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SELECTION OF DESIRABLE MUTANTS IN M_3 GENERATION OF SOYBEAN

G. A. Kankal[1], S. K. Dhapke[2], Shubhangi K. Maraskole[3], Shanti R. Patil[4], D. Y. Upadhyay[5], S. R. Kamdi[6] and

A. V. Navghare[7]

ABSTRACT

An experiment was conducted at experimental farm of Agricultural Botany, College of Agriculture, Nagpur during *kharif* 2017 in M_3 generation with the objectives to estimate genetic parameters and identify superior mutants for further utilization. 62 mutants identified in M_2 generation along with two checks (TAMS-38 and JS-335) were evaluated in M_3 generation in replicated trial with three replications of which only 20 survived and data were recorded on nine traits i.e. germination percentage, mortality percentage, days to flowering, days to maturity, plant height, number of branches plant^{-1}, number of pods plant^{-1}, 100 seed weight and grain yield plant^{-1}. Analysis of variance indicated that the mean square due to between family were highly significant for all traits, revealing the presence of significant genetic variability between the families. Intra class correlation (t) lead to the conclusion that differences between individuals within family is large and each family differentiated distinctly from the other one at lower level in M_3 generation hence, equal weightage to ó^{2}f and ó^{2}w were considered for selection in $M_{3.}$ generation. Selection of superior families followed by selection of individual plants in selected families were considered as the criteria of selection. Thus, fifty four individual plants from 11 families out of 20 mutant families were identified in M_3 generation and were suggested to be raised in progeny rows for one more generation so as to attain homozygosity.

(Key words: Variability, mutants, additive gene action)

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is referred as “Golden bean’’ and “Miracle crop” of 21th century. It is one of the important oilseed as well as legume crop. It contributes more than 50% to the global production of edible oil. Soybean contains 20% oil and 40% protein. Soy protein is rich in all essential amino acids, vitamin A, B and D; health promoting phytochemicals like isoflavones. The soy protein stand unique by supplying all sixteen essential amino acids. Soybean oil is used as an edible oil in Indian diet. It contains low level of saturated fatty acids. Therefore, soybean oil is better for human health. The worldwide increasing demand of soybean is due to its unique composition, excellent nutritional value, health beneûts, and adaptability to varied climatic conditions.

Creation of genetic variability, selection of useful genotype and comparative tests to demonstrate the superiority of selected genotypes are the main three phases of plant breeding procedures. Genetic variability in the treated population is increased primarily through induced mutation. The subsequent selection and testing procedures used in a mutation breeding programmes are same as the plant breeders follow in a hybridization programme (Gaul, 1963).

The segregating material developed through mutation breeding has to be evaluated (M_2 to M_6) till stability is reached, then the selected mutants which are superior have to be evaluated at various locations, considering the general environmental effect and evaluate their adaptability over environment. Handling of advanced generation is important, as it is the efficiency of plant breeder to decide the criteria of selection of the best mutants which have attained homozygosity with increased productivity.

Seed yield is polygenic trait and is highly depended on yield contributing characters *viz*., number of branches plant^{-1}, number of pods plant^{-1} and seed yield plant^{-1}. Seed yield is governed by variability, heritability and genetic advance expressed by such traits and correlation between parameters. Putting this view the present work was framed and was implemented for selecting the high yielding mutants in M_3 generation, with the objectives to estimate between and within family variances in M_3 generation and also to identify superior mutants for yield and yield contributing characters.

1, 3, 5 and 7. P.G. Students, Agril. Botany Section, College of Agriculture, Nagpur, India
2 and 6. Asstt. Professors & Agril. Botany Section, College of Agriculture, Nagpur, India
4. Professor (CAS), Agril. Botany Section, College of Agriculture, Nagpur, India

MATERIALS AND METHODS

Dry healthy and genetically pure seeds of TAMS-38 was used in this study. Four different lots of soybean seed cultivar TAMS-38 were made. Every lot was of 500 g seed weight. The three lots of seeds were sent to Bhabha Atomic Research Centre, Trombay, for irradiation with three different doses i.e. 200 Gy, 250 Gy, 300 Gy of gamma rays and used for raising M_1 during *kharif* 2016 and individual plant in each treatment were harvested separately. The harvested seeds were used to raise M_2 generation in *rabi* 2016 and mutants were identified.

