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Variability studies on M₃ Population of Soybean (*Glycine max* L. Merill.)

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ABSTRACT: An experiment was conducted focussing on creation of variability in soybean crop. Three soybean genotypes were evaluated for variability induced by gamma rays and EMS mutagens for yield and vield attributing traits. Population generated from treatments with four doses of gamma rays and three concentrations of EMS along with control laid into randomized complete block design with three replications for evaluation. The experimental findings revealed that EMS had more pronounced effect in inducing the variability as compared to gamma rays. The higher estimates of GCV, PCV, heritability and GA as per cent mean was recorded by 0.2 per cent EMS treatment for most of the characters like plant height, number of pods per plant, 100 seed weight and seed yield per plant particularly in Soybean genotype TAMS 38 and RSC 10-46, whereas days to 50 % flowering, number of branches per plant, days to maturity, number of seeds per pod, oil content and protein content showed low to moderate magnitude of variability parameters in all soybean genotypes.

Keywords: EMS, Gamma rays, GCV, PCV, Soybean, Variability.

INTRODUCTION

The Soybean (Glycine max (L.) Merrill.) is one of the most important oilseed crops not only in India but in the entire world. Soybean belongs to genus Glycine willd., which is family Leguminoseae, а subfamily Papilionoideae, and tribe Phaseoleae. There are two subgenera of soybeans, Glycine (perennials) and Soja (Moench) F.J. Herm. (annuals). The cultivated soybean-Glycine max and the wild annual soybean-G. soja, comes under subgenus Soja. (Hymowitz, 2004). Cultivated soybean (Glycine max (L.) Merr.) was domesticated by humans from wild soybean G. soja. Glycine max and Glycine soja are cross compatible since both has 20 chromosomes (2n = 40). The primary center of origin of soybean is China.

'Soybean'- A 21st century crop, rich in oil and protein content with versatile nutritional values gaining great importance and popularity among the farmers and in agriculture base industries. This crop also plays important role in Indian economy with export of DOC, oil industries and use in different agricultural commodities. The ease in cultivation and management of soybean crop is another reason for popularity and hence the area under cultivation of this crop is increasing day by day. In India, though the area under cultivation is increasing, the productivity is much less than world's average productivity and major reason is narrow genetic base and limited variability present in the crop. In self-pollinated crops like soybean, artificial induction of variability through mutagenesis is best Patil et al.,

alternative as against the traditional method. Among the various mutagens, gamma rays and ethyl methane sulphonate (EMS) found more effective in inducing variability in crop plants (Khatri et al., 2005). Hence, the present investigation was planned with inducing variability with physical (gamma rays) and chemical (EMS) mutagen and study the effect of these two mutagens on yield and yield contributing characters in M₃ population.

MATERIAL AND METHODS

During M₂ generation after careful screening of individual plants fifteen normal looking healthy plants were harvested from four mutagenic population of gamma rays (viz. 150, 200, 250 and 300 Gy) and three mutagenic population of ethyl methane sulphonate (0.1%, 0.15% and 0.2%) of three soybean genotypes viz. TAMS 38, AMS 1001 and RSC 10-46. These fifteen plants from each mutagenic treatments were threshed separately and advanced to M₃ generation.

The experiment was carried out on the farm of Regional Research Centre (Dr. PDKV) Amravati (MS) during kharif, 2022. The seeds harvested for fifteen selected plants from mutagenic population were sown in randomized complete block design along with respective control in three replications. The observations were recorded on randomly selected plants in each mutagenic population for ten yield and yield attributing traits viz. days to 50% flowering, plant height (cm), number of branches per plant, number of pods per plant,

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number of seeds per pod, days to maturity, 100 seed weight (g), seed yield per plant (g), oil content (%) and protein content (%). Standard method of analysis of variance for randomized block design (Panse and Sukhatme 1969) was followed and data was subjected to variability analysis for estimates of different parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) (h²) and genetic advance as per cent mean (GAM).

RESULTS AND DISCUSSION

The analysis of variance (Table 1) performed showed that mutagenic population of soybean genotypes TAMS 38, AMS 1001 and RSC 10-46 and respective control differed significantly among themselves for various characters under study indicating the significant effect of gamma rays and ethyl methane sulphonate.

