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Generation Mean Analysis Studies in Cowpea (*Vigna unguiculata* L. Walp)

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ABSTRACT: In present investigation on generation mean analysis carried out study on components of variance in two safflower crosses. Except for days to 50% flowering in cross GDVC-2 × LC-1 and pod length in both crosses, the estimate of significant simple scaling tests and joint scaling tests revealed the presence of epistatic gene effects for seed yield and its component characteristics in both crosses. Seed yield and its components were shown to be affected by both additive and non-additive genetic variations, with non-additive gene activity predominating. All three forms of non-allelic interactions contribute more to reducing alleles of dominance × dominance (l) in various characteristics when it comes to epistasis effects. The majority of the characters had duplicate epistasis.

Keywords: Cowpea, Gene action, Generation mean, Scaling Test.

I. INTRODUCTION

Cowpea [*Vigna unguiculata* L. Walp] (2n = 22) is a leguminous crop in the order Fabaceae, subfamily Faboideae (Papillionoideae), tribe Phaseoleae, subtribe Phaseolinae, genus *Vigna*. It is mainly grown in tropical and subtropical regions in the world for vegetable and grains and to lesser extent as a fodder crop. The precise origin of cultivated cowpea is not known. However, Asia and Africa were discussed as domestication site of this crop. But due to presence of most primitive form of wild species and highest genetic diversity of the crop, Southern Africa is proposed as most probable centre of domestication and to be the centre of origin [7].

In plant breeding, understanding gene activity aids in the selection of parents and the selection of an appropriate breeding strategy for genetic improvement of certain quantitative characteristics, as well as the assessment of some other genetic factors. Gene action may be classified into three kinds based on how it affects genetic variance: additive, dominance, and epistatic gene action. Because additive genetic variation is the only genetic variable that reacts to selection in self-pollinating crops like cowpea, it is a need for genetic gain under selection.In addition to additive variation, it has been suggested that non-additive variance (dominance and epistasis) may also be involved in the inheritance of many quantitative characters in cowpea.

II. MATERIALS AND METHODS

The crossing work to obtain two F_1 crosses *viz.,* GDVC-2 × LC-1 and GC-6 × LC-1 involving three diverse patents *viz.,* GDVC-2, GC-6 and LC-1 was undertaken during *kharif*, 2018-19. Back crossing and selfing of F_1 to get F_2 was done during *rabi*, 2018-19. The experimental material comprised of six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 of each of two different cowpea crosses were sown in Randomized Block Design with two replications and data were recorded for ten morphological traits. Each plot has two rows of P1, P2, F1, BC1, BC2, and F2, as well as eight rows of F2. Individual scaling tests (A, B, C, D) as outlined by Hayman and Mather (1955) were employed to evaluate the adequacy of the additive-dominance model in each cross for non-allelic interaction. In addition, the chi-square value for 10 characters in each cross was computed using Cavalli's Joint scaling test technique (1952). If the character's Chi-square value was not significant, it meant there was absence of higher-order interaction or linkage. Various gene effects were calculated in the presence of non-allelic interactions using Hayman's six-parameter model (1958).

III. RESULT AND DISCUSSION

The analysis of variance for generation mean analysis was carried out for ten morphological traits (Table 1). The findings of the analysis of variances between crosses revealed that all of the characters had highly significant differences. The mean sum of square for treatments were extremely significant for all characters in both crosses except days to 50% flowering and pod length in GC-6 × LC-1, according to the outcomes of analysis of variances between generations within crosses. This suggested that there were enough differences in the material to allow for effective selection of all of the characters.

Table 1: Analysis of variance (Mean sum squares) of generation means for 10 characters in cowpea.

