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STUDY ON GENETIC VARIABILITY FOR MORPHOLOGICAL, YIELD CONTRIBUTING AND ROOT NODULATION TRAITS IN SOYBEAN (*Glycine max* (L.) MERRILL.)

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ABSTRACT

An experiment was conducted at All India Coordinated Research Project on Soybean, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani with view to study genetic variability in 35 soybean genotypes along with 5 checks for oil, yield and root nodulation traits. Analysis of variance showed significant genetic variability for all the characters. The present study revealed that the genotypes viz., MACS 1188, MAUS 282, MAUS 417, Dsb 11, DS 2614, PS 1450, PS 1444, RKS 54 exhibited better performance for days to maturity, number of branches, number of pods, plant height, oil content and number of nodules. These characters also showed positive correlation with yield per plant through their direct and indirect effect. Most of these characters exhibited high heritability coupled with high expected genetic advance. Hence, direct selection for these characters in soybean will increase the breeding efficiency. The promising genotypes MACS 1188, MAUS 282, MAUS 417, Dsb 11, DS 2614, PS 1450, PS 1444 and RKS 54 should be evaluated for yield and other characters in future.

Key words : *Genetic variability, genetic advance, GCV, PCV, root nodulation, soybean, yield.*

Soybean (*Glycine max* (L.) Merrill.) often designed as 'golden bean' contains about 20 per cent of oil, 40 per cent high quality proteins, 23 per cent carbohydrates and reasonable amounts of minerals, vitamins and dietary fibers, Since the yield per unit for many conventional crops has perhaps come to a plateau, search for unconventional source of protein rich food and edible oil supply is a necessity and soybean seems the only crop at present, which has the potential to meet the present and future needs of the world for protein and edible oil. Overall improvement in yield, oil and protein content in soybean still remains major task for plant breeders. This can be achieved through selection, efficiency of which mainly depends on the extent of the variability existing in the available material. In applied plant breeding success of the programme may be anticipated if the genetic variability of different selection is known, well in advance. The correlation and path analysis provide information on genetic association of yield contributing characters, which in turn are useful in developing breeding strategies. The information of variability in yield, oil and root nodulation traits will help to manipulate breeding programme for developing a suitable variety.

The present investigation was undertaken to evaluate the genetic variability parameters for morphological, yield and yield components, oil and root nodulation traits in 40 genotypes of soybean.

MATERIALS AND METHODS

The experiment was laid out during *Kharif* 2008-2009 at experimental farm of All India Co-ordinated Research Project on Soybean, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani in Randomized Block Design with three replications. The experimental material comprised of 35 promising newly developed cultivars of soybean developed at different centre of country and five checks *viz.,* Bragg, JS 93-05, JS 335, MAUS 71 and MAUS 81 which were planted by maintaining 45 cm row to row distance and 5 cm plant to plant distance and fertilizer dose of 30:60:30 NPK kg/ha was applied. All the recommended agronomic package of practices was followed for satisfactory crop growth. Five plants were selected randomly from each treatment for recording of observations on morphological characters *viz*., days to flowering, days to 50% flowering, days to maturity, number of branches per plant, plant height (cm); root nodulation characters *viz.,* number of root nodules per plant, nodule dry weight per plant (mg), and main root length (cm) and yield contributing characters *viz.,* 100 grain weight (gm), number of pods per plant, oil content (%), and grain yield per plant. The analysis of variance was done as suggested by (1). The genotypic and phenotypic simple correlation coefficients were worked out from the respective variances and co variances as per method suggested by (2).

RESULTS AND DISCUSSION

Genetic variability is prerequisite in crop improvement programme. The heritable variation is masked by non-heritable variation which creates difficulty in exercising selection. Hence, it becomes necessary to split overall variability into heritable and non-heritable components with the help of certain genetic parameters which may enable the breeder to plan out proper breeding programme since many characters of economic importance are highly influenced by environmental condition. Hence, progress of population mainly depends upon the magnitude of genetic variability present in population. In the present study efforts have been made to analyze the component of variability in different genotypes with an object to exploit it in future breeding programme.

