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Genetic architecture in blackgram [*Vigna mungo* (L). Hepper]

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Abstract
Generation mean analysis study was carried out to estimate the gene action governing inheritance of yield and its components in blackgram using six parameter model. Six generations of a cross NUK-15-02 × NUK-15-09 was studied. Simple scaling test as well as joint scaling test were carried out to check the adequacy of additive-dominance model. Additive gene effect had lower magnitude than dominance gene effect in most of the characters. Additive × additive type of epistatis was found significance for days to first flower, plant height and branches per plant. Dominance × dominance gene interaction was registered significant by days to first flower, days to maturity and plant height. Hereby for the improvement of various characters studied in this cross, followed population improvement approach which takes in to account both additive and non-additive gene action.

Keywords: Generation mean analysis, scaling test, six parameter model, epistatis

Introduction

Blackgram or urd (*Vigna mungo* (L.) Hepper) is one of the most highly prized pulses in tropical countries especially in India. The green pods are eaten as vegetable and they are highly nutritious. It has inevitably marked itself as the most popular pulse and can be most appropriately referred to as the "king of the pulses" due to its mouthwatering taste and numerous other nutritional qualities. Whether it be the very special "Dal makhni" of Punjab or the "Vada Sambhar" of South India, the taste rules the hearts of one and all alike. Indian immigrants have popularized the taste worldwide as well. An erect, sub-erect or trailing, densely hairy, annual herb. The tap root produces a branched root system with smooth, rounded nodules. The pods are narrow, cylindrical and up to six cm long. Urd is pulse crop of many Asian countries and it belongs to tribe phaseolus family fabaceae with chromosome number 2n=22. Blackgram an indigenous African annual legume, having high protein (20-25%). Blackgram can be grown in all types of soil but sandy and sandy loam soils are best suited for it. Black gram's heat-loving nature makes them an ideal mid-summer replenisher of soil organic matter and mineralizable nitrogen. For consumption purpose, it is largely used to make dal from the whole or split, dehusked seeds. The bean is boiled and eaten whole or, after splitting, made into dal; prepared like this it has an unusual mucilaginous texture. In India it is mainly grown in Dadra and Nagar Haveli, Andhara Pradesh, Jarkhand, Bihar, Arunachal Pradesh, Madya Pradesh, Assam, Himachal Prdesh, Rajasthan, Gujarat, Maharashtra, and some regions of Southern India. In India, it occupies about 5279.09 thousand hectares and annual production of urd bean is about 3492.42 thousand tones with 662 kg/ha productivity, while in Gujarat, it occupies about 136.00 thousand ha area with the production of 86.52 thousand tones, with 636 kg/ha productivity in year 2018. (Anon., 2018).

In India, the availability of many improved varieties has boosted production. This indicates that there is still scope to increase yield potential of varieties through genetical improvement. Various biometrical methods have been used by the plant breeder for the selection of suitable parents in their breeding material, of these, generation means analysis provides information on the nature and magnitude of gene action involved in yield and its component characters.

Materials and Methods

The research experiment was conducted during summer-2020 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari. In this experiment six generations *viz.*, P1, P2, F1, F2, BC1 and BC2 of cross involving two diverse genotypes of blackgram were produced and evaluated in Compact Family Block Design with three replications. The crossing program was initiated during Summer-2019 to produce three F1 hybrids among four selected genotypes (Table 3.1); while backcrossing and selfing of F1 was done in Kharif-2019 to obtain BC1, BC2 and F2 generations of respective crosses. Observations were recorded on single plant basis for days to first flower, days to maturity, plant height, branches per plant, pods per plant, seeds per pod and seed yield per plant. Average value for each character was worked out and used for statistical analysis. To confirm presence or absence of epistasis, simple as well as joint scaling test (as described by Hayman and Mather, 1955 [7] and Cavalli, 1952) [2] was carried out. Various gene effects were estimated using six parameter model as suggested by Hayman (1958) [6].

Results and Discussion

The mean values of all the six generations *viz.,* P$_1$, P$_2$, F$_1$, F$_2$, BC$_1$ and BC$_2$ for eleven different characters were first subjected to genetic analysis. The test of adequacy of scale is important because in most of the cases the estimation of additive and dominance components of variances is made assuming the absence of gene interaction.

