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ASSESSMENT OF TRANSGRESSIVE SEGREGANTS FOR YIELD AND YIELD ATTRIBUTING TRAITS IN MUNG BEAN (*VIGNA RADIATA* (L.) R. WILCZEK) IN F$_3$ GENERATION

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ABSTRACT

This study aimed to estimate transgressive segregants in nine mung bean genotypes. The genotypes included four crosses and five parents. Eight morphological traits were examined. The experiment was conducted during the *Kharif* season of 2022 at the Research Farm of Sri Karan Narendra College of Agriculture, Jobner, Jaipur. A randomized block design with three replications was used. Transgressive segregation in desirable directions was observed for all traits in the F$_3$ generation of the crosses. The highest proportion of transgressive segregants was found for pods per plant. Other traits with high transgression included plant height, pod length, clusters per plant, seed yield per plant, 100-seed weight, seeds per pod, chlorophyll content, and pods per cluster. The study concluded that transgressive breeding is effective when desired trait intensity is absent in the parents. This method accumulates favorable genes from both parents. In many cases, the better-parent yield was surpassed, along with improvements in other traits. Significant transgressive segregants for major agronomic traits were observed. MH 421 × RMG 975 showed the highest proportion of desirable segregants. These segregants exhibited substantial improvements in yield. Seed yield per plant increased by up to 52.14% compared to the best parent. The findings show the potential of transgressive breeding to improve green gram productivity.

***Keywords* :** Transgressive segregation, mung bean, F3 generation and seed yield per plant

Introduction

Transgressive segregation is a crucial genetic phenomenon in plant breeding, wherein certain hybrid progeny display traits that surpass the range of both parental lines, leading to superior performance in yield and stress tolerance (Gardner, 1968). This phenomenon is particularly advantageous in breeding programs as it facilitates the emergence of new phenotypes that outperform parent varieties in agronomic traits (Rieseberg *et al.,* 1999). The mechanism behind transgressive segregation typically involves the recombination of advantageous alleles from both parents, allowing the selection of genotypes with enhanced productivity and resilience (Jones and Arnold, 2014).

Green gram (*Vigna radiata* (L.) R. Wilczek) is a vital legume crop in India. Transgressive segregation offers significant potential for boosting yield and improving desirable traits (Singh *et al.,* 2015). Green gram is widely important but faces challenges in production. Limited genetic diversity and susceptibility to abiotic and biotic stresses are major issues and moderate yield levels (Nair *et al*., 2020). Green gram's self-pollinating nature limits genetic diversity. Exploring transgressive segregants can boost yield and stress tolerance (Sharma *et al.*, 2016). This strategy enhances adaptability and supports sustainable farming through nitrogen fixation, benefiting soil health (Mehandi *et al.*, 2019).

This research aims to assess the presence and advantages of transgressive segregation within four diverse green gram crosses, focusing on identifying segregants with superior yield and agronomic traits. This study seeks to evaluate the role of transgressive segregants in advancing green gram breeding programs and in bolstering productivity and resilience.

Materials and Methods

Location: This investigation was conducted at the Research Farm of Sri Karan Narendra College of Agriculture, Jobner, Jaipur, Rajasthan, during the *kharif* season of 2022. The experimental site is situated at an altitude of 450 meters above mean sea level, with a latitude of 26°5’ N and a longitude of 75°28’ E, falling within agro-climatic zone III A (semi-arid eastern plains).

Experimental material: The plant material included four F_3 crosses and five parental genotypes of green gram (*Vigna radiata*), obtained from the Department of Plant Breeding and Genetics, SKN College of Agriculture, Jobner. The genotypes comprised four F_3 crosses: MH 421 x RMG 975, Pusa 9531 x LGG 4604, Pusa 9531 x MH 2-15, and Pusa 9531 x RMG 975. The parental genotypes used were MH 421, Pusa 9531, LGG 4604, RMG 975, and MH 2-15.

Experimental design and layout: The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each of the four F_3 crosses was represented by five rows, while each parent was represented by a single row in each replication. Row length was standardized at 3 meters, with inter-row and intra-row spacing maintained at 30 cm and 10 cm, respectively.

Data collection and observations: Data were recorded from 40 superior selected plants in each F_3 population and 10 randomly plants per parent. The observations recorded in this study included plant height (cm), clusters per plant, pods per cluster, pods per plant. pod length (cm), seeds per pod, 100-seed weight, and seed yield per plant (g).

