TRANSGRESSIVE SEGREGATION ANALYSIS IN F_3 GENERATION IN MUNG BEAN [*Vigna radiata* (L.) Wilczek]

Abstract

The present investigation was conducted to evaluate twelve crosses of mungbean genotypes for eleven characters to access the magnitude of genetic variability and to understand the heritable component of variation for grain yield and its component traits. All the 12 crosses were grown in compact family block design with three replications in each of two environments during *kharif,* 2022. The analysis of variance revealed significant differences among the families for grain yield and all other traits in both the environments. On the other hand, differences among the progenies within a family varied from character to character and environment (E1) to environment (E2). In each of the crosses under study, the seed yield per plant was transgressed simultaneously with one or several other characters. Interestingly, some important and rare transgressive segregants, though low in frequency, were picked up in different crosses. In addition, there were several such combinations of characters in which seed yield per plant was transgressed in conjugation with transgression with other agronomic characters. The details of these rare and critical transgressive segregants are presented in table 4. In E1 the promising transgressive segregants identified were C2P5-7, C2P5-13, C1P4-2, C11P5-6, C11P5-10, C7P4-12, C7P4-13, C3P2-2, C3P2-3, C3P2-5. In E2 the promising transgressive segregants identified were C1P4-10, C1P1-6, C1P5-6, C1P5-10, C12P5-5, C12P1-14, C7P5-7, C11P5-6, C11P5-7, C11P5-10, C10P5-12.The majority of the individuals, whenever increasing parent seed yield per plant was transgressed; there was simultaneous transgression for one or more other yield contributing characters like clusters per plant, pods per cluster, pods per plant, pod length and primary branches per plant, plant height.

Introduction

Mung bean (*Vigna radiata*), a versatile leguminous crop, plays a pivotal role in global agriculture due to its nutritional value and adaptability to diverse climates. According to Karpechenko (1925), it bears the diploid chromosomal number 2n = 2x = 22. According to Vavilov(1926) mungbean is a native of India and Central Asia. Since prehistoric times, it has been grown in these regions. The diploid mungbean (2n = 22) is a member of the Leguminaceae family, Papillionaceae subfamily, genus *Vigna* and species *radiata*. About 18.0 to 32.0 per cent protein and 1 to 5 per cent fat are both found in pulses. Chemical components include proteins, fatty acids, carbohydrates, vitamin B1, vitamin B2, beta-carotene, folic acid, calcium, phosphorus, and iron. Apart from their great nutritional content, they have the unique ability to maintain and restore soil fertility through biological nitrogen fixation and hence play an important role in sustainable agriculture. India accounts for around 25 per cent of global production from 35 per cent of global area under pulses. In India year 2019–20, mungbean occupied roughly 31.15 lakh hectares and produced 23.40 lakh tonnes at a productivity of 798 kg/ha. States that produce a significant amount of mungbean in India include Rajasthan, Maharashtra, Karnataka, Madhya Pradesh, Odisha and Telangana (Anonymous, 2019-20). Rajasthan leads the group in terms of both production and area dedicated to growing mungbean. In Rajasthan, the total area planted with mungbean for 2019–2020 was 23.27 lakh hectares, producing 13.04 lakh tonnes with a productivity of 561 kg/ha (Anonymous, 2019-20). It is primarily grown in the semi-arid and dry regions of Rajasthan, particularly in the districts of Nagaur, Ajmer, Jaipur, Jodhpur, Jalore, Pali, Sikar and Jhunjhunu.

The crop's genetic diversity serves as a valuable resource for breeders aiming to enhance traits such as yield, resistance to diseases, and tolerance to environmental stressors. The identification of transgressive segregants, individuals displaying traits that surpass those of their parental lines, holds great promise for accelerating the breeding process and unlocking novel genetic combinations.

As agricultural challenges intensify and the need for sustainable crop production grows, researchers are increasingly turning to advanced genomic techniques to unravel the intricate genetic architecture of mung bean populations. The identification and characterization of transgressive segregants have emerged as a focal point in this pursuit, offering a deeper understanding of the underlying genetic mechanisms responsible for superior trait expression.

This study embarks on a comprehensive exploration of transgressive segregants in mung bean, employing various selection tools. Understanding the genetic basis of transgressive segregation is crucial for harnessing the full spectrum of mung bean genetic diversity and capitalizing on the hidden potential within its gene pool.

