



# Genetic Variability Studies Based on Morpho-Physiological Traits Related to Temperature; Seedling Growth; Development and Phenology of Soybean [(*Glycine max* (L.) Merrill]

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## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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## ABSTRACT

The present experiment was conducted with an aim to understand genetic variability and heritability among 30 soybean genotypes of different geographical locations during *Kharif* 2019 at TCA, Dholi, Bihar in Randomized Complete Block Design accommodating 30 genotypes randomly in three replicates. These genotypes evaluated for twenty-seven traits: five phenological, nine agronomorphological, eight physiological traits (from field trial) and five physiological traits from laboratory experiment recorded and subjected to statistical and biometrical analyses. Considerable variability was observed for these traits which revealed usefulness of existing genetic variability for all 27 attributes amongst which vigour index II, seedling dry weight, specific leaf weight and 100- seed weight was trust worthy (GCV in close correspondence with PCV; high  $h^2$ bs & high GAM reflecting additive gene action) for selection criteria.

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## 1. INTRODUCTION

Golden bean and miracle crop are most commonly used synonym for soybean [(*Glycine max* (L.) Merrill)]. A fast horizontally expanding, protein + oil source miracle crop, increasingly adopted by farmers, offers opportunity under diverse growing situations in different cropping systems, against abiotic stresses and also as contingent crop, utilized for diversified food and feed purposes. Although it had 40% quality protein (glycine, tryptophan and lysine) and comparatively lesser quantity of (20%) quality oil, it is mainly popular as oilseed crop rather than a pulse crop because of its extraordinary oil qualities viz., no cholesterol, essential heart friendly omega-3 fats etc. Soybean, is globally oldest cultured plant. Historical evidences indicate its use for over 5000 years by human [1].

At present, soybean has acquired global importance and India is the fourth largest country in the world after United States of America, Brazil and Argentina regarding area but fifth regarding total production after China. The productivity of soybean is quite low in our country as compare to top soybean producing countries of the world which is probably due to narrow genetic base of the released varieties as well as their lower genetic yielding potential are the major reasons for low genetic yielding potential. Development of stable genotypes with enhanced seed yield is the most important goal of many soybean breeding programmes. Morphological traits/markers indicate the genetic composition of the cultivar and also the interaction of the genotype with the environment in which it is expressed. The information on genetic variability helps in selecting parents out of new land races, local selection, elite cultivars and exotic germplasm of crop plants for development of new varieties, continuous evaluation for important traits, which in earlier days was exclusively based on the available morphological data [2].

## 2. MATERIALS AND METHODS

The experiment was carried out during *kharif*, 2019 at the farm of Tirhut College of Agriculture, Dholi (25.5°N, 35.40°S and 52.2m MSL) in Muzaffarpur District (North Bihar) located in eco-geographical region I Sub region IV of Bihar. Thirty entries (including 3 checks) were sown in Randomized Complete Block Design. Each plot

consisted three rows of 3-meter length. The row to row and plant to plant distance was 45cm and 5cm, respectively. Trial laid out for 27 (22 field and 5 laboratory screening) morpho-physiological traits viz., germination relative index seedling length (cm), seedling dry weight (g), vigour index I, vigour index II, formation of flower tubercles (days), flower budding (days), first flowering (days), cessation of flower (days), physiological maturity (days), plant height (cm), main shoot length (cm), primary branches plant<sup>-1</sup>, secondary branches plant<sup>-1</sup>, no of clusters plant<sup>-1</sup>, no of pods cluster<sup>-1</sup>, no of pods plant<sup>-1</sup>, pod length(cm), no of seeds pod<sup>-1</sup>, growing degree days(°c), specific leaf weight (g/cm<sup>2</sup>), leaf area index, 100-seed weight (g), harvest-index (%), dry matter efficiency, effective rainfall use efficiency, seed yield plant<sup>-1</sup> (g). Data for individual characters observed, replication-wise and mean data was used for statistical analyses. Genetic variability parameters were calculated as per Burton and de vane [3].