The present work is the continuation of the above mentioned work. The 62 mutants identified in M_2 along with 2 checks (TAMS-38 and JS335) were planted in Randomised Block Design (RBD) with three replications in *kharif* 2017.

Observations on germination per cent, mortality per cent, days to flowering, 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} were recorded on each treatment. For recording germination percentage the number of seeds germinated in each treatment were counted on 12 days after sowing and the germination percentage was calculated as per the formula given below:

$$GP(\%) = \frac{\text{Number of germinated seeds}}{\text{Total number of seeds sown}} \times 100$$

For mortality percentage the number of plants which failed to survive up to flowering from the date of germination were counted and mortality percentage was calculated as per the formula given below:

$$\text{Mortality per cent} = \frac{\text{Number of plants failed to survive upto flowering}}{\text{Number of seeds germinated}} \times 100$$

The data recorded were analyzed statistically for testing the significance of between families and within families variances for all the characters as per the method given by Sharma (2006).

RESULTS AND DISCUSSION

Analysis of variance observed significance of between family and within family genetic variation. The results of this analysis are presented in table 1. The data on the analysis of variance resulted in highly significant mean square due to between family for all nine characters studied i.e. germination percentage, mortality percentage, days to flowering, 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 nine characters which allowed the estimation of genetic parameters. In accordance to this results significant variability between the families were also reported by Patil and Wakode (2011) and Pavadai *et al.* (2010) in soybean.

The intra class correlation (t) estimated in M_3 generation ranged from 0.469 for number of branches plant^{-1} to 0.922 for germination percentage. Highest intra class correlation value was observed for germination percentage (0.922) followed by mortality percentage (0.666), days to maturity (0.573), plant height (0.573), days to flowering (0.540), 100 seeds weight (0.536), seed yield plant^{-1} (0.533), number of pods plant^{-1} (0.492) and number of branches plant^{-1}, (0.469). This revealed that 92 %, 66 % 57 %, 57 %, 54 %, 53 %, 53 %, 49 % and 46 % of variation for germination percentage, mortality percentage, days to maturity, plant height, days to flowering, 100 seed weight, seed yield plant^{-1}, number of pods plant^{-1} and number of branches plant^{-1} respectively were due to differences between the mutant families and 8 %, 34 %, 43 %, 43 %, 46 %, 47 %, 47 %, 51 % and 54 % were due to within families respectively.

This indicated that differences between individuals within a family are large for all the characters but each family distinctly differentiated from other also at higher level except for germination percentage. Therefore, equal weightage was suggested to be assigned to $ó^2f$ and $ó^2w$ in this generation. This indicates that between family selection followed by within family selection will be more rewarding in M_3 generation.

Any appraisal of the breeding material permitting elimination of material of low potential is clearly advantageous because all important programme have limitations and elimination of poor material enhances the probability of finding superior segregants in remaining material (Allard, 1960). Selection for seed yield in soybean based on single characters 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 seven characters viz., seed yield plant^{-1}, number of pods plant^{-1}, number of branches plant^{-1}, 100 seed weight, plant height, days to flowering and days to maturity which showed high GCV, high / moderate heritability and high genetic advance as percentage of mean (Table 2) were considered for selection in M_3 generation. This revealed that the above mentioned seven 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, it was observed that difference between individuals within a family are large and each family is also different from the other but at higher level for all the above mentioned seven characters (seed yield plant^{-1}, number of pod plant^{-1}, number of branches plant^{-1}, 100 seed weight, plant height, days to flowering and days to maturity). Therefore, it is suggested in this study to give equal weightage to $ó^2f$ and $ó^2w$ during

