

Estimates of genetic variability in mutated populations and the scope of selection for yield attributes in *Vigna radiata* (L.) Wilczek

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ABSTRACT

A significant increase in mean values of the fertile branches per plant, pods per plant and seed yield per plant was noticed in mutants of mungbean (*Vigna radiata* (L.) Wilczek) – a self-fertilized crop. Estimates of genetic parameters (genotypic coefficient of variation, heritability and genetic advance) for the yield and its components were higher than the control in two generations. The increased genetic variability for these traits provides great scope for further selection.

KEYWORDS: *Vigna radiata*, induced mutations, genetic variability, yield components, selection.

INTRODUCTION

Grain legumes, commonly known as pulses, occupy a pivotal position in meeting the protein needs of people in developing countries like India. Mungbean (*Vigna radiata* (L.) Wilczek) (Papilionaceae) is an important, self-fertile pulse crop grown all over South East Asia. Due to lack of sufficient natural variability for yield and its component traits in mungbean, conventional methods of breeding have limited scope.

Induced mutations have been used to generate genetic variability and have been successfully utilized to improve yield and yield components of various crops like *Oryza sativa* (Rao & Siddiq 1977; Awan *et al.* 1980; Singh *et al.* 1998), *Hordeum vulgare* (Gustafsson 1963; Ramesh *et al.* 2001), *Triticum durum* (Sakin & Yildirim 2004), *Vicia faba* (Ismail *et al.* 1977), *Cicer arietinum* (Shaikh *et al.* 1982; Sharma *et al.* 1990), *Vigna unguiculata* (Mensah & Akomeah 1992), *Cajanus cajan* (Srivastava & Singh 1996), *Vigna mungo* (Kundu & Singh 1981; Singh & Singh 2001) and *Lens culinaris* (Kumar *et al.* 1995; Rajput *et al.* 2001; Khan *et al.* 2006). These reports show that mutagenesis is a potential tool to be employed for crop improvement.

Development of high-yielding varieties requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value between generations.

In the present study, therefore, an attempt has been made to partition the variance components, especially phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2) and genetic advance (GA) for yield and yield components in M2 and M3 generations of mungbean. These estimates could be useful in developing reliable selection indices.

MATERIALS AND METHODS

A field experiment was conducted during the kharif season of 2003, 2004 and 2005 at the Agricultural Farm, Aligarh Muslim University, Aligarh, India. Seeds of mungbean (*Vigna radiata* (L.) Wilczek) var. PDM-11, presoaked in distilled water for 9 hours, were treated with 0.1%, 0.2% ethylmethane sulphonate (EMS) or 0.01%, 0.02% hydrazine hydrate (HZ) for 6 hours to induce mutations. The untreated seeds presoaked in distilled water for 15 hours were sown as control. The solutions of EMS and HZ were prepared in phosphate buffer (pH 7.0). Chemically treated seeds were thoroughly washed in running tap water to remove the mutagen from the seed surface.

One hundred seeds for every treatment and control were sown in the field in a complete randomized-block design to raise the M₁ generation. Such a field design is most frequently used in plant breeding programmes. The phenotypic variance of the test variety might be influenced partially by soil heterogeneity and partially by environment, and the complete randomized-block design provides an efficient mechanism for Analysis of Variance to account for these sources of variation.

Seeds harvested from individual M₁ plants were sown as M₂ families in three replicates in the field. For raising the M₃ generation, ten M₂ progenies were selected which showed significant deviations in mean values in the positive direction from the mean values of the control, particularly for the yield and yield components of the M₂ generation. Seeds from each selected M₂ progeny were bulked by taking an equal amount of seeds from each M₂ progeny and thoroughly mixing them. A random sample of this bulk was sown to obtain M₃ progeny.

Data collected for fertile branches per plant, pods per plant, the weight of 100 seeds (g) and seed yield per plant (g) in the M₂ and M₃ generations were subjected to statistical analysis in order to assess the extent of induced variation. Significant differences were identified using the Least Significance Difference estimated from the error mean square and tabulated 't' values at the 5% level of significance.

