

## Genetic Divergence and Character Association in Micromutants of Green Gram [*Vigna radiata* (L.) Wilczek] Variety Sujata

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**Abstract:** Twenty five mutants selected from a gamma irradiated population of Green gram variety Sujata were evaluated to assess the genetic divergence among the mutants for nine quantitative traits in M<sub>4</sub> generation. Mutants were grouped in eight clusters based on D<sup>2</sup> values. Three clusters included two mutants whereas one cluster included only one mutant. The clustering pattern of mutants showed that mutants derived from a particular dose of treatment often grouped into different clusters. All the seven clusters (cluster II to VIII) were divergent from the cluster I, the largest group that included the parent variety Sujata. D<sup>2</sup> analysis of genetic divergence showed that branches plant<sup>-1</sup> followed by pod length, yield plant<sup>-1</sup> and plant height were the major contributors to divergence among mutant cultures of Sujata. Correlation coefficients (r) measure the mutual relationship between various quantitative characters on which selection can be based for yield improvement. Path analysis revealed that pods plant<sup>-1</sup> had the highest direct effect followed by branches plant<sup>-1</sup>, 100-seed weight, seeds pod<sup>-1</sup> and pod length on seed yield plant<sup>-1</sup>.

**Key words:** Greengram • Genetic Divergence • Correlation Coefficients • Path Analysis

### INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek] is one of the important short duration pulse crop of India and also an excellent source of high quality protein in Indian diets. But, unfortunately, the production and productivity of the crop is very low due to various reasons. Lack of genetic diversity is one of the bottlenecks in increasing the productivity in green gram. Induction of variability for crop improvement is one of the primary objectives of most of the mutation breeding programmes. Multivariate analysis, which takes into consideration of several quantitative traits, would be more dependable tool in determining the small differences among the micro-mutants as compared to univariate analysis. Multivariate analysis for identification and classification of mutants have earlier been reported by various workers [1-2] in green gram. Inability to recognize small differences in quantitative traits among individual plants visually, association of traits becomes the best alternative to

measure the relationship between traits and provides the degree to which various characters of a crop are associated with seed yield. The correlation between two traits is due to composite effects of selection, linkage and pleiotropy [3]. The usefulness of induced mutations in weakening, strengthening or altering the direction of character association in greengram has earlier been reported in green gram [4-6]. Path coefficient analysis is used in assessing the real contribution of various component traits towards seed yield, so that direction for desired improvement may be developed [7]. Selection based on yield components is advantageous if different yield related traits have been well documented [6]. Therefore, the present investigation was taken up for identification and classification of micromutants through multivariate analysis and to understand the nature, magnitude and direction of association and extent of direct and indirect effects of various quantitative traits on yield in the derived mutants of green gram.

## MATERIALS AND METHODS

Genetically pure, uniform dry seeds (10% of moisture) of green gram cv. Sujata, a derivative of the cross L24-2 x Pusa Baisakhi, determinate in habit, synchronous in maturity (60-65 days duration) having small pods, tolerant to YMV were exposed to 20, 30, 40, 50 and 60 kR doses of gamma rays at the BARC, Trombay. The experiments were conducted in the Instructional Farm of Krishi Vigyan Kendra, Jajpur, Odisha, India. Seeds of each treatment were sown in Randomized Block Design (RBD) with three replications to raise the  $M_1$  generation. The recovered mutants were first advanced to  $M_2$  and  $M_3$  generations. Twenty-five isolated promising lines were advanced to  $M_4$  generation. Observations on days to 50% flowering and days to maturity were taken on plot basis. For other characters like plant height, primary fruiting branches  $\text{plant}^{-1}$ , pods  $\text{plant}^{-1}$ , pod length, seeds  $\text{pod}^{-1}$ , 100 seed weight and seed yield  $\text{plant}^{-1}$ , observations were recorded on ten random plants per culture in each replication. Multivariate analysis of genetic divergence among mutants was done by using Mahalanobis'  $D^2$  statistic and grouping of mutants in to clusters by Tocher's method as suggested by Rao [8]. The genotypic and phenotypic correlation coefficients were estimated according to Singh and Chaudhary [9] and path coefficient analysis was done as per method suggested by Dewey and Lu [10].