## 3. RESULTS AND DISCUSSION

The ANOVA of various traits (Table 1) revealed that there were significant differences among genotypes for all the traits under study. This indicates that exploitable level of genetic variability has been created and genetic base is broadened for most of the important characters among different genotypes developed through hybridization and selection involving diverse parents. The utilization of these diverse genotypes may lead to development of potential and suitable genotypes in future. Similar results have been reported by [4-9] for number of pods per plant and seed yield per plant.

**Genetic variability:** The results (Table-3) revealed that the phenotypic coefficient of variation was found higher in magnitude than that of genotypic coefficient of variation for all the characters under study. Vigour index II recorded the highest genotypic coefficient of variance and phenotypic coefficient of variance followed by seedling dry weight, specific leaf weight, grain yield per plant, effective rainfall use efficiency, leaf area index, 100-seed weight, main shoot length, vigour index I, secondary branches, seeds per pod, seedling length, primary branches, moderate for plant height, pod per plant, harvest index, cluster per plant, pod length, pod per cluster, germination relative index. This revealed that a considerable scope

for improvement of these characters through selection programme. In agreement with the present findings [4,7,10] for number of pods per plant and seed yield per plant, [5] for plant height, [11] for plant height, seed yield per plant and number of pods per plant and [12] for seed yield per plant.

Mean and range of 27 character (Table 2) exhibited considerably wide range of variation among 30 genotypes for studied traits. Many different genotypes in variable number were significantly superior over best check for each character. Harvest index, dry matter efficiency and cluster per plant accommodated highest 7 different genotypes which were significantly superior over best check. Genotype NRC-142 and SL-688 were significantly superior over best check for 8 characters which was highest, followed by both SL-955, VLS-94 for 6 characters.

Low genotypic coefficient of variance and phenotypic coefficient of variance were recorded

for dry matter efficiency, days to tubercle, days to flower budding, days to cessation, days to physiological maturity, days to first flowering, and growing degree days indicating that they are very difficult to improve via selection programme. These results are in confirmation with the findings of [11] for days to 50% flowering and days to maturity.

**Heritability and genetic advance as percentage of mean:** To adjust the variation over environment heritability was calculated and presented in Table 3. High heritability coupled with high genetic advance as percentage of mean was observed for seedling dry weight, vigour index-II, specific leaf weight and 100-seed weight whereas high heritability along with moderate genetic advance was recorded for plant height, main shoot length, secondary branches, seed per pod, leaf area index, effective rainfall use efficiency, vigour index-I and seed yield per plant these results indicate the preponderance of additive gene action may be responsible in the inheritance of the above traits.

**Table 1. ANOVA for all the 27 traits of soybean [*Glycine max* (L.) Merrill]**

SL. No.	Character	Replications (df = 2)	Genotypes (df = 29)	Error (df = 58)
1	DT	0.63	12.67**	1.01
2	DFB	0.57	18.81**	0.58
3	DFF	0.41	11.05**	0.50
4	DC	0.87	39.22**	0.59
5	DPM	1.43	130.37**	2.51
6	PH (cm)	40.13	423.18**	31.27
7	MSL (cm)	5.03	551.13**	31.72
8	PB	5.30	5.22**	1.50
9	SB	1.36	2.09**	0.44
10	C/P	2.29	46.25**	5.07
11	P/C	0.08	0.32**	0.04
12	P/P	50.84	438.82**	92.80
13	PL (cm)	0.03	0.68**	0.03
14	S/P	0.02	0.96**	0.07
15	GDD (°c)	35x10 <sup>-4</sup>	0.21**	41x10 <sup>-4</sup>
16	SLW (g/cm <sup>2</sup> )	5x10 <sup>-7</sup>	83x10 <sup>-6**</sup>	4x10 <sup>-6</sup>
17	LAI	0.25	11.09**	1.78
18	SW(g)	74x10 <sup>-4</sup>	9.84**	0.03
19	HI (%)	0.49	129.47**	9.76
20	DME	26x10 <sup>-5</sup>	0.03**	11x10 <sup>-4</sup>
21	ERUE (kg/ha)	0.45	0.93**	0.13
22	GYPP (g)	18.62	36.67**	5.05
23	GER	57.70	212.37**	15.34
24	SL (cm)	19.33	98.98**	25.34
25	SDW (g)	13x10 <sup>-3</sup>	0.19**	44x10 <sup>-4</sup>
26	V1	27565.47	1077907.94**	244787.37
27	V2	127.54	1551.38**	46.34

