

Short Communication

Generation mean analysis for earliness and yield traits in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) verdcourt)

EG Merin* and S Sarada

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Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt; $2n=24$), a distinct form of cowpea, is one of the most important leguminous vegetable crops originated from Central Africa and widely distributed in India, Indonesia, Philippines and Srilanka. It is an annual food legume belonging to the family Fabaceae and the genus *Vigna*, which comprises of about 80 species. It is called as 'vegetable meat', being a rich and inexpensive source of vegetable protein (3.5 g), calcium (72 mg), iron (2.5 mg), riboflavin (0.09 mg), phosphorus (59 mg) and vitamin A (564 mg 100 g⁻¹ of edible pod). Prerequisite for the effective choice of breeding methodology for developing elite varieties is the understanding of the mode of inheritance of the yield components. Generation mean analysis, which provide the estimates of main gene effects (additive and dominance) along with their digenic interactions (additive × additive, additive × dominance and dominance × dominance) helps to understand the nature of gene effects involved in different traits of concern and accordingly the breeding procedure could be applied in developing superior populations.

The experiment was conducted at the Department of Vegetable Science, College of Agriculture, Vellayani, Thiruvananthapuram, Kerala during 2017-2018. The objective was to study the inheritance and gene action of yield and quality in yard long bean using generation mean analysis. The materials for the study comprised of 6 treatments (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of the hybrid) using the parents, VS 50 (Kakkamoola Local) and VS 34 (Githika). The details of genotypes used as parents are given in Table 1. The experiment was carried out in three parts. In part I, cross VS 50 X VS 34 of yard long bean with high yield and quality characters, selected

based on specific combining ability and *per se* performance. The seeds of the hybrid were produced in a crossing block. In part II, the F_1 hybrid was selfed to produce F_2 progeny. Simultaneously, the F_1 hybrid was backcrossed with the female parent to produce BC_1 generation and the male parent to produce BC_2 generation. In part III, the six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of the hybrid were evaluated in a replicated field experiment using generation mean analysis. The six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) from the cross combination was raised in Randomized Block Design with spacing 1m x 1m. One replication consisted of one row of parents, F_1 , two rows of the back-cross generations BC_1 and BC_2 and four rows of F_2 . Each row consisted of 10 plants and subjected to generation mean analysis (Hayman 1958) followed by scaling test (Mather 1949). Five plants from each treatment in the experimental field were randomly selected and tagged as observational plants. Observations were taken and the average of the five plants worked out in each replication for statistical analysis. Number of days from the date of sowing to the first flowering of observational plants was recorded for days to first flowering. Five pods were selected at random from each observational plant at peak harvest period. Pod length was measured using a twine and scale as distance from the point of pedicel attachment to the apex of the pod. Pod weight was taken from the same pods used for recording pod length. Total number of pods produced per plant till the last harvest was counted and recorded as pods plant⁻¹. Average weight of all pods harvested from the observational plants were taken and expressed as pod yield. Seeds extracted from the dried pod from the peak harvest were counted and expressed as seeds pod⁻¹. The flowering and pod characters were analyzed statistically using generation mean analysis.

Days to first flowering: 'm' was significant and greater than all other effects denoting the significant variation

Department of Vegetable Science, College of Agriculture, Vellayani, Thiruvananthapuram-695522, Kerala

*Corresponding author, Email: merinelzageorge5010@gmail.com

between the treatments for days to first flowering. F_1 was earlier to flower (50.00) while P_1 (53.50) were late. Significance was observed for scales A, B and C and all were acting in the favourable negative direction. Superiority of F_2 over the parents was denoted by the significance with highest value of scale C over all other scales. Dominance effect was acting in the favourable negative direction and had the highest magnitude (Gupta et al. 2017). Hence heterosis breeding would improve the trait and restore early flowering types.