Table 1. Analysis of variance for different characters in M_3 generation

Source of variation	df	Mean sum of squares								
		Germination%	Mortality%	Days to flowering	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	No. of pods plant^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)
Between families	20	1304.02**	1325.92**	15325.94**	84299.03**	13109.06**	110.30**	51398.21**	571.95**	1771.48**
Within families	1239	35.71	190.08	214.76	1032.16	161.07	2.05	868.24	8.13	25.46
Intra class correlation(t)		0.922	0.666	0.540	0.573	0.573	0.469	0.492	0.536	0.533

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

Table 2. Mean performance of 20 mutants along with checks for various characters

Sr. No.	Progeny	Germination %	Mortality %	Days to flowering	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	No. of pod plant^{-1}	100 seed weight (w)	Seed yield plant^{-1} (g)
1	T_1/1	43.78	31.63	46.37	98.00	40.06	2.25	11.68	8.61	3.13
2	T_1/2	44.04	41.09	45.66	97.77	45.77	3.44	26.22	9.24	5.17
3	T_1/3	49.58	45.23	46.00	99.33	42.00	6.00	29.33	6.33	4.56
4	T_1/14	58.83	2.08	43.59	95.83	37.76	3.43	77.78	8.74	13.04
5	T_1/16	37.53	52.77	43.00	102.0	34.00	1.00	12.00	8.00	2.65
6	T_1/22	33.33	8.33	45.20	103.6	23.80	2.80	19.20	8.38	4.32
7	T_2/2	41.50	5.88	45.17	100.1	38.75	2.83	44.79	8.06	7.27
8	T_2/5	40.50	1.96	44.67	97.26	34.03	3.74	85.05	8.25	14.26
9	T_2/6	22.70	12.50	47.00	97.00	38.50	4.00	24.50	7.90	4.20
10	T_2/7	31.83	18.52	50.25	99.25	33.50	3.00	12.00	9.05	3.55
11	T_2/8	34.64	27.78	46.20	104.0	30.00	2.00	13.50	7.70	3.15
12	T_2/18	80.00	3.50	43.30	98.24	42.80	3.00	65.28	8.55	11.93
13	T_2/19	65.95	00.00	42.54	95.81	34.92	3.56	72.15	8.16	13.97
14	T_2/20	62.35	00.00	42.27	95.82	40.12	3.75	84.17	8.70	16.33
15	T_2/21	64.73	00.00	42.58	94.96	37.45	3.58	76.88	8.16	13.80
16	T_2/22	40.42	00.00	44.07	98.27	38.60	3.46	62.53	8.98	10.87
17	T_2/23	43.05	00.00	45.04	97.66	34.75	3.29	63.83	8.27	9.64
18	T_2/24	63.29	00.00	42.19	95.51	35.70	3.42	73.29	8.64	13.31
19	T_3/8	22.29	11.11	50.00	104.0	23.00	2.00	7.00	6.80	1.20
20	T_3/11	49.63	47.78	46.00	102.0	38.33	2.66	15.67	11.23	3.40
21	JS-335	73.33	7.27	40.53	109.1	39.75	3.53	41.57	6.56	9.24
	Mean	47.77	40.25	43.19	98.27	37.95	3.40	64.45	8.24	11.83
	SE_m ±	3.45	7.96	8.46	18.55	7.33	0.83	17.01	1.65	2.91
	CD (5 %)	10.32	23.83	25.34	55.63	21.96	2.45	51.00	4.93	8.71
	CV (%)	12.51	34.25	33.92	32.69	33.44	42.01	45.72	34.59	42.64
	GCV (%)	43.04	48.34	36.74	37.91	38.71	39.45	45.03	37.18	45.59
	PCV (%)	44.82	59.24	50.00	50.06	51.15	57.63	64.17	50.78	62.43
	Heritability (%)	92.21	66.57	53.97	57.34	57.26	46.85	49.23	53.60	53.34
	G.A (per cent of mean)	81.76	66.30	40.84	44.78	45.65	38.08	45.67	41.05	50.09