This research is aspired to provide valuable insights into the identification, characterization, and utilization of transgressive segregants in mung bean breeding programs. The outcomes of this study may pave the way for the development of improved mung bean varieties that exhibit enhanced agronomic performance, resilience to environmental stresses, and heightened nutritional quality, contributing to the sustainable intensification of global agriculture.

Materials and methods

Plant material

The experimental material comprised five individual plants from each of twelve different cross combinations from F_2 generation which were selected on the basis of high grain yield to raise F_3 generation. Each cross was taken as a family and within a cross, individual plants selected were denoted as progenies. All these F_3 materials of mungbean grown were available in the Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner.

All the 12 crosses were grown in compact family block design with three replications in each of two environments during *kharif,* 2022-2023. Experimental plot consisted of 3 m long single row spaced 30 cm apart and plant to plant distance within rows was spaced 10 cm apart. All the recommended cultural and management practices were followed to raise a healthy crop. The study was conducted in two environments one at Experimental Farm of Department of Plant Breeding and Genetics, Sri Karan

Narendra College of Agriculture, Jobner and the other at Agricultural Research Station, Fatehpur, Shekhawati Sikar during *kharif,* 2022-2023. Data were recorded on five randomly selected plants in each row for the characters *viz.* plant height, primary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight, grain yield per plant. Days to 50 per cent flowering and days to maturity were recorded on the basis of individual progeny rows.

Statistical method

The analysis of variance for between families and between progenies within a family was worked out using the method given by Panse and Sukhatme (1978). The data on individual plants for each character were pooled together and means, standard deviations, standard error of means, variances, standard varieties were obtained. The transgressive segregants are identified using the limiting value as given below:

Limiting value:

The limiting value of standard variates corresponding to range of parental means at 5 per cent probability level was calculated so that the segregates beyond this limiting value would be transgressive segregants. The limiting normal deviation value was calculated as follows:

$$\frac{\bar{P}(+) + 1.96\ \delta P(+) - F_3}{\delta F_3}$$

Normal Deviation (N.D.) value =

Threshold value = $\bar{P}^{(+)} + 1.96\ \delta P^{(+)}$

Where,

$\bar{P}^{(+)}$: Mean of increasing parent

$\delta P^{(+)}$: Standard deviation of increasing parent

$\bar{F}_3$: Mean of F_3 generation

δF_3 : Standard deviation of F_3 generation

Results and Discussion

Transgressive segregation is a key strategy for improving crops by plant breeders. Transgressive segregants are occasionally created in F_2, F_3 or later generations due to segregation and recombination through the accumulation of advantageous genes from both parents who participated in the hybridization. Bharathi *et al.* (2019) suggested that the genetic analysis for transgressive segregation in F_2 helps determine the potency of different crosses achieving efficiency in early generation selection and reducing population size in later generations. The favourable genes impacting yield and yield-governing traits combine to create transgressive segregants.

Apart from the frequency of transgressive segregants, the intensities of the characters expressions were achieved by the transgressants in each of the crosses examined. This also provided an insight into the extended limits and intensities of desired character's expression achieved by transgressive breeding. In the present study, in F_3 generations the desirable transgressive segregants were observed in each of the twelve crosses for different characters (Table 1 to Table 3). In environment E1 the highest proportion of individuals transgressed beyond the increasing parent for grain yield per plant was recorded by C7 (36.00%) followed by C3 (33.33%), C1 (20.00%), C4 (18.67%), C11 (16.00%) and C2 (13.33%). In environment E2 the highest proportion of individuals transgressed beyond the increasing parent for grain yield per plant was recorded by C2 (26.67%), C12 (22.67%), C10 (21.33%), C7 (20.00%), C11 (20.00%) and C1 (18.67%). In these families transgressive segregants were also found for other component traits in both the environments.

Karkute and Girase (2013) observed transgressive segregants in mungbean for pods per plant, seed yield per plant, pod length, number of clusters per plant, seeds per pod and 100-seed weight. Reddy *et al*. (2021)observed a good transgressive segregants in a desirable direction for plant height, pods per cluster and harvest index in the crosses. Basamma (2011) reported similar findings for seed yield, seeds per pod and seed weight in urd bean in F_2 and F_3 generations. Shivani *et al.* (2011) observed transgressive segregants in safflower for seed yield, number of capitula per plant and number of seeds per capitulum.

