GENERATION MEAN ANALYSIS FOR PROTEIN CONTENT IN COWPEA

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ABSTRACT

A field experiment was undertaken with a view to know the components of variation for protein content in cowpea [Vigna unguiculata (L.) Walp.]. Six generations, viz., P_1, P_2, F_1, F_2, BC_1 and BC_2 of eight crosses involving sixteen diversified cultivars of cowpea were evaluated for protein content. Scaling test revealed inadequacy of additive-dominance model and presence of epistatic interaction in all the eight crosses. Significant dominance x dominance type of interaction in most of the crosses indicated non-additive type of gene action governing protein content. Opposite signs of h and l indicated presence of duplicate type of epistasis in most of the crosses except Cross II (GC-4 x Pusa komal), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi), which revealed complementary epistasis. Non-additive gene action with presence of epistasis in most of the crosses suggested that selection in later generation would be effective for further improvement in protein content.

KEY WORDS: Cowpea, generation mean analysis, protein content

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is diploid with chromosome number 2n=22 and belongs to family *Fabaceae*. It is one of the oldest sources of human food in form of green pod as well as dry grain and has most likely been used as a crop. Cowpea an indigenous African annual legume is high in protein (25%) and is having good nutritional qualities. The protein in cowpea seed is rich in the amino acids *viz.*, lysine and tryptophan compared to cereal grains; however, it is deficient in methionine and cystine when compared to animal proteins. Therefore, cowpea seed is being valued as a nutritional supplement to cereals and an extender of animal proteins. So, broader objective of this research was to focus on components of variation for protein content in cowpea. As, protein content of cowpea is influenced by both genotype and environmental conditions, the concept of generations mean analysis developed by Hayman (1958) and Jinks and Jones (1958)

for the estimation of genetic components of variation was employed to study the same. Analysis of this technique is based on six different generations of a cross, *viz.*, parents (P_1, P_2), their F_1, F_2 and backcrosses (BC_1, BC_2). The mean values over replications are used for the estimation of gene effects. This technique provides information about the presence or absence of epistasis besides estimation of additive and dominance variances and effects. In crop improvement, only the genetic component of variation is important since only this component is transmitted to the next generation. Components of variation are more useful in predicting the resultant effect of selecting the best individuals and determining the breeding procedure for the improvement of such character.

MATERIALS AND METHODS

The present investigation was carried out to elicit information on components of variation for protein content in cowpea. The experimental material consisting of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the following eight single crosses *viz.*, Cross I (GC-3 x Pusa falguni), Cross II (GC-4 x Pusa komal), Cross III (GC-5 x Anand cowpea), Cross IV (W-203-3 x W 3-1), Cross V (W-502-2 x W-3-2), Cross VI (Phule CP-5040 x W 601), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi). The F_1 hybrids were generated of above eight single crosses during *Rabi* 2012-13 and *Summer* 2013. Backcrossing was done in *Rabi* 2013-14 with its respective parents. Selfing of F_1s was done in the same season (*Rabi* 2013-14) to get F_2s. All the six generations were sown at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari during *Kharif* 2014 in Compact Family Block Design with three replications. Each replication was divided in eight compact blocks. Each eight crosses consisting of six generations were randomly allotted to the blocks. Six generations were than randomly allotted to each plot within a block. Each plot consisted of one row of parents and F_1s, two rows of the backcrosses and four rows of the F_{2S} of each cross. Inter and intra row spacing was kept 45 cm and 10 cm, respectively. Protein content of dry seeds was determined by estimating the nitrogen content following Kjeldhal's method (Jackson, 1967) and multiplying the nitrogen content with a factor 6.25 and expressed on per cent basis for each genotype. The mean values of the protein content were subjected to statistical analysis to study the components of variation.

RESULTS AND DISCUSSION

The analysis of variance for protein content was carried out for each of the eight crosses and the results are presented in Table 1. The mean sum of squares indicated significant differences among the generations of all the eight crosses for protein content indicated sufficient amount of variability was present among all the generations.

