	0.25	41.58
Generations	5	4.27**	7.57*	9.92**	79.79**	0.46*	3.34**	291.86*
Error	10	0.43	1.71	0.93	12.66	0.10	0.40	68.35
Cross II (NCK-13-11 × GC-3)								
Replications	2	0.01	0.32	0.37	3.84	0.34*	0.06	0.08
Generations	5	1.68**	14.87**	9.63*	48.90**	0.31*	3.14**	38.96**
Error	10	0.25	1.83	2.15	4.57	0.08	0.19	2.99
Sources	**d.f.**	**Mean sum of squares**						
		Seeds per pod	**Pod length (cm)**	**100 seed weight (g)**	**Grain yield/plant (g)**	**Harvest index (%)**	**Protein content (%)**	
Cross I (NCK-13-11 × NCK-15-09)								
Replications	2	0.49	0.19	0.14	13.44	1.27	0.07*	
Generations	5	5.84**	3.03**	174.22**	66.99**	4.65*	11.36**	
Error	10	0.79	0.41	0.37	9.13	1.28	0.01	
Cross II (NCK-13-11 × GC-3)								
Replications	2	0.82	0.02	0.05	30.73*	1.56	0.02	
Generations	5	9.65**	2.52*	91.37**	18.15	2.48*	9.54**	
Error	10	1.23	0.48	0.34	6.19	0.60	0.05	

* and **, significant at 5% and 1%, respectively

The majority of the scaling tests for grain yield per plant and its constituent attributes showed a considerable degree of epistasis and the insufficiency of the additive-dominance model to compute different non-allelic gene effects. Consequently, a six-parameter model was utilized to estimate the genetic components, with the exception of cross I (NCK-13-11 × NCK-15-09), which was used to determine the length of the reproductive phase; cross II (NCK-13-11 × GC-3) was used to determine the length of the reproductive phase and the number of branches per plant. The absence of non-allelic interactions was indicated by the non-significance of the scaling test, which suggested using the three-parameter model provided by Jinks and Jones (1958) for genetic component estimation.

Both additive and dominant gene effects were found to be substantial for grain yield per plant and most component traits in both crosses. The dominant gene effect has a larger magnitude than the additive gene effect. For both crossings in the majority of the characters under investigation, the epistasis gene interactions dominance × dominance and additive × additive contributed considerably. In both crosses, duplicate epistasis has been detected, with the exception of plant height. In these cases, we should look for crossovers between different parental lines that would provide complementary epistasis and increase the expression of the characteristic under study, since selection would be limited and the impact of dominant genes may be reduced. Results similar to this one has been reported by Marennavar *et al.* (2015); Singh and Singh (2016); Pathak *et al.* (2016); Thakare *et al.* (2016); Gupta *et al.* (2017); Owusu *et al.* (2018); Pallavi *et al.* (2019); Shinde *et al.* (2021); Victoria *et al.* (2021). Apart from cross I (NCK-13-11 × NCK-15-09), which demonstrated significant outcomes for days to flowering, days to maturity, plant height, 100 seed weight, grain yield per plant, harvest index, and protein content, the current study found that cross II (NCK-13-11 × GC-3) demonstrated significant outcomes for days to flowering, days to maturity, plant height, and harvest index. Both additive and non-additive components affect the inheritance of these characteristics, as evidenced by studies conducted by Nautiyal *et al.* (2015), Singh and Singh (2016); Thakare *et al.* (2016); Gupta *et al.* (2017); Shinde *et al.* (2021); Victoria *et al.* (2021).

Table 2: Estimation of scaling tests and gene effects.

Characters	Crosses	Scaling test					Gene effect						Type of epistasis
		A	B	C	D	χ^2	m	d	h	i	j	l	
Days to flowering	**I**	-3.50**	-1.80*	-3.83**	0.73	**S**	36.15**	-0.63	-3.62**	-1.47	-0.85	6.77**	**D**
	II	-2.90**	-1.27	-4.57**	-0.20	**S**	35.94**	-0.28	-0.10	0.40	-0.82	3.77*	**D**
Days to maturity	**I**	-7.00**	-4.00	-7.70*	1.65	**S**	82.81**	-1.57	-0.63	-3.30	-1.50	14.30**	**D**
	II	-5.07**	-5.23*	-8.67**	0.82	**S**	71.22**	-0.72	-5.33	-1.63	0.08	11.93*	**D**
Reproductive phase duration	**I**	-3.50	-2.20	-3.87	0.92	**NS**	-	-	-	-	-	-	-
	II	-2.17	-3.97	-4.10	1.02	**NS**	-	-	-	-	-	-	-
Plant height (cm)	**I**	10.57*	2.83	23.97**	5.28	**S**	63.39**	4.60	-0.70	-10.57	3.87	-2.83	-
	II	8.33**	-7.73**	19.17**	9.28**	**S**	81.62**	5.45**	-12.15*	-18.57**	8.03	17.97*	-
Branches per plant	**I**	-0.67*	-0.40	-1.87**	-0.40	**S**	3.51**	-0.38*	1.65**	0.80	-0.13	0.27	-
	II	0.07	0.33	0.47	0.03	**NS**	-	-	-	-	-	-	-
Clusters per plant	**I**	-4.30**	-3.27**	-4.80**	1.38**	**S**	5.73**	-1.02**	-1.50	-2.77**	-0.52	10.33**	**D**