Statistical analysis: The statistical analysis of transgressive segregation involved calculating the mean and range for each trait to assess central tendency and variability within the F3 generation. The highest and lowest trait values were used to determine the range, providing insights into the extent of variation among the segregants. Standard deviation, standard error of the mean, and variance were calculated to assess data dispersion, precision of the sample mean, and the extent of variation across different traits. Threshold values were established based on parental means and standard deviations at a 5% probability level to identify transgressive segregants, which exhibited trait values surpassing the parental range.

Results and Discussion

Transgressive Segregation in F_3 Generations

Transgressive segregants were observed among F3 progenies from four direct crosses *viz*., MH 421 × RMG 975, PUSA 9531 × LGG 4604, PUSA 9531 × MH 2-15, and PUSA 9531 × RMG 975. Five parents were involved in these crosses. Observations revealed that desirable transgressive segregants were identified across all eight traits studied (Table 1). Transgressive segregation, arising from recombination and segregation of favorable alleles contributed by both parents, was evident in the F_3 generation (Briggs and Allard, 1953; Gardner, 1968).

The highest proportion of individuals transgressing beyond the increasing parent was observed for pods per plant (10.00–19.17%), followed by plant height (10.83–18.33%), seeds per pod (6.67–13.33%), seed yield per plant (9.17–15.83%), pods per cluster (5.83–11.67%), 100-seed weight (9.17–13.33%), pod length (11.67–15%), and clusters per plant (11.67–14.17%). These results align with findings from earlier studies by Karkute and Girase (2013), who reported significant transgressive segregants for traits such as pods per plant, grain yield, and pod length in mungbean, and Reddy *et al.* (2021), who observed transgressive segregants for plant height, pods per cluster, and harvest index.

Ranking of Crosses Based on Transgressive Segregation

The ranking of the four crosses for their ability to generate transgressive segregants revealed that MH 421 × RMG 975 consistently performed best, ranking first for seven out of nine traits (Table 1). PUSA 9531 × RMG 975 ranked second for four traits, while PUSA 9531 × MH 2-15 secured second place for two traits. PUSA 9531 × LGG 4604 exhibited the least potential, failing to produce top-ranked transgressive segregants for any trait. These results are in agreement with the observations of Smith (1966), who emphasized the importance of utilizing distantly related parents with favorable expressions for desirable traits.

Evaluation of Transgressive Segregants

The crosses (MH 421 × RMG 975, PUSA 9531 × LGG 4604, PUSA 9531 × MH 2-15, and PUSA 9531 × RMG 975) exhibited significant variations in the frequency of transgressive segregants. Among these, MH 421 × RMG 975 produced the highest number of transgressive segregants (19 individuals, 15.83%) for seed yield per plant, followed by PUSA 9531 × MH 2-

15 (15 individuals, 12.5%), PUSA 9531 × RMG 975 (13 individuals, 10.83%), and PUSA 9531 × LGG 4604 (11 individuals, 9.17%). These results align with previous findings by Karkute et al. (2013), who reported a higher frequency of transgressive segregants for yield traits when parents with complementary traits were used. The superior performance of MH 421 × RMG 975 may be attributed to greater genetic diversity between the parents, which enhances the chances of recombination events leading to favorable allele combinations (Briggs and Allard, 1953).

Contribution of Traits to Transgressive Segregation

In cross MH 421 × RMG 975, transgressive segregants were observed not only for seed yield per plant but also for major associated traits such as clusters per plant, pods per plant, and pod length. The presence of favorable additive alleles in both parents likely led to enhanced performance in the progeny. Gardner (1968) emphasized that traits governed by polygenic inheritance, such as seed yield, show higher transgressive segregation due to the combined effects of minor alleles. Conversely, PUSA 9531 × LGG 4604 produced the lowest frequency of transgressive segregants. This could be due to limited genetic variation between the parents or insufficient complementarity in their traits. Similar observations were reported by Reddy *et al.* (2021), who noted reduced transgressive potential in crosses involving genetically similar parents.

Enhanced Trait Intensities in Transgressive Segregants

The evaluation of transgressive segregants across four crosses highlighted significant advancements in character expression intensity compared to their respective increasing parents. These findings underscore the utility of transgressive breeding in extending trait limits and achieving superior genetic recombination.

The highest-performing transgressive segregants achieved seed yields of 10.80 g in MH 421 × RMG 975, 11.35 g in PUSA 9531 × LGG 4604, 10.70 g in PUSA 9531 × MH 2-15, and 9.70 g in PUSA 9531 × RMG 975, far surpassing their respective increasing parents with yields of 6.77 g, 5.50 g, 5.63 g, and 5.62 g. These improvements reflect successful genetic recombination and additive gene action, aligning with findings by Karkute *et al.* (2016) and Sundaram *et al.* (2023). Yadav *et al.* (2021) reported that transgressive segregants in mungbean excelled in seed yield and 100-seed weight due to favorable recombination events. Singh *et al.* (2019) highlighted the utility of transgressive breeding in enhancing mungbean yield and adaptability.

