Genetic Variability and Association of Traits in Soybean (*Glycine max* (L.) Genotypes in Ethiopia

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Abstract

The study was conducted at Jimma andMetu, southwestern Ethiopia during 2019 main cropping season to estimate the extent of genetic variability and association among traits in100soybeangenotypes(Glycine Max (L.). The field experiment was laid down in 10 x10 simple lattice design. The combined analysis of variance revealed the presence of significant (P<0.01) and wide range ofvariation among the tested genotypes for most of the traits. The maximum grain yield per hectare was recorded on genotypes; T1-EL-OS-JM17-E1, T4-EL-LG-65-JM17-A11 and T4-EL-LG-65-JM17-F2(2.50 t/ha each) while the minimum (0.85t/ha) was obtained from T5-EL-LD-77-JM17-D4.High yielding genotypes had a yield advantage of 32.98% and 61.29% compared with the standard checks (Nyala and Clark 63k), respectively. Subsequent 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 (24.80%, 87.85% and 47.95%), number of pods per plant (25.34%, 69.38% and 43.55%) and hundred seed weight (20.74%, 75.29% 37.12%), which denotes, these traits can be improved through direct selection more easily than other traits. Cluster analysis categorized 100 soybean genotypes into five clusters. The maximum inter cluster distance was found between clusters-IV and V, suggesting superior recombinants can be realized by crossing genotypes in these clusters. Principal component analysis (PCA) revealed that, the 1stfour PCA with Eigen values exceeding one were responsible for about 72.62 % of the total variation. Out of the entire variations, 1stPCA and the 2ndPCA accounted for more than two third of the total variations (53.13%). Therefore, discrimination of the genotypes into different clusters was mainly due to number of pod per plant, number of seed per plant, grain yield, plant height, days to flowering, days to maturity and hundred seed weight. Grain yield exhibited significant (P<0.05) and positive phenotypic and genotypic correlation coefficient to days to maturity, plant height , number of pod per plant, number of seed per plant, number of branch per plant and soybean rust. Except days to maturity and frog eye leaf spot, all other traits showed positive direct effect on grain yield. Number of pod per plant and plant height showed positive direct effect and strong positive genotypic correlation coefficient with grain yield. Therefore, these traits should be considered as important selection indices for yield improvement program. Generally, the present study revealed the existence of enormous genetic variability among soybean genotypes for various important morphological traits.

Keywords: GCV, PCV, Heritability, GA, Cluster, Correlation, Path coefficient

Introduction

Soybean (*Glycine max* L., 2n=40) belongs to the genus *Glyicine* in the family *Leguminasae* (Bermard and Weiss, 1973). It is a high value and profitable crop due to its versatile uses. Soybean grain is reach in quality protein (40%) and oil (20%) content (Singh *et al.,* 2008; Fekadu *et al*., 2009). Soybeans represented 59% of the world's vegetable oilseed production (USDA, 2022). The by-product or soy meal is also the main source of protein used for farm animal; livestock, poultry, and pig feeding (Clarke and Wiseman, 2000; Stevanovic *et al*., 2017). Moreover, 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 diseases in cereal rotation system (Graham and Vance, 2003). Therefore, soybean is the crop of great promise for most developing countries faced with extensive malnutrition and food insecurity.

The major producing and supplying countries in the world are Brazil, USA, Argentina and China, accounting for more than 90% of the world production. African producers contribute less than 1% of the world soybeans. South Africa, Nigeria and Zambia are the top soybean producers; While, Ethiopia is the sixth producer on the continent (Cornelius and Goldsmith, 2019).

In Ethiopia, FAFA food factory has been using soybean to prepare balanced food particularly for the most vulnerable subset of impoverished families like women and children (MOA, 2018).The utilization and consumption of locally prepared Soybean-based foods such as porridge; kukis, biscuit, bread, soymilk and yogurt are becoming accepted and popular in the country. According to CSA (2020) report, the estimated area coverage, total production and productivity in Ethiopia was54,543.26 hectare, 125,623.20 ton, and 2.3 ton/ha, respectively. This means, the gap between its potential and national average productivity remains high due to several production constraints. Limited availability of adaptable improved varieties, different biophysical stresses, poor extension services, poor management practices and lack of market access for small scale farmers are the major problems.

Pre-breeding activity in any crop is an art of evaluation of genetic resources with identification their desirable traits (Merriam, 1991). The information obtained on characterization of genetic resources of crop plants is useful, both for breeding and for the purpose of geremplasm conservation (Brown *et al*., 1990). Such knowledge and visualization can be achieved through the study of morphological, structural and functional attributes of germplasm as the carrier of all hereditary characteristics of any given species (Jaramillo and Baena, 2000).The main morphological markers vital to distinguish variation based on external

observation differences in soybean germplasm are days to flowering, days to physiological maturity, plant height, number of pod per plant, number of seed per plant, number of branch per plant, hundred seed weight and grain yield. Oil and protein content are also widely used nutritional values for soybean genetic variability assessment. Therefore, soybean genetic resources with these important traits should be systematically characterized using different genetic variance components and multivariate analysis.

