

# Genetic Variability of Soybean (*Glycine Max* (L) Merrill) Genotypes Under Moisture Stress Areas of Ethiopia

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**Abstract:** Characterization and evaluation soybean genotypes for different traits of interest is important to facilitate the breeding program. The study was conducted using 25 early maturing soybean genotypes at Mehoni, Humera, Jinka, Tiro-afeta, and Gofa, Ethiopia during 2018 main cropping seasons. The objective of the experiment was to estimate genetic variability of these breeding materials. The genotypes were planted using 5x5 simple lattice design and managed as per the soybean recommended agronomic production practices. Data on important traits like days flowering (DTF), days to maturity (DTM), plant height (PH), number of pod per plant (NPP), number of seed per plant (NSP), hundred seed weight (HSW) and yield per hectare (YLD) was recorded. The pooled analysis of variance revealed highly significant difference among locations (L) and genotypes (G). The maximum yield was recorded from genotype; JIM-ALM/CRFD-15-SA (2.30 t/ha) followed by PI417129B (2.27 t/ha), with the yield advantage of (27% and 37%) and (25% and 36%) relative to the checks varieties; Gazale (1.81t/ha) and Nova (1.67t/ha), respectively. Based on earliness of the genotypes, all the tested genotypes were found early with the range of 86 to 105 days. High phenotypic (PCV) and high genotypic coefficients of variation (GCV) were recorded for DTF (148.38% and 142.29%), PH (97.64% and 95.13%), NPP (56.68% and 47.63%), NSP (136.52% and 111.43%), HSW (55.92% and 45.45%) and YLD (133.80% and 92.09%), respectively. While, high PCV (20.78%) with moderate GCV (15.90%) was recorded from DTM. However, the difference between PCV with the corresponding GCV values was relatively higher for NSP and YLD, suggesting high influence of the environment on these traits. High heritability estimates was recorded for DTF (91.95%), NPP (70.62%), NSP (66.62%), and HSW (66.07%), while the remaining showed moderate heritability. High genetic advance as percent of mean (GAM) was found for all the traits studied. Whereas, combined high GCV, high heritability and high GAM were recorded for DTF (142.29%, 91.95% and 281.48%), PH (95.23%, 95.23% and 191.62%), NPP (47.63%, 70.62% and 82.57%), NSP (111.43%, 66.43% and 187.63%) and HSW (45.45%, 66.07% and 76.21%), respectively, which means these traits are controlled more of by additive genes. Generally, the existences of sufficient variability among the evaluated materials create immense opportunity to bring considerable improvement through selection and cross breeding in soybean breeding program.

**Keywords:** Soybean, Physiological Maturity, Moisture Stress, Heritability, Genetic Advance

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## 1. Introduction

Soybean is one of the most important pulses and oil crops for food, feed and industries. It supplies about 60% of the total oil seed crop produced in the world [1]. Its grain is rich in quality protein (35-40%) and Vegetable oil (18-22%) content [2-4]. Similarly, the crop also contains essential vitamins and minerals, which helps to reduce the risk of cardiovascular and some chronic diseases [5, 6]. Therefore, soybean is particularly a crop of great promise for developing

countries faced with extensive malnutrition and food insecurity. The by-product of soy meal is also the main sources of protein for farm animal and aquaculture feeding [7, 8]. In low input farming systems, it is an ideal crop in improving and amending soil properties through nitrogen fixation and the ability to break lifecycles of pests and disease in cereal rotation system [9].

Soybean has the potential to grow under a wide range of climate conditions. It is grown over 122 million-hectare of land with 341.8 million tons of annual production in the

world. The major producer and exporter countries in the globe are Brazil followed by USA, Argentina and China, accounting for almost 90% of the world production [10]. African producers contribute less than 1% of the world soybean. South Africa, Nigeria and Zambia are the top producers, while Ethiopia is the sixth in Africa [11]. Soybean crop introduction and cultivation in Ethiopia was date back to 1950s with the aim of replacing imported soybean flour, inclusion of the crop to the existing farming system and supplementing the diet of Ethiopians [12]. Since then, the utilization and consumption soybean-based foods are becoming popular in Ethiopia. For the last decades, local food processing factory has used soybean to prepare balanced food particularly for women and children [13]. Currently, a number of oil processing industries have been launched in Ethiopia to use soybean as a row material.

