

## INDUCED GENETIC VARIABILITY FOR QUANTITATIVE TRAITS IN *VIGNA RADIATA* (L.) WILCZEK

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### Abstract

Mutations were induced in two mungbean varieties, K-851 and Pusa Baisakhi using sodium azide (SA) as a mutagen. The immediate effects of mutagenic treatments were measured in terms of biological damage caused in  $M_1$  generation. All the mutagenic treatments brought reduction in seed germination, pollen fertility and survival at maturity. Such reduction, with an exception of survival, were found to be dose dependent.

Significant shift in mean values for quantitative characters was observed in  $M_2$  and  $M_3$  generations and genetic parameters were recorded higher for all the treatments in both the generations. A significant positive correlation between various character pairs was observed.

### Introduction

Mungbean (*Vigna radiata* (L.) Wilczek), being a self-fertilized crop, has very limited genetic variability. Low genetic variability for the major characters becomes a limiting factor for its improvement. Induced mutations can provide additional source of variability for quantitative and qualitatively inherited traits in number of crop plants (Brock, 1971). Sodium azide ( $\text{NaN}_3$ ) is well known for its high mutagenic effect in several crops. It is an excellent chemical mutagen, with high solubility in water, strong reaction with and low toxicity to biological materials as compared with alkylating compounds that are usually used for mutation induction in plants (Ando & Neto, 1996). In the present study, attempt has been made to ascertain the magnitude of induced genetic variability following mutagenesis with sodium azide and also magnitude of associations between yield and its component characters in  $M_2$  and  $M_3$  generations.

### Materials and Methods

A field experiment was conducted during kharif season of 2000/01, 2001/02 and 2002/03 at the Agricultural Farm, Aligarh Muslim University, Aligarh, India. Seeds of two mungbean (*Vigna radiata* (L.) Wilczek) varieties, viz., K-851 and Pusa Baisakhi, pre-soaked in distilled water for 9 hours, were treated with 0.01 and 0.02 % of Sodium azide (SA) for 6 hours. Seeds soaked in distilled water were used as control. Seeds harvested from individual  $M_1$  plants were sown as  $M_2$  families in three replications in the field. For raising  $M_3$  generation, such 10  $M_2$  progenies were selected which showed significant deviations in mean values in the positive direction from the mean values of control, particularly for the yield and yield components in  $M_2$  generation. Seeds from each selected  $M_2$  progeny were bulked by taking an equal amount of seeds from all  $M_2$

plants from a single  $M_2$  progeny and thoroughly mixed. A random sample of this bulk was sown to obtain  $M_3$  progeny.

ANOVA was performed to test the significance of variance. Heritability ( $h^2$ ) in broad sense and phenotypic correlation among various character pairs were calculated by the formulae suggested by Singh & Chaudhary (1985) and the genetic advance by the method outlined by Johnson *et al.*, (1955).

## Results and Discussion

### Biological effects in $M_1$

The data recorded on seed germination, pollen fertility and plant survival at maturity in  $M_1$  are presented in Table 1. Both the varieties responded differently to various mutagenic treatments. Percentage inhibition in seed germination was recorded maximum in mungbean var. Pusa Baisakhi than the var. K-851 whereas % reduction in pollen fertility was highest in the var. K-851 in comparison to var. Pusa Baisakhi. Survival percentage of  $M_1$  plants decreased considerably in the mutagenic treatments in both the varieties. However, no dose dependent relationship was noticed. Differential response of the varieties to the mutagenic concentration was reported by Muthusamy & Jayabalan (2002) in *Gossypium hirsutum* and Wani *et al.*, (2004) in *Lens culinaris*. High degree of pollen sterility has been reported in rice after treatments with SA, gamma rays, EMS and HZ (Sarawgi & Soni, 1994). Failure of homologous pairing during meiosis could be the main cause of high pollen sterility. Gaul (1970) has suggested that the chromosomal aberrations are probably the major effect of all mutagenically induced pollen sterility. The actual reason of sterility caused by SA may be gene mutation or invisible deficiencies.

### Fertile branches per plant

There was an increase in the mean values of the fertile branches in  $M_2$  and  $M_3$  generations in both the mungbean varieties K-851 and Pusa Baisakhi (Tables 2 & 3). The mean values were also significantly higher than the controls. The mean number of fertile branches were recorded higher in  $M_3$  than in  $M_2$  generation. Singh & Chaturvedi (1990) showed increase in mean values of number of primary branches in *Lathyrus sativus* from  $M_2$  to  $M_3$  using NMU as a mutagen.

### Number of pods

A comparison of number of pods in the treated and control population (Tables 2 & 3) showed that the mean values significantly increased in all the treatments of SA in both the varieties. In  $M_3$ , significantly higher mean value (10.77 pods per plant) was noted with 0.02% SA in the var. K-851. The increase in variability for number of pods per plant following mutagenic treatments has been reported in *Lathyrus sativus* (Waghmare & Mehra, 2000) and in *Vigna mungo* (Singh *et al.*, 2000).