Sources	d.f	DF	DM	PH	NBPP	NPPP	NSPP	PL	TW	HI	SYPP
Analysis of variance between crosses											
Replication	1	0.04	0.17	0.96	0.01	1.94	0.67	0.02	0.08	10.58	3.47
Treatment	12	11.06**	93.59**	374.09**	4.18**	25.69**	5.64**	2.49**	2.7**	67.64**	19.93**
Error	12	0.19	0.2	8.69	0.15	1.63	0.62	0.07	0.03	6.24	1.41
Analysis of variance between generations within cross											
GCVC-2 × LC-1											
Replication	1	0.18	0.001	30.7	0.07	0.006	0.08	0.001	0.04	1.91	1.10
Treatment	5	16.28**	169.6**	602.23**	6.64**	46.96**	4.63*	2.23**	1.12**	26.47	31.93**
Error	5	0.20	0.22	49.01	0.28	2.25	0.90	0.05	0.04	8.73	0.62
GC-6 × LC -1											
Replication	1	0.00083	0.44	7.05	0.12	3.03	0.20	0.0052	0.024	17.52	5.41
Treatment	5	0.092	20.3*	213.8**	3.26**	14.25*	7.25**	0.25	3.32**	38.34*	7.15*
Error	5	0.21	0.38	8.29	0.032	1.38	0.41	0.07	0.023	3.73	1.66

*Significant at 5 % level, ** Significant at 1 % level; DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); NBPP = Number of branches per plant; NPP = Number of pod per plant; NSPP = Number of seeds per pod; PL= Pod length (cm); TW = Test weight (g); HI = Harvest index (%);SYPP = Seed yield per plant (g)

The scaling test and joint scaling test revealed that the assumption of a simple additive-dominance model was not met in most of the crosses for all of the characteristics investigated, indicating the presence of digenic interaction in the inheritance of these traits. For analysis this suggested a six-parameter model with three digenic interaction parameters. When the basic additive-dominance model failed to explain the variance in generation means. Table 2 displays the gene effect for both crosses.

For trait days to 50% flowering, non-significant estimates of all scales in the cross, GDVC-2 × LC-1 indicating absence of non-allelic interaction, whereas significant estimates of all the scale in the cross, GC-6 × LC-1 indicating presence non allelic interaction. Both additive and dominance gene effects were significant with relative greater magnitude of additive component for days to 50 % flowering was in the cross, GC-6 × LC-1. However only dominance effects in positive direction in the cross, GDVC-2 × LC-1. Among the epistatic interaction all three type of gene effects were observed for this character in the cross, GC-6 × LC-1 with presence of duplicate epistatic in the expression of this traits. This suggest importance of both additive and non-additive gene effects with preponderance of dominance effect and duplicate type of gene interaction responsible for inheritance of this traits, [4]. The presence of non-allelic interaction for days to maturity was indicated by significant estimation of A, C, and D scales in cross, GDVC-2 × LC-1 and A, B, C, and D scales in cross, GC-6 × LC-1. The importance of additive and non-additive gene action was demonstrated by significant values of additive and dominant gene effects. The additive × additive and additive × dominance gene effects were highly significant in the cross GDVC-2 × LC-1, and the additive x additive gene effect was highly significant in the cross GC-6 × LC-1. The inheritance of this character was caused by complementary epistasis for GDVC-2 × LC-1 and duplicate epistasis for GC-6 × LC-1, [2].

Significant values for scale A, B, and C in the GDVC-2 × LC-1 cross and A, B, C, and D in the GC-6 × LC-1 cross, as well as a significant X^2 value in both crossings, indicating the possibility of non-allelic interaction. In both crosses, the significant ‘m’ from the generation mean analysis revealed that six generations were significantly different in terms of plant height. In both crosses, the estimates of dominating effects were significant, with positive and larger magnitudes for plant height. Among the epistatic interaction significant and positive additive × dominance and dominance × dominance in the cross, GDVC-2 × LC-1 and additive × additive, additive × dominance and dominance × dominance effects were observed for this trait. The dominance gene effects and dominance × dominance types of interaction was significant in positive direction in both the crosses revealing epistasis was predominantly of complementary type. The results are similar to other investigation also reported [10]. For number of branches per plant estimates of simple scaling tests B, C and D in the cross, GDVC-2 × LC-1 and A, C and D in the cross, GC-6 × LC-1 were significant indicating presence of non-allelic gene interaction. The estimates of gene effects revealed that in cross, GDVC-2 × LC-1, dominance, additive × additive and additive × dominance and in the cross, GC-6 × LC-1, dominance, additive × additive, additive × dominance and dominance × dominance effects were highly significant. The opposite sign of dominance (h) and dominance × dominance (I) component in both the crosses showed duplicate type of epistasis for this trait [11].