Table 3. Superior mutants selected in M_3 generation

Sr.No.	Doses of Mutagon	Mutant progeny in M_2	No. of plants selected in M_3	Individual plant selected in M_3	Character of selected mutants	Seed yield plant^{-1}	No. of pods plant^{-1}	100 seed weight (g)	No. of branches plant^{-1}	Days to maturity	Plant height(cm)
1	200 Gy	T_1/3	1	T_1/3-1	Tall	5.6	40	6.4	6	104	62
2		T_1/14	7	T_1/14-1	High yield	27.6	138	11.6	5	98	42
3				T_1/14-5	Dwarf	5.4	27	7.4	3	98	25
4				T_1/14-6	Early	13.9	73	7.2	4	92	46
5				T_1/14-7	High yield & More number of pods	34.7	216	9.6	6	97	43
6				T_1/14-9	High yield & More number of pods	28.8	192	9.3	5	93	39
7				T_1/14-10	High yield	26.5	148	9.6	4	96	34
8				T_1/14-14	Dwarf	7.8	53	8.0	6	93	21
9	250 Gy	T_2/2	1	T_2/2-1	More branching	18.2	141	8.5	6	102	46
10		T_2/5	7	T_2/5-1	More branching	16.6	93	7.1	8	93	38
11				T_2/5-2	High yield & Early	35.0	187	10.4	6	92	38
12				T_2/5-3	More branching & More number of pods	34.0	217	10.6	7	92	36
13				T_2/5-4	More branching, More number of pods & High yield	39.9	236	10.6	8	92	41
14				T_2/5-5	High yield & More number of pods	35.7	212	9.4	5	102	37
15				T_2/5-6	High yield	27.1	149	9.5	4	102	40
16				T_2/5-7	Dwarf	9.9	46	9.8	4	96	22
17		T_2/18	5	T_2/18-4	Dwarf	11.4	72	8.1	3	102	22
18				T_2/18-7	High yield	25.8	112	9.0	5	97	42
19				T_2/18-10	Early	23.0	83	9.9	3	90	46
20				T_2/18-11	More branching	20.8	81	9.9	6	93	46
21				T_2/18-12	Early	13.9	52	6.5	4	91	48
22		T_2/19	11	T_2/19-1	Early	26.0	98	7.8	5	89	40
23				T_2/19-2	High yield & More branching	35.3	146	10.5	8	97	41
24				T_2/19-3	High yield	27.1	117	8.2	6	93	42
25				T_2/19-4	High yield & More branching	30.8	165	9.7	6	100	45
26				T_2/19-5	High yield	25.6	160	8.8	5	98	36
27				T_2/19-6	High yield	24.4	146	9.2	5	98	33
28				T_2/19-7	High yield	24.1	93	8.2	4	97	36
29				T_2/19-8	Early & More branching	21.3	147	7.6	6	92	33
30				T_2/19-10	Dwarf	12.4	49	9.2	4	104	23
31				T_2/19-13	More branching	27.0	123	9.3	6	97	36
32				T_2/19-14	Early	8.5	47	5.9	3	90	35

Contd.