Introduction and local hybridization are paramount important sources of germplasm to initiate soybean variety development program in Ethiopia. Since the inception of soybean research in Ethiopia, a number of germplasm were enhanced from these two methods. So far, genetic variability study was conducted on some soybean germplasmin the country by different researchers, each reported the presence of considerable genetic variations among the tested genotypes(Abush *et al*., 2017;Yechalew *et al*., 2021; Mesfin, 2018; Masreshaw *et al*., 2021; Abady *et al*.,2013;Aditya*et al.*,2011).As the genetic materials are always updated from different sources in different year, the previous genetic information do not totally infer other set of genetic resources. Considering the above facts, the present investigation was necessitated to undertaken the comprehensive assessment of the genetic diversity among the introduced soybean genotypes in Ethiopia.

Materials and Methods

The field experiment was conducted at Metu and Jimma, south western Ethiopia during2019 main cropping season. Metu has an altitude of 1558m.a.s.l. and the mean annual temperature ranges from 12.7-28.9 ^{0}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^{o}c with its mean annual rainfall of 1,572mm.The major soil type in southwest Ethiopia is Nitosols (Paulos, 2001). 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(Abush*et al*., 2017). One hundred soybean genotypes including two standard check varieties (Nyala and Clark-63K) were evaluated in this study using simple lattice design. The genotypes were introduced from external source as breeding material (table 1).