Clusters per plant is a vital trait for branching and reproductive success and showed remarkable improvements. PUSA 9531 X LGG 4604 recorded the highest (8 clusters), followed by crosses PUSA 9531 X MH 2-15 and PUSA 9531 X RMG 975 (7 clusters each) and MH 421 X RMG 975 (6 clusters). These values significantly exceeded the parental means of 3.53 to 3.77 clusters. Studies by Yadav *et al.* (2021) and Kumar *et al.* (2022) attribute such improvements to favorable epistatic interactions and enhanced recombination frequency during gametogenesis in mungbean.

The number of pods per plant was maximized in PUSA 9531 X LGG 4604 (42 pods), with the remaining crosses producing 36 pods each. These values outperformed the parental means, indicating the potential of transgressive breeding to enhance pod development. This improvement corroborates findings by Singh *et al.* (2020), who highlighted the importance of selecting transgressive segregants in improving pod-related traits for enhanced yield in mungbean. Moderate increases in pod length were observed with MH 421 X RMG 975 achieving a maximum of 9.30 cm against its parental mean of 7.77 cm. Seed-related traits also improved, PUSA 9531 × RMG 975 recorded the highest seeds per pod (15), surpassing the parental mean of 12.37 seeds. These results align with Yadav *et al.* (2022), who emphasized the role of polygenic inheritance and complementary gene action in boosting reproductive efficiency through transgressive segregation.

Notable enhancements in 100-seed weight were recorded, with values reaching 4.40 g in crosses MH 421 X RMG 975 and PUSA 9531 X RMG 975, significantly exceeding the parental means (3.32 to 3.87 g). These findings are consistent with Dhakal *et al.* (2020), who reported that transgressive segregants often exhibit higher seed weight due to the accumulation of favorable alleles influencing seed size and density.

Simultaneous transgressive segregation for two or more characters in each of the four crosses

The analysis of transgressive segregants across the four crosses revealed notable genetic improvements in several yield-contributing traits, particularly seed yield per plant, clusters per plant, pods per cluster, pods per plant, pod length, and seeds per pod (Table 3). In most instances, when transgression was observed for seed yield per plant, other important yield-related characters also exhibited transgressive behavior. These findings highlight the interdependence of seed yield with other critical components, such as the number of clusters per plant, pods per cluster, and pod length.

A significant proportion of transgressive segregants (12.5% for MH 421 X RMG 975, 9.16% for PUSA 9531 X MH 2-15) exhibited transgression for seed yield per plant alone, while other individuals showed simultaneous transgression for seed yield and multiple components, including clusters per plant, pods per cluster, and pods per plant. 0.83% of individuals in MH 421 X RMG 975, PUSA 9531 X LGG 4604 and PUSA 9531 X MH 2-15 showed transgression for seed yield per plant alongside clusters per plant, pods per cluster, pods per plant, pod length, and seeds per pod, indicating a broader range of genetic improvements.

This study supports previous findings on mungbean, showing that genetic improvements in seed yield are linked with enhancements in other yield components like pods per plant and seeds per pod (Singh *et al*., 2020; Yadav *et al*., 2021). The consistent transgression of multiple traits suggests shared genetic pathways or epistatic interactions (Sarker *et al*., 2019). The genetic interdependence of seed yield with traits like clusters per plant and pod length, observed in this study, aligns with earlier research (Sundaram *et al*., 2023; Reddy *et al*., 2021). This emphasizes the potential of transgressive breeding for simultaneous yield improvements.

Promising Transgressive Segregants in F3 Generation of Four Mungbean Crosses

Among the transgressive segregants, several plants showed substantial improvements in seed yield per plant, as well as other yield-contributing traits such as clusters per plant, pods per cluster, pods per plant, and pod length. In the cross MH 421 × RMG 975, plant No. 77 exhibited a remarkable 52.14% increase in seed yield per plant compared to the best parent involved in the cross (Table 4). This plant also showed higher values for clusters per plant and pods per plant, indicating that improvements in seed yield were accompanied by enhancements in other agronomically important traits. Similarly, in the cross PUSA 9531 × LGG 4604, plant No. 27 showed a 70% increase in seed yield, with a significant improvement in clusters per plant and pods per cluster. This suggests that selection for transgressive segregants can simultaneously improve multiple yield traits, leading to an overall better-performing plant.

