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Variability Studies in M_3 Generation of Soybean

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A B S T R A C T

The present study was conducted with the objectives to estimate genetic parameters in M_3 generation of soybean. The experiment was conducted at the farm of Agricultural Botany Section, College of Agriculture, Nagpur during *kharif* 2017 in M_3 generation. 62 mutants along with two checks (TAMS-38 and JS-335) were evaluated in M_3 generation in three replications of which only 20 survived. Data were recorded on 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}. Genetic parameters estimated revealed that 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 where the characters influenced by additive gene action as they exhibited high genotypic coefficient of variation, moderate to high heritability along with high genetic advance as percentage of mean. Hence, those characters were identified for selection of better individual mutant from the progenies.

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 stands 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 benefits, and adaptability to varied climatic conditions.

Soybean belonging to the family Leguminosae, subfamily Papilionoideae, and genus *Glycine* (L.). It has become an increasingly important agricultural commodity with a steady increase of annual production worldwide. In 1999, the global production of soybean was 155.1 million metric tonnes, with the major producers being the United States, Brazil, Argentina, China, and India (Anonymous, 2000). However, the United States has become the world leader (Liu, 1997), producing about half of the total world soybean crop. India ranked 5th position in respect to area and production of soybean. The largest soybean producing states in India are Madhya Pradesh, Maharashtra and Rajasthan. Maharashtra ranks second in area and production.

The cultivar TAMS-38 is taken for study because, this cultivar is recommended as a high yielder and better adoptable in the area of Vidarbha. Induction of mutation in this cultivar and creation of variability would be a better source for selection of desirable mutants in yield and yield contributing characters. 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 crop, the induced mutation is proved to be most effective. Therefore, it is our prime need to develop resistance and high yielding cultivar. Putting this view the present work was framed and was implemented with the objective to estimate genetic parameters in M_3 generation in order to find the extent of variability in M_3 generation.

Materials and Methods

Dry healthy and genetically pure seeds of TAMS-38 were used in this study. Four different lots of soybean seeds 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 of gamma rays treatment. These seed were treated by three different doses of gamma rays i.e. 200 Gy, 250 Gy, 300 Gy (Co^{60} at BARC Trombay, Mumbai) and used for raising M_1 during *kharif* 2016 and individual plant in each treatment were harvested separately. The harvested seed 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 (Table 1) 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. All the cultural practices were followed to raise a good crop.

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 from 12 days after sowing and the germination percentage was calculated as per the formula given below:

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

For mortality percentage the number of plants which failed to survive up to flowering from the date of germination was 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 used for estimation of mean, range, genotypic variance, phenotypic variance, genotypic and phenotypic coefficient of variation (GCV and PCV) as per formula given by Burton (1953), heritability percentage as per Hanson *et al.,* (1956) and genetic advance as per Robinson *et al.,* (1949).

Results and Discussion

Sixty two putative mutants identified in M_2 generation were evaluated in M_3 generation out of which only 20 survived (Table 1).

Hence, observations were recorded on these 20 families for nine characters and genetic parameters were estimated.

The grand mean recorded for 20 mutants along with two checks were found to be 47.77 per cent for germination, 40.25 per cent for mortality, 43.19 days for flowering, 98.27 days for maturity, 37.95 cm for plant height, 3.40 for number of branches plant^{-1}, 64.45 for number of pods plant^{-1}, 8.24 g for 100 seed weight and 8.07 g for seed yield plant^{-1} (Table 2).

High range of 78.05 was exhibited for number of pods plant^{-1}, followed by germination percentage (57.71) and mortality percentage (52.77) which indicated that wide range of variation were functioning for these characters. In accordance to these results wide range of variation for yield and yield component were also reported by Gobinath and Pavadai (2015), Pavadai (2015) and Hoa and Giang (2012) in soybean.

The phenotypic variance and phenotypic coefficient of variation was observed to be far higher than genotypic variance and genotypic coefficient of variation for all nine characters studied (Table 2 and Fig.1). This indicated the higher influence of environment in the phenotypic expression of these characters. Similar to this results higher influence of environment on germination percentage, days to flowering, days to maturity, plant height, number of branches plant^{-1}, number of pods palnt^{-1} and seed yield plant^{-1} were also reported by Patil and Wakode (2011), Malek *et al.,* (2014) and Patil and Sharma (2016) in soybean.