Table 1.Detailsof the100 Soybean genotypes

Geno	Designation	Description	Source of materials	Geno	Designation	Description	Source of material
1	T1-EL-OS-JM17-A13	Inbred line	USA	51	T4-EL-LG-65-JM17-C15	Inbred line	USA
2	T1-EL-OS-JM17-A15	Inbred line	USA	52	T4-EL-LG-65-JM17-C18	Inbred line	USA
3	T1-EL-OS-JM17-B11	Inbred line	USA	53	T4-EL-LG-65-JM17-C20	Inbred line	USA
4	T1-EL-OS-JM17-B14	Inbred line	USA	54	T4-EL-LG-65-JM17-E24	Inbred line	USA
5	T1-EL-OS-JM17-C2	Inbred line	USA	55	T4-EL-LG-65-JM17-F2	Inbred line	USA
6	T1-EL-OS-JM17-D4	Inbred line	USA	56	T4-EL-LG-65-JM17-G1	Inbred line	USA
7	T1-EL-OS-JM17-D6	Inbred line	USA	57	T4-EL-LG-65-JM17-G9	Inbred line	USA
8	T1-EL-OS-JM17-D14	Inbred line	USA	58	T4-EL-LG-65-JM17-G27	Inbred line	USA
9	T1-EL-OS-JM17-E1	Inbred line	USA	59	T4-EL-LG-65-JM17-I14	Inbred line	USA
10	T1-EL-OS-JM17-E2	Inbred line	USA	60	T5-EL-LD-77-JM17-A2B	Inbred line	USA
11	T1-EL-OS-JM17-E3	Inbred line	USA	61	T5-EL-LD-77-JM17-A5	Inbred line	USA
12	T1-EL-OS-JM17-E5	Inbred line	USA	62	T5-EL-LD-77-JM17-A7	Inbred line	USA
13	T1-EL-OS-JM17-E6	Inbred line	USA	63	T5-EL-LD-77-JM17-A9	Inbred line	USA
14	T1-EL-OS-JM17-E13	Inbred line	USA	64	T5-EL-LD-77-JM17-A11	Inbred line	USA
15	T1-EL-OS-JM17-E15	Inbred line	USA	65	T5-EL-LD-77-JM17-A14	Inbred line	USA
16	T1-EL-OS-JM17-E18	Inbred line	USA	66	T5-EL-LD-77-JM17-A15	Inbred line	USA
17	T1-EL-OS-JM17-E23	Inbred line	USA	67	T5-EL-LD-77-JM17-A17	Inbred line	USA
18	T1-EL-OS-JM17-E27	Inbred line	USA	68	T5-EL-LD-77-JM17-B16	Inbred line	USA
19	T1-EL-OS-JM17-E28	Inbred line	USA	69	T5-EL-LD-77-JM17-C1	Inbred line	USA
20	T1-EL-OS-JM17-G13	Inbred line	USA	70	T5-EL-LD-77-JM17-C3	Inbred line	USA
21	T1-EL-OS-JM17-H6	Inbred line	USA	71	T5-EL-LD-77-JM17-C4	Inbred line	USA
22	T1-EL-OS-JM17-H9	Inbred line	USA	72	T5-EL-LD-77-JM17-C6	Inbred line	USA
23	T1-EL-OS-JM17-H12	Inbred line	USA	73	T5-EL-LD-77-JM17-C7	Inbred line	USA
24	T2-EL-LG-90-JM17-I12	Inbred line	USA	74	T5-EL-LD-77-JM17-C25	Inbred line	USA
25	T2-EL-LG-90-JM17-I15	Inbred line	USA	75	T5-EL-LD-77-JM17-D4	Inbred line	USA
26	T2-EL-LG-90-JM17-I22	Inbred line	USA	76	T5-EL-LD-77-JM17-E10	Inbred line	USA
27	T3-EL-LG-63-JM17-A1	Inbred line	USA	77	T5-EL-LD-77-JM17-E25	Inbred line	USA
28	T3-EL-LG-63-JM17-A3	Inbred line	USA	78	T5-EL-LD-77-JM17-E27	Inbred line	USA
29	T3-EL-LG-63-JM17-A8	Inbred line	USA	79	T5-EL-LD-77-JM17-F3	Inbred line	USA
30	T3-EL-LG-63-JM17-A10	Inbred line	USA	80	T5-EL-LD-77-JM17-F4	Inbred line	USA
31	T3-EL-LG-63-JM17-A17	Inbred line	USA	81	T5-EL-LD-77-JM17-F11	Inbred line	USA
32	T3-EL-LG-63-JM17-A22	Inbred line	USA	82	T5-EL-LD-77-JM17-F15	Inbred line	USA
33	T3-EL-LG-63-JM17-A28	Inbred line	USA	83	T5-EL-LD-77-JM17-F27	Inbred line	USA