Parameters estimated were the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h²) and expected genetic advance (GA). All were estimated in the standard manner, except genetic advance. The estimate of the expected genetic advance (GA, expressed as a percentage of the mean value) with an assumed 1% selection intensity was computed by the formula of Allard (1960) as suggested by Khan (1979), namely:

$$GA = k. \sigma_p. h^2$$

where,

h² = broad-sense heritability

σ_p = phenotypic standard deviation of the mean performance of the treated population

k = 2.64, constant for 1% selection intensity (i.e. the highest-performing 1% are selected).

In this experiment we judged that 1% was approximately the correct level.

RESULTS

There was a significant increase in the mean fertile branches per plant in all the mutagen treatments over the control in both M₂ and M₃ generations (Tables 1 & 2). EMS treatments were more effective in increasing the mean values and genetic variability than HZ in both the generations. The highest coefficient of phenotypic (18.2%) and genotypic (15.0%) variability was recorded with the 0.2% EMS treatment, whereas the highest heritability estimate (72.6%)

was observed with 0.02% HZ in the M₃ generation (Table 2). The expected genetic advance was more pronounced in EMS-treated populations than HZ in both the generations.

The mean values of the number of pods per plant in treated populations differed significantly ($p = 0.05$) from the control in both M₂ and M₃ generations. EMS treatments were found to be more effective than HZ treatments. With regards to genetic parameters, variability was higher in EMS treatments. EMS at 0.1% concentration gave the maximum values of the genetic parameters in both generations (Tables 1 & 2).

The weight of 100 seeds is a reliable measure of yielding ability in pulses. Although the mean 100-seed weight showed a positive shift, the difference was not significant over the control (Tables 1 & 2). The values of the coefficients of variation (phenotypic and genotypic), heritability and expected genetic advance increased in the treated population as compared to control. The highest values were observed in EMS treatments.

The grain yield of a crop is a complex trait, the result of interactions of various parameters. The data on seed yield per plant presented in Tables 1 & 2, show that there was a general increase in the mean values for each treatment in both the generations. The mean in the treated population significantly differed from that of the control. The highest coefficient of genotypic variation, heritability and expected genetic advance were observed in EMS treatments than HZ treatments.

Table 1: Estimates of mean values (\bar{X}), shift in \bar{X} , phenotypic (PCV) and genetic (GCV) coefficient of variation, heritability (h^2) and genetic advance (GA) for seed yield and its components in the M₂ generation of mungbean. C.D. = critical difference at the 5% level of significance

Treatment	Mean \pm S.E.	Shift in \bar{X}	PCV(%)	GCV(%)	h^2 (%)	GA(% of \bar{X})
Fertile branches per plant						
Control	6.38 \pm 0.12	-	9.4	2.4	6.7	1.7
0.1% EMS	9.40 \pm 0.24	+ 3.02	16.9	10.0	34.8	19.7
0.2% EMS	10.10 \pm 0.26	+ 3.72	16.4	8.6	27.5	14.9
0.01% HZ	8.62 \pm 0.23	+ 2.24	13.7	8.8	41.0	14.7
0.02% HZ	8.23 \pm 0.22	+ 1.85	10.1	4.2	17.4	4.5
C.D. (p=0.05)		0.33				
Pods per plant						
Control	45.96 \pm 0.55	-	6.8	3.0	20.1	3.6
0.1% EMS	57.23 \pm 0.83	+11.27	10.5	7.5	50.9	14.1
0.2% EMS	59.14 \pm 0.85	+13.18	10.3	7.2	49.3	13.3
0.01% HZ	54.25 \pm 0.65	+ 8.29	8.9	6.1	47.3	11.0
0.02% HZ	50.97 \pm 0.62	+ 5.01	7.7	4.9	40.1	8.1
C.D. (p=0.05)		1.18				
100-seed weight (g)						
Control	3.70 \pm 0.02	-	4.0	2.3	29.2	3.1
0.1% EMS	3.87 \pm 0.08	+ 0.17	15.5	9.7	38.9	15.8
0.2% EMS	4.03 \pm 0.09	+ 0.33	16.8	12.2	52.2	23.1
0.01% HZ	3.97 \pm 0.09	+ 0.27	14.9	9.1	37.1	14.5
0.02% HZ	3.94 \pm 0.08	+ 0.24	15.2	9.4	38.9	15.6
C.D. (p=0.05)		0.35				
Seed yield per plant (g)						
Control	8.40 \pm 0.12	-	7.6	3.9	26.8	5.4
0.1% EMS	11.20 \pm 0.20	+ 2.80	12.9	9.3	50.9	20.8
0.2% EMS	11.74 \pm 0.24	+ 3.34	12.4	8.9	51.2	16.7
0.01% HZ	9.93 \pm 0.19	+ 1.53	12.9	7.5	34.4	11.5
0.02% HZ	9.66 \pm 0.18	+ 1.26	13.1	7.7	35.0	12.1
C.D. (p=0.05)		0.31				

