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GENERATION MEAN ANALYSIS FOR QUALITY TRAITS IN FODDER COWPEA [*VIGNA UNGUICULATA* (L.) WALP]

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SUMMARY

The objective of the present investigation was to estimate genetic variation and type of gene action controlling quality traits of two cowpea crosses *viz*., C 74 × C 88 and C 74 × CL 400 by six parameter generation mean analysis. The quality traits studied were green fodder yield, dry matter yield, crude protein (%), acid detergent fibre (%) and neutral detergent fibre (%). The results indicated that the mean effects were highly significant and the traits were quantitatively inherited. Additive and dominant gene effects are highly significant for all traits. The high magnitude of additive x additive gene effect suggests the pedigree method is best suitable breeding method for development of high yielding fodder cultivars with better quality traits.

Key words : Cowpea, Quality traits, generation mean analysis

Cowpea is a multipurpose crop, grown for pods as a vegetable, seed as pulse, leaves as fodder, in mixed farming for nitrogen fixation and green manure for soil improvement (Roy *et al.,* 2016, Arya *et al*., 2021). In Punjab, Cowpea is generally grown as a summer fodder crop and is cultivated from March to July. Cowpea is a rich source of protein and provide high-quality food for ruminants (Kulkarni *et al*., 2018; Panchta *et al*., 2021). It is a rich source of tryptophan and lysine amino acids which are present in plant storage proteins. The leaves of cowpea are rich in vitamins and minerals which makes it a perfect food material for animal consumption. The leaves contain 22-30% crude protein and haulms contain 13-17% protein. The leaves are rich in several antioxidants as well, it includes tocopherols, flavonoids, anti-cancer agents and lycopene (Shetty *et al*., 2013).

Development of high fodder yielding cowpea varieties would be helpful to farmers for sustainable livestock farming (Rachie, 1985, Vu *et al*., 2017). To develop high yielding fodder cowpea genotypes, a better understanding of the gene action involved in the inheritance of fodder traits is essential (Nguyen *et al*., 2019; Panchta *et al*., 2020) which ultimately helpful in the breeding of new high yielding genotypes/ varieties (Arya *et al*., 2008). Therefore, the objective of present study was to understand the gene action and inheritance patterns of fodder quality traits and identify appropriate strategies for transferring these traits to elite lines of cultivated cowpea.

MATERIALS AND METHODS

Breeding material

The study was carried out at the experimental farm of Forage, Millets and Nutrition Section. Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab from July to September 2020. The cowpea genotypes Cowpea 74, C88 and CL 400 were used to develop two sets of six basic generations (P1, P2, F1, F2, BC1 and BC2). Two crosses (Cowpea 74 x C 88) and (Cowpea 74 x CL 400) were made between and during *Kharif* 2018. Their generations *viz*. F1, F2, BC1 and BC2 were made in *Kharif* 2019 in the controlled environment. Each generation was harvested separatelyand the seed of each generation was stored for sowing in the following year.

Experimental design

Six generations of two crosses were sown in randomized complete-block design with three replications and recommended agronomic practices were followed. Parental lines and their F_1s were grown in five-row plots while F_2, BC1 and BC2 were sown in 15-row plots with 3 m length. A total of 15 randomly selected plants from parents and their F_1s and 60 plants from F_2, BC1 and BC2 were tagged in each replication and samples were taken for the following quality trait analysis:

1. Green fodder yield (GFY) (g/plant) was recorded at the flower initiation stage by taking 10 randomly selected plants.
2. Dry matter yield (DMY) (g/plant). The 200 g fresh weight sample was dried in the oven at 55 degree Celsius and the oven dried weight was recorded. Dry matter % was obtained as percent of oven dried weight to 200 g.

Dry matter yield (g/plant) = Dry matter % x Green fodder yield (g/plant)

3. Crude protein content (CP) (%)

The dried grinded sample was sent to ARC-IIC for analysis of nitrogen content. The method used to determine the nitrogen % of cowpea was Kjeldahl digestion procedure (Mackenzie and Wallace, 1954). The percent crude protein content was estimated using the relationship:

Crude protein % = N% × 6.25

4. Acid detergent fibre (ADF) (%)

To calculate ADF %, the method given by Georing and Van Soet (1970) was followed.

ADF (%) = loss of weight after ignition (g) × 100 / weight of the sample (g)

5. Neutral detergent fibre (NDF) (%)

To calculate NDF %, the method given by Georing and Van Soet (1970) was followed.