34	T3-EL-LG-63-JM17-B4	Inbred line	USA	84	T5-EL-LD-77-JM17-F28	Inbred line	USA
35	T3-EL-LG-63-JM17-B6	Inbred line	USA	85	T5-EL-LD-77-JM17-G7	Inbred line	USA
36	T3-EL-LG-63-JM17-B1	Inbred line	USA	86	T5-EL-LD-77-JM17-G18	Inbred line	USA
37	T3-EL-LG-63-JM17-C1	Inbred line	USA	87	T5-EL-LD-77-JM17-G29	Inbred line	USA
38	T3-EL-LG-63-JM17-E8	Inbred line	USA	88	T5-EL-LD-77-JM17-H1	Inbred line	USA
39	T3-EL-LG-63-JM17-E14	Inbred line	USA	89	T5-EL-LD-77-JM17-H3	Inbred line	USA
40	T3-EL-LG-63-JM17-E17	Inbred line	USA	90	T5-EL-LD-77-JM17-H30	Inbred line	USA
41	T3-EL-LG-63-JM17-E30	Inbred line	USA	91	T5-EL-LD-77-JM17-H31	Inbred line	USA
42	T3-EL-LG-63-JM17-E31	Inbred line	USA	92	T5-EL-LD-77-JM17-H43	Inbred line	USA
43	T3-EL-LG-63-JM17-FI1	Inbred line	USA	93	T5-EL-LD-77-JM17-H44	Inbred line	USA
44	T3-EL-LG-63-JM17-F29	Inbred line	USA	94	T5-EL-LD-77-JM17-I3	Inbred line	USA
45	T3-EL-LG-63-JM17-I31	Inbred line	USA	95	T5-EL-LD-77-JM17-I22	Inbred line	USA
46	T3-EL-LG-63-JM17-I36	Inbred line	USA	96	T5-EL-LD-77-JM17-I24	Inbred line	USA
47	T4-EL-LG-65-JM17-A8	Inbred line	USA	97	T5-EL-LD-77-JM17-I34	Inbred line	USA
48	T4-EL-LG-65-JM17-A11	Inbred line	USA	98	T5-EL-LD-77-JM17-I35	Inbred line	USA
49	T4-EL-LG-65-JM17-A13	Inbred line	USA	99	Nyala	Check variety	-
50	T4-EL-LG-65-JM17-B8	Inbred line	USA	**100**	Clarck 63K	Check variety	-

Each genotype was planted in a plot of two rows and four meter length with regular spacing of 5cm between plants and 60cm between rows. Planting was done with two seeds per hill and latter thinned to one plant /hill at 2-3 weeks after emergence. All the agronomic management practices were applied for the experiment as per the recommendation.

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}) were recorded. Disease for bacterial blight, 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**.** 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. Analysis for simple lattice design was performed using the SAS program software. The total variability for the traits was quantified using pooled analyses of variance over two locations using the following model:

$$\mathbf{P_{ijkt} = \mu + l_t + r_{i(t)} + b_{j(i)(t)} + g_k + +(gl)_{kt} + e_{ijkt}}$$

where P_{ijkt}= phenotypic value of k^{th} genotype under i^{th} replication at t^{th} location and j^{th} incomplete block with replication i, location t; l_t= t^{th} location; $r_{i(t)}$ = the effect of replication i with location t; $b_{j(i)(t)}$= the effect of incomplete block j with in replication i and location t; g_k= the effect of k^{th} genotype; μ= grand mean and $(gl)_{kt}$= the interaction effects and e_{ijkt}= random error.