Table 2: Estimates of mean values (\bar{X}), shift in \bar{X} , phenotypic (PCV) and genetic (GCV) coefficient of variation, heritability (h^2) and genetic advance (GA) for seed yield and its components in the M_3 generation of mungbean. C.D. = critical difference at the 5% level of significance

Treatment	Mean \pm S.E.	Shift in \bar{X}	PCV(%)	GCV(%)	h^2 (%)	GA(% of \bar{X})
Fertile branches per plant						
Control	6.47 \pm 0.13	-	11.5	3.0	6.7	2.0
0.1% EMS	11.50 \pm 0.22	+ 5.03	15.6	12.5	64.1	26.3
0.2% EMS	11.87 \pm 0.26	+ 5.40	18.2	15.0	67.5	32.2
0.01% HZ	10.55 \pm 0.19	+ 4.08	12.6	10.5	68.9	22.9
0.02% HZ	10.01 \pm 0.14	+ 3.54	14.6	10.3	72.6	23.1
C.D. (p=0.05)		0.58				
Pods per plant						
Control	45.90 \pm 0.10	-	6.6	2.8	17.8	3.1
0.1% EMS	60.17 \pm 0.72	+14.27	11.6	10.7	84.1	25.8
0.2% EMS	62.26 \pm 0.76	+16.36	11.3	10.1	79.8	23.5
0.01% HZ	55.95 \pm 0.57	+10.05	10.4	9.6	84.3	23.2
0.02% HZ	53.10 \pm 0.46	+ 7.20	7.9	7.0	77.8	16.2
C.D. (p=0.05)		2.30				
100-seed weight (g)						
Control	3.65 \pm 0.02	-	3.9	2.1	30.3	3.0
0.1% EMS	3.95 \pm 0.08	+ 0.30	19.0	16.2	72.7	36.4
0.2% EMS	4.11 \pm 0.09	+ 0.46	17.5	13.8	61.5	28.4
0.01% HZ	3.89 \pm 0.09	+ 0.24	18.4	14.5	62.7	30.2
0.02% HZ	3.98 \pm 0.07	+ 0.33	16.3	13.6	70.4	30.0
C.D. (p=0.05)		0.49				
Seed yield per plant (g)						
Control	8.56 \pm 0.10	-	7.6	3.9	26.2	5.2
0.1% EMS	12.98 \pm 0.34	+ 4.42	21.0	18.0	73.3	40.6
0.2% EMS	13.66 \pm 0.29	+ 5.10	19.1	16.5	74.6	37.4
0.01% HZ	10.85 \pm 0.24	+ 2.29	16.5	12.3	56.2	24.4
0.02% HZ	10.70 \pm 0.21	+ 2.14	14.5	10.7	54.9	21.0
C.D. (p=0.05)		0.74				

