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PERFORMANCE OF SOYBEAN MUTANTS FOR YIELD AND YIELD COMPONENTS

Vaishnavi Deshmukh[1], M. P. Meshram[2] and R. N. Deshmukh[3]

ABSTRACT

The present investigation was taken to study the "Performance of soybean mutants for yield and yield components". The experimental material comprised of 20 soybean mutant lines along with 2 checks TAMS-38 and JS-335. The experiment was conducted at Shankar nagar, Research field of Agricultural Botany Section, College of Agriculture, Nagpur during *kharif* 2019. Mutant lines with checks were evaluated for days to 1stflower, days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, number of pods plant^{-1}, 100 seed weight, oil content and seed yield plant^{-1}. Mutant line number 10 (T2/2/1-1) and mutant line number 14 (T2/5/1-1) were isolated as superior lines over all the mutant lines compared with checks for further soybean breeding programme.

(Key words : *per se* performance, mutant line, breeding)

INTRODUCTION

Soybean is also known as "Gold of soil" due to its various qualities such as ease in cultivation, less requirement of fertilizers and labor resulting in high cost:benefit ratio.*Glycine max* is probably polyploid in its origin although the exact nature of its origin is yet to be understood (Darlington and Janaki Ammal, 1945). It is categorized as an oilseed rather than a pulse, despite being the rich source of protein and used as food and feed by the human as well as livestock across the globe.

This soybean has grown within China used for more than 4000 years (Hymowitz, 1970). Soybean being predominantly self-fertilized, inherent variability in this crop may not be sufficient to develop new varieties possessing different desirable characters.It carries a very high nutritional value which contains about 40% proteins, possessing high level of essential amino acids except methionine and cystine, 20% oil rich in polyunsaturated fatty acids specially omega-6 and omega-3 fatty acids, 6 to 7% total minerals, 5 to 6% crude fibre and 17 to 19% carbohydrates (Chauhan *et al*., 1988).

Besides, it has a number of nutraceutical compounds such as tocopherol, iron, vitamin B-complex, lecithin and isoflavones such as daidzein, genistein of glycitin made it one of the most valuable agronomic crops in the world (Khan and Tyagi, 2013). Yield and related characters are controlled by the polygenic system. Under such situation, mutation breeding is now playing an important role in developing new genetic resource and breakage of unwanted linkages.

The cultivar TAMS-38 was taken for the study because this cultivar is recommended as high yielding, better adoptable into the area of Vidarbha but highly susceptible to root rot and moderately susceptible to YMV (Yellout mosai & virus). This situation heads breeders on to new breeding technologies. The breeding objective in soybean is to develop varieties with high yield, early maturity, disease, and insect resistant. To achieve these objectives and bring about desired genetic improvements in the crop, the induced mutation is proved to be most effective. Therefore, it is our prime need to develop high yielding cultivar. Putting this view, the present work was framed and was implemented by selecting the high yielding mutants in M_7 generation.

MATERIALS AND METHODS

The experiment was conducted at Research field of Agril. Botany Section, College of Agriculture, Nagpur during *kharif* 2019.Inreplicated trial using Randomized Block Design replicated thrice in *kharif* 2019-20 all the harvested seed from each (20) mutants of M_6 generation along with 2 checks (TAMS-38 and JS-335) were sown to raise M_7 generation.All the recommended cultural practices were followed to raise a good crop.

The data on days to first flower, days to 50 % flowering, days to maturity, plant height (cm), number of branches plant^{-1}, number of pods plant^{-1}, 100 seed weight

1. P.G. Student,Agril. Botany Section, College of Agriculture Nagpur, Maharashtra
2. Asst. Professor, Agril. Botany Section, College of Agriculture, Nagpur
3. Head, Dept. of Botany, NAC&S College, Parner, Maharashtra

(g), oil content (%) and seed yield plant^{-1}(g) were recorded.Analysis of variance (Table 1) for these characters worked out and *per se* performance (Table 2) evaluated, as per the methodology suggested by Panse and Sukhatme (1954).