The vast majority of low land to mid land agro ecology of Ethiopia is the potential arable land suitable for soybean production. The entire low to mid altitude maize belt areas are also appropriate for soybean production [14]. However, area coverage (54,543.26 hectare) and annual soybean production (125,623.20 ton) in Ethiopia is below its potential [15] and the country is still spending many on the import of edible oil to meet the domestic demands.

Adaptation of plants to the local environment with all its physical and biological stresses is the substance of evolution. Environmental adversity in relation to crop productivity can be viewed as the cause of stress on a particular genotype, and it will vary with the genotypes. Stress resistance can be divided into "avoidance" and "tolerance." [16]. In the USA, losses for major crops due to physical environmental factors were calculated as 66.5% (compared to 9.3% for losses to all biological factors of diseases, insects, and weeds) [17]. Current breeding programs generally have a major component involving two or three of these objectives-overcoming disease susceptibility, insect susceptibility, and physical factor limitation to yield. Based on their maturity period, Soybean genotypes are classified in to early, medium and late maturing groups. Early maturing genotypes are suitable for moisture stress areas and also suited for double cropping for long duration rainfall condition. Due to climate

change drought spell is increasing across soybean growing locations and limited genetic information to develop widely adapted variety for high temperature and moisture stress area one of the determinant factors for low production and productivity in the country. Therefore, it is a high time to look early maturing varieties for moisture stress areas. Based on such justification, the current study was undertaken to evaluate and estimate the genetic variability of the early maturing soybean genotypes for morphological traits under moisture stress agro ecologies of Ethiopia.

## 2. Materials and Methods

The experiment was conducted at Mehoni, Humera, Jinka, Tiro-afeta and Areka during 2018 cropping season. The description of experimental location is stated in Table 1. Twenty-five soybean genotypes along with check varieties (Nova and Gazele) were evaluated in this experiment. All the tested soybean genotypes except genotype JM-ALM/CRFD-15-SA were introduced from USA. Genotype; JM-ALM/CRFD-15-SA, is recombinant inbred line developed by JARC. The genotypes which started with PI designation were introduced with objective to screen for rust resistance/tolerance in Ethiopian condition because they have same resistance gene during introduction and were advanced from rust resistance trials based on their earliness. While the rest were just introduced as breeding materials (Table 2).

The field experiment was conducted using 5x5 simple lattice designs for all testing locations. Planting was done in a plot of four rows with 4m length and with regular spacing of 5 cm between plants and 60cm between rows. Two seeds per hill were placed carefully to ensure the first germination and thinning was made at 2-3 weeks after emergence. NPS fertilizer was applied during sowing at the recommended rate of 122 kg /hectare and the rest agronomic management was done as per the recommendation. The following important agronomic characters like Days to Flowering, Plant Height (cm), Number of Pod per plant, Number of Seed per plant, hundred seed weight (gm) and Grain Yield (t/ha) were recorded according to the random sampling methods. All the data were collected from the middle two harvestable rows.

Table 1. Description of experimental locations.

Location	Altitude	longitude	Latitude	Temperature		Annual rain fall
				min	max	
Mehoni	1571	39°38'38"	12°47'56"	18	25	750mm
Jinka	1920	036°00"	05°00"	16	27	1274mm
Humera	586	36°36'29"	14°17'26"	19	36	6111mm
Tiro-afeta	1768	07°49' 0"	037°13' 0"	18	26	1829mm
Areka (Gofa)	1774	7°4'00"	7°42'00"	13	28	1298 mm

Climate –data-org, 2019

Table 2. Soybean bean genotypes tested at five locations during 2018.

Nº.	Genotypes	source	Maintainer	Testing Location
1.	PI594760B	introduced from USA	JARC/EIAR	Mehoni
2.	PI567104B	introduced from USA	JARC/EIAR	Jinka
3.	PI567054C	introduced from USA	JARC/EIAR	Humera
4.	PI417089A	introduced from USA	JARC/EIAR	Tiro-afeta