Genotypic coefficient of variation exhibited high category for all the characters studied. The high genotypic coefficient of variation for mortality percentage (48.34%), seed yield plant^{-1} (45.59%), number of pods plant^{-1} (45.03%), germination percentage (43.04%), number of branches plant^{-1} (39.45%), days to flowering (36.74%), 100 seed weight (37.18%), days to maturity (37.91%) and plant height (38.71%) were observed.

Similarly phenotypic coefficient of variation was also observed to be high for different characters. High phenotypic coefficient of variation was observed for number of pods plant^{-1} (64.17%), seed yield plant^{-1} (62.43%), mortality percentage (59.24%), number of branches plant^{-1} (57.63%), plant height (51.15%), 100 seed weight (50.78%), days to maturity (50.06%), days to flowering (50.00%) and germination percentage (44.82%). In accordance to these results high genotypic coefficient of variation and phenotypic coefficient of variation for number of pods plant^{1}and seed yield plant^{-1} were also reported by Malek *et al.*,(2014) and Patil and Sharma (2016) in soybean.

The estimate of heritability and genetic advance estimated in material consisting 20 mutants along two checks for nine characters are reported in table 2 and fig. 2. Heritability per cent ranged from 46.85% (number of branches plant^{-1}) to 92.21% (germination percentage). High heritability was recorded for germination percentage (92.21%) and mortality percentage (66.57).

Table.1 Details of treatments (Mutants) used in the study

Doses of Mutagen	Sr. No.	Mutants to be grown	Character of Progeny
200Gy	*1	T_1/ 1	High yielding and Disease free mutant
	*2	T_1/ 2	Broad and flattered leaves, More branched, High yielding mutant
	*3	T_1/ 3	More branched mutant
	4	T_1/4	Narrow pod shape
	5	T_1/ 5	Healthy and More branched mutant
	6	T_1/ 6	Tall, ovule leaves shape, and More branched mutant
	7	T_1/ 7	Dwarf mutant
	8	T_1/ 8	Disease free and High yielding mutant
	9	T_1/ 9	Early flowering and Early maturity mutant
	10	T_1/ 10	Tall and More branched mutant
	11	T_1/ 11	Early flowering, More branched mutant
	12	T_1/ 12	Early maturity, Small leaves mutant
	13	T_1/ 13	Early flowering mutant
	*14	T_1/ 14	More branches, Dark wrinkle rough leaves mutant
	15	T_1/ 15	More branched, Small leaves and Brown pubescence mutant
	*16	T_1/ 16	Dwarf mutant
	17	T_1/ 17	More branches, Good plant type
	18	T_1/ 18	Dwarf plant and Early flowering mutant
	19	T_1/ 19	Oblong leaves and More branched mutant
	20	T_1/ 20	Two seeded pod and Small leaves mutant
	21	T_1/ 21	More branches and Healthy mutant
	*22	T_1/ 22	Dwarf mutant
	23	T_1/ 23	Anthocynin strip pigment, Wrinkle leaf shaped mutant
	24	T_1/ 24	Tall plant and Disease free mutant
	25	T_1/ 25	High yielding mutant
	26	T_1/ 26	Late flowering mutant
	27	T_1/ 27	Leafy mutant, oblong leaf shape mutant
250Gy	28	T_2/ 1	Early flowering, Early maturity and Disease free mutant
	*29	T_2/ 2	High yielding and More branched mutant

	30	T_2/ 3	High yielding and More branched mutant
	31	T_2/ 4	Early flowering and Early maturity mutant
	*32	T_2/ 5	Early maturity, Brown pubescence and Disease free mutant
	*33	T_2/ 6	Dark green rough and wrinkle leaves mutant
	*34	T_2/ 7	High yielding and Small leaves mutant
	*35	T_2/ 8	High yielding and 100% colour less hylum
	36	T_2/ 9	High yielding and Disease free mutant
	37	T_2/ 10	Tall plant and Disease free mutant
	38	T_2/ 11	Tall plant, Rough and wrinkle leaves mutant
	39	T_2/ 12	Disease free and Late maturity mutant
	40	T_2/ 13	Healthy plant and High yielding mutant
	41	T_2/ 14	Early flowering and More branched mutant
	42	T_2/ 15	Healthy plant and Small leaves mutant
	43	T_2/ 16	Healthy plant and late flowering mutant
	44	T_2/ 17	Dwarf mutant
	*45	T_2/ 18	More branches and High yielding mutant
	*46	T_2/ 19	Healthy and High yielding mutant
	*47	T_2/ 20	More branched mutant
	*48	T_2/ 21	More branches and High yielding mutant
	*49	T_2/ 22	Early flowering mutant
	*50	T_2/ 23	Early flowering and More branched mutant
	*51	T_2/ 24	Late maturity mutant
300Gy	52	T_3/ 1	Early flowering and High yielding mutant
	53	T_3/ 2	High yielding and More branched mutant
	54	T_3/ 3	Rough leaves and More branched mutant
	55	T_3/ 4	High yielding, Early flowering and Early maturity mutant
	56	T_3/ 5	Ventral leaves surface and Early maturity mutant
	57	T_3/ 6	Early flowering and Dwarf mutant
	58	T_3/ 7	Disease free, Small and hairy leaves mutant
	*59	T_3/ 8	Late flowering and Late maturity mutant
	60	T_3/ 9	Tall mutant
	61	T_3/ 10	Dwarf mutant
	*62	T_3/ 11	Late flowering and Late maturity mutant
Control			TAMS-38
			JS-335