RESULTS AND DISCUSSION

The mean sum of squares due to genotypes were highly significant for all the characters studied (Table 1). This reveals that the genotypes had significant amount of genetic variability among themselves for seed yield plant^{-1} and other yield components, which allow the further estimation of different parameters for all nine characters.

Overall mean performance i.e. *per se* performance (Table 2) showed significant difference between characters. Average mean of days to 1st flower was 39.61, days to 50% flowering (47.34), days to maturity(99.60), plant height (58.90 cm), number of branches plant^{-1} (2.78), number of pods plant^{-1} (56.99), 100 seed weight (14.24g), oil content (18.05%), seed yield plant^{-1} (13.43g). Mean performance taken into the consideration two mutant lines were isolated as promising genotypes over the best check i.e. TAMS-38 (seed yield plant^{-1} 13.36 g, plant height 51.86 cm, number of branches plant^{-1} 3.06 and number of pods plant^{-1} 54.86. Mutant line number 10 was found to be significantly superior over mean for seed yield plant^{-1} (16.79 g), plant height (64.93) cm and at par for number of branches plant^{-1} (3.06). Mutant line number 14 was found to be significantly superior over mean for seed yield plant^{-1} (16.92 g), number of pods plant^{-1} (73.60) and plant height (60.86 cm).

Considering all the characters studied for M_7 mutant lines of soybean, mutant line number10 (T2/2/1-1) and mutant line number 14 (T2/5/1-1) (Plate 1 and 2) respectively, showed significant superior mean for identification, purification and multiplication and as promising breeding parents (donors) in soybean breeding programme.Bisane *et al*. (2019) stated that 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,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). Individual plants from 41 families selected in M_4 generation were suggested to be raised in progeny rows for one more generation so as to attain homozygosity. Lande *et al*. (2018) reported that chlorophyll mutants, early flowering, late flowering, early maturing, late maturing, dwarf, tall, increased root length, increased 100 seed weight, more branched mutants isolated as ecological and morphological mutants from variety TAMS-38. High yielding mutant with 12 g to 17 g yield as against 4.40 g in control were isolated mutants evaluated for their breeding behaviour in further generation and their utilization in improvement in soybean.

Koraddi and Basavaraja (2019) studied variability, heritability and genetic advance in 13 genotypes of soybean for yield and yield component traits. Observations on 11 characters were recorded. Analysis of variance revealed highly significant differences among the genotypes for the all characters, the range was maximum for plant height (39.27-77.73) followed by number of pods plant^{-1} (35.87-61.40). Malek *et al*. (2014) studied genetic variability and genetic diversity among 27 soybean mutants and four mother genotypes. Analysis of variance revealed significant differences among the mutants and mothers for nine morphological traits. All the nine morphological traits showed highly significant (5ØCÜ d" 0.01) variations indicating the presence of sufficient amount of genetic variability among the mutants for all the studied traits.

Akram *et al*. (2011) investigated and carried out at the experimental farm of Sakha Research Station, Kafr El-Sheikh, during 2009 and 2010 seasons to study the performance of 15 soybean genotypes for yield and its related traits and reported highly significance between plant height, days to maturity, number of branches plant^{-1}, 100 seed weight and number of pods plant^{-1}. Arshad *et al*.(2006) evaluated thirty three soybean genotypes for days to flowering, days to maturity, pod length, number of branches, number of unfilled, filled pods and total pods, 100 seed weight and seed yield. Grain yield (kg ha^{-1}) was estimated on the basis of 12 m^2 plot size, analysis of variance and mean performance for yield and its components revealed significant differences among all the genotypes for all the characters.