The data recorded in M3 generation on ten yield and yield contributing traits along with oil and protein content was statistically analysed for determination of different variability parameters viz. mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h²) (broad sense) and genetic advance as per cent of mean (GAM). The treatment means were found to be significantly deviated from control mean in all mutagenic treatments of all population. The effect of gamma rays and EMS in positive as well as negative direction was observed for all the characters except days to 50% flowering in RSC 10-46, number of branches plant⁻¹ in TAMS 38 and AMS 1001, days to maturity in AMS 1001 and RSC 10-46 where only positive shift over control was gained. Deviation in mean from control treatment was also reported by Dhanavel et al. (2012); Gobinath and Pavadai (2015).

The wider range induced by the effect of different dose/concentration of gamma rays and EMS against the respective control population was also noticed for almost all traits in M_3 population of three soybean genotypes. Wider range in positive direction implies greater scope of improvement through selection. These results are in close agreement with findings of Khan and Tyagi (2010); Geeta and Wakode (2011).

The success of any crop improvement initiative is mostly determined by the level of genetic diversity and heritability present in the source material. The genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV), which give information on the relative amount of variation in various traits, are used to quantify the extent of variability. Therefore, an analytical evaluation of metrical components is required in order to acquire a clear understanding. Heritability information by itself may not be helpful in identifying the qualities that are being selected because heritability is also impacted by environment. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson *et al.*, 1955).

In present investigation, the estimated value of phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the **Patil** et al. **Biological Forum – An International Jou**

traits, indicating that variation is not only due to genotype but also due to environmental influence. Similar result was also reported by Shakthi et al. (2021). The magnitude of genotypic coefficient of variation and phenotypic coefficient variation was found low for days to 50% flowering, days to maturity, oil content and protein content, it was low to moderate for number of branches plant⁻¹, number of seeds per pod⁻¹ and 100 seed weight whereas moderate to high values were recorded for Plant height, number of pods plant⁻¹ and seed yield plant⁻¹ in all M₃ population (Table 2). The low estimates of variability parameters implies that there is influence of environmental factors and selection may not be effective for the same. Privanka et al. (2021); Patel et al. (2014); Bhuiyan et al. (2021) also reported low variability estimates for different polygenic characters in crop plants whereas low to moderate estimates were earlier reported by Raina et al. (2022).

Transmission of character from parent to offspring can be predicted through estimates of heritability and high heritability values infers low environmental influence having ample scope for improvement through selection on the basis of per se performance, but the selection on the basis of heritability accompanied with genetic advance as per cent mean will be more rewarding in complex traits.

In present study, high heritability coupled with high genetic advance as per cent mean was exhibited by plant height, number of branches plant⁻¹, number of pods plant⁻¹, number of seeds per pod⁻¹, 100 seed weight and seed yield plant⁻¹, moderate to high heritability with moderate GAM was observed for days to 50% flowering and oil content whereas low magnitude of GAM was for days to maturity and protein content in almost all mutagenic treatment (Table 1). According to Singh and Narayanan (2002), high heritability coupled with high genetic advance is indicative of the fact that the heritability is most likely the result of additive gene effects and that selection may be successful. Geetha Patil and Wakode (2011); Nang Htwe Kham et al. (2015); Sofia (2020); Chaturvedi et al. (2021) earlier also found the highe heritability with high GAM for quantitative traits which support the findings of present study.

In M_3 generation, as regards to mutagens, ethyl methane sulphonate has produced comparatively more variability by exhibiting high estimates of variability in most of the traits particularly in soybean genotype TAMS 38 and RSC 10-46 (Table 3). Nawale (2004); Bolbhat and Dhumal (2012) also reported that chemical mutagen was more effective in inducing variability.

As shown in Table 4, 0.2 per cent EMS treatments induced higher magnitude of GCV, PCV, heritability and GA as per cent mean in major polygenic traits as compared to other mutagenic treatments particularly in soybean genotype TAMS 38 and RSC 10-46. Accumulation of favourable genes with additive effects may results in high estimates of variability parameters in particular mutagenic treatment. Sapna Rajderkar (2021), also reported similar results in soybean.

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Table 1: Analysis of variance for ten quantitative characters of M₃ population of three soybean genotypes.