Partitioning of the total variation into components due to genotype (δg^2), environment (δe^2) and genotype by environment interaction (δge^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* (1955) as:

PCV= [σp/ x] x100

GCV= [σg/ x] x100

Where σp= phenotypic standard deviation (σg + σe), σg=genotypic standard deviation, σe= environmental standard deviationand$x$ = grand mean for the trait 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 (1960) as:

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

$$H^2 = \frac{\sigma g2}{\left[\sigma g2 + \frac{\sigma ge2}{e} + \frac{\sigma e2}{er}\right] x100}$$

Where $\sigma p^{2=}$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*(1955) 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.

Mean data for each trait was subjected to multivariate analysis techniques. Cluster analysis was employed using SAS statistical package. Genetic divergence to estimate the genetic distance between clusters was determined using the generalized Mahalanobis's D^2 statistics (Mahalanobis, 1936). The D^2 values obtained for pairs of clusters were considered as the calculated values of Chi-square (X^2) and tested for significance both at 1% and 5% probability levels against the tabulated value of X^2 for 'P' degree of freedom, where P is the number of traits considered (Singh and Chaudhary, 1987). The principal components (PC) analysis was employed in order to minimize the traits into a new set of linearly combined measurements and to identify the traits contributing large part of the total variation among the genotypes. The analysis was performed by using SAS software. In this analysis, only PCs with Eigen values greater than one were considered as important for the total variations.

Correlation analysis was also performed using SAS statistical package to determine the level of associations among the studied traits. Path coefficient analysis was calculated using the formula suggested by (Dewey and Lu, 1959). To determine direct and indirect effect of different variables on yield as:

$rij = Pij + \Sigma rikPkj$

Where; rij = is the mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficients Pij = is the component of direct effects of the independent trait (i) on the dependent trait (j) ΣrikPkj = is summation of components of indirect effect of a given independent trait via all other independent traits.

Result and Discussions

Combined analysis of variance

The results from the combined analysis of variance across two locations has presented in table 2. The pooled analysis of variance revealed that, the mean square due to location was significant ($P \leq 0.01$) for all the traits except number of branches per plant, indicating the distinct nature of the two test locations. Mean squares due to genotype were differed significantly ($P \leq 0.01$) with respect to all the traits except for bacterial blight, meaning genotypes were responded differently for each trait.

Mean squares due to location x genotype were significant for plant height, soybean rust, frog eye leaf spot and hundred seed weight, implying genotypes exhibited different relative performance in each location for these traits.

Table 2. Mean squares of the combined analysis of variance for yield and related traits of100 soybean genotypes at two locations, evaluated during 2019

Source of variations	DF	Traits											
		DTF	DTM	PH	NPP	NSP	NBP	LG	SR	BB	FLS	HSW (gm)	YLD (t/ha)
Loc	1	214.6*	7992.4**	15601.3**	727.9**	7905.9**	0.44	11.90**	386.12**	9.61**	930.25**	249.96**	13.54**
Rep(Loc)	2	23.2ns	14.4 ns	499.2**	1211.2**	6233.7**	2.68**	0.09 ns	11.80**	2.89**	30.25**	0.524 ns	3.22**
Block(Loc*Rep)	36	52.4 ns	13.9	63.8**	42.5*	474.0*	0.46 ns	0.12*	1.08 ns	0.47**	2.23**	8.11**	0.27**
Geno	99	56.3*	34.3**	156.3**	76.9**	512.7**	0.76**	0.11*	2.05**	0.32 ns	0.72**	11.54**	0.34**
Loc*Geno	99	44.4 ns	10.7 ns	34.3**	29.3 ns	332.9 ns	0.39 ns	0.11*	2.22**	0.32 ns	0.72**	4.06*	0.18 ns
Error	162	44.5	9.5	11.5	27.9	287.67	0.34	0.08	1.22	0.24	0.43	3.04	0.141

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, SP= NBP=number of branch per plant, LG=lodging, SH=shattering ,SR=soybean rust, CBB=common bacterial blight, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= grain yield ton ha-1

Performance of soybean genotypes for yield and related traits

The performance of the genotypes (table 3) ranged widely for number of seed (30.15-118.65), days to flowering (26.75-66.75), grain yield (0.85-2.5 t/ha), plant height (33.35-67.30 cm), number of pods(15.70-37.70), days to maturity (115.50-130.75), hundred seed weight (8.78-17.53gm), soybean rust (2.0-5.0), frog-eye leaf spot (1.5-4.0),number of branch (2.90-5.30),crop lodging(1.17-2.0) and bacterial blight (1.16-2.0) (table 3).More than 56% and 80% of the tested soybean genotypes had mean yield exceeding the standard check varieties (Nyala and Clark 63k), respectively. The maximum yield was recorded on genotypes T1-EL-OS-JM17-E1, T4-EL-LG-65-JM17-A11 and T4-EL-LG-65-JM17-F2 (2.50 t/ha each) followed by T3-EL-LG-63-JM17-E14 (2.40 t/ha). The high yielding genotypes had a yield advantage of 32.98% and 61.29% compared with the standard checks (Nyala and Clark 63k), respectively.