Plate 1. Mutant line number 10 (T2/2/1-1)

Plate 2. Mutant line number 14 (T2/5/1-1)

Table 1. Analysis of variance (mean sum of squares) for different characters under study in soybean

		Mean sum of squares								
Sources of variation	**D.F***	**Days to 1st flower**	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of branches plant-1**	**No. of pods plant-1**	**100 seed weight (g)**	**Oil content (%)**	**Seed yield plant-1(g)**
Replications	**2**	**0.060**	**3.469**	**4.606**	**1.302**	**0.132**	**49.783**	**1.414**	**0.005**	**4.841**
Treatments	**21**	**7.420****	7.126**	15.290**	92.152**	0.637**	111.691**	1.616**	1.818**	10.907**
Error	42	3.040	3.056	4.129	11.732	0.061	41.477	0.458	0.001	3.851

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

Table 2. Mean performance of selected 20 mutant lines along with 2 checks for various characters

Mutant line no.	Pedigree	Days to 1st flower	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant-1	Number of pods plant-1	100 seed weight (g)	Oil content (%)	Seed yield plant-1 (g)
1	T2/5/8-1	41.00	47.33	99.33	53.06	2.80	52.73	12.90	19.73	13.56
2	T2/19/2-1	39.67	45.66	96.00	52.20	3.40	52.93	14.16	19.43	13.55
3	T2/5/4-1	36.00	45.33	98.33	62.20	3.70	63.26	14.43	18.07	14.28
4	T2/20/6-1	37.33	46.00	97.00	55.26	2.76	59.80	14.27	17.47	15.48
5	T2/20/7-1	40.67	46.66	101.33	61.53	2.73	52.86	14.72	18.04	13.38
6	T2/20/6-1	40.00	46.33	98.66	62.26	2.20	62.46	15.21	17.70	14.42
7	T2/5/3-2	39.33	45.66	96.66	65.20	2.33	57.53	15.04	17.21	15.02
8	T2/20/12-1	39.67	46.33	101.66	66.13	2.86	61.66	13.87	18.56	14.72
9	T2/21/6-1	40.67	47.66	101.00	62.46	1.40	57.46	13.50	18.10	13.64
10	T2/2/1-1	40.33	49.00	98.66	64.93	3.06	59.60	15.01	16.95	16.79
11	T2/18/2-1	41.67	49.66	99.00	61.60	2.66	59.80	14.79	16.43	14.98

12	T2/23/5-1	40.33	48.33	102.33	62.86	3.20	47.13	14.70	18.24	11.54
13	T2/20/10-1	38.67	47.00	99.00	64.46	2.86	57.93	14.55	18.41	12.02
14	T2/5/1-1	37.67	45.66	100.00	60.86	2.73	73.60	13.12	18.03	16.92
15	T2/23/5-3	39.33	47.66	99.33	59.66	3.13	58.73	13.84	17.65	13.45
16	T2/19/4-2	40.67	49.00	100.33	54.40	3.00	53.00	13.84	17.41	10.86
17	T2/5/5-1	36.67	46.00	98.00	58.60	2.40	50.26	13.85	18.33	10.60
18	T2/20/11-1	38.33	45.66	100.66	53.60	2.93	45.73	12.91	18.42	10.74
19	T2/20/4-1	40.33	48.00	98.00	57.00	2.73	59.13	14.12	17.51	13.37
20	T2/21/15-1	41.67	50.00	97.33	61.46	2.66	61.20	14.53	17.81	12.80
TAMS-38	Check	40.00	48.66	103.66	51.86	3.06	54.86	15.72	18.62	13.36
JS-335	Check	41.33	50.00	105.00	44.20	2.53	52.06	14.15	19.10	9.90
Mean		39.61	47.34	99.60	58.90	2.78	56.99	14.24	18.05	13.43
S.E(m) ±		1.010	1.00	1.17	1.97	0.14	3.71	0.39	0.02	1.13
CD (5%)		3.06	2.98	3.34	5.64	0.40	10.61	1.11	0.07	3.23

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