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Genetic Variability in Soybean (*Glycine Max* L.) Genotypes for Morphological Traits in Southwestern Ethiopia

Masreshaw Yirga, Yechalew Sileshi

Ethiopian Institutes of Agricultural Research, Jimma Agricultural Research, Pulse and Oil Research Division, Jimma, Ethiopia

Email address:

yirgamasresha@gmail.com (Masreshaw Yirga)

Abstract: Genetic variability assessment in is paramount important for soybean variety development program. The field experiment was conducted at Jimma and Metu, south western Ethiopia for two year during 2017-2018 main cropping season to estimate the extent of genetic variability in 64 soybean genotypes for morpho-agronomic traits. The trial was laid down in simple lattice design. The combined analysis of variance revealed the presence of significant ($P<0.01$) variation among the tested genotypes for all the traits. The maximum grain yield per hectare was recorded on variety; Coker240 (3.09 t/ha each) followed by genotype PI567104B (3.00 t/ha), PI567054C (2.85 t/ha) and G 7955-C3RPP (2.82 t/ha), while the minimum yield was scored from PI416826A (1.33t/ha). The performance of the tested genotypes also showed resistance to moderately resistance to soybean rust. Maximum disease score was recorded from genotype PI567090 (25.52%), while the minimum was from PI594538A (3.78%). combined high genotypic coefficients of variation (GCV), high heritability (H^2) and high genetic advance as present of mean (GAM) were recorded for plant height (71.48%, 98.51% and 146.36%), number of pod (79.58%, 89.39% and 155.22%), number of seed (113.92%, 88.49% and 221.09%), hundred seed weight (62.28%, 74.10% and 110.60%) and grain yield (36.97%, 83.22% and 69.57%), which denotes, these traits can be improved through direct selection more easily than other traits. Therefore, this research finding showed the existence of enormous genetic variability among soybean genotypes for various important morphological traits.

Keywords: GCV, PCV, H^2, GA

1. Introduction

Soybean (*Glycine max* L., 2n=40) belongs to the genus *Glycine* in the family *Leguminasae* [1]. Soybean is one the multipurpose grain legume crop which has a potential to deliver a multifaceted impact on sustainable agriculture systems, household food, nutrition, feed and income for smallholder farmers faced with food and nutritional insecurity particularly in sub-Saharan Africa (SSA) including Ethiopia. Its unic nature of the crop is high grain nutritional value with quality protein (35-40%) and vegetable oil (18-22%) content as well as its biological nitrogen fixing ability [2-4]. Soybean has a potential to be grown widely from lowland to midland maize belt agro ecology of Ethiopia.

Currently, soybean is one of the national strategic crops for its combination of higher edible oil yield and cake for animal feed per hectare as compared to other oil crops. Farmers also showed a high interest in soybean farming, mainly because of its suitability to different soil types and the high market demand from exporters and domestic millers. The export of unprocessed soybean (86000ton) generates approximately US$45million in foreign exchange [5]. Currently, number of holders (177, 940.0), area coverage (83,797.2 hectare) and annual soybean production (208,676.4 ton) with its productivity (2.5 ton/ha) has better progress as compared to the previous decade's trend in Ethiopia [6]. However, there is still a high the gap between actual productivity and its potential due to several limiting factors like lack of widely adaptable varieties and poor management practices.

So far, a number of germplasm was enhanced through introduction and local crossing methods in Ethiopia. some parts of soybean germplasm were morphologically characterized by different researchers [7-12], each reported the presence of considerable genetic variations among the tested genotypes. Therefore continues characterization of soybean germplasm is very important for effective conservation and efficient

exploitation of through selection and crossing in soybean variety development prorgam. Considering these facts, the study was conducted to estimate the extent of genetic variability among soybean with respect to morhophlogical traits.

2. Materials and Methods

The field experiment was conducted at Metu and Jimma, Southwestern Ethiopia during 2019 main cropping season. Metu has an altitude of 1558 m.a.s.l. and the mean annual temperature ranges from 12.7-28.9°C with annual rainfall of 1829 mm, while Jimma has an altitude of 1754 m.a.s.l with the average annual temperature of from 26.3-26.3°C with its mean annual rainfall of 1,572mm. The major soil type in southwest Ethiopia is Nitosols [13]. Metu site is characterized by strong soil acidity and low phosphorus level (1.92) with the PH of 4.82, while Jimma is characterized by moderate soil acidity and phosphorus level (4.9) with the PH

of 5.46 [7]. Sixty four soybean genotypes including three standard check varieties (AFGAT, Clark-63K and Nyala) were evaluated in this study using simple lattice design. The genotypes were introduced from external source as rust tolerant genotypes (Table 1).