N°.	Genotypes	source	Maintainer	Testing Location
5.	PI200466	introduced from USA	JARC/EIAR	Areka (Gofa)
6.	PI203398	introduced from USA	JARC/EIAR	
7.	LD13-00833	introduced from USA	JARC/EIAR	
8.	SA13-3135	introduced from USA	JARC/EIAR	
9.	LD10-10198	introduced from USA	JARC/EIAR	
10.	LD13-07022	introduced from USA	JARC/EIAR	
11.	F6 LG06-5920 x LG04-6000	introduced from USA	JARC/EIAR	
12.	LG04-4468 x U02-242055	introduced from USA	JARC/EIAR	
13.	F6 LG04-4717 x LG05-4292	introduced from USA	JARC/EIAR	
14.	PI416873B	introduced from USA	JARC/EIAR	
15.	PI471904	introduced from USA	JARC/EIAR	
16.	PI417129B	introduced from USA	JARC/EIAR	
17.	PR-143-(14)	introduced from USA	JARC/EIAR	
18.	KS4895	introduced from USA	JARC/EIAR	
19.	F6 LG03-3020/LG03-3780	introduced from USA	JARC/EIAR	
20.	PI594172A	introduced from USA	JARC/EIAR	
21.	F6 LG05-4321x LG05-4550	introduced from USA	JARC/EIAR	
22.	JM-ALM/CRFD-15-SA	recombinant inbred line	JARC/EIAR	
23.	Gazale	introduced from USA	JARC/EIAR	
24.	Nova	introduced from USA	JARC/EIAR	
25.	F6LG04-5187/LG05-4092	introduced from USA	JARC/EIAR	

Prior to proceeding with the analysis of variance (ANOVA), homogeneity test was made for each variable using the  $F_{\max}$  test and then all the data considered were subjected to combined analysis of variance (ANOVA) over

environment for simple lattice design, which was performed using the SAS program software. The total variability for the traits was quantified using pooled analyses of variance over five locations using the following model.

$$P_{ijkt} = \mu + y + l_t + r_{i(t)} + b_{j(i)(t)} + g_k + (gy)_k + (yl)_t + (gl)_{kt} + (ylg)_{tk} + e_{ijkt}$$

where  $P_{ijmkt}$  = phenotypic value of  $k^{\text{th}}$  genotype under  $i^{\text{th}}$  replication at  $t^{\text{th}}$  location and  $j^{\text{th}}$  incomplete block with replication  $i$ , location  $t$ ;  $l_t = t^{\text{th}}$  location;  $r_{i(t)}$  = the effect of replication  $i$  with in location  $t$ ;  $b_{j(i)(t)}$  = the effect of incomplete block  $j$  with in replication  $i$ , location  $t$ ;  $g_k$  = the effect of  $k^{\text{th}}$  accession;  $\mu$  = grand mean and  $(gy)_k$ ,  $(yl)_t$ ,  $(gl)_{kt}$  and  $(ylg)_{tk}$  = the interaction effects and  $e_{ijkt}$  = random error. Partitioning of the total variation into components due to genotype ( $\delta g^2$ ), environment ( $\delta e^2$ ) and genotype by environment interaction ( $\delta ge^2$ ) deviations was performed from the analyses of variance by calculating the expected mean squares and similarly the components from pooled analysis of variance across locations were calculated. The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson *et al* [18] as:

$$PCV = [\sigma_p / x] \times 100$$

$$GCV = [\sigma_g / x] \times 100$$

Where  $\sigma_p$  = phenotypic standard deviation ( $\sigma_g + \sigma_e$ ),  $\sigma_g$ =genotypic standard deviation,  $\sigma_e$ = environmental standard deviation and  $x$  = grand mean for the character  $x$ ; PCV and GCV = phenotypic and genotypic coefficients of variation respectively.

Estimate of heritability

Broad-sense heritability ( $H^2$ ) for traits was estimated for pooled analyses over two locations using the formula adopted by Allard [19] as:

$$\sigma_p^2 = \sigma_g^2 + \sigma_{ge}^2/e + \sigma_e^2/re.$$

$$H^2 = \frac{\sigma_g^2}{\left[ \sigma_g^2 + \frac{\sigma_{ge}^2}{e} + \frac{\sigma_e^2}{er} \right]} \times 100$$

Where  $\sigma_p^2$  = phenotypic variance,  $\sigma_g^2$  = genotypic variance,  $\sigma_{ge}^2$  = variance genotype by environment interaction,  $\sigma_e^2$  = 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* (1955) as:

$$GA = k\sigma_p^2$$

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

Where  $k$  = the standardized selection differential at 5% selection intensity ( $k = 2.063$ ),  $\sigma_p$  = phenotypic standard deviation,  $h^2$  = Heritability and  $x$  = Grand mean.