The mean performance of different characters studied is presented in Table-1. Analysis of variance showed significant genetic variability for all the characters. Early maturity was recorded by VLS 72 (75.33 days), VLS 71 (82 days), MACS 1188 (82 days), Himso 1678, TS 5 and Himso 1677 (84 days). The genotypes TS 2, MAUS 282, BAUS 96, PS 1450, Himso 1676 (3.86), VLS 71(3.33), Himso 1678, PS 1454 and PS 1444 (3.00) recorded maximum number of braches per plant. Number of pods per plant were higher in MACS 1188 (61.66), RKS 52(57.00), NRC 80 (56.00), AMS 1 (52.66), JS (SH) 2002-14 (52.33) and MACS 1184 (48.00). High oil content were recorded by VLS 71 (24.00%), JS (SH) 2002-11 (22.98%), MACS 1039 (22.54%), and JS (SH) 2002-14 (22.47%). Nodule dry weight per plant and number of nodules per plant were higher in MACS 1188 (57.66 and 28.33 mg), MAUS 417 (47 and 22.66 mg), JS (SH) 2002-14 (43.66 and 21.77 mg), RKS 52 (45 and 19.77 mg).The strain MAUS 417 (17.21 gm), DS 2614 (17.09 gm), Dsb 11 (16.40 gm), MACS 1188 and PS 1450 (15.62 gm) recorded highest grain yield per plant.

Range of variability : In general wide range of variability was observed for all the characters (Table 2). In soybean significant amount of genetic variability has been reported by (3) for characters days to 50% flowering, days to maturity, plant height, pods per plant, 100 grain weight and grain yield per plant. Similarly, (4) reported highly significant difference for all the 10 characters in 55 genotypes of soybean.

Estimates for phenotypic variance are higher than genotypic variance in all the characters. High genotypic and phenotypic variances were observed for the character for number of pods per plant followed by plant height, nodule dry weight per plant, days to maturity, number of nodules per plant and days to flowering. The results of present findings are in agreement with those of (5). (6) observed high values of genotypic and phenotypic variance for pods per plant, 100 grain weight and days to maturity, (7) for number of nodule and nodule dry weight in soybean. The lowest genotypic and phenotypic variances were observed for the characters number of branches per plant and oil content. These finding are in conformity with the findings of (8).

Genotypic and phenotypic coefficient of variation : In the present investigation, GCV estimates were lower than PCV indicating that these characters responded more to environmental fluctuations. Similar trend of results were reported by (5). Therefore, there is ample scope for selection for increased expansion of PCV and GCV values as there is great influence of environmental factors.

In the present study, high genotypic and phenotypic coefficient of variation were observed for the character *viz.,* number of pods per plant, number of branches, number of nodules per plant, nodule dry weight per plant, plant height and 100 grain weight. These results are in conformity with those reported by (3) for nodules per plant and nodule dry weight. High magnitude of variation was observed for number of branches per plant, nodule dry weight, number of branches per plant and number of nodules per plant indicating better scope for genetic improvement of these traits.

Heritability and genetic advance : The heritability estimates along with expected genetic advance are more useful in predicting yield under phenotypic selection than heritability estimates alone (2). In the present study the range of heritability (bs) was from 59.40 per cent for days to 50% flowering to 99.68 per cent for oil content (Table-2). The character days to maturity, number of pods, plant height, root length, nodule dry weight (mg), 100 grain weight, number of nodules per plant and oil content recorded higher (>70%) broad sense heritability. High heritability estimates were reported for number of branches per plant, days to maturity, plant height by (5), number of pods/plant and grain yield per plant by (6), days to flowering by (9), for 100 grain weight and days to 50% flowering by (3) for grain yield by (9) and for oil content by (10).