## RESULTS AND DISCUSSIONS

The basic pre-requisite in multivariate analysis and grouping of genotypes in to different clusters is the existence of significant differences among the genotypes. Twenty-five mutants of Sujata differed significantly in respect of all the nine quantitative characters observed. The  $D^2$  values for all the 325 paired combinations among twenty-six entries of Sujata ranged from 2.66 between SS5-9 and SS6-9 to 154.68 between SS3-3 and SS6-11. On the basis of average  $D^2$ , contribution of characters to divergence was high for branches/plant followed by pod length, yield  $\text{plant}^{-1}$ , plant height, 100-seed weight, days to 50% flowering, days to maturity, seeds  $\text{pod}^{-1}$  and pods  $\text{plant}^{-1}$ . Twenty-six cultures including the parent were grouped in to eight diverged clusters (Table 1). Cluster I, the largest group, included the parent variety Sujata and 7 mutant cultures (two cultures from 20 kR treatments, three from 50 kR, one each from 40 kR and 60 kR

treatments). Cluster II was the second largest group comprising 5 mutant cultures derived from all the mutagenic treatments except 20 kR dose. Clusters III included 3 mutant cultures derived from 40 kR and 60 kR dose treatments, while clusters IV included 3 mutant cultures derived from 20 and 30 kR mutagenic doses. Cluster V, VI and VII included 2 cultures each derived from all the mutagenic treatments except 50 kR dose of treatment. Cluster VIII was a monogenotypic cluster having only one culture derived from 30 kR dose of treatment. The clustering pattern of mutants showed that mutants derived from a particular dose of treatment often grouped into different clusters and grouping into different genetic clusters indicated the diverse nature of the mutants.

Highest inter-cluster distance was observed between clusters III and V followed by clusters III and VI and clusters III and VII (Table 2). The minimum inter-cluster distance between clusters I and II indicated their genetic closeness. The maximum intra-cluster divergence was observed in cluster VII, followed by cluster IV, cluster II, cluster VI, cluster III, cluster V and cluster I.

The cluster mean for nine quantitative characters of four clusters (cluster II, V, VI and VII) of mutant cultures of Sujata showed higher mean yield than Cluster I, which included the parent variety (Table 3). Cluster II included 5 cultures where as other three clusters included 2 cultures each. Cluster VI, which included only two mutant cultures (SS2-14 and SS3-12) showed highest seed yield  $\text{plant}^{-1}$  (3.60 g). This Cluster showed highest character means for branches  $\text{plant}^{-1}$  and pods  $\text{plant}^{-1}$  and second highest for pod length and 100-seed weight. Cluster VII, represented by 2 mutant cultures (SS4-12, SS6-24), showed the second highest seed yield (3.47 g  $\text{plant}^{-1}$ ) with highest character means for pod length, seeds  $\text{pod}^{-1}$  and 100-seed weight and second highest for branches  $\text{plant}^{-1}$ . The lowest seed yield  $\text{plant}^{-1}$  of 1.84g as observed for cluster III, was represented by three mutant cultures with highest character means for days to 50% flowering, days to maturity and lowest branches  $\text{plant}^{-1}$ , plant height and pods  $\text{plant}^{-1}$ . Use of multivariate analysis for identification of parents in different crop improvement programmes has been reported earlier in green gram by many workers [1-2,7]. The present investigation revealed the presence of wide genetic diversity among the mutants derived from gamma irradiation.

Table 1: Groups for mutant cultures of Sujata in different clusters.

Cluster No	Number of cultures	Name of the culture
I	8	SS2-10, SS2-18, SS4-5, SS5-3, SS5-9, SS5-15, SS6-9, Sujata (Control)
II	5	SS3-19, SS4-18, SS5-13, SS5-21, SS6-17
III	3	SS4-23, SS6-2, SS6-11
IV	3	SS2-4, SS2-8, SS3-8
V	2	SS3-3, SS4-9
VI	2	SS2-1, SS3-12
VII	2	SS4-12, SS6-2
VIII	1	SS3-14

Table 2: Intra-and inter-cluster average D<sup>2</sup> of mutant cultures of Sujata

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	17.33	27.29	37.58	35.15	50.60	62.35	56.39	49.73
II	2.89	49.85	45.98	48.57	60.29	60.69	46.87	
III	19.18	69.42	124.92	118.87	100.15	53.44		
IV	23.78	54.07	62.74	91.91	48.04			
V	18.63	38.58	49.81	91.37				
VI	20.87	38.20	54.35					
VII	32.67	70.47						
VIII	----							

Underline figures are intra-cluster distances.