In each of the above crosses under study, the seed yield per plant was transgressed simultaneously with one or several other characters. Interestingly, some important and rare transgressive segregants, though low in frequency, were picked up in different crosses. In addition, there were several such combinations of characters in which seed yield per plant was transgressed in conjugation with transgression with other agronomic characters. The details of these rare and critical transgressive segregants are presented in table 4. In E1 the promising transgressive segregants identified were C2P5-7, C2P5-13, C1P4-2, C11P5-6, C11P5-10, C7P4-12, C7P4-13, C3P2-2, C3P2-3, C3P2-5. In E2 the promising transgressive segregants identified were C1P4-10, C1P1-6, C1P5-6, C1P5-10, C12P5-5, C12P1-14, C7P5-7, C11P5-6, C11P5-7, C11P5-10, C10P5-12.

It is clear from (Table 4 and Table 5) that in the majority of the individuals, whenever increasing parent seed yield per plant was transgressed; there was simultaneous transgression for one or more other yield contributing characters like clusters per plant, pods per cluster, pods per plant, pod length and primary branches per plant, plant height. The obvious reason for this could be that seed yield per plant has been dependent on the number of clusters per plant, pods per cluster, pods per plant, pod length and seeds per pod alternatively. Similar findings were also reported by Karkute and Girase (2013), Karkute *et al.* (2016), Marwiyah *et al*. (2020), Reddy *et al*. (2021) and Reddy *et al.* (2022) in mungbean, Basamma (2011) and Chauhan *et al.* (2018) in urd bean and Shivakumar *et al*. (2013) and Sundaram *et al.* (2023) in chickpea. It can be concluded that the genes of these characters are linked to each other. Whether it is linkage drag or dependency of seed yield per plant on some of the seed yield components, it could be safely inferred that the selection of transgressive segregants for clusters per plant, pods per cluster, pods per plant, pod length and primary branches per plant will automatically lead to increase in seed yield per plant in mungbean.

Table 1 Frequency of transgressive segregants for eight characters in F_3 generation of twelve crosses in E1 and E2 environments

S. No.	C1		C2		C3		C4		C5		C6		C7		C8		C9		C10		C11		C12	
	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Plant height	-	10	-	-	-	-	-	-	10	-	-	-	15	-	15	-	-	-	-	-	-	-	-	11
Primary branches per plant	15	15	6	-	3	3	-	5	-	-	-	-	-	8	-	3	8	-	3	-	-	8	-	3
Clusters per plant	-	-	17	-	-	-	-	20	-	-	-	-	-	-	10	15	-	-	-	-	15	-	-	15
Pods per cluster	-	14	-	15	-	-	-	10	15	-	15	-	-	11	12	-	15	-	10	-	-	-	-	-
Pods per plant	22	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	25	25	15	15	-	-	-	-
Pod length	-	-	15	-	-	-	-	-	-	24	-	26	-	-	-	-	-	-	-	-	-	-	11	-
Seeds per pod	-	-	-	-	-	14	-	16	15	-	10	16	-	-	13	-	-	10	10	-	-	-	-	-
Grain yield per plant	15	14	10	20	25	-	14	-	-	-	-	-	27	15	-	-	-	-	-	16	12	15	-	27

Table 2aPercentage of transgressive segregants for eight characters in F_3 generation of twelve crosses in E1 and E2 environments

Characters	C1		C2		C3		C4		C5		C6	
	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Plant height	-	13.33	-	-	-	-	-	-	13.33	-	-	-
Primary branches per plant	20.00	20.00	8.00	-	4.00	4.00	-	6.67	-	-	-	-
Clusters per plant	-	-	22.67	-	-	-	-	26.67	-	-	-	-
Pods per cluster	-	18.67	-	20.00	-	-	-	13.33	20.00	-	20.00	-
Pods per plant	29.33	26.67	-	-	-	-	-	-	-	-	-	-
Pod length	-	-	20.00	-	-	-	-	-	-	32.00		34.67
Seeds per pod	-	-	-	-	-	18.67	-	21.33	20.00	-	13.33	21.33
Grain yield per plant	20.00	18.67	13.33	26.67	33.33	-	18.67	-	-	-	-	-

Table 2b Percentage of transgressive segregants for eight characters in F_3 generation of twelve crosses in E1 and E2 environments