In the cross PUSA 9531 × MH 2-15, plant No. 83 exhibited a 77.61% higher seed yield than the best parent, along with higher values for pods per plant, clusters per plant, and pod length. This result is consistent with findings from recent studies on mungbean, which indicate that improvements in yield are often linked with the enhancement of other key traits, such as pod number and pod length (Singh *et al.,* 2020; Yadav *et al.,* 2021). Likewise, in the cross PUSA 9531 × RMG 975, plant No. 82 demonstrated a 47.68% increase in seed yield along with higher expression of multiple yield components, highlighting the potential of transgressive breeding to enhance both seed yield and associated traits.

These results align with recent research on mungbean, which has shown that seed yield is genetically linked with traits such as pod number, pod length, and clusters per plant. Singh *et al.* (2020) and Yadav et al. (2021) observed similar correlations, where improvements in seed yield were accompanied by increases in other yield components, suggesting that these traits are genetically interdependent. Furthermore, the concept of transgressive segregation, where segregants express extreme values beyond those of the parents, has been well-documented in mungbean breeding programs. According to Sarker *et al.* (2019), transgressive breeding enables the expression of superior genotypes due to favorable recombinations and epistatic interactions, which may explain the observed improvements in both seed yield and related traits.

Transgressive breeding in mungbean holds considerable promise for improving not only seed yield but also other important agronomic traits. This approach could be particularly beneficial in regions where mungbean is a staple crop and a primary source of protein (Sharma *et al.,* 2020).

Conclusion

The study on transgressive segregation in the F3 generation of mungbean crosses demonstrated the significant potential of utilizing transgressive breeding to enhance seed yield and associated traits. The cross MH 421 × RMG 975 consistently produced the highest number of desirable transgressive segregants across multiple traits, including seed yield, clusters per plant, pods per plant, and pod length, highlighting the importance of genetic diversity and favorable recombination. These findings align with previous research, emphasizing the interdependence of yield components and the role of transgressive breeding in improving multiple traits simultaneously. The results suggest that transgressive breeding could be a valuable strategy for improving mungbean productivity, particularly in regions where the crop is a major source of protein.

Table 1 : Threshold values and transgressive segregation in mungbean crosses

Character	N.D.	Threshold value	Desirable transgressive segregants		Range in value of T.S.
			Frequency	T.S. %	
MH 421 X RMG 975					
Plant height (cm)	44.96	56.34	22	18.23	57 to 68
Clusters per plant	0.11	4.59	15	12.50	5 to 6
Pods per cluster	0.29	4.71	14	11.67	5 to 6
Pods per plant	15.01	17.47	23	19.17	18 to 36
Pod length (cm)	-10.19	7.93	14	11.67	8.00 to 9.30
Seeds per pod	-5.50	13.31	9	7.50	14 to 14
100-seed weight (g)	-15.64	3.99	15	12.50	4.10 to 4.40
Seed yield per plant (g)	2.01	7.24	19	15.83	7.40 to 10.80
PUSA 9531 X LGG 4604					
Plant height (cm)	39.19	52.13	14	11.67	53 to 70
Clusters per plant	1.31	4.55	17	14.17	5 to 8
Pods per cluster	-0.41	4.60	7	5.83	5 to 6
Pods per plant	13.06	14.96	20	16.67	15 to 42
Pod length (cm)	-12.87	7.64	18	15.00	7.65 to 8.53
Seeds per pod	2.69	13.08	8	6.67	14 to 14
100-seed weight (g)	-14.61	3.56	11	9.17	3.70 to 4.00
Seed yield per plant (g)	2.91	6.54	11	9.17	6.60 to 11.35
PUSA 9531 X MH 2-15					
Plant height (cm)	40.19	49.44	13	10.83	55 to 67
Clusters per plant	1.09	4.51	16	13.33	5 to 7
Pods per cluster	-1.12	4.41	8	6.67	5 to 6
Pods per plant	11.22	13.19	19	15.83	15 to 36
Pod length (cm)	-12.22	7.72	16	13.33	7.75 to 8.55
Seeds per pod	-3.65	12.88	16	13.33	13 to 13
100-seed weight (g)	-6.98	3.56	14	11.67	3.60 to 4.10
Seed yield per plant (g)	1.82	6.30	15	12.50	6.40 to 10.70
PUSA 9531 X RMG 975					
Plant height (cm)	49.58	56.34	17	14.17	58 to 88
Clusters per plant	0.94	4.59	14	11.67	5 to 7
Pods per cluster	-1.08	4.71	9	7.50	5 to 6
Pods per plant	15.13	17.47	12	10.00	20 to 36
Pod length (cm)	-10.62	7.83	15	12.50	7.90 to 8.80
Seeds per pod	-0.63	13.31	16	13.33	14 to 15
100-seed weight (g)	-8.51	3.84	16	13.33	4.00 to 4.40
Seed yield per plant (g)	1.60	6.31	13	1.60	6.50 to 9.70

Table 2: The extended limits achieved by transgressive segregants in respect of various characters in F_3 generation of four crosses.