Days to first flower

Scaling test A, B and D were found significant which indicated the non-allelic gene action, and also significance of both simple scaling test as well as χ^2 value of joint scaling test indicates inadequacy for additive dominance model. Dominance (h), additive × additive (i) and dominance × dominance (l) interaction were found highly significant. The result of best fit model indicates the presence of significant additive (d), dominance (h) and two types of non-allelic interactions *viz.*, additive × additive (i) and dominance × dominance (l). On the basis of sign of (h) and (l), duplicate type of gene action was found responsible for inheritance of this trait. The result indicated that additive (d), dominance (h) and epistatic component of genetic variance play major role in the inhetitance of this trait. Similar result was also found by Rehman *et al.* (2009), Bhagirath *et al.* (2013) [1] and Gupta *et al.* (2017) [4].

Days to maturity

Among all four scales, only B scaling test was found significant and χ^2 value of joint scaling test was also significant. Based on result of six parameter model, dominance (h) and dominance × dominance (l) parameters were observed significant. Result of best fit model indicated highly significant value of additive (d) and dominance (h) component of genetic variance. The result showed that in the governance of this character additive (d), dominance (h) and dominance × dominance (l) type of epistatis had significance importance. These findings are in accordance with Durga Prasad and Murugan (2015) [3], Kachave *et al.* (2015) [8] and Gupta *et al.* (2017) [4].

Plant height (cm)

For this chraracter scaling tests A and C were highly significant which indicated the presence of epistasis. As far as estimation of genetic component is concerned additive (d) components was observed highly significant, while only one interaction dominance × dominance (l) was found highly significant. According to reduced model by omitting non-significant parameter, all parameters *viz.*, additive, dominance, additive × dominance and dominance × dominance were found highly significant except additive × additive. Inheritance of this character was governed by duplicate type of gene action which, revealed that the character was influence by additive (d), dominance (h) as well as epistatic component. Similar results were also reported by Khattak *et al.* (2004) [11], Khan *et al.* (2007) [10], Tchiagam *et al.* (2011) [14] and Kachave *et al.* (2015) [8].

Branches per plant

Significance of C and D scaling test as well as highly significant χ^2 value of joint scaling test revealed presence of non-allelic gene effect in the inheritance this trait. Additive (d), dominance (h) and additive × additive (i) gene effects found highly significant in six parameter model as well as in best fit model. The result showed that the character was governed by additive, dominance as well as additive × additive type of epistasis. These findings are similar with the findings of Singh and Dikshit (2003) [13], Haque *et al.* (2013) [5] and Gupta *et al.* (2017) [4].

Pods per plant

Scaling tests A and D were found significant which indicated presence of non-allelic interaction. But, result of joint scaling test was more reliable than the scaling test; in this test χ^2 value was observed non-significant, which indicate absence of non-allelic interaction and adequacy of three parameter model for the inheritance of trait under consideration.

Seeds per pod

Scaling test C and χ^2 value of joint scaling test were found significant which revealed that character was influenced by non-allelic interactions. All the genetic parameters in six parameter model were found non-significant. However, result of best fit model indicated significant estimate of additive (d), additive × additive (i) and additive × dominance (j). The result indicated that additive and additive type of epistasis play major role in the governance of this trait. Similar results were also found by Haque *et al.* (2013) [5], Kachave *et al.* (2015) [8] and Gupta *et al.* (2017) [4].

Seed yield per plant (g)

Out of four, only one scaling test C was found significant and result of joint scaling test depicted significance of χ^2 value. The result of six parameter model shows that dominance (h) components was significant and other genetic components registered non-significant value. The same components were also found significant in best fit model indicated that the character was govern by only dominant gene action. Similar results were also reported by Rehman *et al.* (2009) [12], Bhagirath *et al.* (2013) [1] and Kachave *et al.* (2015) [8].