**Table 1. Effect of SA on seed germination, pollen fertility and plant survival in M<sub>1</sub> generation.**

Variety	Treatment	% age inhibition in seed germination	% age reduction in pollen fertility	% plant survival at maturity
<b>K-851</b>	Control	-	-	86.67
	0.01% SA	8.69	13.28	68.00
	0.02% SA	16.04	17.75	76.67
<b>Pusa Baisakhi</b>	Control	-	-	90.25
	0.01% SA	14.12	10.68	74.00
	0.02% SA	19.58	14.54	76.60

**Table 2. Estimates of mean values ( $\bar{X}$ ), shift in  $\bar{X}$ , coefficient of variation, heritability ( $h^2$ ) and genetic advance (GA) for different characters in M<sub>2</sub> generation of *Vigna radiata* (L.) Wilczek.**

Treatment	Mean $\pm$ S.E.	Shift in $\bar{X}$	PCV (%)	GCV (%)	$h^2$ (%)	GA (% of $\bar{X}$ )
<b>Var. K-851</b>						
<b>Number of fertile branches</b>						
Control	5.60 $\pm$ 0.19	0.00	20.30	13.50	44.10	23.67
0.01% SA	6.63 $\pm$ 0.22	+1.03	24.88	15.35	38.06	24.99
0.02% SA	6.45 $\pm$ 0.21	+0.85	23.42	14.94	40.69	25.15
<b>CD (p=0.05)</b>		<b>0.83</b>				
<b>Number of pods</b>						
Control	48.57 $\pm$ 1.41	0.00	6.64	4.00	36.29	6.36
0.01% SA	57.47 $\pm$ 0.57	+8.90	10.05	8.16	65.92	17.48
0.02% SA	56.27 $\pm$ 0.59	+7.70	7.26	5.01	47.50	9.13
<b>CD (p=0.05)</b>		<b>5.19</b>				
<b>Total plant yield (g)</b>						
Control	09.61 $\pm$ 0.18	0.00	6.50	4.35	44.79	4.80
0.01% SA	12.83 $\pm$ 0.10	+3.22	7.04	6.05	73.97	13.75
0.02% SA	13.59 $\pm$ 0.08	+3.98	8.59	7.50	76.23	17.28
<b>CD (p=0.05)</b>		<b>0.38</b>				
<b>Var. Pusa Baisakhi</b>						
<b>Number of fertile branches</b>						
Control	7.00 $\pm$ 0.34	0.00	22.82	14.20	42.35	24.39
0.01% SA	8.30 $\pm$ 0.27	+1.30	25.90	20.20	60.82	41.58
0.02% SA	7.40 $\pm$ 0.33	+0.40	31.09	21.30	46.94	38.54
<b>CD (p=0.05)</b>		<b>0.97</b>				
<b>Number of pods</b>						
Control	53.77 $\pm$ 1.52	0.00	7.35	4.33	34.70	6.73
0.01% SA	59.10 $\pm$ 0.57	+5.33	7.40	5.20	49.38	9.65
0.02% SA	57.40 $\pm$ 0.55	+3.63	7.42	5.96	64.58	12.65
<b>CD (p=0.05)</b>		<b>2.77</b>				
<b>Total plant yield (g)</b>						
Control	09.99 $\pm$ 0.24	0.00	13.64	3.91	8.22	2.96
0.01% SA	10.92 $\pm$ 0.13	+0.93	10.19	7.20	49.92	13.43
0.02% SA	10.88 $\pm$ 0.15	+0.89	10.45	7.96	58.00	15.99
<b>CD (p=0.05)</b>		<b>0.46</b>				

PCV = Phenotypic coefficient of variation.

GCV = Genotypic coefficient of variation.

**Table 3. Estimates of mean values ( $\bar{X}$ ), shift in  $\bar{X}$ , coefficient of variation, heritability ( $h^2$ ) and genetic advance (GA) for different characters in  $M_3$  generation of *Vigna radiata* (L.) Wilczek.**