Perusal of *per se* performance for protein content as depicted in Table 2 showed that highest protein content in

F_1s was recorded for cross Cross VII (CDP-108 x W-4) 31.96 per cent followed by cross VIII (Cowpea Sabra x Waghai Krushi) 28.57 per cent, cross II (GC-4 x Pusa komal) 23.82 per cent and cross III (GC-5 x Anand cowpea) 23.14 per cent (Table 2). In the present study, the mean of the F_1s were higher than both the parents in all the eight crosses indicating presence of over dominance for inheritance of protein content. The mean values of F_2s were higher than F_1s in Cross IV (W-203-3 x W 3-1), Cross V (W-502-2 x W-3-2) and Cross VI (Phule CP-5040 x W 601) indicating absence of inbreeding depression, while Cross I (GC-3 x Pusa falguni), Cross II (GC-4 x Pusa komal), Cross III (GC-5 x Anand cowpea), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi) showed lower F_2 means as compared to F_1 indicating presence of inbreeding depression. Cross I (GC-3 x Pusa falguni), Cross IV (W-203-3 x W 3-1), Cross V (W-502-2 x W-3-2), Cross VI (Phule CP-5040 x W 601) and Cross VII (CDP-108 x W-4) in BC_1 generation and Cross IV (W-203-3 x W 3-1) and Cross VI (Phule CP-5040 x W 601) in BC_2 generation were found to be either closer or higher than parents and/or F_1s revealed that genes for the protein content were present in respective parents, while rest of all the crosses in BC_1 and BC_2 generation showed the presence of epistatic interaction.

Scaling tests A, B, C and D were significant which revealed inadequacy of additive-dominance model and presence of non-allelic/epistatic interactions for inheritance of protein content in all the crosses (Table 3). Additive effect was non-significant for all the crosses, but additive x additive type of epistatic interaction was found significant in crosses IV, V, VI and VII and dominance effect was significant for the crosses IV, VI and VII. Significant and positive dominance x dominance type of interaction in most of the crosses indicated non-additive type of gene action governing protein content. Opposite signs of *h* and *l* indicated presence of duplicate type of epistasis in most of the crosses except Cross II (GC-4 x Pusa komal), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi), which revealed complementary epistasis. Similar kind of results were also reported by Noubissie *et al.* (2011), Tchiagam *et al.* (2011), Adeyanju *et al.* (2012) and Akhshi *et al.* (2014) for protein content in cowpea.

CONCLUSION

From the results and discussion, it can be concluded that non-additive gene action with presence of epistasis in most of the crosses suggested that delayed selection between families would be more meaningful as due to inbreeding additive genes could be fixed for further improvement in protein content.

REFFERENCES

Adeyanju, A. O.; Ishiyaku, M. F.; Echekwu, C. A. and Olarewaju, J. D. (2012).

Generation mean analysis of dual purpose traits in cowpea [*Vigna unguiculata* (L.) walp]. *African J. Biotechnol.*, **11**(46): 10473-10483.

Akhshi, N.; Cheghamirza, K.; Nazarian, F. F. and Ahmadi, H. (2014). Generation mean analysis for yield components in common bean. *Iranian J. Plant Physiol.*, **4** (3): 1079-1085.

Hayman, B. I. (1958). The separation of epistatic from additive and dominance variation in generation. *Hered.*, **12**: 371-390.

Jackson, M. L. (1967). Soil Chemical Analysis, Prentice Hall Int., New Delhi.

Jinks, J. L. and Jones, R. M. (1958). Estimation of the components of heterosis. *Genet.*, **43**: 223-234.

Noubissie, J. B. T.; Youmbi, E.; Njintang, N. Y.; Bell, J. M. and Maina, A. N. (2011). Generation mean analysis of seed sucrose content in cowpea [*Vigna unguiculata* (L.) Walp.]. *Asian J. Agric. Sci.*, **3**(6): 475-480.

Tchiagam, J. B. N.; Youmbi, E.; Njintang, N. Y.; J. M. and Maina, A. N. (2011). Generation means analysis of seed sucrose content in cowpea [*Vigna unguiculata* (L.) Walp.]. *Asian J. Agric. Sci.*, **3** (6): 475-480.