Table 1: Estimates of scaling test and joint scaling test for various characters in blackgram of cross NUK-15-02 × NUK-15-09

Character	Simple scaling test			Joint scaling test				χ^2 value
	A	B	C	D	m	d	h	
Days to first flower	-4.73**±1.23	-2.73*± 1.22	-1.60 ±1.91	2.93**±0.89	64.62**±0.36	0.90**±0.34	-5.91**±0.69	19.46**
Days to maturity	-1.20±1.34	-4.20**±1.45	-2.86±2.21	1.26±0.97	82.64**±0.41	-1.25**±0.15	-3.28**±0.66	8.40*
Plant height (cm)	-15.26**±2.04	-16.00**±2.51	-21.46**±4.41	4.90**±1.82	34.59**±0.33	-6.43**±0.27	-14.74**±1.55	67.79**
Branches per plant	-0.93±0.72	0.13±0.65	-3.20**±1.18	-1.20*±0.50	5.28**±0.20	-0.93**±0.18	1.43**±0.41	11.86**
Pods per plant	4.46*±2.14	0.53±2.52	-3.06±3.37	-4.03*±1.90	14.76**±0.62	0.76±0.64	4.30**±1.05	8.24
Seeds per pod	-0.66±0.44	0.66±0.45	1.20*±0.58	0.60±0.34	6.67**±0.11	0.47**±0.12	0.96**±0.19	10.52*
Seed yield per plant	-0.35±0.75	-0.90±0.86	-2.65*±1.31	-0.70±0.60	5.01**±0.20	-0.77**±0.20	-0.45±0.97	1.29*

Table 2. Estimates of gene effects for various characters in blackgram for cross NUK-15-02 × NUK-15-093

Character	Six parameter model (Hyaman, 1958)					
	m	d	h	i	j	l
Days to first flower	62.08**±0.31	0.23±0.63	-11.23**±1.92	-5.86**±1.78	-1.00±0.76	13.33**±3.18
Days to maturity	81.06**±0.34	-0.26±0.69	-5.30*±2.13	-2.53±1.94	1.50±0.84	7.93*±3.56
Plant height (cm)	27.51**±0.74	-5.73**±1.04	-16.36**±3.99	-9.80**±3.64	0.36±1.21	41.06**±6.08
Branches per plant	5.50**±0.19	-1.26**±0.32	4.20**±1.10	2.40*±1.00	-0.53±0.40	-1.60±1.76
Pods per plant	-	-	-	-	-	-
Seeds per pod	7.36**±0.10	-0.06±0.27	-0.26±0.72	-1.20±0.69	-0.66±0.30	1.20±1.22
Seed yield per plant	5.10**±0.21	-0.49±0.42	2.90*±1.30	1.40±1.21	0.27±0.48	-0.14±2.15

Table 3: Best fit model for various characters in blackgram for cross NUK-15-02 × NUK-15-09

Character	Best fitting model model (Mather and jink)					
	m	d	h	i	j	l
Days to first flower	71.04**±1.83	0.93**±0.34	-24.59**±4.77	-5.88**±1.78	-	13.35**±10.17
Days to maturity	82.64**±0.41	-1.25**±0.39	-3.28**±0.81	-	-	-
Plant height (cm)	45.71**±3.59	-6.00**±0.53	-56.67**±8.62	-9.58**±3.55	-	40.55**±5.85
Branches per plant	3.80**±0.53	-0.97**±0.18	3.58**±0.83	1.73**±0.58	-	-
Pods per plant	-	-	-	-	-	-
Seeds per pod	7.39**±0.07	0.59**±0.13	-	-0.83**±0.16	-1.36*±0.60	-
Seed yield per plant	5.18**±0.21	-	2.90*±1.30	-	-	-

Conclusion
The significance of C scaling test for seed yield per plant and its components characters indicated the presence of appreciable amount of epistasis and inadequacy of additive-dominance model. For seed yield per plant and most of the component characters both additive and dominance gene effects were found to be significant. In present study non-allelic interactions along with additive and dominant component played pertinent role in determination of various characters in blackgram. In general, involvement of both additive and non-additive gene effects for most of the characters suggested that it would be desirable to adopt biparental mating followed by population improvement method of breeding involving conventional breeding approach of selection of superior recombinants and their inter-mating for the development of elite homozygous recombinants having high quality and high yielding potentiality. Thus, population improvement approaches involving inter mating of selected plant in advance generation like biparental mating and diallel selective mating design that take care of both additive and non-additive gene actions are more promising for the improvement of various characters studied.

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