Sr.No.	Doses of Mutagon	Mutant progeny in M_2	No. of plant selected in M_3	Individual plant selected in M_3	Character of selected mutants	Seed yield plant^{-1}	No. of pod plant^{-1}	100 seed weight (g)	No. of branches plant^{-1}	Days to maturity	Plant height(cm)
33		T_2/20	6	T_2/20-1	High yield	26.0	167	8.4	5	102	52
34				T_2/20-2	More branching	19.9	133	8.1	6	103	36
35				T_2/20-6	More branching	24.8	121	7.9	6	93	42
36				T_2/20-14	High yield	28.8	123	10.4	5	93	42
37				T_2/20-15	High yield & More branching	28.1	172	8.8	6	91	40
38				T_2/20-16	More branching	15.9	115	7.4	7	92	31
39		T_2/21	7	T_2/21-1	High yield, More branching & More number of pods	36.9	207	9.8	7	98	42
40				T_2/21-6	More branching	24.8	121	7.9	6	93	42
41				T_2/21-7	Early	22.4	97	8.2	6	91	38
42				T_2/21-9	More branching & More number of pods	27.1	203	9.4	7	93	41
43				T_2/21-10	High yield, More branching & More number of pods	38.5	221	9.9	7	97	32
44				T_2/21-11	Early	19.9	122	8.1	6	88	34
45				T_2/21-15	Early	22.2	107	7.9	5	90	38
46		T_2/22	2	T_2/22-1	High yield	24.3	131	11.4	4	98	42
47				T_2/22-2	Early	12.2	83	9.6	3	90	39
48		T_2/23	1	T_2/23-5	More branching	20.4	164	8.4	7	97	40
49		T_2/24	6	T_2/24-2	Dwarf	10.0	112	7.8	3	102	22
50				T_2/24-4	Early	18.1	109	8.2	5	91	38
51				T_2/24-6	High yield	23.9	179	9.9	5	105	35
52				T_2/24-8	Early & More branching	26.0	151	8.0	6	90	38
53				T_2/24-11	High yield	21.3	112	9.6	4	96	36
54				T_2/24-12	Dwarf	14.0	78	8.1	4	95	24
55	Checks			TAMS-38	-	12.8	56	7.2	4	104	40
56				JS-335	-	13.3	59	6.3	4	109	41
Total			54								

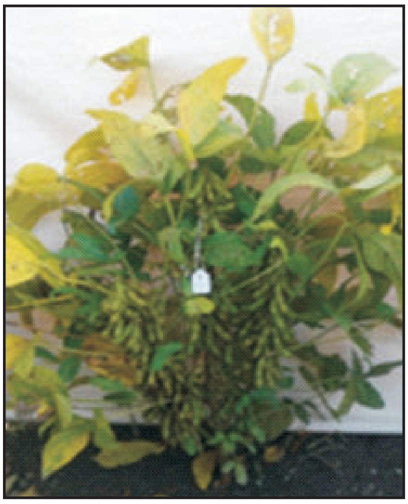
Tall (T_1/3-1)

Dwarf (T_2/19-10)

Dwarf (T_1/14-14)

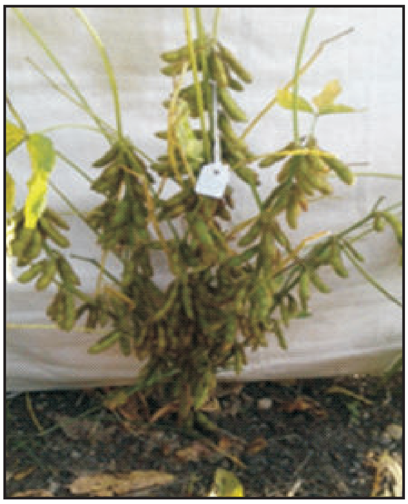
Early (T_2/21-10)

More branches (T_1/14-7)



More pods (T_2/5-4)

More pods (T_2/5-4)



High yielding (T_1/5-2)

High yielding (T_2/19-2)

selection in M_3 generation. Therefore, selections of superior families followed by selection of individual plants in selected families were considered as the criteria of selection. Based on these criteria 54 individual plants were selected from 11 families (Fig. 1) out of the total 20 families studied. The performances of these selected individual plants are presented in table 3, and plate 1. It is observed from the table that the seed yield plant^{-1} of selected individuals ranged from 5.4 to 39.9 g, number of pods plant^{-1} from 27 to 236. Similarly 100 seed weight from 6.4 to 11.6 g, number of branches plant^{-1} from 3 to 8, days to maturity from 88 to 105 and plant height from 21 to 62 cm.

It is inferred from this study that, as additive gene action was found to be predominant for yield and yield components, the selected 54 individual plants from M_3 generation could 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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