### 3. Results and Discussion

The results from the combined analysis of variance across the five locations are presented in table 3. The pooled analysis variance revealed that, the mean square due to location (L) and genotype (G) was highly significant ( $P \leq 0.01$ ) for all the traits considered, indicating the distinct nature of the five test locations and the traits were responded differently to each of the soybean genotypes tested under different moister deficient areas of Ethiopia. The possible reasons for the significant difference among the genotypes for the traits might be due to genetic difference among the

genotypes. The existences of sufficient variability among the evaluated materials create immense opportunity to bring considerable improvement through selection and cross breeding in the future soybean improvement program.

Mean squares due to the interaction between location and genotype were non-significant for all traits, meaning that the soybean genotypes exhibited consistent relative performance in each location in a year. The significant difference observed for measured traits in this study were in agreement with the finding of earlier authors who reported considerable genetic variability within the soybean genotypes for yield, disease resistance and growth characters [20-24].

The performance of the genotypes ranged widely for days to flowering (42-58), days to maturity (88-105), total plant height (28.56-74.05), number of pod per plant (24.3-42.27), number of seed per plant (22.89-66.04), hundred seeds weight (12.27-21.15gm) and yield per hectare (0.8-2.3 ton/ha). Out of these important traits, highest ranges were obtained for number of seed per plant followed by plant height, number of pod per plant, days to flowering and days to maturity, which played important role in the total variability of tested soybean genotypes.

The maximum yield was recorded from genotype; JIM-ALM/CRFD-15-SA (2.3t/ha) followed by PI417129B (2.27ton/ha), and PR-143-(14) (2.09 ton/ha), which exhibited a yield advantage of (27% and 37%), (25% and 36%) and (15% and 25%), from the standard checks; Gazale (1.81t/ha) and Nova (1.67t/ha) respectively.

Based on earliness of the genotypes, all the genotypes exhibit early physiological maturity with the range of 86 to 105 days to flowering. The outstanding genotypes; JIM-ALM/CRFD-15-SA and PI417129B also found to be earlier (95 and 94 maturity date respectively) than the standard check Gazale (102 days to maturity), but not from check Nova (86 days). Generally, all the tested genotypes were fitted with the earliness concepts; hence, there is an opportunity to find genotypes among the tested entries that perform better than the existing varieties in moisture stressed areas and/or to use them as parents for hybridization programs.

### 3.1. Estimation of Genotypic and Phenotypic Coefficients of Variation

Table 5 presents grand means, the estimates of genotypic and phenotypic variance, genotypic (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability ( $H^2$ ), genetic advance (GA) and genetic advance expressed as percent of mean (GAM). The ranges for PCV and GCV were (15.9%-142.29%) and (20.78%-148.38%), respectively. The present finding illustrated that, PCV was higher than GCV for all the studied traits, suggesting the observed variation in the soybean genotypes were both the combination of genotypic and environment effect. According to Deshmukhs *et al.* [25] descriptions, High phenotypic and genotypic coefficients of variation were recorded for days to flowering (148.38% and 142.29%), plant height (97.64% and 95.13%), number of pod per plant (56.68% and 47.63%), number of

seed per plant (136.52% and 111.43%), hundred seed weight (55.92% and 45.45%) and yield per hectare (133.80% and 92.09%), 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; While, high PCV (20.78%) with moderate GCV (15.90%) was recorded from days to maturity.

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 [26]. Accordingly, the difference between PCV with the corresponding GCV values was relatively higher for number of seed per plant and gain yield, suggesting the high influence of the environment on these traits. Though, the difference between PCV and GCV was comparatively low for plant height, days to flowering, number of pod per plant and hundred seed, indicating the minimal influence of environment on the expression of these traits. Therefore, selection based on phenotypic performance would be effective to bring considerable improvement in these traits. The current finding is in agreement with Neelima *et al.* [24] who reported high GCV and PCV for number of pod, number of seed, plant height and hundred seed weight.