Note: (*) mutants are survived

Table.2 Genetic parameters estimates for different characters in M_3 generation

Parameters	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)
Mean	47.77	40.25	43.19	98.27	37.95	3.40	64.45	8.24	11.83
Range	22.29-80.00 (57.71)	0.00-52.77 (52.77)	40.53-50.25 (9.71)	94.96-109.08 (14.11)	23-45.77 (22.77)	1-6 (5)	7-85.05 (78.05)	6.33-11.23 (4.9)	1.20-16.33 (15.13)
Genotypic variance	422.77	378.61	251.85	1387.78	215.80	1.80	842.16	9.39	29.10
Phenotypic variance	458.47	568.69	466.60	2419.94	376.87	3.85	1710.41	17.53	54.55
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	39.05	26.68	17.64	44.00	17.32	1.29	29.43	3.38	5.92
G.A (per cent of mean)	81.76	66.30	40.84	44.78	45.65	38.08	45.67	41.05	50.09

Fig.1 GCV and PCV per cent estimated in M_3 generation

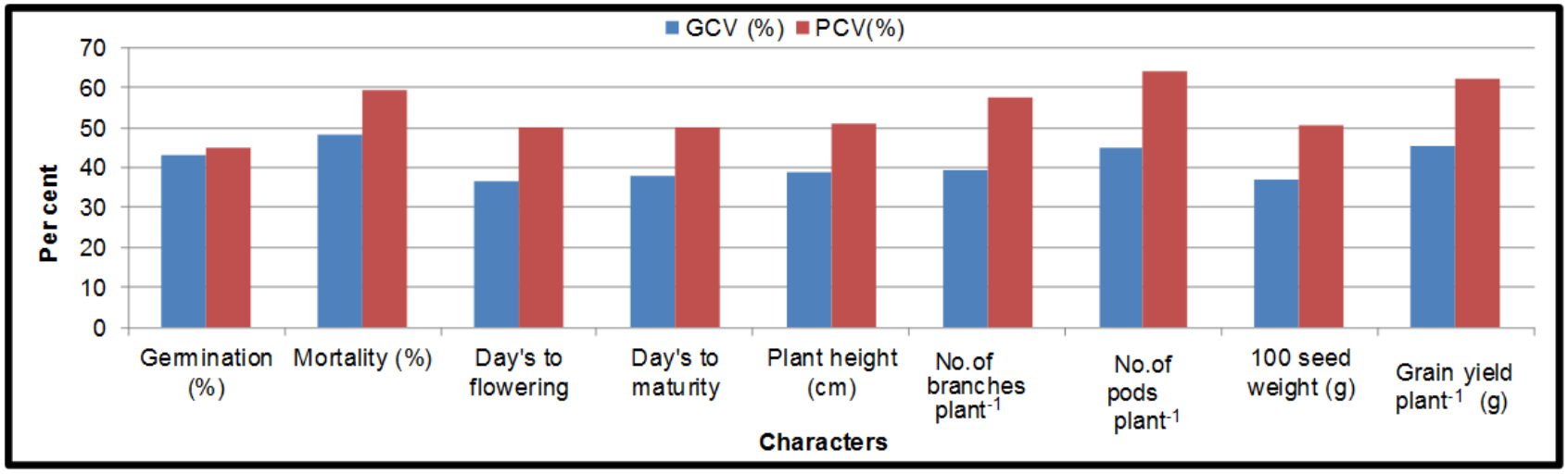
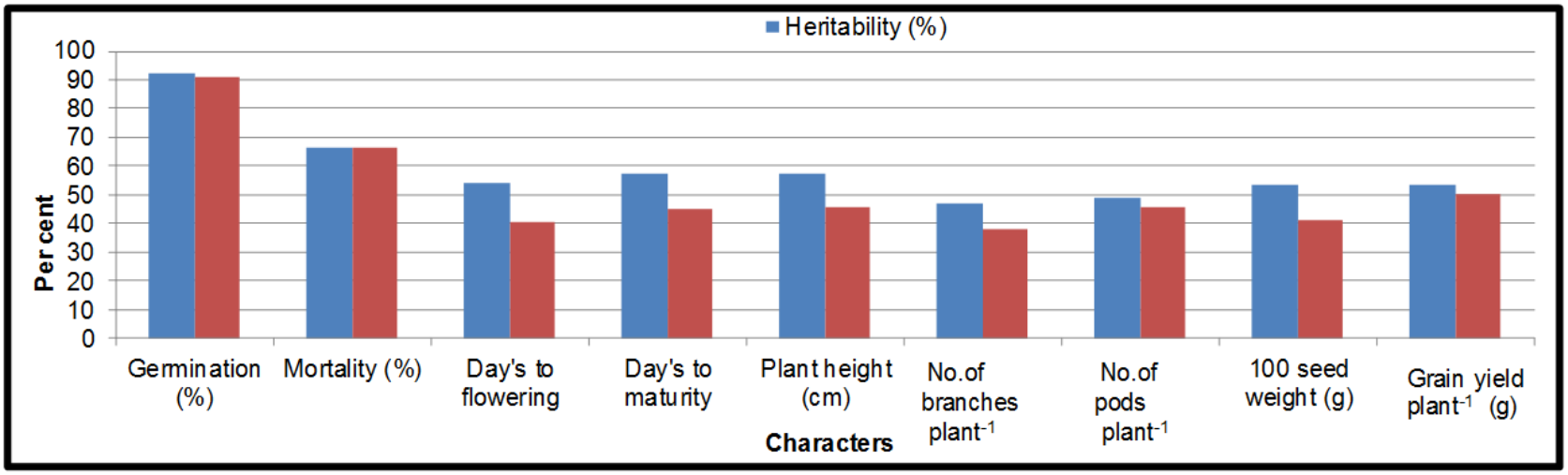