Pod length (cm): Significant variation was observed among the generations for pod length as shown by the significant value of 'm'. Pod length was highest for P_1 (65.99 cm) and lowest pod length was recorded for P_2 (60.58 cm). Significance was observed for scales B and C in favourable positive direction among which scale B had the highest magnitude, which implies that F_1 is better than the second parent. The predominance of dominance gene action revealed that reliance should be placed on heterosis breeding for the improvement of pod length (Nagaraj et al. 2002).

Pod weight (g): Significance of 'm' denoted wide variation for pod weight among the generations. The highest mean values for pod weight was recorded by BC_1 (47.22 g) and the lowest values by P_2 (27.33 g). Significance was observed for all the scales A, B, C and D in favourable positive direction except D, which was negative. The highest magnitude of scale C denotes the betterment of F_2 over the parents. Significance was observed for all the genetic components, among which additive, dominance, and additive x additive were positive while additive x dominance and dominance x dominance were in negative direction. Dominance gene action had the highest magnitude. Since dominance effect was predominant, heterosis breeding could be used for the improvement of the trait in accordance with Adeyanju (2009).

Table 1. Yard long bean accessions used as parental lines

Sl. No.	Accession No.	Accession Name	Source	Character
1	VS 50	Kakkamoola Local	Kakkamoola, Thiruvananthapuram	High yield, long pods
2	VS 34	Githika	College of Agriculture, Vellayani	High yield and fruit weight

Table 2. Significance of specific scales

Sl. No	Scales	Significance
1	A, B or both scales	Presence of all three types of epistasis, viz. A x A, A x D and D x D
2	C scale	Dominance x Dominance type of epistasis (I)
3	D scale	Additive x Additive type of epistasis (i)
4	C and D scales	Additive x Additive (i) and Dominance x Dominance (I)

Pods Plant⁻¹: The generations differed significantly for pods plant⁻¹ as given by significant 'm' value. F_1 produced highest number of pods plant⁻¹ (84.00), while P_1 (32.67) the lowest. All the scales were significant, among which scale C had the highest magnitude in positive direction indicating that F_2 is better than the parents. Though all the genetic components displayed significance, additive and dominance x dominance effect were negative while dominance, additive x additive and additive x dominance were positive of which dominance effect had the highest value. Predominance of dominance effect suggested that heterosis breeding would improve the trait. These results agree with the findings of Ushakumari et al. (2010) and Gupta et al. (2017) who suggested the presence of non-additive action for controlling the trait.

Pod yield (g plant⁻¹): The main objective of any breeding programme is higher yield and in the present study it was recorded in terms of pod yield (g plant⁻¹). Significant difference was observed among the six generations for pod yield plant⁻¹, since 'm' value was significant and greater than all other effects. Among the treatments, yield plant⁻¹ was highest for F_1 (1210.51 g) and lowest yield plant⁻¹ was recorded by P_2 (642.61 g). Positive significance was noticed for scales A, C and D, of which scale C had the highest magnitude, which implies the superiority of F_2 over both the parents. Further analysis of genetic components showed the significance of additive, dominance, additive x additive and additive x dominance of which dominance had the highest positive value, underlines the suitability of exploiting heterosis breeding, as observed in earlier studies of Adeyanju (2009).

Seeds Pod⁻¹: Wide variation was observed between the treatments for number of seeds pod⁻¹, 'm' value being significant. Maximum number of seeds pod⁻¹ was observed in F_1 (22.33). Least number of seeds pod⁻¹ was recorded by P_1 (19.17). Significance was observed for scales A, B and D, among which scale D had the highest magnitude in favourable positive direction which implies the superiority of F_2 over the backcrosses BC_1 and BC_2 . The analysis of genetic components revealed the significance of additive, dominance, additive x additive and dominance x dominance effects of which dominance x dominance type of epistasis was in favourable positive direction with highest value. Predominance of dominance x dominance effect indicated the suitability of hybridization and selection for the improvement of the trait, which was in accordance with the earlier reports of non-additive gene actions in controlling the trait by Nagaraj et al. (2002) and Singh et al. (2006).