Characters	C7		C8		C9		C10		C11		C12	
	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Plant height	20.00		20.00	-	-	-	-	-	-	-	-	14.67
Primary branches per plant	-	10.67	-	4.00	10.67	-	4.00	-	-	10.67	-	4.00
Clusters per plant	-	-	13.33	20.00	-	-	-	-	20.00	-	-	20.00
Pods per cluster	-	14.67	16.00	-	20.00	-	13.33	-	-	-	-	-
Pods per plant	-	-	-	-	33.33	33.33	20.00	20.00	-	-	-	-
Pod length	-	-	-	-	-	-	-	-	-	-	14.67	-
Seeds per pod	-	-	17.33	-	-	13.33	13.33	-	-	-	-	-
Grain yield per plant	36.00	20.00	-	-	-	-	-	21.33	16.00	20.00	-	22.67

Table 3aThreshold value, range of segregants and range of $F_3$for eight characters in F_3 generation of twelve crosses in E1 and E2 environments

Crosses		C1		C2		C3		C4		C5		C6	
Characters		E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Plant height	TV	-	66.37	-	-	-	-	-	-	77.22	-	-	-
	RS	-	67.00 to 76.00	-	-	-	-	-	-	77.80 to 94.80	-	-	-
	F_3	-	40.50 to 76.00	-	-	-	-	-	-	64.10 to 94.80	-	-	-
Primary branches per plant	TV	1.36	2.13	1.23	-	1.12	2.51	-	2.63	-	-	-	-
	RS	2 to 3	3 to 4	2	-	2	3	-	3	-	-	-	-
	F_3	1 to 3	2 to 4	0 to 2	-	0 to 2	1 to 3	-	1 to 3	-	-	-	-
Clusters per plant	TV	-	-	6.51	-	-	-	-	5.17	-	-	-	-
	RS	-	-	7 to 9	-	-	-	-	6 to 7	-	-	-	-
	F_3	-	-	3 to 9	-	-	-	-	3 to 7	-	-	-	-
Pods per cluster	TV	-	5.15	-	5.15	-	-	-	5.15	4.14	-	4.36	-
	RS	-	6 to 7	-	6 to 7	-	-	-	6 to 7	5 to 6	-	5	-
	F_3	-	4 to 7	-	4 to 7	-	-	-	3 to 7	2 to 6	-	2 to 5	-
Pods per plant	TV	21.49	20.38	-	-	-	-	-	-	-	-	-	-
	RS	22 to 29	21 to 28	-	-	-	-	-	-	-	-	-	-
	F_3	11 to 29	13 to 28	-	-	-	-	-	-	-	-	-	-
Pod length	TV	-	-	8.22	-	-	-	-	-	-	8.13	-	8.19
	RS	-	-	8.70 to 10.30	-	-	-	-	-	-	8.50 to 9.40	-	8.50 to 9.60
	F_3	-	-	5.80 to 10.30	-	-	-	-	-	-	5.90 to 9.40	-	6.20 to 9.60
Seeds per pod	TV	-	-	-	-		11.64	-	11.39	10.92	-	12.34	11.80
	RS	-	-	-	-		12 to 14	-	12 to 14	11 to 14	-	13 to 14	12 to 14
	F_3	-	-	-	-		10 to 14	-	11 to 14	9 to 14	-	9 to 14	10 to 14
Grain yield per plant	TV	4.97	4.91	4.97	4.91	4.97	-	4.97	-	-	-	-	-
	RS	4.98 to 6.07	5.50 to 6.02	5.41 to 5.77	5.22 to 5.99	5.23 to 5.85	-	5.51 to 6.12	-	-	-	-	-
	F_3	2.07 to 6.07	2.09 to 6.02	3.19 to 5.77	2.57 to 5.99	1.63 to 5.85	-	2.10 to 6.12	-	-	-	-	-

Table 3b Threshold value, range of segregants and range of $F_3$for eight characters in F_3 generation of twelve crosses in E1 and E2 environments