	Mean sum of squares				
Sr. No.	Source of variation	Replication	Treatment	Error	
	Degrees of freedom	2	23	46	
1.	Days to 50% flowering	0.491	7.715**	0.182	
2.	Plant height (cm)	1.710	90.755**	0.660	
3.	Number of branches plant ⁻¹	0.010	1.279**	0.004	
4.	Number of pods plant ⁻¹	3.420	214.683**	5.687	
5.	Number of seeds pod ⁻¹	0.006	0.077**	0.002	
6.	Days to maturity	0.702	19.371**	0.327	
7.	100 seed weight (g)	0.025	0.919**	0.028	
8.	Seed yield per plant (g)	0.020	14.686**	0.091	
9.	Oil content (%)	0.074	1.023**	0.040	
10.	Protein content (%)	0.242	0.752**	0.137	

Table 2: Variability estimates for different characters in all three soybean genotypes.

Sr. No.	Character	Range	Mean	GCV and PCV	\mathbf{h}^2	GAM
1.	Days to 50% flowering	Deviated from control	Wide	Low	Moderate to high	Moderate
2.	Plant height (cm)	Deviated from control	Wide	High	High	High
3.	Number of branches plant ⁻¹	Deviated from control	Wide	Low to high	High	High
4.	Number of pods plant ⁻¹	Deviated from control	Wide	High	High	High
5.	Number of seeds pod ⁻¹	Deviated from control	Wide	Low to moderate	High	High
6.	Days to maturity	Deviated from control	Wide	Low	Moderate to high	Low
7.	100 seed weight (g)	Deviated from control	Wide	Moderate to high	High	High
8.	Seed yield plant ⁻¹ (g)	Deviated from control	Wide	High	High	High
9.	Oil Content (%)	Deviated from control	Wide	Low	Moderate to high	Low to moderate
10.	Protein Content (%)	Deviated from control	Wide	Low	High	High

Table 3: Characters showing high estimates of variability parameters due to mutagenic treatments in M₃ generation of soybean.

Mutagens	Gamma rays	EMS	
Genotypes	s Characters showing high estimates of variability parameters		
TAMS 38	Days to 50% flowering, Number of branches plant ⁻¹ and days to maturity	Plant height, number of pods plant ⁻¹ , number of seeds pod ⁻¹ ,100 seed weight, seed yield plant ⁻¹ , oil content and protein content	
AMS 1001	Days to 50% flowering, Plant height, number of pods plant ⁻¹ , days to maturity,100 seed weight and oil content	Number of branches plant ⁻¹ , number of pods plant ⁻¹ , seed yield plant ⁻¹ and protein content	
RSC 10-46	Number of branches plant ⁻¹ , number of seeds pod ⁻¹ and days to maturity,	Days to 50% flowering, Plant height, number of pods plant ⁻¹ , 100 seed weight, seed yield plant ⁻¹ , oil content and protein content	

Table 4: Mutagenic treatment showing higher estimates of variability parameters for different characters in three soybean genotypes during M3 generation.

Sr. No.	Characters	TAMS 38	AMS 1001	RSC 10-46
1.	Days to 50% flowering	200 Gy Gamma rays	300 Gy Gamma rays	0.2 % EMS
2.	Plant height (cm)	0.2 % EMS	300 Gy Gamma rays	0.2 % EMS
3.	Number of branches plant ⁻¹	150 Gy Gamma rays	0.1 % EMS	200 Gy Gamma rays
4.	Number of pods plant ⁻¹	0.2 % EMS	0.15 % & 0.2 % EMS	0.2 % EMS
5.	Number of seeds pod ⁻¹	0.15 % EMS	200 Gy Gamma rays	300 Gy Gamma rays
6.	Days to maturity	150 Gy Gamma rays	300 Gy Gamma rays	300 Gy Gamma rays
7.	100 seed weight (g)	0.2 % EMS	250 Gy Gamma rays	0.2 % EMS
8.	Seed yield plant ⁻¹ (g)	0.2 % EMS	0.2 % EMS	0.2 % EMS
9.	Oil Content (%)	0.2 % EMS	300 Gy Gamma rays	0.2 % EMS
10.	Protein Content (%)	0.2 % EMS	0.15 % EMS	0.2 % EMS

CONCLUSIONS

Ethyl methane sulphonate mutagen found effective in inducing variability and in characters showing high estimates of variability simple selection may be rewarding.

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