

GENETIC STUDIES IN M₄ POPULATION OF SOYBEAN CULTIVAR TAMS-38

Ritik D. Bisane¹, Sandeep R. Kamdi², Rajesh D. Deotale³, Milind P. Meshram⁴, Shanti R. Patil⁵,
Vasant S. Pawar⁶ and Pradnya P. Bambodkar⁷

ABSTRACT

Mutation breeding is an effective approach in improvement of the crop having a narrow genetic base such as soybean by creating variability. Therefore, the present study was conducted with an objective to estimate between and within a family variation, estimate genetic parameters and identify superior mutants for further utilization. In *kharif* 2017, 104 mutants identified in M₃ generation were evaluated along with two checks (TAMS-38 and JS-335) in M₄ generation in two replications at the experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. Data were recorded on yield and yield contributing traits. Analysis of variance indicated that the mean square due to between family were highly significant for all traits revealed the presence of significant genetic variability between the families. In the present investigation, high PCV and GCV and high to moderate heritability coupled with high genetic advance as a percentage of mean were observed in seed yield plant⁻¹, number of pods plant⁻¹, 100 seed weight, plant height and days to maturity. This indicates the minimum influence of environment in the expression of these traits and prevalence of additive gene action in their inheritance. Hence, these traits are amenable for simple selection. Thus, 141 mutants were selected from TAMS-38 variety treated with different doses of gamma rays (T₁= 200 Gy, T₂= 250 Gy and T₃= 300 Gy). Due to the predominance of additive gene action for yield and yield component, those individual plants from 41 families selected in M₄ generation were suggested to be raised in progeny rows for one more generation so as to attain homozygosity.

(Key words: Soybean, gamma rays, variability, heritability, genetic advance as percentage of mean, M₄ mutants)

INTRODUCTION

Soybean (*Glycine max* L.) possess a very high nutritional value. Soybean is the world's foremost provider of protein and oil (Nagarajan *et al.*, 2017). It contains about 20 % oil and 40% protein. Soybean protein is rich in valuable amino acid lysine (5%) in which most of the cereals are deficient (Pavadai *et al.*, 2010).

It is referred to "the miracle golden bean" as well as "the protein hope of the future" because of its high nutritive value as it is a good source of unsaturated fatty acids, minerals like calcium and phosphorus including vitamin A, B, C and D thus, it can meet up various nutritional needs. Being an important source of raw materials for various industries, soybean plays a very important role in changing the scenario of the industrial sector. Cultivated soybean one of the major crop is used for human foods and animal feed. Hence, the development of high yielding varieties specific to a particular eco-geographic situation is of paramount importance (Nagarajan *et al.*, 2017).

But soybean being predominantly self-fertilized, inherent variability in this crop may not be sufficient to develop new varieties possessing different desirable characters. The absence of stable male sterile lines and vulnerability of their flowers to artificial manipulation renders production of large-scale variability through hybridization and intermating a laborious exercise. Due to lack of sufficient nature variability for yield and its component traits in soybean, conventional methods of breeding have limited scope. Induction of mutation into this cultivar and creation of variability would be a better source for the selection of desirable mutants for yield and yield contributing characters. The cultivar TAMS-38 was for the study because this cultivar is recommended as high yielding, better adoptable into the area of Vidarbha. The assessment of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h₂) and genetic advance (GA%) is a pre-requisite criterion for effective selection. Hence, the important objective in soybean improvement is oriented to develop varieties which have high yielding potential.