Fig.2 Heritability and G.A as percentage of mean estimated in M_3 generation



Moderate heritability was observed for days to maturity (57.34%), plant height (57.26%), days to flowering (53.97%), 100 seed weight (53.60), seed yield plant^{-1} (53.34%), number of pods plant^{-1} (49.23%) and number of branches plant^{-1} (46.85%). High to moderate estimate of heritability for above traits suggested less influence of environmental factor in the expression for these traits. In accordance to these results high heritability for yield and yield components were also reported by Basavaraja *et al.*,(2008), Pavadai *et al.,* (2010), Hoa and Giang (2012) and Patil and Sharma (2016) in soybean.

Genetic advance as a percentage of mean were high for germination percentage (81.76%), mortality percentage (66.30%), seed yield plant^{-1} (50.09%), number of pods plant^{-1} (45.67%), plant height (45.65%), days to maturity (44.78%), 100 seed weight (41.05%), days to flowering (40.84%) and number of branches plant $^{-1}$ (38.08%). Similar to these results high genetic advance as a percentage of mean was also reported by Khan and Goyal (2009), Malek *et al.*,(2014), Meshram *et al.*, (2013) and Pavadai *et al.*, (2010) in soybean.

The results obtained in this study revealed that mortality percentage, exhibited high genotypic coefficient of variation, high heritability along with high genetic advance as percentage of mean. Similarly, germination percentage, exhibited high genotypic coefficient of variation, high heritability with high genetic advance as a percentage of mean. Another character seed yield plant^{-1} also exhibited high genotypic coefficient of variation and high genetic advance as a percentage of mean along with moderate heritability. Similarly high GCV, moderate heritability and high genetic advance as percentage of mean were also observed for days to flowering, days to maturity, plant height, number of branches plant^{-1}, number of pods plant^{-1} and 100 seed weight. This indicated that all these characters were influenced by additive gene action operating in the expression of these traits in M_3 generation and hence can be used as criteria for making selection.

It is concluded from this study that in M_3 generation of soybean 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 were identified as the traits with additive gene action and can be used for selection better individual mutant from the progenies based on genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance.

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