Therefore, traits which obtained highest ranges were played important role in the total variability of soybean genotypes. Indicating, the scope for selection of these traits for further breeding works. In agreement with this result wide range of variation for number of pod, grain yield and plant height, number of seed and hundred seed weight was reported by Abush*et al* (2017) and Neelima*et al* (2018).

Table 3. Range and Mean values of yield and other morphological traits of 100 soybean genotypes evaluated across two sites.

		Trait											
No.	**Designation**	**DTF**	**DTM**	**PH**	**NPP**	**NSP**	**NBP**	**LG**	**SR**	**BB**	**FLS**	**HSW**	**yld**
1	T1-EL-OS-JM17-A13	56.75	119.75	45.63	32.93	66.60	4.25	1.38	3.50	1.00	2.00	12.18	2.08
2	T1-EL-OS-JM17-A15	57.50	122.50	46.08	33.20	59.38	4.35	1.13	4.00	1.00	2.00	11.23	1.98
3	T1-EL-OS-JM17-B11	57.00	120.75	40.18	29.50	56.40	3.80	1.00	3.50	2.00	2.50	12.43	1.78
4	T1-EL-OS-JM17-B14	57.00	121.00	48.48	31.75	60.00	4.20	1.25	4.50	1.00	2.50	11.93	2.18
5	T1-EL-OS-JM17-C2	55.25	120.25	44.33	32.30	63.63	3.50	1.00	3.50	1.00	2.00	10.05	2.33
6	T1-EL-OS-JM17-D4	57.00	121.00	49.73	30.63	55.60	3.70	1.25	3.50	1.00	3.50	11.63	1.90
7	T1-EL-OS-JM17-D6	58.00	124.25	53.75	33.35	65.13	4.00	2.00	3.00	1.00	2.00	12.03	2.00
8	T1-EL-OS-JM17-D14	57.50	126.50	51.55	29.05	54.90	4.05	1.25	4.00	1.00	2.00	13.53	1.40
9	T1-EL-OS-JM17-E1	56.50	121.50	49.33	37.70	72.43	4.45	1.25	4.00	1.00	2.00	10.93	2.50
10	T1-EL-OS-JM17-E2	57.00	121.50	60.45	33.20	63.18	3.90	1.50	4.00	1.50	2.50	11.00	2.25
11	T1-EL-OS-JM17-E3	57.00	125.50	50.85	31.10	63.13	3.95	1.25	4.50	1.00	2.50	13.03	1.78
12	T1-EL-OS-JM17-E5	57.50	124.50	43.43	30.50	51.95	3.95	1.13	2.50	1.00	2.50	11.98	1.83
13	T1-EL-OS-JM17-E6	26.75	120.75	41.40	29.28	56.88	4.05	1.00	3.50	1.00	2.50	12.13	1.85
14	T1-EL-OS-JM17-E13	56.50	122.50	42.40	29.38	55.53	3.30	1.13	3.00	1.00	2.50	11.23	1.80
15	T1-EL-OS-JM17-E15	57.50	120.75	43.40	28.25	55.48	3.85	1.00	2.50	2.00	2.00	11.93	1.50
16	T1-EL-OS-JM17-E18	56.00	119.00	49.73	32.10	60.33	3.85	1.13	4.50	1.50	2.50	12.80	1.98
17	T1-EL-OS-JM17-E23	55.50	120.00	41.10	35.00	72.55	3.65	1.00	2.50	1.00	2.00	11.15	1.63
18	T1-EL-OS-JM17-E27	57.50	121.25	55.35	33.70	67.60	4.15	1.63	3.00	1.00	2.50	11.45	2.15
19	T1-EL-OS-JM17-E28	56.75	120.75	53.13	31.75	64.13	4.40	1.38	2.50	1.00	3.00	12.38	2.20
20	T1-EL-OS-JM17-G13	56.25	120.50	51.03	34.20	68.35	4.25	1.25	4.50	1.00	1.50	12.48	2.38
21	T1-EL-OS-JM17-H6	56.50	121.25	44.03	31.50	59.53	4.35	1.25	3.50	1.00	2.00	12.03	2.35
22	T1-EL-OS-JM17-H9	56.00	120.75	45.75	36.83	71.38	4.30	1.00	3.00	1.00	2.00	12.55	2.10
23	T1-EL-OS-JM17-H12	59.75	126.25	56.00	34.75	73.23	4.15	1.50	3.00	2.00	2.50	14.15	2.35
24	T2-EL-LG-90-JM17-I12	56.00	127.00	62.15	33.45	65.30	4.45	1.00	2.50	1.00	2.00	12.43	1.98
25	T2-EL-LG-90-JM17-I15	57.75	124.25	51.55	27.53	53.13	4.20	1.00	4.00	1.00	2.50	14.28	1.98
26	T2-EL-LG-90-JM17-I22	55.00	124.25	58.65	27.33	44.30	4.35	1.13	3.00	1.00	2.50	16.18	1.65
27	T3-EL-LG-63-JM17-A1	55.25	129.25	52.45	32.70	60.65	4.60	1.00	2.50	1.00	2.00	12.93	1.83
28	T3-EL-LG-63-JM17-A3	55.00	121.25	52.40	22.10	36.95	4.25	1.00	2.50	1.50	3.00	16.25	1.50
29	T3-EL-LG-63-JM17-A8	59.00	127.00	61.45	37.15	67.48	4.20	1.25	3.00	1.00	2.00	14.40	1.85
30	T3-EL-LG-63-JM17-A10	58.75	129.75	58.70	32.85	55.83	3.90	1.25	4.00	1.50	2.50	14.40	2.00
31	T3-EL-LG-63-JM17-A17	56.00	125.75	55.23	31.95	118.65	4.00	1.00	2.50	1.00	3.00	11.83	1.85
32	T3-EL-LG-63-JM17-A22	54.00	128.25	50.85	31.38	62.35	3.45	1.00	2.00	1.00	1.50	14.85	1.95
33	T3-EL-LG-63-JM17-A28	55.50	127.25	57.90	26.33	58.28	3.75	1.25	2.50	1.00	2.50	15.25	2.08
34	T3-EL-LG-63-JM17-B4	58.00	130.75	57.10	29.85	54.98	3.90	1.13	4.50	1.00	2.00	14.85	2.15
35	T3-EL-LG-63-JM17-B6	56.50	123.50	48.38	27.85	52.20	3.95	1.50	3.00	1.00	3.50	13.45	1.75
36	T3-EL-LG-63-JM17-B1	56.50	124.50	48.10	23.93	44.93	4.25	1.13	3.50	1.00	2.00	13.83	1.88