Predominance of dominance gene action was observed

Table 3: Generation means (\pm SE), Scale values (\pm SE), and estimates of genetic component (\pm SE) in yard long bean

	Days to First Flowering	Pod Length (cm)	Pod Weight (g)	Pods Plant ⁻¹	Yield (g plant ⁻¹)	Seeds Pod ⁻¹
Generation means						
P ₁	53.50 \pm 0.17	65.99 \pm 0.04	35.33 \pm 0.17	32.67 \pm 0.73	707.95 \pm 2.62	19.17 \pm 0.30
P ₂	53.00 \pm 0.10	47.86 \pm 0.39	27.33 \pm 0.26	45.67 \pm 1.45	642.61 \pm 14.22	20.33 \pm 0.17
F ₁	50.00 \pm 0.19	62.16 \pm 0.48	37.89 \pm 0.15	84.00 \pm 0.87	1210.51 \pm 24.55	22.33 \pm 0.67
F ₂	50.17 \pm 0.21	62.50 \pm 0.30	42.22 \pm 0.14	75.67 \pm 0.70	1018.46 \pm 5.99	21.67 \pm 0.30
BC ₁	50.60 \pm 0.21	63.91 \pm 0.45	47.22 \pm 0.14	80.67 \pm 0.41	1071.52 \pm 11.52	19.77 \pm 0.27
BC ₂	50.03 \pm 0.21	61.22 \pm 0.21	45.66 \pm 0.17	78.67 \pm 0.30	913.87 \pm 1.48	20.00 \pm 0.20
Scale values						
A	-2.29* \pm 0.50	-0.34 \pm 1.01	21.22* \pm 0.35	44.67* \pm 1.40	224.57* \pm 33.77	-1.95* \pm 0.91
B	-2.94* \pm 0.47	12.42* \pm 0.75	26.11* \pm 0.46	27.67* \pm 1.80	-25.39 \pm 28.53	-2.67* \pm 0.80
C	-5.82* \pm 0.93	11.82* \pm 1.58	30.44* \pm 0.70	56.33* \pm 3.66	302.27* \pm 56.52	2.50 \pm 1.83
D	-2.93 \pm 0.51	-0.13 \pm 0.77	-8.44* \pm 0.35	-8.00* \pm 1.49	51.54* \pm 16.69	3.56* \pm 0.69
Genetic components						
m	52.66* \pm 1.02	56.66* \pm 1.56	14.45* \pm 0.72	23.17* \pm 3.07	778.36* \pm 34.15	26.86* \pm 1.39
d	0.25* \pm 0.10	9.07* \pm 0.20	4.00* \pm 0.15	-6.50* \pm 0.81	32.67* \pm 7.23	-0.58* \pm 0.17
h	-7.31* \pm 2.44	17.85* \pm 3.87	87.66* \pm 1.80	149.17* \pm 6.86	528.25* \pm 90.71	-16.26* \pm 3.25
i	0.59 \pm 1.01	0.27 \pm 1.55	16.89* \pm 0.71	16.00* \pm 2.96	-103.08* \pm 33.37	-7.11* \pm 1.38
j	0.65 \pm 0.62	-12.76* \pm 1.06	-4.89* \pm 0.54	17.00* \pm 1.92	249.96* \pm 27.37	0.72 \pm 0.75
l	4.65* \pm 1.50	-12.35* \pm 2.53	-64.22* \pm 1.13	-88.33* \pm 4.19	-96.11 \pm 73.17	11.73* \pm 2.27
E	D	D	D	D	D	D

E: Epistasis

D: Duplicate type of epistasis

*Significant at 5% level

for most of the characters pointed out the suitability of heterosis breeding for the improvement of the trait. Seeds pod⁻¹ was predominated by dominance x dominance interaction suggested the use of hybridization followed by selection as the appropriate breeding method. Duplicate type of epistasis was observed for all the traits, as shown by the opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

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