Table 1: Analysis of variance of protein content (%) for six generations in eight crosses of cowpea

Source	d.f.	Mean sum of square							
		Cross I	Cross II	Cross III	Cross IV	Cross V	Cross VI	Cross VII	Cross VIII
Replication	2	1.29	1.70	1.54	0.60	0.93	0.64	0.13	3.12
Generation	5	2.11**	4.83**	3.56**	3.48**	1.64**	3.07**	73.15**	25.02**
Error	10	0.34	0.44	0.40	0.17	0.24	0.18	0.44	0.82

Where,

Cross I (GC-3 x Pusa falguni), Cross II (GC-4 x Pusa komal), Cross III (GC-5 x Anand cowpea), Cross IV (W-203-3 x W 3-1), Cross V (W-502-2 x W-3-2), Cross VI (Phule CP-5040 x W 601), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi)

**Significant at 5% level and ** Significant at 1% level*

Table 2: *Per se* performance of six generations in eight crosses of cowpea for protein content (%)

Cross	Generations						S.Em ±	CD
	P_1	P_2	F_1	F_2	BC_1	BC_2		
Protein content (%)								
I	19.97	21.63	22.00	20.89	20.05	20.43	0.34	1.06
II	21.46	23.39	23.82	21.30	20.81	21.22	0.38	1.21
III	20.90	22.73	23.14	21.15	20.52	20.92	0.37	1.15
IV	16.73	17.80	18.04	19.97	18.41	18.73	0.24	0.74
V	18.39	19.76	20.12	20.48	19.15	19.49	0.28	0.90
VI	16.94	18.05	18.31	20.03	18.53	18.85	0.24	0.77
VII	19.60	22.00	31.96	18.84	19.90	20.35	0.38	1.20
VIII	24.75	27.85	28.57	22.23	22.21	22.58	0.52	1.65

Where,

Cross I (GC-3 x Pusa falguni), Cross II (GC-4 x Pusa komal), Cross III (GC-5 x Anand cowpea), Cross IV (W-203-3 x W 3-1), Cross V (W-502-2 x W-3-2), Cross VI (Phule CP-5040 x W 601), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi)

Table 3: The results of scaling test and estimates of gene effects forprotein content (%) in eight crosses of cowpea

Cross	A	B	C	D	*m*	*d*	*h*	*i*	*j*	*l*	Gene action
Protein content (%)											
I	-1.87	-2.76*	-2.05	1.29	20.89**	-0.38	-1.39	-2.59	0.9	7.22*	Duplicate
II	-3.67**	-4.77**	-7.28**	0.58	21.3**	-0.41	0.24	-1.16	1.11	9.6**	Complementary
III	-2.99**	-4.02**	-5.32*	0.85	21.15**	-0.4	-0.37	-1.69	1.03	8.7**	Duplicate
IV	2.06*	1.63	9.28**	2.8**	19.97**	-0.32	-4.82**	-5.6**	0.43	1.91	Duplicate
V	-0.21	-0.89	3.53	2.32*	20.48**	-0.35	-3.6	-4.64*	0.68	5.74*	Duplicate
VI	1.8*	1.35	8.5**	2.68**	20.03**	-0.33	-4.54*	-5.35**	0.46	2.2	Duplicate
VII	-11.77**	-13.27**	-30.16**	-2.56**	18.85**	-0.45	16.26**	5.12**	1.51	19.93**	Complementary
VIII	-8.9**	-11.26**	-20.81**	-0.32	22.23**	-0.37	2.91	0.64	2.37	19.52**	Complementary

Where,

Cross I (GC-3 x Pusa falguni), Cross II (GC-4 x Pusa komal), Cross III (GC-5 x Anand cowpea), Cross IV (W-203-3 x W 3-1), Cross V (W-502-2 x W-3-2), Cross VI (Phule CP-5040 x W 601), Cross VII (CDP-108 x W-4) and Cross VIII (Cowpea Sabra x Waghai Krushi)

****Significant at 5% level and** ** Significant at 1% level***

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