Table3. (Continued)

		Trait											
No.	**Designation**	**DTF**	**DTM**	**PH**	**NPP**	**NSP**	**NBP**	**LG**	**SR**	**BB**	**FLS**	**HSW**	**YLD**
37	T3-EL-LG-63-JM17-C1	56.75	124.25	49.83	28.53	53.63	4.20	1.13	3.50	1.00	2.50	14.30	1.88
38	T3-EL-LG-63-JM17-E8	59.50	127.00	55.05	28.88	49.25	4.10	1.00	3.50	1.00	2.00	14.43	1.68
39	T3-EL-LG-63-JM17-E14	55.25	119.25	40.33	24.10	47.90	2.95	1.00	3.50	1.50	2.50	13.93	2.40
40	T3-EL-LG-63-JM17-E17	55.75	121.75	44.80	25.65	47.15	3.95	1.25	2.50	1.00	3.00	16.35	1.50
41	T3-EL-LG-63-JM17-E30	54.75	124.50	46.15	25.40	45.75	3.95	1.13	2.50	1.00	2.00	17.10	1.98
42	T3-EL-LG-63-JM17-E31	56.00	120.75	47.35	27.88	57.25	4.50	1.00	5.00	1.00	2.50	13.23	2.20
43	T3-EL-LG-63-JM17-FI1	53.50	120.50	52.83	32.68	57.13	3.50	1.38	3.00	1.00	2.00	16.23	1.88
44	T3-EL-LG-63-JM17-F29	58.00	125.00	55.05	32.68	58.73	4.40	1.00	2.50	1.00	2.50	16.70	2.03
45	T3-EL-LG-63-JM17-I31	57.50	122.50	49.23	28.50	50.80	4.80	1.50	3.50	1.00	3.50	11.08	1.98
46	T3-EL-LG-63-JM17-I36	56.50	119.25	41.95	29.48	53.85	4.10	1.00	3.00	1.00	2.50	15.30	1.68
47	T4-EL-LG-65-JM17-A8	56.25	124.00	52.70	35.00	74.75	4.20	1.25	4.50	1.50	3.50	13.43	2.23
48	T4-EL-LG-65-JM17-A11	56.00	122.50	54.45	32.13	63.03	4.65	1.38	4.50	1.00	2.00	15.50	2.50
49	T4-EL-LG-65-JM17-A13	56.50	121.50	47.38	31.10	60.35	4.20	1.50	4.50	1.00	2.50	13.93	2.13
50	T4-EL-LG-65-JM17-B8	56.50	121.25	49.83	31.20	58.23	4.35	1.25	4.00	1.00	2.50	14.23	1.70
51	T4-EL-LG-65-JM17-C15	56.75	124.00	51.38	27.15	52.43	3.60	1.00	3.00	1.50	2.50	14.40	1.65
52	T4-EL-LG-65-JM17-C18	58.25	125.00	58.53	28.83	51.33	3.55	1.50	4.00	1.00	2.00	17.00	2.20
53	T4-EL-LG-65-JM17-C20	59.00	123.50	57.03	29.33	58.00	3.20	1.13	3.25	1.00	2.00	15.93	2.03
54	T4-EL-LG-65-JM17-E24	55.00	119.50	37.08	26.15	46.10	3.25	1.13	3.50	1.00	3.00	11.93	1.63
55	T4-EL-LG-65-JM17-F2	57.25	122.50	65.75	29.65	57.43	4.60	1.38	2.50	1.00	3.00	15.20	2.50
56	T4-EL-LG-65-JM17-G1	55.50	120.00	50.03	25.80	52.48	4.20	1.25	4.50	1.00	3.00	12.40	1.98
57	T4-EL-LG-65-JM17-G9	55.25	120.75	49.35	26.75	47.30	3.90	1.25	4.50	1.00	2.00	14.88	2.18
58	T4-EL-LG-65-JM17-G27	55.50	120.75	45.18	31.25	64.80	3.75	1.75	4.50	1.00	2.00	12.88	2.13
59	T4-EL-LG-65-JM17-I14	56.00	121.50	46.25	25.45	47.65	3.60	1.13	2.00	1.00	2.00	14.83	1.80
60	T5-EL-LD-77-JM17-A2B	55.25	121.00	46.43	23.53	44.53	3.40	1.13	3.00	1.00	2.00	15.65	1.68
61	T5-EL-LD-77-JM17-A5	54.75	121.75	55.78	27.95	49.80	4.25	1.25	2.50	1.50	2.50	13.13	1.60
62	T5-EL-LD-77-JM17-A7	55.00	119.75	53.30	26.60	52.20	3.60	1.13	3.50	1.00	2.50	15.03	2.03
63	T5-EL-LD-77-JM17-A9	55.00	121.25	49.13	23.00	39.20	3.90	1.00	3.00	1.50	2.00	15.98	1.88
64	T5-EL-LD-77-JM17-A11	55.25	120.75	58.70	24.85	49.73	3.70	1.13	3.50	1.00	2.50	16.75	2.08
65	T5-EL-LD-77-JM17-A14	54.00	121.00	51.63	25.33	52.38	3.70	1.25	3.50	1.00	2.00	16.70	2.13
66	T5-EL-LD-77-JM17-A15	56.25	121.75	53.00	26.25	47.00	4.00	1.13	3.50	1.00	2.50	14.63	1.85
67	T5-EL-LD-77-JM17-A17	55.75	122.50	46.25	21.00	42.23	3.35	1.00	2.50	1.50	3.00	16.68	1.43
68	T5-EL-LD-77-JM17-B16	54.00	122.25	45.25	24.38	46.28	3.55	1.00	2.00	1.00	2.50	16.08	
69	T5-EL-LD-77-JM17-C1	54.50	118.75	40.55	21.45	37.25	3.90	1.00	2.00	1.00	3.00	15.85	1.33
70	T5-EL-LD-77-JM17-C3	53.75	119.00	42.90	17.55	33.00	2.90	1.00	3.00	1.50	4.00	15.13	1.35
71	T5-EL-LD-77-JM17-C4	53.75	117.00	41.40	15.70	30.15	3.30	1.38	2.50	1.00	3.50	15.73	1.33
72	T5-EL-LD-77-JM17-C6	55.00	120.50	47.65	24.30	46.15	3.70	1.13	3.50	1.00	2.50	14.88	1.93