Each genotype was planted in a plot of four rows and four meter length with regular spacing of five cm between plants and 60cm between rows. All the agronomic management practices were applied for the experiment as per the recommendation.

Data was recorded on Agronomic traits such as days to flowering, days to maturity, plant height (cm), number of pod per plant, number of seed per plant, number of branch per plant, crop lodging, shattering hundred seed weight (gm) and grain yield (t ha-1). Disease for soybean rust and frog eye leaf spot data was also recorded. The scoring system was 1-9 scale (1=immune, 9=susceptible, then 1-3=resistant, 4-6=moderately resistant and 7-9 = susceptible.

Table 1. *Details of the 64 Soybean genotypes.*

Geno.	designation	description	Source of materials	Geno.	designation	description	Sourceof materials
1	PI567099A	pure line	USA	33	PI567025A	USA	pure line
2	G 7955-C3RPP (C1)	Pipe line	USA	34	PI605838	USA	pure line
3	MKSOY-2N white (C2)	Variety	USA	35	PI567090	USA	pure line
4	PI605823	pure line	USA	36	PI605773	USA	pure line
5	PI567020A	pure line	USA	37	PI416810	USA	pure line
6	PI567102B	pure line	USA	38	PI605854B	USA	pure line
7	PI471904	pure line	USA	39	PI594767A	USA	pure line
8	PI567039	pure line	USA	40	PI566989A	USA	pure line
9	PI567058D	pure line	USA	41	PI200466	USA	pure line
10	PI605824A	pure line	USA	42	PI635999	USA	pure line
11	PI578457A	pure line	USA	43	PI423960A	USA	pure line
12	PI567046C	pure line	USA	44	PI417208	USA	pure line
13	PI615445	pure line	USA	45	PI567059	USA	pure line
14	PI567180	pure line	USA	46	PI567053	USA	pure line
15	PI606405	pure line	USA	47	PI567068A	USA	pure line
16	PI594760B	pure line	USA	48	PI567034	USA	pure line
17	PI605891A	pure line	USA	49	PI567189A	USA	pure line
18	PI567104B	pure line	USA	50	PI594538A	USA	pure line
19	PI567054C	pure line	USA	51	AFGAT (C5)	Ethiopia	Variety
20	PI605891B	pure line	USA	52	PI230970	USA	pure line
21	PI567069A	pure line	USA	53	PI615437	USA	pure line
22	Cocker 240	pure line	USA	54	PI416886	USA	pure line
23	PI606397B	pure line	USA	55	PI417085	USA	pure line
24	PI567056A	pure line	USA	56	PI203398	USA	pure line
25	PI628932	pure line	USA	57	PI423972	USA	pure line
26	PI587905	pure line	USA	58	PI423960B	USA	pure line
27	PI567061	pure line	USA	59	PI507004	USA	pure line
28	PI567024	pure line	USA	60	PI340898A	USA	pure line
29	PI605865B	pure line	USA	61	PI416873B	USA	pure line
30	PI416826A	pure line	USA	62	PI506677	USA	pure line
31	PI506939	pure line	USA	63	Clarck	Ethiopia	Variety
32	PI587880A	pure line	USA	64	Nyal	Ethiopia	Variety

Data Analysis for simple lattice design was performed using the R-program software. The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson *et al* [14] as:

$$PCV= [\sigma p/ x] \times 100$$

$$GCV= [\sigma g/ x] \times 100$$

Where σp= phenotypic standard deviation (σg + σe), σg=genotypic standard deviation, σe= environmental standard deviation and x = grand mean for the trait x; PCV and GCV =phenotypic and genotypic coefficients of variation respectively.