Table 3: Cluster mean for nine quantitative characters in Sujata

Clu-ster No.	Number of culture	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches plant <sup>-1</sup>	Pods plant <sup>-1</sup>	Pod length (cm)	Seeds pod <sup>-1</sup>	100-seeds weight (g)	Yield plant <sup>-1</sup> (g)
I	8	38.81	71.00	27.17	2.55	8.85	5.77	8.74	2.79	2.23
II	5	41.02	73.15	33.22	2.97	9.73	5.67	8.81	2.64	2.44
III	3	41.48	73.26	24.68	1.96	7.00	5.73	8.84	2.84	1.84
IV	3	37.78	71.15	25.95	2.42	8.41	4.99	7.74	2.82	1.98
V	2	38.50	69.89	35.49	3.53	11.28	5.67	8.45	2.98	3.00
VI	2	40.72	73.11	28.52	3.91	11.57	5.69	8.45	3.11	3.60
VII	2	40.56	72.89	33.65	3.59	10.28	6.47	9.58	3.32	3.47
VIII	1	40.11	71.78	26.60	3.20	9.73	4.85	7.40	3.00	2.20

Table 4: Phenotypic correlation (r<sub>p</sub>) and genotypic correlation (r<sub>g</sub>) among the quantitative traits in the mutant cultures of Sujata in M<sub>4</sub> generation

Character	Correlation	Days to maturity	Plant height	Branches plant <sup>-1</sup>	Pods plant <sup>-1</sup>	Pod length	Seeds pod <sup>-1</sup>	100-seed weight	Yield plant <sup>-1</sup>
Days to 50% flowering	r <sub>p</sub>	0.798**	0.171	0.278	0.203	0.337	0.311	0.094	0.291
	r <sub>g</sub>	0.845**	0.163	0.260	0.269	0.448*	0.353	0.060	0.297
Days to maturity	r <sub>p</sub>	0.105	0.116	0.045	0.186	0.250	0.055	0.152	
	r <sub>g</sub>	0.072	0.103	0.063	0.221	0.254	0.070	0.153	
Plant height	r <sub>p</sub>	0.370	0.391*	0.310	0.318	0.042	0.430*		
	r <sub>g</sub>	0.397*	0.467*	0.339	0.361	0.024	0.477*		
Branches/plant	r <sub>p</sub>	0.906**	0.266	-0.002	0.460*	0.907**			
	r <sub>g</sub>	1.013**	0.298	-0.030	0.535**	0.961**			
Pods/plant	r <sub>p</sub>	0.173	-0.026	0.182	0.843**				
	r <sub>g</sub>	0.131	-0.040	0.267	0.882**				
Pod length	r <sub>p</sub>	0.716**	0.412*	0.497**					
	r <sub>g</sub>	0.863**	0.496**	0.535**					
Seeds/pod	r <sub>p</sub>	0.096	0.249						
	r <sub>g</sub>	0.127	0.231						
100-seed weight	r <sub>p</sub>	0.542**							
	r <sub>g</sub>	0.594**							

\*Significant at P = 0.05,

\*\*Significant at P = 0.01

Table 5: Direct and indirect effects of component traits on their phenotypic correlation with seed yield of mutants of Sujata in M<sub>4</sub> generation

Character	Days to 50% flowering	Days to maturity	Plant height	Branches/Plant	Pods/Plant	Podlength	Seeds/pod	100-seed weight	r <sub>p</sub> with yield/plant
Days to 50% flowering	-0.070	0.060	0.005	0.084	0.103	0.043	0.044	0.023	0.291
Days to maturity	-0.056	0.074	0.003	0.035	0.023	0.023	0.036	0.014	0.152
Plant height	-0.012	0.008	0.030	0.112	0.198	0.039	0.045	0.010	0.430
Branches/plant	-0.019	0.009	0.011	0.302	0.458	0.036	-0.000	0.114	0.907
Pods/plant	-0.014	0.003	0.012	0.274	0.505	0.022	-0.004	0.045	0.843
Pod length	-0.024	0.014	0.009	0.080	0.087	0.126	0.102	0.102	0.497
Seeds/pod	-0.022	0.019	0.010	-0.001	-0.013	0.090	0.143	0.024	0.249
100-seeds weight	-0.007	0.004	0.001	0.139	0.092	0.052	0.014	0.247	0.542

Residential effect = 0.254. R<sup>2</sup> = 93.573%. Bold and underline figures indicate direct effect of that component character on seed yield/plant.

The character association studies among nine quantitative traits revealed that the genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic correlation coefficients for most of the character pairs (Table 4). Twelve of the thirty-six phenotypic correlation estimates and sixteen of the thirty-six genotypic correlation estimates were significant. The phenotypic and genotypic correlation ( $r_p$  and  $r_g$ ) estimates showed that plant height, branches plant<sup>-1</sup>, pods plant<sup>-1</sup>, pod length and 100-seed weight had highly significant positive correlation with seed yield plant<sup>-1</sup>. The phenotypic and genotypic correlation between other characters including seeds pod<sup>-1</sup> and seed yield plant<sup>-1</sup> was positive. The association of days to 50% flowering and days to maturity were positive and highly significant. Plant height showed significant and positive association with pods plant<sup>-1</sup> where as positive association with other characters. Branches plant<sup>-1</sup> showed positive significant association with pods plant<sup>-1</sup> and 100-seed weight, but negative association with seeds pod<sup>-1</sup>. Pod length showed significant positive association with seeds pod<sup>-1</sup> and 100-seed weight. Similar results have been reported earlier in green gram [5-7,11-13]. Achakzai and Panizai [14] and Achakzai [15] also obtained similar trend of results for mash-bean and pea cultivars, respectively.