In present study for all the important characters the heritability estimates were very high. However, as in broad sense heritability the contribution of dominance and epitasis are also included. Such estimate alone does not hold the repeatability of expression of characters in the selection programme. Similarly, the broad sense heritability estimates are prone to change from location to location and interaction with the environment. The heritability estimates for yield contributing characters were also reported by (2). The high heritability estimates are associated with low expected genetic advance indicating the non additive genetic control. Association of heritability, expected genetic advance and genotypic coefficient of variability has been reported by several workers including (8). High heritability estimates coupled with high expected genetic advance were observed for number of branches per plant and plant height by (5) for number of pods per plant and grain yield per plant. (9) for days to flowering and days to maturity. (3) for plant height and pods per plant. (11) for 100 grain weight and (12) for 50% flowering. High heritability also observed for number of nodules per plant, nodule dry weight and root length.

Table-1 : Mean performance of genotypes for yield and yield contributing characters in soybean.

Entry	Morphological characters					Root nodulation characters			Yield and yield contributing characters			
	Days to flowering	Days to 50 % Flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of nodules per plant	Nodule dry wt. (mg)	Root length (cm)	Oil content (%)	100 grain weight (gm)	Number of pods per plant	Yield per plant (gm)
2	3	4	5	6	7	8	9	10	11	12	13	14
Dsb 11	38.33	41.33	93.33	41.33	2.80	10.22	27.67	22.05	21.09	13.33	32.00	16.40
JS(SH) 2002-11	33.67	36.67	85.33	41.67	2.00	9.44	23.00	17.83	22.98	12.00	23.33	12.61
MAUS- 417	40.67	43.67	96.67	48.67	2.13	22.66	47.00	18.21	22.27	13.00	29.00	17.22
VLS 72	30.33	33.33	75.33	31.33	3.27	8.66	18.33	18.55	19.67	9.60	21.00	4.77
Himso 1678	32.33	35.33	84.00	35.00	3.00	10.33	23.67	20.42	22.23	13.00	29.33	14.58
PS 1454	35.67	38.67	92.00	40.00	3.13	18.77	38.33	21.77	21.06	14.00	31.00	14.23
MACS 1039	37.67	40.67	94.00	44.00	3.87	10.11	23.33	20.13	22.54	13.70	24.67	14.19
BAUS 96	38.67	41.67	94.00	61.67	3.00	13.00	28.00	18.99	21.20	12.50	46.67	13.97
DS 2613	33.67	36.67	85.00	48.33	2.07	12.44	28.67	18.94	22.38	13.10	44.67	12.41
MAUS 282	36.67	39.67	91.67	43.00	3.39	12.11	28.33	22.61	21.02	13.30	45.67	15.70
JS 20-14	34.67	37.67	87.00	40.33	2.07	9.11	23.33	16.61	21.04	10.33	19.33	10.68