Broad-sense heritability (H^2) for traits was estimated for pooled analyses over two locations using the formula adopted by Allard [15] as:

$$\sigma p^2 = \sigma g^2 + \sigma ge^2/e + \sigma e^2/re.$$

$$H^2 = \frac{\sigma g2}{\left[\sigma g2 + \frac{\sigma ge2}{e} + \frac{\sigma e2}{er}\right] \times 100}$$

Where σp^2 = phenotypic variance, σg^2 = genotypic variance, σge^2 = variance genotype by environment interaction, σe^2 = environmental variance, e= number of environment and r= number of replications.

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, was estimated in accordance with the methods illustrated by Johnson et al [14] as:

$$GA = k\sigma pH^2$$

$$GAM = (GA/x) \times 100$$

Where k = the standardized selection differential at 5% selection Intensity (k = 2.063), σp = phenotypic standard deviation, H^2 =Heritability and x = Grand mean.

3. Results and Discussion

3.1. Analysis of Variance

The combined analysis of variance across locations and year is presented in Table 2. The analysis of variance showed that mean squares due genotype was significant (P≤ 0.01) for all the traits, indicating genotypes were responded differently for each trait. Means squares due to genotype x location x year interaction found significant effect (P≤ 0.01) for hundred seed weight (HSW), soybean rust disease (SR) and grain yield (YLD). Generally, the observed variability of agronomic traits is dependent on genetic factors, environmental variables and the interaction factor.

Table 2. Mean squares of the combined analysis of variance for yield and related traits of 64 soybean genotypes at two location, evaluated during 2017-2018.

source of variation	Df	DTF	DTM	PH	NPP	NNSP	HSW	Rust	YLD (t/ha)
Geno.	63	692.06**	927.72**	4344.80**	1452.52**	14867.35*	14867.35**	164.85**	14867.35**
Location	1	2516.06**	6202.20**	239.67ns	427.78ns	8294.72ns	8294.72**	22911.38**	8294.7**
Year	1	5466.66**	1582.03**	843.83*	6496.86**	370559.55**	370559.55**	117.24ns	370559.55**
Location: Rep.: Block	28	26.85ns	23.58ns	302.06*	507.80ns	5880.32ns	5880.32ns	100.18**	5880.32ns
Geno.: Location	63	17.48ns	60.42ns	72.05ns	432.77ns	1261.313ns	1261.31**	164.85**	1261.31**
Geno.: Year	63	58.55**	121.46**	383.96**	632.40ns	11487.84*	11487.84**	97.30**	11487.84**
Location: Rep.	2	14.063ns	107.28ns	1066.13ns	1485.79ns	13037.81ns	13037.81ns	19.16ns	13037.81ns
Location: Year	1	2501.60**	6159.85**	262.81**	2843.55*	20289.00*	20289.000**	116.09ns	20289.00**
Geno.: Location: Year	63	17.74ns	59.40ns	67.29ns	235.53ns	721.46Ns	721.46**	97.27**	721.46**
Residuals	226	21.87	49.99	169.77	525.72	4220.95	4220.95	53.75	4220.95

Where, * = significant at (P≤0.05) and **= significant at (P≤.01), loc=location, Geno=genotype, Df=degree of freedom, DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP= number of seed per plant, SR=soybean rust, HSW=hundred seed weight, YLD= grain yield per [ha-1]

Based on the combined mean performance of the genotypes over environment (Table 3), variety Coker240 scored maximum grain yield (3.09 t/ha) followed by genotype PI567104B (3.00 t/ha), PI567054C (2.85 t/ha) and G 7955-C3RPP (2.82 t/ha), while the minimum yield was scored from PI416826A (1.33t/ha). The performance of the tested genotypes also showed resistance to moderately resistance to soybean rust. Maximum disease score was recorded from genotype PI567090 (25.52%), while the minimum was from PI594538A (3.78%). Latest physiological maturing genotype was genotype PI567104B (145.37 days) followed by PI567102B (144.75 days) and PI578457A (144.44 days), while the earliest genotype was PI615437 (104.58 days). Highest plant height was recorded from PI567104B (149.01 cm) followed by PI340898A (134.74 cm), while the lowest was recorded from genotype PI507004 (44.24 cm).

Table 3. Range and Mean values of yield and other morphological traits of 64 soybean genotypes evaluated across two sites during 2017-2018.