### 3.2. Heritability and Genetic Advance

Gadde (2002) generally classified heritability estimates as low (<30%), moderate (30-60%) and high (>60%). Based on this classification, plant height (95.13%), days to flowering (91.95%), number of pod (70.62%), number of seed (66.62%), and hundred seed weight (66.07%) exhibited high heritability estimates. On the other hand, moderate broad sense heritability estimates were observed for days to maturity (58.52%) and grain yield per hectare (47.99%). Similar to the current finding high heritability estimates on plant height, hundred seed weight and number of pod was reported by [20, 24, 27].

As stated by Johnson *et al* [18] the genetic advance as the percent of mean was categorized as low (0-10%), medium (10-20%) and high ( $\geq 20\%$ ). As per this suggestion, the highest GAM was observed for days to flowering (281.48%), followed by plant height (191.62%), number of seed (187.63%), yield per hectare (132.40%), and number of pod (82.57%), hundred seed weight (76.21%) and days to maturity (25.09%).

High heritability estimates accompanied by the high genetic advance is usually more helpful in predicting increase under selection than heritability estimates alone [18]. Accordingly, combined high GCV, high heritability and high GAM were recorded for days to flowering (142.29%, 91.95% and 281.48%), plant height (95.23%, 95.23% and 191.62%), number of pod (47.63%, 70.62% and 82.57%), number of seed (111.43%, 66.43% and 187.63%) and hundred seed weight (45.45%, 66.07% and 76.21%), respectively, which means these traits are controlled more of by additive genes [28].

Hence, this trait can be improved through direct selection more easily than other traits. Similar to this investigation, high heritability combined with high GAM for plant height and hundred seed weight was reported by Abush *et al.* [20], while Aditya *et al.* [27] and Neelima *et al.* [24] were reported combined High heritability with high GAM for plant height and number of pod. Whereas, days to maturity and grain

yield showed moderate heritability (58.52% and 47.99%) along with high genetic advance (25.09% and 132.46%), respectively, suggests that those traits are governed by both additive and non-additive (dominant, epistemic) type of gene action [29], therefore, cross breeding is the best alternative method rather than simple selection for improvement of such kind of traits.

**Table 3.** Mean squares of combined analysis of variance for 7 traits of 25 soybean genotypes evaluated in 2018 main cropping season across five locations of Ethiopia.

Traits	MSL (df=)	MSG (df=)	MSGxL (df=)	MSE (df=)	CV (%)
FD (days)	717.01**	5235.76**	1619.1ns	20.61	9.55
MD (days)	1429.73**	293.46**	66.26ns	73.1	9.1
PH (cm)	684.5**	1918.79**	104.03ns	176.5	30.5
PP (count)	869.5**	383.42**	101.47ns	125.7	34.5
SP (count)	12766.38**	4091.35**	898.6ns	1185.01	40.24
HW (g)	281.23**	63.89**	6.48ns	6.61	15.2
YD (q)	22.55**	2.49**	0.16ns	0.38	37

Where, \* = significant at ( $P \leq 0.05$ ), and \*\* = highly significant at ( $P \leq 0.01$ ), MSL = mean Squares of locations, MSG = mean squares of genotypes, MSGxL = mean square of genotype x location interaction, MSE = mean squares of error, CV = coefficient of variation. FD = days to 50% flowering, MD = days to maturity, PH = plant height, PP = pod per plant, SP = seed per plant, HW = hundred seed weight, YD = yield per ha-1, and df = degree of freedom.