Treatment	Mean $\pm$ S.E.	Shift in $\bar{X}$	PCV (%)	GCV (%)	$h^2$ (%)	GA (% of $\bar{X}$ )
<b>Var. K-851</b>						
<b>Number of fertile branches</b>						
Control	05.82 $\pm$ 0.14	0.00	16.55	10.96	43.83	19.15
0.01% SA	07.97 $\pm$ 0.26	+2.15	23.30	16.29	48.88	30.07
0.02% SA	07.40 $\pm$ 0.24	+1.58	22.30	15.24	46.68	27.48
<b>CD (p=0.05)</b>		<b>0.72</b>				
<b>Number of pods</b>						
Control	49.53 $\pm$ 1.31	0.00	5.02	2.85	32.28	4.28
0.01% SA	59.13 $\pm$ 0.42	+9.60	6.19	5.39	75.99	12.41
0.02% SA	60.30 $\pm$ 0.42	+10.77	5.69	4.79	70.57	10.62
<b>CD (p=0.05)</b>		<b>6.32</b>				
<b>Total plant yield (g)</b>						
Control	09.98 $\pm$ 0.06	0.00	2.00	1.10	30.28	1.59
0.01% SA	13.77 $\pm$ 0.05	+3.79	12.96	9.96	51.05	17.46
0.02% SA	13.94 $\pm$ 0.03	+3.96	13.51	10.03	55.11	19.65
<b>CD (p=0.05)</b>		<b>0.14</b>				
<b>Var. Pusa Baisakhi</b>						
<b>Number of fertile branches</b>						
Control	07.50 $\pm$ 0.19	0.00	17.41	10.52	36.51	16.78
0.01% SA	09.30 $\pm$ 0.31	+1.80	26.03	20.99	65.05	44.70
0.02% SA	09.70 $\pm$ 0.36	+2.20	31.66	27.00	72.73	60.79
<b>CD (p=0.05)</b>		<b>0.41</b>				
<b>Number of pods</b>						
Control	54.83 $\pm$ 0.94	0.00	8.65	5.29	37.39	8.54
0.01% SA	63.13 $\pm$ 0.68	+8.30	9.39	8.22	76.53	18.98
0.02% SA	64.00 $\pm$ 0.82	+9.17	9.59	7.41	59.59	15.09
<b>CD (p=0.05)</b>		<b>3.96</b>				
<b>Total plant yield (g)</b>						
Control	10.53 $\pm$ 0.18	0.00	8.80	3.59	16.64	3.87
0.01% SA	11.64 $\pm$ 0.15	+1.11	11.82	8.79	55.28	17.25
0.02% SA	11.93 $\pm$ 0.17	+1.40	11.34	8.57	57.10	17.09
<b>CD (p=0.05)</b>		<b>0.49</b>				

PCV = Phenotypic coefficient of variation.

GCV = Genotypic coefficient of variation.

### Total plant yield

The data on the total yield per plant show that there was an increase in the mean values for each treatment in both the varieties (Tables 2 & 3). However, mean values increased considerably in the var. K-851 as compared to the var. Pusa Baisakhi in both  $M_2$  and  $M_3$ . In majority of experiments, reduction in mean seed yield per plant in  $M_2$  and  $M_3$  has been reported (Scossiroli *et al.*, 1966; Singh *et al.*, 2000). The reduction in mean seed yield may be due to higher frequency of mutations with persistent negative effects for yield contributing traits. Increase in mean seed yield in  $M_3$  over the  $M_2$  and control

could be a result of directed selection for yield exercised in M<sub>2</sub> generation. Waghmare & Mehra (2000) achieved considerably increased mean yield in M<sub>3</sub> after gamma ray and EMS treatments in *Lathyrus sativus*.

The yield, as such, is a complex manifestation of large number of genes involved in physiochemical processes of the plant system. Induced mutations can contribute to the physiological efficiency of the plant for grain yield by generation of more favourable correlations between various yield components (Waghmare & Mehra, 2000). A comparison of mutated and control population of the two varieties of mungbean revealed that a significant increase in positive correlations between the number of fertile branches and pods, the number of fertile branches and the total plant yield and the number of pods and the total plant yield were observed with the mutagenic treatments (Table 4). It was also observed that the negative association between number of fertile branches and pods (var. K-851) and the number of pods and the total plant yield (var. Pusa Baisakhi) in control population was broken down after SA treatments in M<sub>3</sub> generation. This was highly desirable from the point of view of improvement of more than one trait. Such desirable changes in association with yield contributing characters have also been reported in *Cicer arietinum* by Kharkwal (2003).

Assessment of variance has been the most dependable statistical measure to find the mutagenic effect on the polygenes. Estimation of various genetic parameters viz., genotypic coefficient of variation (GCV), heritability (h<sup>2</sup>) and genetic advance (GA) for three quantitative characters of the two varieties of mungbean provided ample evidence that mutagenic treatments could alter mean values and create additional genetic variability for quantitative traits. In the present study, number of pods and total plant yield showed high heritability but moderate to low genetic advance in both the varieties. These results indicated that these characters were under the control of non-additive gene action and they will not respond to early selection. High heritability coupled with high genetic advance was observed for fertile branches per plant in the var. Pusa Baisakhi. High heritability and genetic advance for a character would indicate the predominance of additive gene action on the trait and as such this trait is likely to respond effectively to phenotypic selection (Johnson *et al.*, 1955; Sheeba *et al.*, 2003).

**Table 4. Phenotypic correlation between various character pairs in M<sub>3</sub> generation of *Vigna radiata* (L.) Wilczek.**

Variety	Treatment	Fertile branches/ plant Vs. pods/plant	Fertile branches/ plant Vs. total plant yield (g)	Pods/plant Vs. total plant yield (g)
<b>K-851</b>	Control	- 0.512	0.263	0.910
	0.01% SA	0.674**	0.610	0.974**
	0.02% SA	0.512*	0.614*	0.943*
<b>Pusa Baisakhi</b>	Control	0.308	0.480	- 0.200
	0.01% SA	0.718**	0.831**	0.758**
	0.02% SA	0.694**	0.750**	0.756**

\*Significant at 5% level.

\*\*Significant at 1% level.

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