No.	Designation	Trait							
		DTF	DTM	PH	NPP	NSP	SR (%)	HSW	yld
1	PI567099A	72.98	124.45	119.04	54.95	121.80	8.98	8.60	1.79
2	G 7955-C3RPP (C1)	63.54	131.56	106.23	44.70	95.15	12.67	18.83	2.82
3	MKSOY-2N white (C2)	68.76	138.47	94.80	71.06	121.28	9.33	15.39	1.76
4	PI605823	72.40	135.63	81.40	45.40	107.03	4.36	14.89	2.14
5	PI567020A	72.58	136.74	120.66	52.52	127.07	18.91	11.49	2.37
6	PI567102B	79.01	144.75	144.37	96.53	154.43	10.08	11.35	2.23
7	PI471904	68.01	130.76	109.40	53.57	116.38	11.19	13.19	2.83
8	PI567039	72.82	128.45	110.66	34.62	81.73	8.58	12.77	2.53
9	PI567058D	69.58	133.71	114.31	43.51	126.41	8.52	13.32	2.28
10	PI605824A	65.61	120.69	105.23	37.88	84.92	9.62	12.95	1.83
11	PI578457A	67.94	144.44	116.19	36.95	75.05	13.64	14.04	1.96
12	PI567046C	68.87	124.74	97.11	45.86	179.65	8.24	11.88	2.49
13	PI615445	64.48	119.25	85.22	34.35	73.85	9.55	14.35	2.05
14	PI567180	58.90	116.19	81.54	33.27	60.56	9.73	16.03	1.73
15	PI606405	61.40	118.89	75.04	29.89	56.12	8.01	15.42	1.75

No.	Designation	Trait							
		DTF	DTM	PH	NPP	NSP	SR (%)	HSW	yld
16	PI594760B	63.23	122.00	98.49	46.43	112.50	8.12	15.29	2.27
17	PI605891A	61.82	119.77	84.54	29.67	64.39	12.11	14.91	2.38
18	PI567104B	79.18	145.37	149.01	74.61	143.37	11.48	12.30	3.00
19	PI567054C	68.82	127.19	98.76	52.83	118.26	8.95	12.65	2.85
20	PI605891B	66.43	134.13	98.05	44.49	95.72	12.54	13.58	2.54
21	PI567069A	79.08	140.30	104.69	58.82	130.23	16.76	8.42	2.36
22	Cocker 240	59.51	124.58	86.00	33.99	65.47	21.17	18.50	3.09
23	PI606397B	65.41	126.71	76.72	38.17	72.27	21.21	14.74	2.45
24	PI567056A	87.39	142.03	120.84	62.20	123.61	21.91	9.67	2.00
25	PI628932	54.95	124.19	63.93	32.38	61.47	13.05	17.40	1.77
26	PI587905	59.06	112.85	56.90	63.07	246.25	6.46	13.86	2.02
27	PI567061	71.14	134.75	113.45	52.51	131.25	8.14	15.60	2.49
28	PI567024	65.23	121.15	99.92	38.73	179.61	18.58	16.07	2.45
29	PI605865B	63.12	118.29	89.47	40.41	90.36	14.10	15.76	2.63
30	PI416826A	47.19	108.68	51.68	18.67	44.07	9.87	14.11	1.33
31	PI506939	67.44	131.60	106.25	45.29	112.51	5.81	12.91	2.71
33	PI587880A	54.95	124.90	72.98	44.67	98.41	5.99	20.60	1.76
34	PI567025A	69.17	130.09	109.63	42.11	100.26	10.35	12.51	2.15
35	PI605838	72.50	129.30	110.85	48.84	109.62	9.79	12.86	2.41
36	PI567090	82.55	138.17	133.98	64.09	136.72	25.52	10.70	2.18
37	PI605773	59.29	125.79	88.44	42.79	103.29	10.63	16.31	2.08
38	PI416810	56.50	115.27	117.88	34.69	66.44	14.70	18.88	2.71
39	PI605854B	63.86	123.70	83.20	41.76	80.60	11.49	15.68	2.55
40	PI594767A	63.34	111.25	61.18	37.76	80.55	6.99	12.07	2.13
41	PI566989A	75.23	134.51	92.64	53.99	115.87	18.26	12.41	2.05
42	PI200466	49.49	113.89	71.89	43.45	100.89	12.56	19.25	2.35
43	PI635999	62.57	125.38	88.58	31.72	68.05	8.76	19.25	1.98
44	PI423960A	56.86	120.99	84.79	39.62	86.67	10.08	14.97	2.39
45	PI417208	55.61	108.42	66.35	32.06	134.55	14.06	21.90	2.56
46	PI567059	59.89	114.25	89.23	39.80	93.01	8.74	15.27	2.09
47	PI567068A	75.68	125.42	105.89	67.51	298.52	8.86	8.32	1.84
48	PI567034	54.54	108.52	77.76	33.65	73.09	11.17	11.58	2.07
49	PI567189A	61.37	120.46	83.81	40.94	95.20	9.99	14.12	2.16
50	PI594538A	55.45	108.45	52.25	30.62	72.54	3.78	18.86	2.51
51	Afgat (C5)	64.81	131.70	99.82	52.08	121.19	14.77	13.88	2.42
52	PI230970	59.44	131.85	101.06	60.85	152.68	5.89	12.35	2.62
53	PI615437	63.86	104.58	72.29	41.10	92.05	7.23	15.39	2.35
54	PI416886	50.43	106.72	44.87	28.43	71.17	10.01	18.39	1.78
55	PI417085	61.63	123.68	91.28	32.67	75.18	10.34	22.01	2.97
56	PI203398	58.14	122.29	87.52	40.38	82.52	8.44	14.63	2.47
57	PI423972	70.32	126.64	94.00	44.93	107.26	15.35	16.26	2.08
58	PI423960B	50.89	116.96	73.34	34.50	78.30	12.89	19.73	2.29
59	PI507004	49.07	109.11	44.24	20.48	31.49	6.92	19.40	2.04
60	PI340898A	88.65	145.51	134.74	56.51	116.67	15.08	11.26	1.99
61	PI416873B	48.49	106.00	55.95	27.82	119.57	8.37	20.48	2.02
62	PI506677	53.31	108.65	57.39	29.60	74.16	9.34	24.01	2.19
63	Clarck	63.50	124.75	77.39	42.99	103.48	24.14	15.36	2.41
64	Nyal	58.15	115.11	65.88	34.21	70.02	21.82	15.43	2.68
	maximum	88.65	145.51	149.01	96.53	298.52	25.52	24.01	3.09
	mean	64.57	124.48	91.50	43.84	104.40	11.69	14.93	2.27
	minimum	47.19	104.58	44.24	18.67	31.49	3.78	8.32	1.33
	CV	7.24	5.68	14.24	52.30	62.23	62.72	11.15	17.51
	LSD (5%)	4.61	6.97	12.84	22.59	64.01	7.22	1.64	0.39
	P-value	**	**	**	*	**	**	**	**