	II	2.37**	0.63	5.33**	1.17**	**S**	6.13**	-0.47	-3.00**	-2.33**	0.87	-0.67	**-**
Pods per plant	**I**	-19.53**	-33.47**	-41.43**	5.78**	**S**	17.55**	-4.15**	-3.12	-11.57**	6.97	64.57**	**D**
	II	2.93**	-3.50	-6.13**	-2.78	**S**	14.94**	-2.27	5.02	5.57	3.22	-5.00	**-**
Seeds per pod	**I**	4.93**	5.00**	7.23**	-1.35**	**S**	12.95**	-0.62*	3.28**	2.70**	-0.03	-12.63**	**D**
	II	6.73**	0.47	0.20	-3.50**	**S**	13.05**	2.00**	9.80**	7.00**	3.13	-14.20**	**D**
Pod length (cm)	**I**	0.73**	1.46**	-2.24**	-2.22**	**S**	14.08**	-0.04	6.74**	4.44**	-0.37	-6.63**	**D**
	II	2.46**	-0.05	1.83	-0.29	**S**	15.46**	0.83	2.46*	0.57	1.26	-2.98	**D**
100 seed weight (g)	**I**	-2.05**	7.05**	-2.46**	-3.73**	**S**	13.45**	6.59**	2.21*	7.46**	-4.55	-12.47**	**-**
	II	-12.43**	0.42	0.64	6.33**	**S**	17.07**	1.31**	-17.25**	-12.65**	-6.43	24.66**	**D**
Grain yield per plant (g)	**I**	-12.11**	-17.57**	-25.96**	1.86	**S**	30.66**	3.37**	5.64	-3.72	2.73	33.40**	**D**
	II	-	-	-	-	**-**	-	-	-	-	-	-	**-**
Harvest index (%)	**I**	-2.86*	-2.82*	-10.65**	-2.49**	**S**	35.25**	-0.27	7.22**	4.97**	-0.02	0.71	**-**
	II	-0.84	-2.79**	-4.64*	-0.51	**S**	36.88**	-0.15	0.90	1.01	0.98	2.62	**-**
Protein content (%)	**I**	1.14**	-3.88**	-8.15**	-2.71**	**S**	17.60**	1.49**	1.58**	5.41**	2.51	-2.67**	**-**
	II	4.06**	4.90**	9.90**	0.47	**S**	23.16**	0.44**	1.33*	-0.93	-0.42	-8.04**	**D**

CONCLUSIONS

In a nutshell, non-allelic interactions were important in determining the numerous features of cowpea, along with additive and dominant components. The majority of the traits exhibiting digenic interaction were shown to depend heavily on duplicate gene activity. In this kind of scenario, it would be challenging for the breeder to use traditional breeding techniques, such creating straightforward crossings and using the straight pedigree approach to exploit them, to obtain potential segregants that are superior to the involved parents. Breeding procedure involving multiple crosses, biparental crosses may be restores to get transgressive segregants. This is especially important to develop good pure lines having superiority in different characters.

Acknowledgement. Department of Genetics and Plant Breeding (NMCA) and Pulse and Castor Research Station, Navsari Agricultural University graciously provided the required resources for the experiments, which the authors gratefully thank.
Conflict of Interest. None.

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How to cite this article: K.S. Mungra, P.A. Vavdiya, Y.V. Naghera, D.A. Chauhan and M.R. Prajapati (2023). Genetic Analysis for Yield and other Important Characters Related to Yield in Cowpea (*Vigna unguiculata* (L.) Walp.). *Biological Forum – An International Journal, 15*(11): 533-536.