DISCUSSION

Induction of mutations affecting quantitative characters can be inferred by the estimation of mean and genetic parameters: genotypic coefficient of variation, heritability and expected genetic advance in the mutagen treated populations (Khan 1985). In recent years there have been a number of attempts to assess mutagen-induced genetic variability in quantitative traits of different crop plants such as *Oryza sativa* (Kaul & Kumar 1983), *Cajanus cajan* (Srivastava & Singh 1993), *Vigna unguiculata* (Gunasekaran *et al.* 1998), *Vigna mungo* (Singh *et al.* 2000), *Lathyrus sativus* (Waghmare & Mehra 2000), *Lens culinaris* (Solanki & Sharma 2001) and *Cicer arietinum* (Khan & Wani 2005).

In the present study, the variability in the treated population was higher than the control for all the quantitative traits, namely fertile branches per plant, pods per plant, 100-seed weight and seed yield per plant. The increase in the number of pods was due to an increase in the number of flowers. Flower shedding was not noticed in the mutants. Similar increases in the number of pods of some other varieties of mungbean has been reported by Tickoo & Chandra (1999) using ethylmethane sulphonate, nitrosomethyl urea, hydroxylamine and gamma rays as mutagens.

The weight per 100 seeds showed no significant increase over control in the M_2 and M_3 generations. These results are contrary to the earlier findings of Scossiroli (1964) and Khan (1985). However, no significant improvement in grain weight was reported by Potdukhe *et al.*

(1994) in durum wheat after gamma rays treatment. In the present study, increase in the mean values of various traits may be due to the selection of normal-looking plants in M_2 which led to elimination of aberrant plants and also due to changes induced at genetic level. Gaul (1964) suggested that the selection process should be delayed until the M_3 or later generations following mutagenic treatment. However, here the selection of progenies on the basis of desirable mean and greater variance in the early generation was found to be highly useful, leading to the desirable improvement of yield and its components in the M_3 generation.

High phenotypic and genotypic variances in the quantitative traits in all the mutagenic treatments indicate better chances for selection to be successful. The genotypic coefficient of variation measures the range of genetic variability shown by the plant trait and helps to compare the genetic variability present in various traits. However, with the genotypic coefficient of variation alone it is not possible to determine the amount of variation that is heritable. The heritable portion of the variation was determined with the aid of heritability estimates. The values of heritability increased and differed from trait to trait. The seed yield per plant exhibits high heritability. Kaul & Kumar (1983) obtained low heritability values for grain yield in rice. The disparity in the results could be due to the fact that heritability is a property not only of a character but also of the population and the environment to which the genotypes are subjected to. Therefore, its ultimate value depends on the magnitude of all the components of variance. The high estimates of heritability in the quantitative traits has been found to be useful from the point of view of plant breeding, as this enables selection to be based on phenotypic performance.

Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance is usually more helpful than the heritability value alone in predicting the resultant effect of selecting the best individuals. In the present study, high heritability coupled with high genetic advance was noticed for all the quantitative traits. Genotypic coefficient of variation, heritability and expected genetic advance showed a considerable increase in the treated population for all the traits. Therefore, these traits have high selection value and can be exploited for the improvement of mungbean.

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الملخص العربي

موهد رافيق واني و ساميولاه خان

معمل الطفرات الوراثية - قسم علم النبات - جامعة الجاره الاسلامية - الجاره - الهند

أثبتت الدراسة زيادة معنوية في القيم الوسطية لعدد الأفرع، عدد القرون وإنتاجية البذور في طفرات أحد أنواع نبات الفول وهو النوع فيجانا راديانا والذي يعتبر من الأنواع ذاتية التلقيح. أيضا لوحظ أن هناك زيادة معنوية في العناصر والتباين الوراثي في النبات وإنتاجيته بالمقارنة بالمجموعة الضابطة. أوضحت الدراسة أن هذه الزيادة في الاختلافات الوراثية في هذه الطفرات سوف يكون لها مردود كبير في عمليات الانتخاب المستقبلية لهذا النوع.