Significant estimates of C and D scale in cross, GDVC-2 × LC-1 and A, C and D scale in cross, GC-6 × LC-1 and significant X^2 values in both the crosses indicated presence of non-allelic gene interaction for number of pods per plant. The genetic parameters *viz.,* dominance, additive x additive and dominance × dominance in the cross, GDVC-2 × LC-1 and additive, dominance, additive × additive and dominance × dominance gene effects in the cross, GC-6 × LC-1 were highly significant. The dominance and dominance × dominance had apposite sign indicating the presence of duplicate gene interaction in both crosses for this trait. In both the crosses dominance and additive × additive gene effects were responsible for inheritance of number of pods per plant. In some reports, reported both additive and non-additive type of gene action with duplicate type of epistatic for improvement of this trait [11].

For trait number of seeds per pod, estimates of scale A, B and C scale in cross, GDVC-2 × LC-1 and D in cross, GC-6 × LC-1 and significant X^2 values in both the crosses indicated presence of non-allelic gene interaction for this trait. Dominant effects were highly significant in both crosses, however additive effects was significant in cross, GDVC-2 × LC-1. Among the epistatic gene interaction, additive × additive effects with complementary gene action for the cross GDVC-2 × LC-1 and additive × dominance and dominance × dominance effects with duplicate gene action were observed for this trait. According to reported, that additive, dominance and epistatic effect were responsible for inheritance of seed per pods [8]. Non-significant scaling tests and X^2 values demonstrated that there was no non-allelic interaction for the trait pod length (cm) in both crosses, implying that the additive-dominance model was adequate. In the cross GC-6 × LC-1, the genetic characteristics, such as dominance impact, were determined to be positive and significant. The dominance effect was shown to be positive in the GDVC-2 × LC-1 cross [11].

Scaling tests B and C in the GDVC-2 × LC-1 cross, as well as C and D in the GC-6 × LC-1 cross, were extremely significant, and the X2 value for the additive-dominance model was significant in both crosses. The genetic characteristics, namely the dominance effect, were positive and larger than the additive effects in the GDVC-2 × LC-1 cross. Only the additive × dominance impact was significant among the epistatic effects. The presence of duplicate gene action was revealed by the opposite sign of dominance and dominance × dominance effects. The dominance, additive × additive, and dominance × dominance effects in the cross, GC-6 × LC-1, were all highly significant. The impacts of dominance × dominance were greater than the effects of dominance. This feature was found to be caused by a duplicate form of gene interaction [10]. The presence of non-allelic interaction as indicated by highly significant estimates of scaling tests A, C, and D in the cross, GDVC-2 × LC-1 and A and C in the cross, GC-6 × LC-1 for trait, harvest index (%). For both crosses, the joint scaling test yielded a highly significant chi square. Both crosses had highly substantial dominant effects, while the GC-6 × LC-1 cross had a highly significant additive effect. In both crosses, all three types of digenic interaction were highly significant. The cross GDVC-2 × LC-1, on the other hand, exhibited a complimentary type of gene action for this characteristic, whereas the cross GC-6 × LC-1 revealed a duplicate type of gene action, [1].

The estimation of scales B and C in the cross, GDVC-2 × LC-1, and C and D in the cross, GC-6 × LC-1, for trait seed yield per plant (g), suggesting the presence of non-allelic interaction. In both crosses, the joint scaling produce a relatively significant chi square value. Both additive and dominant gene effects were significant, although the additive gene effect in the GDVC-2 × LC-1 cross was negative in direction. Additive × dominance and dominance × dominance gene effects were significant in the cross, GDVC-2 × LC-1, while additive × additive and dominance × dominance gene effects were significant in the cross, GC-6 × LC-1. In both crosses, dominant effects and dominant × dominant type gene interactions were significant. However, negative and positive directions in the cross GDVC-2 × LC-1 and positive direction in the cross GC-6 × LC-1 revealed epistasis was predominantly of duplicate and complementary types, respectively. The current findings are consistent with [9].

Table 2: Estimates of gene effects in two crosses of cowpea for 10 characters.