\*\*& \* Significant of  $P = 0.01$  and  $P = 0.05$  F-value at  $.01=5.42$  &  $.05=3.33$

**Table 2. Range and mean performance of 30 soybean genotypes for 27 characters**

CHARACTERS	DT	DFB	DFE	DC	DPM	PH	MSL	PB	SB
	1	2	3	4	5	6	7	8	9
Mean	30.067	37.889	43.289	55.222	107.733	65.167	54.700	7.479	3.425
Range	25.667-35.000	32.667-41.667	40.000-47.000	50.000-66.333	93.667-116.333	42.667-92.667	33.667-81.000	4.683-10.447	1.527-4.930
Minimum Genotype	25.667 VLS-94	32.667 VLS-94	40.000 NRC 142	50.000 NRC 142	93.667 NRC 142	42.667 ShalimarSoy1	33.667 VLS-94	4.683 RKS-18	1.527 PS - 1347
Maximum Genotype	35.000 RSC 11-17	41.667 RSC 1071 NRC128,12	47.000 NRC-128	66.333 AMS- 2014	116.333 SL 1074	92.667 NRC-137	81.000 NRC-137, RSC 1071	10.447 SL 955	4.930 SL 955
No. of significantly Superior Genotypes (vis-à-vis best check)	3	4	4	3	3	4	5	3	4
Name(s) of Genotypes	VLS-94 SL-688	VLS-94 NRC-142	NRC-142 PS-1092	NRC-142 VLS-94	NRC-142 Shalimar soy-1	NRC-137 MACS-1493	NRC-137 RSC-1071	SL 955 Pusa 9712	SL 955 PS- 1092
	NRC-142	PS-1343 PS-1092	VLS-94 SL-688	SL-688	RSC-1103	RSC-1071 NRC-12	MACS-1493 RSC-11-15	JS 9305	SL-688 RSC- 1052
Best Check	JS-9752, RKS-18	JS-9752	JS-335	RKS-18	JS-335	JS-9752	NRC-12 JS-9752	JS-9752	JS-335

Cont...

CHARACTERS	C/P	P/C	P/P	PL	S/P	GDD	SLW	LAI	SW
	10	11	12	13	14	15	16	17	18
Mean	26.227	3.120	78.756	3.328	2.797	18.244	0.015	6.819	7.179
Range	19.733-34.057	2.467-4.200	62.399-105.041	2.400-4.400	1.773-3.887	17.891-18.812	0.007-0.031	4.790-11.007	4.500-11.197
Minimum Genotype	19.733 NRC 142	2.467 PS-1572	62.399 RSC 1103	2.400 AMS-2014	1.773 RSC 11-7 RSC 11-17	17.891 SL 1074	0.007 NRC-12	4.790 RKS-18	4.500 Shalimar Soy -1
Maximum Genotype	34.057 SL 955	4.200 NRC-136	105.041 NRC-136	4.400 NRC SL-1	3.887 Pusa 9712	18.812 NRC 142	0.031 RSC 1071	11.007 SL 955	11.197 SL 1028
No. of significantly Superior Genotypes (vis-à-vis best check)	7	6	6	6	6	6	2	5	1
Name(s) of Genotypes	SL-688 MACS-1493 AMS-2014 Pusa 9712 ShalimarSoy1 NRC-128 NRC-137 JS-335	NRC-136 VLS-94 PS-1092 RSC-11-17 SL-688 SL-1028 JS-9752	NRC-136 ShalimarSoy1 SL-688 NRC-137 MACS-1493 AMS-2014 JS-335	NRC SL-1 ShalimarSoy1 NRC-12 PS-1092 PS-1572 PS -1347 RKS-18	Pusa 9712 NRC SL-1 PS-1092 RSC 1071 SL 955 PS-1572 JS-9752	NRS-142 RSC 11-7 RSC 1103 ShalimarSoy1 RSC 11-17 VLS-94 RKS-18	RSC-1071 RSC 11-7 Pusa 9712 JS 9305 SL-1074	SL 955 SL 688 Pusa 9712 JS 9305 SL-1074	SL-1028
Best Check	JS-335	JS-9752	JS-335	RKS-18	JS-9752	RKS-18	JS-335	JS-9752	JS-335

Cont...