1, 6 and 7. P.G. Students, Botany Section, College of Agriculture, Nagpur

2, 4 and 5. Asstt. Professors, Botany Section, College of Agriculture, Nagpur

3. Professor, Botany Section, College of Agriculture, Nagpur

MATERIALS AND METHODS

Four different lots of dry, healthy and genetically pure seeds of TAMS-38 were made and each lot consists of 500 g seed weight. These seeds were treated by three different doses of gamma rays i.e. 200 Gy, 250 Gy and 300 Gy (Co^{60} at BARC Trombay, Mumbai) and used for raising M_1 during *kharif* 2016 and individual plants in each treatment were harvested separately. The harvested seeds were used to raise M_2 generation in *rabi* 2016 and mutants were selected for various morphological and yield traits. M_3 generation were raised in *kharif* 2017 for studying their behaviour. The present work is the continuation of the above-mentioned work. In *kharif* 2018-19 all the harvested seeds from each selected (104) mutants of M_3 generation along with 2 checks (TAMS-38 and JS-335) were sown to raise M_4 generation in replicated trial using Randomized Block Design replicated twice. Plot size was 1.8×2 Sq. mt. Three rows were allotted for each mutant and check with 20 plants row⁻¹. The row to row distance was 60 cm and plant to plant distance 10 cm respectively. The sowing was undertaken on the fertile and well levelled piece of land at research farm, Botany section, College of Agriculture, Nagpur. Twenty plants in checks and mutant lines were randomly selected in each replication and observations were recorded for germination percentage, days to first flower, days to maturity, plant height (cm), number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight (g) and seed yield plant⁻¹(g). The data recorded during M_4 generation were subjected to the statistical analysis i.e., mean, range, genotypic variance, phenotypic variance, heritability (broad sense) (Hanson *et al.* 1956), genotypic coefficient of variation (%), phenotypic coefficient of variation (%) (Burton and Devane, 1953), genetic advance (GA) (Robinson *et al.*, 1949), genetic advance as percentage of mean (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

The data regarding analysis of variance of 104 mutant families and two genotypes as check with respect to 8 quantitative characters are presented in table 1. Analysis of variance indicated significant difference between families. The data on the analysis of variance revealed that the mean sum of squares due to mutants was highly significant for all the characters studied indicated the presence of variability among the experimental materials for germination percentage, days to first flower, days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹. This indicated the presence of significant genetic variability between the families for all eight characters. This allowed further estimation of genetic parameters. Pavadai *et al.* (2010), Malek *et al.* (2014), Kumar *et al.* (2017) and Li *et al.* (2017) were reported significant variability between the families in soybean.

The intra class correlation (t) estimated in M_4 generation ranged from 0.339 for number of branches

plant⁻¹ to 0.769 for germination percentage. Highest intra class correlation value was observed for germination percentage (0.769) followed by seed yield plant⁻¹ (0.471), number of pods plant⁻¹ (0.414), days to maturity (0.411), plant height (0.405), 100 seed weight (0.375), days to first flower (0.360) and number of branches plant⁻¹ (0.339). This revealed that 76.9%, 47.1%, 41.4%, 41.1%, 40.5%, 37.5%, 36.0% and 33.9% of variation for germination percentage, seed yield plant⁻¹, number of pods plant⁻¹, days to maturity, plant height, 100 seed weight, days to first flower and number of branches plant⁻¹ respectively were due to differences between the mutant families and 23.1%, 52.9%, 58.6%, 58.9%, 59.5%, 62.5%, 64% and 66.1% were due to within families. This indicated that family distinctly differentiated from others and differences between individuals within a family were also large for all characters except germination percentage as obtained from 't' estimated. Therefore, equal importance was suggested to be assigned to σ^2_f (variance between families) and σ^2_w (variance within families) in this generation. This indicates that between family selection followed by within family selection will be more rewarding in M_4 generation.

Data regarding estimates of genetic parameters in M_4 generation for eight characters are presented in table 2. Significant differences were observed between the progenies for all the eight characters studied. The coefficient of variation (CV) ranged from 13.27 to 49.40% for various characters (Table 2). The lowest coefficient of variation (≤ 20) was observed for the character germination percentage (13.27) which showed the best genetic potential and its genetic influence. The high coefficient of variation was observed for seed yield plant⁻¹ (49.40), number of pods plant⁻¹ (45.83), number of branches plant⁻¹ (37.96), plant height (33.52), 100 seed weight (33.48), days to maturity (29.67) and days to first flower (27.77) which indicates more influence of environmental fluctuation. Pavadai *et al.* (2010), Malek *et al.* (2014) and Nagarajan *et al.* (2017) also observed high CV and the influence of environment on yield and yield component in soybean.