3.2. Estimation of Genotypic and Phenotypic Coefficients of Variation

The estimates of genetic variance components (GCV, PCV, H^2, GA &GAM) presented in table 4. This finding showed that, PCV was higher than GCV for most of studied traits, suggesting the observed variation was the combined of effect of genotypic and environment factor. According to [16] descriptions, high PCV and GCV were recorded all of the traits except number of pod which recorded low PCV (10.0%) and high GCV (79.58%) respectively. High PCV and GCV indicated, the genotype could be reflected by the phenotype, which means selection will be effective based on the phenotypic performance for these traits.

However, the extent of the environmental influence on any character is indicated by the magnitude of the differences between PCV and GCV. Large differences reflect high environmental influence, while small differences reveal high

genetic influence [17]. Accordingly, the difference between PCV with the corresponding GCV values was relatively higher for number of pod and soybean rust, suggesting the high influence of the environment on these traits. While the difference between PCV and GCV was relatively low for the remaining traits, which means selection based on phenotypic performance would be effective to bring considerable improvement in these traits. The current finding is in agreement with Masreshaw et al [11, 12] and Neelima et al [18] who reported high GCV and PCV for number of pod, number of seed, plant height and hundred seed weight.

3.3. Heritability and Genetic Advance

According to Gadde [19], heritability estimate was classified as low (<30%), moderate (30-60%) and high (>60%). Based on this classification plant height (98.51%), number of pod (89.39%) and number of seed (88.49%), grain yield (83.22%) and hundred seed weight (74.10) found high heritability estimates. Moderately heritable traits were exhibited for days to flowering (57.05%) and days to maturity (40.89%), while soybean rust was found very low heritable trait (1.45%). Similar to the current finding high heritability estimates on plant height, days to maturity, hundred seed weight and number of pod was reported by [7, 8, 11, 18, 20].