CHARACTERS	HI	DME	ERUE	GYP	GER	SL	SDW	V1	V2
	19	20	21	22	23	24	25	26	27
Mean	39.85	1.33	1.89	11.53	86.76	28.24	0.56	2463.34	49.27
Range	29.27-50.34	1.18-1.52	1.21-3.51	6.54-21.00	62.66-96.33	15.83-38.70	0.17-1.05	1495.60-3503.70	6.05-93.17
Minimum Genotype	29.27 NRCSL1	1.18 NRCSL1	1.21 RKS-18	6.54 RSC 11-17	62.66 NRCSL1	15.83 RSC 1103	0.17 RSC 1052	1495.60 VLS-94	6.05 NRCSL-1
Maximum Genotype	50.34 NRC-136	1.52 ShalimarSoy1	3.51 NRC-136	21.00 NRC-136	96.33 JS-9752	38.70 SL 955	1.05 NRC 142	3503.70 SL 955	93.17 NRC 142
No. of significantly Superior Genotypes (vis-à-vis best check)	7	7	5	5	4	3	4	3	1 (At par)
Name(s) of Genotypes	NRC-136 ShalimarSoy1 PS-1092 RSC-11-17 RSC 11-15 RSC 1071 PS -1347 JS-9752	Shalimar soy 1 RSC-11-17 RSC-11-7 RSC-11-03 NRC-136 PS-1347 VLS-94 JS-9752	NRC-136 SL-955 NRC-137 NRC-128 MACS1493 NRC-128 JS-9752	NRC-136 SL-955 NRC-137 MACS1493 NRC-128 JS-9752	PS-1572 PS-1347 JS-20-116 RSC11-03 JS-9752	SL-955 NRC-137 NRC-136 RSC-1071 JS-335	NRC-142 JS-20-116 MACS1493 RSC-1071 JS-9752	SL-955 NRC-137 NRC-136 NRC-136 JS-335	NRC-142 NRC-137 NRC-136 NRC-136 JS-9752
Best Check	JS-9752	JS-9752	JS-9752	JS-9752	JS-9752	JS-335	JS-9752	JS-335	JS-9752

Table 3. Genetic parameters of 27 morpho-physiological parameters of soybean [*Glycine max* (L.) Merrill]

SN	Character	Genotypic Variance ( $\sigma^2g$ )	Phenotypic Variance ( $\sigma^2p$ )	Genotypic coefficient of Variance (GCV)	Phenotypic coefficient of Variance (PCV)	Heritability Broad Sense ( $h^2$ )	Genetic Advance (G A) at 5%	Genetic advance as per cent of Mean
1	DT	3.888	4.900	6.558	7.363	79.30	3.618	12.033
2	DFB	6.074	6.664	6.505	6.813	91.20	4.847	12.794
3	DFF	3.516	4.019	4.332	4.631	87.50	3.613	8.346
4	DC	12.879	13.469	6.499	6.646	95.60	7.229	13.090
5	DPM	42.621	45.135	6.060	6.236	94.40	13.069	12.131
6	PH	130.64	161.911	17.539	19.526	80.70	21.150	32.455
7	MSL	173.137	204.860	24.055	26.166	84.50	24.919	45.556
8	PB	1.242	2.745	14.901	22.153	45.20	1.544	20.648
9	SB	0.549	0.997	21.641	29.158	55.10	1.133	33.087
10	C/P	13.727	18.798	14.127	16.532	73.00	6.522	24.868
11	P/C	0.094	0.140	9.833	12.010	67.00	0.517	16.583
12	P/P	115.34	208.149	13.637	18.319	55.40	16.469	20.911
13	PL	0.216	0.249	13.956	14.999	86.60	0.890	26.749
14	S/P	0.296	0.372	19.449	21.808	79.50	1.000	35.732
15	GDD	0.069	0.074	1.444	1.486	94.50	0.528	2.892
16	SLW	0.000	0.000	34.112	36.810	85.90	0.010	65.120
17	LAI	3.101	4.888	25.823	32.421	63.40	2.889	42.372
18	SW	3.271	3.308	25.191	25.334	98.90	3.705	51.600
19	HI	39.903	49.666	15.851	17.683	80.30	11.664	29.268
20	DME	0.008	0.009	6.868	7.311	88.30	0.177	13.291
21	ERUE	0.266	0.404	27.194	33.535	65.80	0.861	45.426
22	GYPP	10.538	15.593	28.132	34.221	67.60	5.498	47.642
23	GER	65.676	81.020	9.340	10.374	81.10	15.031	17.323
24	SL	24.545	49.893	17.538	25.004	49.20	7.158	25.340
25	SDW	0.062	0.067	44.267	45.815	93.40	0.496	88.109
26	V1	277706.800	522494.200	21.393	29.344	53.20	791.431	32.128
27	V2	501.679	548.025	45.458	47.512	91.50	44.146	89.597