The estimates of genotypic and phenotypic coefficient of variation are necessary to understand the role of environmental influence on different traits. The estimates of genotypic coefficient of variation were lesser than the estimates of phenotypic coefficient of variation indicating the environmental influence over the characters studied. Genotypic coefficient of variation exhibited high category for all the characters studied. The high GCV and PCV were observed for seed yield plant⁻¹, number of pods plant⁻¹, plant height, number of branches plant⁻¹, 100 seed weight, days to maturity, germination percentage and days to first flower. High genotypic coefficient of variation and phenotypic coefficient of variation were reported by Malek *et al.* (2014) and Nagarajan *et al.* (2017) in soybean for plant height, number of pods plant⁻¹ and seed yield plant⁻¹, Kumar *et al.* (2017) for number of pods plant⁻¹ and seed yield plant⁻¹, Malek *et al.* (2014) for plant height, Khan and Goyal (2009b) in soybean for days to first flower, Chandra

Table 1. Analysis of variance for different characters in M_4 generation

Sources of variation	df	Mean sum of squares							
		Germination (%)	Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g) plant ⁻¹	Seed yield plant ⁻¹
Between families	105	544.71**	2988.60**	22191.03**	2436.83**	25.43**	12188.29**	213.95**	568.99**
Within families	4134	71.22	127.21	767.20	86.41	1.18	416.80	8.55	15.53
Intra class correlation (t)		0.769	0.360	0.411	0.405	0.339	0.414	0.375	0.471

** Significant at 1% level * Significant at 5% level

Table 2. Genetic parameters estimate for different characters in M_4 generation

Parameters	Germination (%)	Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹
Mean	63.61	40.61	93.36	27.73	2.86	44.54	8.73	7.97
Range	25.50-90.50	35.00-46.90	85.80-102.20	19.14-43.85	2.00-3.78	17.80-87.20	6.50-11.35	2.07-16.71
SE _(m) ±	5.97	7.98	19.59	6.57	0.77	14.44	2.07	2.79
CD (5 %)	16.54	22.11	54.29	18.22	2.13	40.01	5.73	7.73
CV (%)	13.27	27.77	29.67	33.52	37.96	45.83	33.48	49.40
GCV (%)	24.19	20.83	24.79	27.64	27.20	38.51	25.94	46.63
PCV (%)	27.59	34.71	38.66	43.45	46.69	59.86	42.35	67.93
h ² (%)	76.87	35.99	41.11	40.47	33.92	41.38	37.51	47.12
GA	24.36	6.27	19.59	6.39	0.54	14.62	1.75	3.61
GAM	38.30	15.44	20.99	23.05	19.00	32.83	20.04	45.26