Crosses	m	d	h	i	j	l	Types of Epistasis
Days to 50 % flowering							
GDVC 6 × LC-1	45.75**±0.18	-5.70±0.07	12.35±0.75	--	---	---	
GC-2 × LC-1	50.00**±0.15	0.20**±0.14	-1.3**±0.67	-1.40**±0.67	-0.050**±0.16	2.10**±0.85	Duplicate
Days to maturity							
GDVC 6 × LC-1	100.4**±0.20	-13.10**±0.1	-8.90**±0.82	-12.20**±0.82	-1.20**±0.11	-2.60±1.71	Complementary
GC-2 × LC-1	101.8**±0.11	-1.60**±0.31	-5.80**±0.79	-6.20**±0.78	3.10±0.32	2.20±1.36	Duplicate
Plant height							
GDVC 6 × LC-1	54.00**±0.56	-4.60±1.05	0.90**±3.13	-26.80±3.09	16.30**±1.16	83.40**±4.89	Complementary
GC-2 × LC-1	44.10**±0.50	-0.90**±1.11	19.10**±9.63	1.80**±3.00	12.00**±1.19	13.40**±5.15	Complementary
Number of branches per plant							
GDVC 6 × LC-1	11.22**±0.22	0.30±0.10	-11.80**±0.93	-13.10**±0.93	1.60*±0.12	11.10±1.00	Duplicate
GC-2 × LC-1	10.84**±0.10	0.30±0.07	-12.46**±0.42	-12.76**±0.42	0.80**±0.07	14.36**±0.49	Duplicate
Number of pod per pant							
GDVC 6 × LC-1	18.93**±0.45	-3.90±0.26	25.53**±1.92	16.48**±1.89	1.75±0.39	-19.18*±2.20	Duplicate
GC-2 × LC-1	18.62**±0.09	-0.50**±0.67	17.00**±1.42	10.90**±1.39	0.60±0.67	-4.50**±2.76	Duplicate
GDVC 6 × LC-1	11.50**±0.06	-0.10*±0.18	-3.95*±0.48	-2.00*±0.43	1.85±0.21	-2.00±0.43	Complementary
GC-2 × LC-1	11.74**±0.23	-1.30±0.26	4.72*±1.10	4.02±1.06	0.90**±0.28	-4.02**±1.53	Duplicate
Pod length (cm)							
GDVC 6 × LC-1	12.22**±0.09	-0.70±0.05	4.45±0.38	--	--	--	
GC-2 × LC-1	12.94**±0.08	-0.20±0.11	2.49*±0.24	--	--	--	
100 seed weight (g)							
GDVC 6 × LC-1	11.28±0.08	-0.20±0.047	4.21±0.35	2.86±0.35	-0.95**±0.06	-3.96±0.39	Duplicate
GC-2 × LC-1	13.03**±0.01	0.20±0.04	2.13**±0.12	0.68**±0.10	-1.55±0.05	-2.78*±0.23	Duplicate
Harvest index (%)							
GDVC 6 × LC-1	45.55**±1.18	-7.65±0.73	3.14**±4.97	5.10**±4.95	-4.51*±0.81	3.94**±5.65	Complementary
GC-2 × LC-1	41.80**±0.73	0.80**±0.89	35.40**±3.50	40.20**±3.43	3.05**±0.93	-51.40**±4.82	Duplicate
Seed yield per plant (g)							
GDVC 6 × LC-1	17.28**±0.19	-3.50**±0.32	25.08*±1.02	21.08±1.01	1.00**±0.36	-18.88*±1.55	Duplicate
GC-2 × LC-1	18.43**±0.67	2.00**±0.21	5.48**±2.75	3.88**±2.73	3.50±0.33	5.72**±2.88	Complementary

*Significant at 5 % level, ** Significant at 1 % level.

IV. CONCLUSION

The study on both crosses provided information about the genetic components of variance, this helped in deciding proper breeding procedure for improvement. In both crosses, significant individual and joint scaling tests revealed epistatic gene effects for seed yield and its component traits. With a prevalence of non-additive gene actions, both additive and non-additive genetic variations were reported to be essential for seed yield and its components. All three types of non-allelic interactions contribute more to lowering alleles of dominance × dominance (I) in some traits when it comes to epistasis effects. The majority of the characters had duplicate epistasis. These characters might be improved through recurrent selection in bi-parental progenies that would help in exploiting the duplicate type of non-allelic interaction. For the traits governing additive gene effect can be improved through pedigree method of selection.

V. FUTURE SCOPE

The study of gene action through generation mean analysis helps in deciding suitable breeding procedure for improvement of given crosses in respect to seed yield and other yield contributing characters.

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