PS 1444	35.67	38.67	92.00	35.33	3.00	11.67	24.67	19.77	19.79	12.00	37.33	14.34
TS 5	32.67	35.67	84.00	61.33	2.80	8.89	18.33	18.50	21.54	10.33	40.00	11.45
Himso 1677	33.00	36.00	84.00	38.67	2.87	13.75	29.00	15.77	22.24	13.67	22.67	12.24
MACS 1184	38.33	41.33	96.00	33.33	2.00	14.97	31.33	20.38	22.11	14.30	48.00	15.19
NRC 80	40.33	43.33	96.00	51.67	3.13	10.38	26.67	21.49	21.67	12.00	56.00	13.27
VLS 71	32.33	34.67	82.00	33.00	3.33	8.22	23.00	17.11	24.00	17.00	25.33	13.73
RKS 54	41.67	44.67	96.67	52.00	1.80	14.00	32.00	19.50	21.24	9.00	43.67	14.34
MACS 1140	36.67	39.67	92.00	54.33	3.00	11.20	29.33	16.05	20.23	13.33	45.67	14.19
JS(SH) 2002-14	33.33	36.33	84.00	44.33	2.00	21.78	43.67	21.77	22.47	12.50	52.33	13.19
TS 2	38.33	41.33	94.00	62.33	3.87	14.88	30.33	17.39	19.11	13.33	32.33	14.08
PS 1450	37.67	44.00	94.00	42.67	3.87	9.66	23.33	21.39	20.21	14.33	28.67	15.62
DS 2614	45.67	48.67	102.00	62.00	2.00	12.77	28.33	19.22	20.92	12.67	37.00	17.09
NRC 79	36.33	39.33	93.33	43.33	2.87	10.11	26.00	17.88	20.16	13.67	33.00	14.62
AMS 1	39.67	42.67	94.00	51.33	2.00	12.33	26.67	18.39	20.49	11.67	52.67	14.77
KDS 321	34.67	37.67	85.67	41.33	2.00	8.00	19.00	16.11	18.72	11.30	29.00	11.19
NSO 383	34.67	37.67	87.33	46.00	2.00	12.11	24.67	15.39	20.17	14.00	30.33	12.69
RKS 52	40.33	43.33	96.00	50.00	2.00	19.78	45.00	17.33	20.75	11.33	57.00	13.60
Himso 1676	32.33	35.33	85.33	38.67	3.87	12.44	30.33	17.22	20.29	15.67	31.33	12.88
JS 20-18	33.67	36.67	84.00	31.33	2.00	10.00	25.67	16.11	18.83	12.77	44.67	9.06
MACS 1188	23.67	47.33	98.67	53.67	2.93	28.33	57.67	20.61	19.81	14.00	61.67	15.63
NRC 81	32.33	35.33	82.00	33.33	3.00	15.77	36.00	20.61	21.10	14.00	29.67	13.36
JS 20-05	32.33	35.33	84.67	35.33	2.00	8.66	20.00	18.11	19.51	12.67	26.00	11.02
NSO 29	39.00	41.33	94.00	44.67	2.07	14.00	32.67	18.72	19.23	16.00	31.67	12.61
AMS 19	36.67	39.67	90.67	72.33	2.13	14.88	31.00	21.55	19.31	18.00	30.00	14.50
Checks												
Bragg	36.67	39.67	92.00	43.67	2.00	13.44	43.00	14.83	19.99	11.50	33.00	13.88
JS 93-05	34.33	37.33	88.00	40.00	2.93	14.55	30.33	19.66	20.75	13.33	22.33	13.00
JS 335	38.33	41.33	92.00	47.00	1.80	19.22	26.00	21.39	20.91	14.00	39.33	16.43
MAUS 71	37.67	40.67	93.67	43.33	2.07	12.88	28.00	17.94	20.29	12.33	52.00	14.93
MAUS 81	39.67	42.67	98.00	51.67	2.00	14.44	34.00	15.44	20.95	12.33	32.00	14.77
G.Mean	36.01	39.58	90.36	45.33	2.64	13.25	29.64	18.79	20.86	13.02	36.28	13.61
SE +	1.446	1.528	1.797	1.792	0.209	0.346	0.069	0.039	0.457	2.765	1.117	0.954
CD at 5 %	4.004	4.231	4.973	4.960	0.580	0.959	0.193	0.108	1.365	7.653	3.091	2.643

Table-2 : Parameters of genetic variability for yield and yield contributing characters in Soybean.