Table 3. Superior mutants selected in M₄ generation

Sr. No.	Individual plant selected in M ₄	Seed yield plant ⁻¹	No. of yield plant ⁻¹	100 seed weight (g)	Days to maturity	Sr. No.	Individual plant selected in M ₄	Seed yield plant ⁻¹	No. of yield plant ⁻¹	100 seed weight (g)	Days to maturity
1	T ₁ /14/1/1	18.7	90	9.1	96	42	T ₂ /18/2/24	17.9	95	10.6	90
2	T ₁ /14/1/3	27.7	145	11.0	96	43	T ₂ /18/15/3	15.7	55	13.2	88
3	T ₁ /14/1/4	18.3	93	9.2	96	44	T ₂ /18/15/4	14.2	70	13.2	88
4	T ₁ /14/1/33	13.8	61	8.5	97	45	T ₂ /18/15/32	18.3	52	11.7	88
5	T ₁ /14/1/34	14.1	90	8.7	97	46	T ₂ /19/2/1	12.3	52	11.2	89
6	T ₁ /14/2/2	19.7	120	9.1	93	47	T ₂ /19/3/21	12.5	125	8.5	95
7	T ₁ /14/2/4	13.9	102	9.2	92	48	T ₂ /19/3/22	9.3	120	8.2	95
8	T ₁ /14/2/6	19.7	130	11.0	93	49	T ₂ /19/5/21	21.4	104	8.2	96
9	T ₁ /14/2/24	23.5	106	8.1	91	50	T ₂ /19/5/31	16.4	90	8.5	97
10	T ₁ /14/2/32	15.5	66	12.3	91	51	T ₂ /19/5/33	16.5	91	9.5	95
11	T ₁ /14/7/5	22.0	102	12.8	94	52	T ₂ /19/13/1	21.5	96	8.2	93
12	T ₁ /14/7/24	19.9	80	10.1	95	53	T ₂ /19/13/2	19.8	119	7.9	94
13	T ₁ /14/7/25	10.2	42	8.7	94	54	T ₂ /19/13/25	20.0	93	9.5	92
14	T ₁ /14/8/1	12.5	68	9.9	94	55	T ₂ /20/1/2	21.2	89	8.5	90
15	T ₁ /14/8/5	11.5	92	7.5	94	56	T ₂ /20/1/5	21.8	105	8.8	90
16	T ₁ /14/9/3	14.9	93	11.1	92	57	T ₂ /20/1/9	21.2	94	8.5	90
17	T ₁ /14/9/6	12.6	90	7.9	91	58	T ₂ /20/1/21	23.9	118	7.9	91
18	T ₁ /14/9/8	13.3	88	11	95	59	T ₂ /20/1/24	21.1	106	8.5	91
19	T ₁ /14/10/2	18.4	78	13	93	60	T ₂ /20/5/1	20.0	106	10	90
20	T ₁ /14/10/3	16.2	110	8.1	92	61	T ₂ /20/5/2	22.1	95	8.5	91
21	T ₁ /14/10/4	17.9	75	9	93	62	T ₂ /20/5/3	18.0	113	8.1	90
22	T ₁ /14/10/7	12.1	85	7.6	93	63	T ₂ /20/5/6	26.1	100	7.5	89
23	T ₁ /14/10/27	13.3	90	8.5	90	64	T ₂ /20/5/21	24.2	111	11	90
24	T ₁ /14/2/21	13.2	89	13	90	65	T ₂ /20/5/22	22.3	124	10	91
25	T ₁ /14/1/1	16.6	100	11.4	90	66	T ₂ /20/5/23	20.3	101	9.5	90
26	T ₁ /14/1/2	19.2	83	9.2	92	67	T ₂ /20/8/21	24.6	171	9.4	94
27	T ₁ /14/1/3	15.5	91	10	92	68	T ₂ /20/8/23	19.4	102	8.5	93
28	T ₁ /14/1/4	23.5	123	10	89	69	T ₂ /20/8/24	20.0	120	10	95
29	T ₁ /14/1/21	17.5	81	8.5	92	70	T ₂ /20/8/26	21.4	113	8.4	94
30	T ₂ /5/1/4	20.6	72	9.5	86	71	T ₂ /21/9/32	16.5	40	6.9	90
31	T ₂ /5/1/25	21.6	83	9.7	87	72	T ₂ /21/10/1	13.9	60	8.3	94
32	T ₂ /5/4/2	13.7	90	9.0	89	73	T ₂ /21/11/1	17.1	97	8.3	92
33	T ₂ /5/4/24	14.8	92	9.1	89	74	T ₂ /21/11/3	18.7	96	10	93
34	T ₂ /5/5/1	23.5	132	13.1	91	75	T ₂ /21/11/29	21.1	97	9.5	92
35	T ₂ /5/5/3	21.2	89	8.6	91	76	T ₂ /5/2/9	16.1	86	9.4	92
36	T ₂ /5/5/26	22.7	101	8.3	89	77	T ₂ /5/2/11	16.7	83	10	92
37	T ₂ /5/5/27	18.7	100	8.2	89	78	T ₂ /5/2/21	16.4	106	9.4	91
38	T ₂ /18/2/2	23.3	92	9.3	89	79	T ₂ /5/2/25	27.8	97	12.1	93
39	T ₂ /18/2/4	21.9	115	11.8	90	80	T ₂ /5/3/21	17.5	85	9	91
40	T ₂ /18/2/22	17.8	122	11.8	91	81	T ₂ /5/3/22	15.4	71	8	90
41	T ₂ /18/2/23	24.6	124	11.8	90	82	T ₂ /5/4/1	19.1	102	10	90

contd...