Path analysis of the component traits partitioned the yield components into direct and indirect effects that reflected on the nature of their associations and the relative importance of the component traits in determining the yield. The direct effects of pods plant<sup>-1</sup> had the highest direct effect on seed yield followed by branches plant<sup>-1</sup>, 100-seed weight, seeds pod<sup>-1</sup> and pod length (Table 5). The direct effect of days to 50% flowering on seed yield was negative, but of very low magnitude (less than 0.070) whereas days to maturity and plant height on seed yield were positive but with very low magnitude. The correlation estimates of branches plant<sup>-1</sup>, pods plant<sup>-1</sup>,

pod length and 100-seed weight with seed yield plant<sup>-1</sup> were largely explained by their direct effects on yield and the indirect effects via other traits, generally of very low magnitude. Though plant height had fairly high correlation coefficient with yield, its direct effect on yield was very low. The correlations with yield were much influenced by indirect effects via other traits, more prominently through pods plant<sup>-1</sup> and branches plant<sup>-1</sup>, respectively. These findings were in broad conformity with the findings of earlier workers [5-7].

Based on correlation coefficients and path analysis, it is concluded that pods plant<sup>-1</sup>, branches plant<sup>-1</sup>, 100-seed weight, seeds pod<sup>-1</sup> and pod length appeared to be the major yield contributing parameters and therefore due consideration should be given to these characters in a planned mutation breeding approach for further yield improvement in green gram.

## REFERENCES

1. Mohapatra, B.K., M.P. Singh, R.P. Puri and C.S. Kalia, 1983. Comparative spectrum and frequencies of induced variability in green gram. Intl. Congress of Genetics, New Delhi, India, 1: 311.
2. Mohapatra, B.K., R.C. Misra and B. Baisakh, 1987. Genetic divergence among different lines of greengram. J. Orissa Botanical Sci., 9: 11-16.
3. Sakai, K.I. and A. Suzuki, 1964. Induced mutations and pleiotropy of genes responsible for quantitative traits in rice. Radit. Bot., 4: 141-151.
4. Khan, I.A., 1985. Correlation and path coefficient analysis of yield components in mungbean (*Phaseolus aureus* Roxb.). Bot. Bull. Acad. Sci., 26: 13-20.
5. Baisakh, B., B.K. Mohapatra and R.C. Misra, 1989. Variability and correlation and path coefficient analysis in mutant lines of greengram. Andhra Agric. J., 36: 182-186.

6. Idress, A., M.S. Sadiq, M. Hanil, G. Abbas and S. Haider, 2006. Genetic parameters and path co-efficient analysis in mutated generation of mungbean, *Vigna radiata* L. Wilczek. J. Agric. Res., 44(3): 181-189.
7. Makeen, K., G.B. Suresh, G.R. Lavany and A. Kumari, 2009. Genetic divergence and character association in micromutants of urdbean (*Vigna mungo* L.) variety T9. Academic J. Plant Sci., 2(3): 205-208.
8. Rao, C.R., 1952. Advance stastical methods in biometric research. John Wiley and Sons. New York.
9. Singh, R.K. and B.D. Chaudhary, 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India, pp: 57-78.
10. Dewey, D.R. and H.K. Lu, 1959. A correlation and path coefficient analysis of components of crested wheat grass seed productions. Agron. J., 51: 515-518.
11. Seth, S. and B.D. Chaudhary, 1989. Irradiation for branching in mungbean (*Vigna radiata*). Indian J. Heredity, 21(1-2): 40-42.
12. Singh, A.K. and R.M. Singh, 2007. Mutagenic effectiveness and efficiency of gamma rays and ethyl methane sulphonate and their synergetic effects in mungbean [*Vigna radiata* (L.) Wilczek]. Crop Research, 34: 1-3.
13. Momin, B.W. and R.C. Misra, 2004. Induced variability, character association and path coefficient analysis in mutant cultures of green gram. *Enviro. and Ecolo.*, 22(3): 608-611.
14. Achakzai, A.K.K. and M.K. Panizai, 2007. Effect of row spacing on growth, yield and yield components of Mash-bean. Sarhad J. Agric., 23(1): 5-10.
15. Achakzai, A.K.K., 2012. Effects of various levels of nitrogen fertilizer on some vegetative growth attributes of Pea (*Pisum sativum* L.) cultivars. Pak. J. Bot., 44(2): 655-659.