Note : DT=Days to tubercle formation, DFB=Days to flower budding, DFF = Days to First flowering, DC=Days to cessation , DPM = Days to Physiological maturity, PH = Plant height (cm), MSL = Main shoot length (cm), PB = Number of primary branches per plant, SB = Number of secondary branches per plant, C/P = Number of cluster per plant, P/C = Number of pods per cluster, P/P = Number of pods per plant , PL= Pod length (cm), S/P=Seed per pod ,GDD=Growing degree days, SLW=Specific leaf weight , LAI=Leaf area index, SW = 100 - seed weight (g), HI = Harvest- index (%), GY = Grain yield per plant(g), DME=Dry matter efficiency, ERUE=Effective rainfall use efficiency, GER=Germination relative index, SL=Seedling length , SDW=Seedling dry weight , VI=Vigour index I, VII=Vigour index II

High heritability with low genetic advance for days to tubercle formation, days to first flowering, days to flower budding, days to cessation of flowering, days to physiological maturity, growing degree days, pods per cluster, pods per plant, pod length, harvest index, dry matter efficiency and germination relative index and medium heritability with low genetic advance was recorded for primary branches and seedling length. These findings indicate that in the inheritance of these traits non-additive gene action may be involved. In agreement with the present investigation, high heritability was also reported by [13] high heritability coupled with high genetic advance have also been reported by [6] for plant height, 100 seed weight, pod length, seeds per pod, seed yield per plant, harvest index and biological yield. [14] for seed yield per plant and biological yield per plant. [15] for plant height, number of seeds per plant, 100-seed weight. [6] observed high heritability for seed yield, seed dry weight, days to maturity, and 100-seed weight. [17] for days to 50 % flowering observed, high heritability and moderate genetic advance.

On the basis of heritability and genetic advance as % of mean, the present investigation suggests that selection may be effective for the improvement of traits viz., plant height, main stem length, cluster per plant, pod length, seed per pod, specific leaf weight, 100-seed weight, harvest index, seedling dry weight and vigour index II, days to tubercles formation, days to flower budding, days to cessation, days to physiological maturity, dry matter efficiency, germination relative index, secondary branches per plant, pod per plant, leaf area index, effective rainfall use efficiency, grain yield per plant, vigour index I, pod per cluster because these traits are governed by additive gene action. Whereas, later generation selection may be effective for days to first flowering, growing degree days, no. of primary branches and seedling length because in the inheritance of these traits preponderance of non-additive gene action was found.

#### 4. CONCLUSION

Present study offers scope for utilizing variability present in studied 30 soybean genotypes, including three checks, for 27 pheno-morpho-physiological traits for genetic enhancement of soybean. Variability, in general and its heritable part, in particular is important than total phenotypic variability for any selection targeted trait. Vigour index-I, seedling dry weight, specific

leaf weight and 100-seed weight were predominantly governed by additive gene action (GCV in close correspondence with PCV, high  $h^2$ bs and high GAM). Selection for these traits would be more realistic as both  $h^2$ bs and GAM explain the genetic gain over unselected base population.

#### DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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