Sr. No.	Individual plant selected in M_1	Seed yield plant ⁻¹	No. of yield plant ⁻¹	100 seed weight (g)	Days to maturity	Sr. No.	Individual plant selected in M_1	Seed yield plant ⁻¹	No. of yield plant ⁻¹	100 seed weight (g)	Days to maturity
83	T ₂ /5/4/3	20.8	103	12	96	116	T ₂ /19/3/22	17.3	91	10.6	92
84	T ₂ /5/4/24	21.1	98	9	91	117	T ₂ /19/3/27	17.2	91	10.5	92
85	T ₂ /5/4/26	20.0	77	10.1	91	118	T ₂ /20/1/1	14.2	131	9.3	97
86	T ₂ /5/5/1	10.6	66	8.5	90	119	T ₂ /20/1/2	11.1	110	11.8	97
87	T ₂ /5/5/21	10.4	73	10.1	89	120	T ₂ /20/1/3	13.3	95	10.6	97
88	T ₂ /5/5/22	15.3	70	9.1	90	121	T ₂ /20/1/4	13.8	100	10.2	98
89	T ₂ /18/2/1	16.1	93	10.1	100	122	T ₂ /20/1/21	18.0	100	11.7	97
90	T ₂ /18/2/2	12.2	77	11.1	100	123	T ₂ /20/1/22	17.4	79	8.8	98
91	T ₂ /18/2/21	19.6	99	9.2	102	124	T ₂ /20/1/23	14.8	85	9.4	98
92	T ₂ /20/2/2	9.1	77	8.1	101	125	T ₂ /20/1/24	17.6	83	8.2	98
93	T ₂ /20/2/4	8.2	54	7.5	102	126	T ₂ /20/6/1	15.6	81	9.5	93
94	T ₂ /20/4/5	23.1	108	11.1	98	127	T ₂ /20/6/2	20.3	132	9.1	92
95	T ₂ /20/4/17	20.1	74	13.5	97	128	T ₂ /20/6/3	18.2	112	8.5	93
96	T ₂ /20/12/1	10.8	92	7.1	95	129	T ₂ /20/6/21	13.0	90	8.1	93
97	T ₂ /20/12/21	10.6	96	7.5	95	130	T ₂ /20/6/23	19.5	96	10.2	93
98	T ₂ /21/15/3	10.8	89	8.1	87	131	T ₂ /21/1/1	23.1	135	9.5	91
99	T ₂ /21/15/21	7.8	67	7.2	88	132	T ₂ /21/1/22	22.1	102	10.1	91
100	T ₂ /18/1/1	12.5	84	11.1	98	133	T ₂ /21/1/23	18.1	120	10.5	90
101	T ₂ /18/1/6	11.8	84	11.4	98	134	T ₂ /24/1/1	24.6	95	11.1	105
102	T ₂ /18/2/2	15.7	93	12.1	98	135	T ₂ /24/1/2	17.7	64	10.2	105
103	T ₂ /18/2/11	16.2	74	8.6	98	136	T ₂ /24/1/3	17.9	64	10.9	102
104	T ₂ /18/2/21	18.3	87	12.2	98	137	T ₂ /24/1/6	18.8	72	9.5	101
105	T ₂ /18/2/22	17.9	104	11.1	98	138	T ₂ /24/1/22	13.7	111	9.2	102
106	T ₂ /18/10/2	14.1	81	11.1	95	139	T ₂ /24/1/24	15.1	108	10.1	102
107	T ₂ /18/10/3	18.6	82	8.2	95	140	T ₂ /24/1/25	14.3	106	11.1	102
108	T ₂ /18/10/27	13.1	78	8.2	96	141	T ₂ /24/1/27	14.2	141	10.1	101
109	T ₂ /19/2/19	22.9	73	11.1	97	142	T ₂ /24/1/28	22.4	120	9.9	102
110	T ₂ /19/3/1	15.6	89	9.3	90	143	T ₂ /24/1/31	14.2	97	9.5	101
111	T ₂ /19/3/2	16	95	9.5	91	144	T ₂ /24/1/32	18.1	82	9.2	101
112	T ₂ /19/3/3	17.7	79	11	92	145	TAMS-38 (c)	12.2	65	8.2	95
113	T ₂ /19/3/4	17.2	89	10	92	146	JS-335 (c)	14.1	64	9.0	96
114	T ₂ /19/3/6	15.6	83	8.5	91						
115	T ₂ /19/3/21	16.4	79	11.5	92						
						Total-144					