Characters	Range	General mean	Genotypic variance (62g)	Phenotypic variance (62g)	GCV (%)	PCV (%)	Heritability (%)	GA	EGA (%)
Days to flowering	30.33-45.66	36.01	12.34	18.62	9.76	11.99	66.29	5.89	16.36
Days to 50 % flowering	33.33-48.66	39.57	10.26	17.27	8.09	10.50	59.40	5.08	12.85
Days to maturity	75.33-102.00	90.35	29.81	39.50	6.04	6.96	75.47	9.76	10.81
Plant height (cm)	31.33-72.33	45.33	87.97	97.61	20.69	21.79	90.13	18.34	40.46
Number of branches per plant	1.80-3.93	2.64	0.52	0.53	27.38	27.76	97.28	1.46	55.63
100 grain weight (gm)	9.00-18.00	13.02	3.12	3.25	13.58	13.86	95.95	3.56	27.40
Number of pods per plant	19.33-61.66	36.28	115.02	137.96	29.56	32.37	83.37	20.17	55.60
Oil content (per cent)	18.72-24.00	20.86	1.45	1.45	5.78	5.79	99.68	2.47	11.88
Nodule dry wt.(mg)	18.33-57.67	13.24	18.85	19.48	32.77	33.31	96.78	8.79	66.41
Number of nodules per plant	8.00-28.33	29.64	67.51	71.32	27.72	28.49	94.65	16.46	55.55
Root length (cm)	15.39-22.61	18.79	4.36	4.72	11.11	11.56	92.36	4.13	22.00
Yield per plant (gm)	4.77-17.21	13.61	4.15	6.88	14.97	19.28	60.29	3.25	23.95

Thus from the foregoing discussion it is clear that the characters oil content, number of branches per plant, number of nodules per plant, nodule dry weight per plant, plant height and root length recorded high heritability and high expected genetic advance, indicating the presence of additive gene action and effective in phenotypic selection. Thus while exploiting genetic variability a due weightage should be given to these characters.

REFERENCES

1. Panse, V. G. and Sukhate, P. V. (1967). Statistical Methods for Agricultural Workers, ICAR Publication, New Delhi,pp 359.
2. Johnson, H. H., Robinson, H. F. and Comstock, R. E. (1955). Genotypic and phenotypic correlation in soybean and their implication in selection. *Agron. J., 47:* 477-485.
3. Mahajan, C.R., Patil, P. A., Mehetre, S. S. and Ghatge, R. D. (1994). Genotypic and phenotypic variability and heritability of some quantitative characters in soybean. *Ann. Agric. Res., 15(1):* 41-44.
4. Gohil, V. N., Pandya, H. M. and Mehta, D. R. (2006). Genetic variability for seed yield and its component traits in soybean. *Agric.Sci. Digest, 26(1):* 73-74.
5. Bangar, N. D., Mukhedkar, G. D., Lad, D. B. and Mukhedkar, D.G. (2003). Genetic variability, correlation and regression studies in soybean. *J. Maharashtra Agric. Univ., 28(3):* 320-321.
6. Sirohi, S. P. S., Sanjai M. and Singh, S. P. (2007). Genetic variability, correlation and path analysis for seed yield and its components in soybean. *Prog. Agric., 7(1/2):* 119-123.
7. Sharma, P., Inderjit S., Veena K. and Sarvjeet S. (2007). Genotypic variability and association studies for growth, symbiotic parameters and grain yield in summer mungbean. *Crop Improv., 34(2):* 166-169.
8. Bhaushan, B., Sharma, S. P. and Ranwah, B. R. (2006). Genetic variability, heritability and genetic advance in soybean. *National J. Pl. Improv., 8(1):* 94-95.
9. Sharma, S. M., Rao, S. K. and Goswami, U. (1983). Genetic variation, correlation and regression analysis and their implications in selection of exotic soybean. *Mysore J. Agric. Sci., 17:* 26-30.
10. Bartley, B.G. and Weber, C.R. (1952). Heritable and non-heritable relationship and variability of agronomic characters in successive generations of soybean crosses. *Agron. J., 44:* 487-493.
11. Taware, S.P., Raut, V. M., Halvankar, G. B. and Patil, V. P. (1995). Phenotypic variability and character association in some vegetable soybean varieties. *J. Maharashtra Agric, Univ., 20(3):* 454.
12. Jangale, C. D., Birari, S. P. and Apte, U. B. (1994). Genetic variability and heritability in soybean . *Agric. Sci. Digest, 14(2):* 117-120.

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