NDF (%) = loss of weight after ignition (g) × 100 / weight of the sample (g)

Statistical analysis

The collected data were subjected to analysis of variance (ANOVA) to test the equality of different generations of a cross. To understand distribution pattern of fodder yield in different crosses were subjected to frequency analysis using 5% of high fodder yielding parent as class range. The generation mean analysis was performed using Mather and Jinks (1971) method.

The expected generation means were calculated as follows:

P1 = m + d F2 = m + (1/2)h
P2 = m - [d] B1 = m + (1/2)d + (1/2)h
F1 = m + [h] B2= m - (1/2)d + (1/2)h

Where,

m= general mean
d= sum of additive effect
h= sum of dominance effects

ABC scaling test (Mather, 1949) and least square method (Hayman, 1960) was tested for adequacy of additive-dominance model by t-test at 5% and 1% level of significance by computing variance of generation means as follows:

$V_A = 4VB_1 + VP_1 + VF_1$
$V_B = 4VB_{2+} V P_2 + VF_1$
$V_{C=} 16VF_2 + 4VF_1 + VP_1 + VP_2$

Where,

A, B, C= Scaling test parameters and V= variance of generation means respectively.

When any scale deviate from zero, additive – dominance model is considered as inadequate due to presence of non-allelic interactions and six parameter models is used.

The mean of each character is indicated as follows:

$$Y = m + C_1[d] + C_2[h] + C_3[i] + C_4[j] + C_5[1] + e$$

Y= the mean of one generation
m= the mean of all generations
d= the sum of additive effects
h= the sum of dominance effects
i= the sum of additive x additive interactions
j= sum of additive x dominance
1= the sum of dominance x dominance
C_1, C_2...C_5 are the coefficients of genetic parameters.

The significance of the genetic effect was tested using t-test at 5% and 1% level of significance.

RESULTS AND DISCUSSION

The mean performance of all six generations (Table 1 and 2) indicates that the mean performance of F1 was higher than both the parents for neutral detergent fibre and intermediate between both the parents for all remaining characters (green fodder yield, dry matter yield, crude protein and acid detergent fibre) in both the crosses. Transgressive segregants were present for all characters under investigation for both crosses. Backcrosses perform almost similar to both parents in cross 1 whereas, backcrosses were superior to both

TABLE 1
Mean performance of cross 1 (GC 89 x C 88)

Population	GFY	DMY	CP	ADF	NDF
C74	52.21	6.20	10.23	39.69	49.90
C 88	115.68	13.82	12.79	36.67	43.95
F1	95.24	13.15	11.78	38.96	60.41
F2	135.46	13.89	13.88	36.57	46.98
BC1	122.17	19.29	11.30	35.33	47.97
BC2	114.37	22.23	11.02	32.86	52.19
MP	83.94	10.01	11.51	38.18	46.92
SE	3.48	0.95	0.98	0.27	1.14

TABLE 2
Mean performance of cross 2 (GC 89 x CL 400)

Population	GFY	DMY	CP	ADF	NDF
C74	50.33	5.86	10.97	43.43	50.64
CL 400	99.55	12.3	11.37	37.27	50.36
F1	95.31	8.98	13.66	37.14	54.05
F2	101.63	11.37	13.15	34.72	52.49
BC1	98.68	19.68	11.26	43.76	55.01
BC2	137.1	18.27	9.96	44.84	57.15
MP	74.94	9.08	11.17	40.35	50.5
SE	0.86	0.26	0.24	0.61	0.30

the parents for characters like dry matter yield, acid detergent fibre and neutral detergent fibre in cross 2.

The significant values for A, B and C scaling test in both the crosses were observed (Table 3 and 4). The results for scaling test with level of significance indicate that the additive – dominance model is inadequate and epistatic interactions were present in both the crosses. So, the six parameter test was employed to estimate gene action using generation means of all six generations (P1, P2, F1, F2, BC1 and BC2).

The results indicate (Table 5 and 6) that all the characters under investigation are highly significant for overall mean which indicates that these traits are quantitatively inherited. Additive [d] and dominance [h] gene effects are significant for all the traits and both were important for inheritance of these traits. However, the dominance [h] gene effect is several times higher than additive [d] gene effect which suggests that the dominance [h] gene effect plays

TABLE 3
Scaling tests in Cross 1 (GC 89 x C 88)

Characters	A	B	C
GFY	296.89±3.39	257.82*±2.29	181.48*±3.30
DMY	19.22**±1.28	0.06**±0.02	9.21**±0.44
CP	0.58**±0.77	-2.54**±0.96	8.92**±1.51
ADF	-7.99**±2.51	-9.90**±1.76	-7.99*±4.09
NDF	-15.55**±1.67	0.01±1.89	-26.75**±3.69

*,** : significance at 5 and 1 per cent respectively.