Characters	Highest intensity of character expression in four crosses			
	F_3			
	MH 421 X RMG 975	PUSA 9531 X LGG 4604	PUSA 9531 X MH 2-15	PUSA 9531 X RMG 975
Plant height (cm)	68 (54.77)	70 (51.27)	67 (47.93)	88 (54.77)
Clusters per plant	6 (3.77)	8 (3.57)	7 (3.53)	7 (3.77)
Pods per cluster	6 (3.83)	6 (3.7)	6 (3.43)	6 (3.83)
Pods per plant	36 (14.53)	42 (13.33)	36 (12.17)	36 (14.53)
Pod length (cm)	9.30 (7.77)	8.53 (7.27)	8.55 (7.45)	8.80 (7.5)

Seeds per pod	14 (12.37)	14 (11.37)	13 (12)	15 (12.37)
100-seed weight (g)	4.40 (3.87)	4.00 (3.32)	4.10 (3.32)	4.40 (3.68)
Chlorophyll content (SPAD meter)	52.10 (45.73)	47.80 (43.96)	53.00 (47.31)	49.00 (43.72)
Seed yield per plant (g)	10.80 (6.77)	11.35 (5.5)	10.70 (5.63)	9.70 (5.62)

*Figures in the bracket are the mean values of increasing parent for respective characters.

Table 3: Rare and important transgressants

Cross No.	Frequency of transgressants (%)	Characters for which transgression was simultaneous
MH 421 X RMG 975	0.83	Seed yield per plant + clusters per plant + pods per cluster + pods per plant + pod length + seeds per pod
PUSA 9531 X LGG 4604	0.83	
PUSA 9531 X MH 2-15	0.83	
PUSA 9531 X RMG 975	0.83	
MH 421 X RMG 975	0.83	Seed yield per plant + clusters per plant + pods per cluster + pods per plant + pod length
PUSA 9531 X LGG 4604	0.83	
PUSA 9531 X MH 2-15	0.83	
PUSA 9531 X RMG 975	0.83	
MH 421 X RMG 975	1.66	Seed yield per plant + clusters per plant + pods per cluster + pods per plant
PUSA 9531 X LGG 4604	0.83	
PUSA 9531 X MH 2-15	1.66	
PUSA 9531 X RMG 975	1.66	
PUSA 9531 X RMG 975	0.83	Seed yield per plant + clusters per plant
MH 421 X RMG 975	12.50	Seed yield per plant alone
PUSA 9531 X LGG 4604	6.66	
PUSA 9531 X MH 2-15	9.16	
PUSA 9531 X RMG 975	6.66	

Table 4 : Promising transgressive segreagants having combinations of desirable attributes

Characters	Plant No.	Plant height	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100-seed weight	Seed yield per plant	% yield increased over increasing parent
Cross - 1 (MH 421 x RMG 975)										
F_3	77	54.00	6.00*	6.00*	36.00*	8.10*	14.00*	3.70	10.30*	52.14
MH 421		42.73	3.17	3.13	13.53	7.77	12.27	3.87	6.77	
RMG 975		54.77	3.77	3.83	14.53	7.50	12.37	3.68	5.62	
Cross - 2 (PUSA 9531 x LGG 4604)										
F_3	27	51.00	8.00*	6.00*	42.00*	7.65*	14.00*	3.20	9.35*	70.00
PUSA 9531		45.63	3.53	3.43	12.17	7.27	11.37	3.32	5.24	
LGG 4604		51.27	3.57	3.70	13.33	7.18	11.03	3.31	5.50	
Cross - 3 (PUSA 9531 X MH 2-15)										
F_3	83	44.00	7.00*	5.00*	35.00*	7.95*	13.00*	2.70	10.00*	77.61
PUSA 9531		45.63	3.53	3.43	12.17	7.27	11.37	3.32	5.24	
MH 2-15		47.93	3.37	3.17	10.77	7.45	12.00	3.26	5.63	
Cross - 4 (PUSA 9531 X RMG 975)										
F_3	82	73.00*	6.00*	5.00*	30.00*	8.10*	14.00*	3.60	8.30*	47.68
PUSA 9531		45.63	3.53	3.43	12.17	7.27	11.37	3.32	5.24	
RMG 975		54.77	3.77	3.83	14.53	7.50	12.37	3.68	5.62	

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