C : check

et al. (2015) in chickpea for 100 seed weight, Malek *et al.* (2014) in soybean for branches plant⁻¹ and Zuge *et al.* (2017) in soybean for days to maturity.

The coefficient of variation indicates only the extent of variability existing for various characters but does not give any information regarding the heritable proportion of it. Hence, the amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified phenotypically. In the present study, broad sense heritability, which includes both additive and non-additive gene effects (Hanson *et al.*, 1956), was estimated.

High heritability was recorded for germination percentage (76.87%). Moderate heritability was observed for seed yield plant⁻¹, number of pod plant⁻¹, days to maturity, plant height, 100 seed weight, days to first flower and number of branches plant⁻¹. High to moderate estimate of heritability for the above traits suggested less influence of environmental factor in the expression for these traits. Pavadai *et al.* (2010), Nagarajan *et al.* (2017) and Kumar *et al.* (2017) were reported high to moderate heritability for yield and yield components in soybean.

Genetic advance as a percentage of mean were moderate to high for all the characters under the present study. Genetic advance as a percentage of mean were high for seed yield plant⁻¹, germination percentage, number of pods plant⁻¹, plant height, days to maturity and 100 seed weight. High genetic advance as a percentage of mean were reported in soybean by Malek *et al.* (2014), Nagarajan *et al.* (2017) and Kumar *et al.* (2017) for number of pods plant⁻¹ and seed yield plant⁻¹, Malek *et al.* (2014) for plant height, Khan and Goyal (2009b) for days to maturity and by Malek *et al.* (2014), Nagarajan *et al.* (2017) and Kumar *et al.* (2017) for 100 seed weight. Moderate genetic advance as per cent of mean was recorded for days to first flower and number of branches plant⁻¹. Malek *et al.* (2014) was reported moderate genetic advance as a percentage of mean for days to first flower and for number of branches plant⁻¹ by Pavadai *et al.* (2010), Nagarajan *et al.* (2017) and Kumar *et al.* (2017) in soybean.

Selection for seed yield in soybean based on single character may not be effective. On the other hand, it is very cumbersome process for a breeder to involve a large number of component characters simultaneously in the selection programme hence, knowledge of major yield components is necessary for involving effective selection criteria. In the present study only five characters *viz.*, seed yield plant⁻¹, number of pods plant⁻¹, 100 seed weight, plant height and days to maturity which showed high GCV, high to moderate heritability and high genetic advance as percentage of mean were considered for selection in M₄ generation. This revealed that the above mentioned five characters were influenced by additive gene action and selection would be effective in improving these traits, hence were considered as criteria for selection in this study.

Between family variance, within family variance and intra class correlation (t) when considered, revealed that δ^2_f and δ^2_w should be given equal weightage for characters *viz.*, seed yield plant⁻¹, number of pods plant⁻¹, 100 seed weight, plant height and days to maturity. Therefore, selections of superior families followed by the selection of individual plants in selected families were considered as the criteria of selection. Based on these criteria out of 104 M₄ mutants families, 144 individual plants were selected from 41 families (Table 3.). In this study as additive gene action was found to be predominant for yield and yield components, it is suggested that the selected 144 individual plants from M₄ generation should be raised in progeny rows for one more generation so that homozygosity will be attained and superior progenies can be then selected for forwarding to yield traits in the next generation.

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