TABLE 4
Scaling tests in Cross 2 (GC 89 x CL 400)

Characters	A	B	C
GFY	149.35±0.09	78.93*±0.11	47.25**±0.02
DMY	24.51**±0.05	15.26**±0.01	9.38**±0.03
CP	1.50**±0.56	-2.11**±0.43	8.95**±1.03
ADF	6.95*±0.09	15.27*±0.04	-16.08**±0.04
NDF	5.32**±0.11	9.89**±1.32	0.87**±1.27

*,** : significance at 5 and 1 per cent respectively.

important role in genetic variations. Except for crude protein in both crosses and acid detergent fibre in cross 1 where additive [d] gene effect is higher then dominance [h] gene effect. This indicates the importance of additive genes in inheritance of these traits. The selection for such traits where additive gene effect is much higher then non-additive ones would be more effective in early segregating generations. Above findings were supported by Arya *et al*. (2009).

The negative values observed in most cases either with main effects; [d] and [h] or the non-allelic interactions; [i], [j] and [l]. This indicates that the alleles of less valued traits were over dominant to the alleles controlling high valued traits. However, it could be detected that the effects of additive and dominant genes were in the opposite direction with respect to its sign. This was true for all traits in both crosses, except green fodder yield and dry matter yield in cross 2.The high magnitude of additive x additive gene affect [i] for green fodder yield suggests pedigree method and selection in later generations.

In both crosses for all studied traits, it could

TABLE 5
Estimation of components of generation mean of different models for cross 1 (C74 x C 88)

Comp.	m	[d]	[h]	[i]	[j]	[1]	X^2	Type of Epistasis
GFY	135.46**±0.68	-12.20**±1.91	382.51**±4.80	371.22±4.22	19.53**±2.0	-92.93**±8.34	1.67**	D
DMY	13.89**±0.08	-2.92**±0.98	30.61**±2.00	27.46**±2.02	0.88**±0.98	-64.15**±3.87	1.05**	D
CP	13.88**±0.33	0.28*±0.53	-10.61**±1.75	-10.89**±1.72	1.56**±0.58	12.85**±2.63	0.89**	D
ADF	36.57**±0.80	2.46**±1.11	-9.11**±4.10	-9.89**±3.90	0.95**±1.36	27.78**±6.06	1.35**	D
NDF	46.98**±0.61	-4.80**±1.02	24.70*±3.32	11.21**±3.19	-7.78**±1.14	4.32**±5.11	0.33*	C

*,** : significance at 5 and 1 per cent respectively, C means complementary gene action and D manes Duplicate gene action.

TABLE 6
Estimation of components of generation mean of different models for cross 2 (C74 x CL 400)

Comp.	m	[d]	[h]	[i]	[j]	[1]	X^2	Type of Epistasis
GFY	97.63**±0.67	11.58**±1.64	200.81*±4.35	181.03**±4.15	35.20**±1.68	-409.31**±7.3	1.56**	D
DMY	11.37**±0.23	1.41**±0.58	30.28**±1.54	30.48**±1.49	4.62**±0.66	-70.15*±2.62	0.12**	D
CP	13.15**±0.22	1.60**±0.29	-10.08**±1.11	-9.57**±1.08	1.81**±0.33	10.18**±1.57	0.93**	D
ADF	34.72±0.41	-1.08**±0.68	35.09**±2.22	38.30**±2.15	-4.16**±0.75	-60.52**3.35	0.5**	D
NDF	52.49**±0.26	-2.14**±0.78	17.88**± 1.96	14.37**± 1.89	-2.28**±0.86	-29.55**±3.46	0.37**	D

*,** : significance at 5 and 1 per cent respectively, C means complementary gene action and D manes Duplicate gene action.

be observed that the signs of dominance [h] and dominance x dominance [l] gene effects were opposite, except NDF in cross 1 suggesting duplicated type of non-allelic interaction in these traits. Complementary type of non-allelic interactions was present for NDF in cross 1. Similar study was carried in pearl millet by Arya *et al*. (2008).

CONCLUSIONS

From the present investigation, it could be concluded that dominant gene effect plays important role in controlling genetic variation of green fodder yield, dry matter and neutral detergent fibre whereas additive gene were predominant for the crude protein. The pedigree method is suggested for the development of fodder variety due to presence of high magnitude of additive x additive gene effects.

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