**Table 4.** Mean of yield and yield related parameters of PNVT soybean in the year 2018 over location.

Trt. No	Designations	DTF	DTM	PH (cm)	NPP	NSP	HSW (gm)	YLD (t/ha)
1	PI594760B	50	98	49.29	32.97	49.40	15.41	1.15
2	PI567104B	58	105	74.05	42.27	57.29	12.93	0.96
3	PI567054C	54	98	60.60	31.13	32.65	12.27	1.97
4	PI417089A	48	94	57.46	31.16	24.43	19.41	1.63
5	PI200466	46	90	45.31	24.55	22.89	18.85	1.30
6	PI203398	50	97	47.45	31.99	37.83	18.01	1.74
7	LD13-00833	44	88	35.72	36.13	45.68	15.66	1.24
8	SA13-3135	44	88	28.56	36.88	54.00	18.22	1.19
9	LD10-10198	44	90	37.47	37.45	51.32	14.83	1.29
10	LD13-07022	43	88	34.37	36.00	55.36	18.47	1.74
11	F6 LG06-5920 x LG04-6000	42	90	30.02	29.89	44.92	18.03	0.80
12	LG04-4468 x U02-242055	44	89	36.81	33.64	52.59	16.13	1.45
13	F6 LG04-4717 x LG05-4292	44	89	35.59	33.27	42.19	15.63	1.17
14	PI416873B	45	91	34.39	24.89	26.88	21.15	1.29
15	PI471904	52	100	65.40	33.79	37.57	13.54	1.82
16	PI417129B	51	94	44.35	40.45	66.04	14.56	2.27
17	PR-143-(14)	50	99	53.55	41.65	53.02	18.35	2.09
18	KS4895	52	98	32.69	32.71	44.61	17.26	1.93
19	F6 LG03-3020/LG03-3780	44	90	34.47	29.15	37.81	16.92	1.58
20	PI594172A	47	90	35.53	24.30	27.83	17.08	1.03
21	F6 LG05-4321x LG05-4550	44	92	39.49	25.64	32.23	17.79	2.08
22	JM-ALM/CRFD-15-SA	50	95	39.38	30.24	31.69	17.63	2.30
23	Gazale (1)	48	102	53.90	43.40	113.0	18.30	1.81
24	Nova (C2)	44	86	54.50	50.20	129.2	12.90	1.67
25	F6LG04-5187/LG05-4092	44	93	35.41	28.84	39.07	16.98	1.68
	min	42.00	86.30	28.56	24.30	22.89	12.27	0.80
	max	58.00	105.0	74.05	50.20	129.20	21.15	2.30
	Mean	47.24	93.37	43.83	33.70	48.38	16.65	1.57
	LSD	5.66	10.66	16.57	13.98	42.93	3.21	0.77
	CV	9.55	9.10	30.50	34.50	40.24	15.20	37.00

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, HSW = hundred seed weight, YLD = yield per ha-1, CV, Coefficient of variation, LSD, Least significant difference.

**Table 5.** Estimates of variance components for 7 traits of 25 soybean genotypes.

Traits	Range Min	Max	Mean	( $\sigma^2_g$ )	( $\sigma^2_p$ )	H (%)	GCV (%)	PCV (%)	GA	GAM (%)
DTF	42.00	58.00	47.24	4518.8	4914.3	91.95	142.29	148.38	132.98	281.48
DTM	86.30	105.00	93.37	220.4	376.6	58.52	15.90	20.78	23.43	25.09
PH	28.56	74.05	43.83	1742.3	1831.5	95.13	95.23	97.64	83.99	191.62

Traits	Range		Mean	$(\sigma^2_g)$	$(\sigma^2_p)$	H (%)	GCV (%)	PCV (%)	GA	GAM (%)
	Min	Max								
NPP	24.30	50.20	33.70	257.7	365.0	70.62	47.63	56.68	27.83	82.57
NSP	22.89	129.20	48.38	2906.3	4362.7	66.62	111.43	136.52	90.78	187.63
HSW	12.27	21.15	16.65	57.3	86.7	66.07	45.45	55.92	12.69	76.21
YLD	0.80	2.30	1.57	2.1	4.4	47.99	92.69	133.80	2.08	132.46

$(\sigma^2_g)$ =genotypic variance,  $(\sigma^2_p)$ =phenotypic variance, H= broad sense 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, HSW=hundred seed weight, YLD= yield per ha-1.

## 4. Conclusions

In this investigation, 25 early maturing soybean genotypes were tested across locations. The pooled analysis variance revealed that, the mean square due to location (L) and genotype (G) was highly significant ( $P \leq 0.01$ ) for all the traits considered. The maximum yield was recorded from genotypes JIM-ALM/CRFD-15-SA (2.3t/ha) followed by PI417129B (2.27ton/ha), and PR-143-(14) (2.09 ton/ha), which exhibited a yield advantage of (27% and 37%), (25% and 36%) and (15% and 25%), from the standard checks; Gazale (1.81t/ha) and Nova (1.67t/ha) respectively. Based on earliness of the genotypes, all the tested genotypes were early with the range of (86 to 105.0days). Combined high GCV, high heritability and high GAM were recorded for days to flowering, plant height, number of pod, number of seed and hundred seed weight, respectively, which means these traits are controlled more of by additive genes. Generally, the existences of sufficient variability among the evaluated materials create immense opportunity to bring considerable improvement through selection and cross breeding in the future soybean improvement program.

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