Genetic advance as the percent of mean (GAM) is categorized as low (0-10%), medium (10-20%) and high (≥20%) Johnson et al (1955). According to this category, the highest GAM was recorded for number of seed (221.09%) followed by number of pod (155.22%), plant height (146.36%), hundred seed weight (110.60%), grain yield (69.57), days to flowering (62.66), days to maturity (31.23%). In contrast, low estimates of GAM were recorded for soybean rust (17.45). Traits which showed low heritability, GCV and low

GAM were under high environmental influence; hence selection based on such traits would be less effective.

According to Johnson et al [15] high heritability estimates with high genetic advance is usually more helpful in predicting increase under selection than heritability estimates alone. Regarding this suggestion, Accordingly, combined high GCV, high heritability and high GAM were recorded for plant height (71.48%, 98.51% and 146.36%), number of pod (79.58%, 89.39% and 155.22%), number of seed (113.92%, 88.49% and 221.09%), hundred seed weight (62.28%, 74.10% and 110.60%) and grain yield (36.97%, 83.22% and 69.57%), which means these traits are controlled more of by additive genes [21]. Hence, this trait can be improved through direct selection more easily than other traits. Similar to this result, high heritability combined with high GAM for plant height and hundred seed weight was reported by Abush et al [7], while Aditya et al [22] and Neelima et al [18] were reported combined High heritability with high GAM for plant height and number of pod. Masreshaw et al (2021) also reported combined high GCV, high heritability and high GAM for days to flowering, plant height, number of pod, number of seed and hundred seed weight.

However, other traits showed low to moderate heritability along with low genetic advance, suggests that those traits are influenced by environmental effects and are most likely governed by both additive and non-additive (dominant, epistemic) type of gene action [23], this would make complicated to improve these traits through simple selection, to the extent that cross breeding is the best alternative method for improvement of such kind of traits. Saravanan et al [24] also suggested that if a trait is controlled by non-additive type of genes then selection for this trait should be postponed and performed safely in advanced/succeeding generations.

***Table 4.** Estimates of variance components for 8 traits of 100 soybean genotypes.*

| Traits | range | | mean | (σ²g) | (σ²p) | H (%) | GCV (%) | PCV (%) | GA | GAM (%) |
	Min	Max								
DTF	88.65	47.19	64.57	674.32	1181.96	57.05	40.21	53.24	40.46	62.66
DTM	145.51	104.58	124.48	868.32	2123.61	40.89	23.67	37.02	38.87	31.23
PH	149.01	44.24	91.50	4277.51	4342.27	98.51	71.48	72.02	133.92	146.36
NPP	96.53	18.67	43.84	1216.99	1361.43	89.39	79.58	10.00	68.04	155.22
NSP	298.52	31.49	104.40	14145.89	15985.20	88.49	113.92	121.10	230.82	221.09
Rust	25.52	3.78	11.69	67.58	4674.18	1.45	70.33	584.87	2.04	17.45
HSW	24.01	8.32	14.93	86.43	116.64	74.10	62.28	72.35	16.51	110.60
YLD	3.09	1.33	2.27	0.70	0.85	83.22	36.97	40.53	1.58	69.57

(σ2g)=genotypic variance, (σ2P)=phenotypic variance, H= broad since heritability, GCV=genotypic coefficient of variance, PCV= phenotypic coefficient of variance, GA=genetic advance, GAM= genetic advance as percent of mean, DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP= number of seed per plant, SR= SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha⁻¹

4. Conclusions

The current morphological variability test of soybean genotypes were found diverse in terms of different traits. Combined high genotypic coefficients of variation (GCV), high heritability (H²) and high genetic advance as present of mean (GAM) were recorded for for plant height (71.48%,

98.51% and 146.36%), number of pod (79.58%, 89.39% and 155.22%), number of seed (113.92%, 88.49% and 221.09%), hundred seed weight (62.28%, 74.10% and 110.60%) and grain yield (36.97%, 83.22% and 69.57%). Hence, this trait can be improved through direct selection more easily than other traits. Hence this research will enhance the utilization of variation present with in soybean genotypes for crossing and selection program.

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