Crosses		C7		C8		C9		C10		C11		C12	
Characters		E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Plant height	TV	66.73	-	68.92	-	-	-	-	-	-	-	-	59.16
	RS	67.20 to 76.60	-	69.30 to 85.70	-	-	-	-	-	-	-	-	60.00 to 74.00
	F_3	50.70 to 76.60	-	44.30 to 85.70	-	-	-	-	-	-	-	-	41.00 to 74.00
Primary branches per plant	TV	-	2.51	-	2.24	1.36	-	2.22	-	-	2.24	-	2.63
	RS	-	3	-	4	2	-	3	-	-	4	-	3 to 4
	F_3	-	1 to 3	-	1 to 4	0 to 2	-	0 to 3	-	-	1 to 4	-	1 to 4
Clusters per plant	TV	-	-	6.40	5.82	-	-	-	-	6.40	-	-	4.27
	RS	-	-	7 to 9	6 to 9	-	-	-	-	7 to 9	-	-	5 to 10
	F_3	-	-	4 to 9	2 to 9	-	-	-	-	4 to 9	-	-	1 to 10
Pods per cluster	TV	-	5.82	4.87	-	4.52	-	4.14	-	-	-	-	-
	RS	-	6 to 7	5 to 6	-	5 to 6	-	5 to 7	-	-	-	-	-
	F_3	-	3 to 7	2 to 6	-	2 to 6	-	3 to 7	-	-	-	-	-
Pods per plant	TV	-	-	-	-	19.05	18.73	21.28	19.79	-	-	-	-
	RS	-	-	-	-	20 to 25	19 to 25	22 to 28	20 to 25	-	-	-	-
	F_3	-	-	-	-	11 to 25	11 to 25	14 to 28	12 to 25	-	-	-	-
Pod length	TV	-	-	-	-	-	-	-	-	-	-	7.73	-
	RS	-	-	-	-	-	-	-	-	-	-	7.50 to 9.00	-
	F_3	-	-	-	-	-	-	-	-	-	-	6.20 to 9.00	-
Seeds per pod	TV	-	-	11.80	-	-	12.10	13.80	-	-	-	-	-
	RS	-	-	12 to 14	-	-	13 to 14	14	-	-	-	-	-
	F_3	-	-	10 to 14	-	-	9 to 14	10 to 14	-	-	-	-	-
Grain yield per plant	TV	4.52	4.88	-	-	-	-	-	4.88	4.42	4.64	-	4.98
	RS	4.55 to 5.79	5.31 to 5.77	-	-	-	-	-	5.31 to 5.77	4.50 to 5.97	5.47 to 6.01	-	5.17 to 6.13
	F_3	2.28 to 5.79	3.09 to 5.77	-	-	-	-	-	3.09 to 5.77	3.27 to 5.97	3.09 to 6.01	-	2.79 to 6.13

TV: Threshold value, RS: Range of segregants, F_3: Range of F_3

Table 4 Frequency and percentage of simultaneous transgressive segregation (T.S) for grain yield per plant in combination with other characters in E1

S. No.	Character combination	Cross	Plant no.	F_3	
				Frequency	per cent of T. S
1	Grain yield per plant + primary branches per plant + clusters per plant + pod length	C2	C2P5-7	1	1.33
2	Grain yield per plant + clusters per plant + pod length	C2	C2P5-13	1	1.33
3	Grain yield per plant + primary branches per plant + pods per plant	C1	C1P4-2	1	1.33
4	Grain yield per plant + clusters per plant	C11	C11P5-6 C11P5-10	2	2.66
5	Grain yield per plant + plant height	C7	C7P4-12 C7P4-13	2	2.66
6	Grain yield per plant + primary branches per plant	C3	C3P2-2 C3P2-3 C3P2-5	3	4.00
	Total			10	13.33

Table 5 Frequency and percentage of simultaneous transgressive segregation (T.S) for Grain yield per plant in combination with other characters in E2

S. No.	Character combination	Cross	Plant No	F_3	
				Frequency	per cent of T. S
1	Grain yield per plant + primary branches per plant + pods per cluster + plant height + pods per plant	C1	C1P4-10	1	1.33
2	Grain yield per plant + primary branches per plant + pods per cluster + pods per plant	C1	C1P1-6	1	1.33
3	Grain yield per plant + pods per plant + pods per cluster	C1	C1P5-6 C1P5-10	2	2.66
4	Grain yield per plant + primary branches per plant + plant height + clusters per plant	C12	C12P5-5	1	1.33
5	Grain yield per plant + primary branches per plant + plant height	C12	C12P1-14	1	1.33
6	Grain yield per plant + clusters per plant + primary branches per plant	C7	C7P5-7	1	1.33
7	Grain yield per plant + primary branches per plant	C11	C11P5-6 C11P5-7 C11P5-10	3	4.00
8	Grain yield per plant + pods per cluster	C2	C2P5-6 C2P5-10	2	2.66
9	Grain yield per plant + pods per plant	C10	C10P5-12	1	1.33
	Total			13	17.33

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