Table3. (Continued)

No.	Designation	Trait											
		DTF	**DTM**	**PH**	**NPP**	**NSP**	**NBP**	**LG**	**SR**	**BB**	**FLS**	**HSW**	**YLD**
74	T5-EL-LD-77-JM17-C25	53.50	116.50	42.75	22.10	42.08	3.35	1.13	3.50	1.00	3.50	14.83	1.58
75	T5-EL-LD-77-JM17-D4	55.50	116.75	33.35	20.50	42.48	5.30	1.00	2.50	1.50	4.00	10.63	0.85
76	T5-EL-LD-77-JM17-E10	54.50	117.25	37.13	19.05	35.20	3.20	1.25	2.00	2.00	3.00	14.83	1.20
77	T5-EL-LD-77-JM17-E25	56.00	119.75	35.58	21.20	40.90	3.85	1.25	3.50	1.00	3.00	12.30	1.30
78	T5-EL-LD-77-JM17-E27	55.25	122.25	45.25	22.38	42.58	3.05	1.13	3.50	1.00	2.00	17.53	1.53
79	T5-EL-LD-77-JM17-F3	54.00	115.50	41.68	21.45	40.75	3.30	1.00	2.50	1.00	3.00	15.68	1.55
80	T5-EL-LD-77-JM17-F4	54.25	120.25	46.05	26.50	47.03	3.85	1.38	3.50	1.00	3.00	15.53	1.65
81	T5-EL-LD-77-JM17-F11	55.50	118.50	39.53	26.25	47.80	3.60	1.13	3.00	1.00	3.00	14.33	2.00
82	T5-EL-LD-77-JM17-F15	54.75	118.25	40.43	22.15	39.78	3.40	1.00	2.50	1.50	3.00	14.95	1.65
83	T5-EL-LD-77-JM17-F27	39.00	121.25	45.10	25.98	52.70	3.30	1.00	3.00	1.00	2.00	15.05	1.25
84	T5-EL-LD-77-JM17-F28	55.25	122.00	47.15	22.65	42.40	3.85	1.13	3.50	1.00	3.50	13.95	1.63
85	T5-EL-LD-77-JM17-G7	55.00	120.50	44.65	23.25	41.10	3.85	1.00	3.50	1.50	2.50	16.78	1.75
86	T5-EL-LD-77-JM17-G18	54.25	122.50	40.43	23.10	44.95	3.90	1.25	3.00	1.00	2.50	14.65	1.25
87	T5-EL-LD-77-JM17-G29	55.75	118.25	44.93	21.15	40.15	3.35	1.13	2.50	1.50	2.50	14.80	1.48
88	T5-EL-LD-77-JM17-H1	55.25	119.25	36.30	21.50	40.18	3.40	1.00	2.00	1.00	2.50	13.73	1.20
89	T5-EL-LD-77-JM17-H3	55.50	119.50	42.48	26.40	51.03	3.70	1.00	2.50	1.00	2.50	15.45	1.75
90	T5-EL-LD-77-JM17-H30	54.25	119.50	40.13	23.90	44.23	3.30	1.00	4.00	2.00	3.00	12.73	1.40
91	T5-EL-LD-77-JM17-H31	54.25	116.50	41.40	22.20	43.70	3.60	1.13	3.00	1.00	3.00	15.80	1.65
92	T5-EL-LD-77-JM17-H43	56.00	122.75	53.28	30.30	57.43	4.35	1.25	3.00	1.00	2.50	14.55	2.03
93	T5-EL-LD-77-JM17-H44	55.25	121.25	40.48	24.85	44.75	3.35	1.00	3.00	1.50	3.50	12.73	1.25
94	T5-EL-LD-77-JM17-I3	53.25	122.50	51.55	24.30	47.98	3.40	1.00	2.00	1.50	2.00	17.43	1.65
95	T5-EL-LD-77-JM17-I22	55.00	122.75	58.15	24.63	47.25	3.65	1.00	2.00	1.00	2.50	15.55	1.58
96	T5-EL-LD-77-JM17-I24	55.75	122.50	54.35	25.85	50.13	3.70	1.25	2.50	1.00	2.00	14.48	2.13
97	T5-EL-LD-77-JM17-I34	55.25	116.25	43.43	25.65	41.48	3.83	1.00	2.50	1.50	3.50	15.85	1.75
98	T5-EL-LD-77-JM17-I35	54.75	119.50	41.68	19.50	37.65	3.05	1.00	2.50	1.00	3.50	15.30	1.18
99	Nyala	59.50	126.75	50.35	28.88	53.78	3.85	1.00	2.00	1.50	2.00	15.38	1.80
100	Clarck 63K	66.75	130.00	67.30	30.70	59.80	4.55	1.75	3.50	2.00	1.50	8.78	1.55
	minimum	**26.75**	**115.50**	**33.35**	**15.70**	**30.15**	**2.90**	**1.00**	**2.00**	**1.00**	**1.50**	**8.78**	**0.85**
	mean	**55.61**	**121.93**	**48.53**	**27.62**	**53.00**	**3.88**	**1.17**	**3.20**	**1.16**	**2.53**	**14.06**	**1.82**
	maximum	**66.75**	**130.75**	**67.30**	**37.70**	**118.65**	**5.30**	**2.00**	**5.00**	**2.00**	**4.00**	**17.53**	**2.50**
	R2 (%)	**62.75**	**89.86**	**93.68**	**78.46**	**72.48**	**71.75**	**79.8**	**82.21**	**71.54**	**94.97**	**83.59**	**80.73**
	CV	**11.99**	**2.61**	**10.91**	**22.84**	**35.22**	**15.80**	**24.35**	**35.39**	**45.81**	**34.78**	**13.13**	**21.96**
	LSD	**9.31**	**4.29**	**5.85**	**7.38**	**23.68**	**0.85**	**0.39**	**1.54**	**0.69**	**0.91**	**2.43**	**0.14**
	P-value	**NS**	**	**	*	**	**	**	**	**NS**	**	**	**

CV, Coefficient of variation, R2, Coefficient of determination, LSD, Least significant difference. *, ** denote significance difference at 5% and 1% probability levels, respectively; NS: non-significant.

Estimation of genotypic and phenotypic coefficients of variation

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)presented in table 4.The ranges for PCV and GCV were (4.68%-46.88%) and (4.08%-24.38%), respectively. The present finding illustrated that, PCV was higher than GCV for all studied traits, suggesting the observed variation in the soybean genotypes were both the combination of genotypic and environment effect. According to Deshmukhs *et al*(1986) descriptions, high phenotypic and genotypic coefficients of variation were recorded for number of seed (40.62% and 28.3%),number of pod (30.43% and 25.34%), soybean rust(46.88% and 28.47%), frogeye leaf spot (43.97% and 21.29%), plant height (26.45% and 24.80%), hundred seed weight (23.90% and 20.74%), 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 (Akinwale*et al*.,2011). Accordingly, the difference between PCV with the corresponding GCV values was relatively higher for frog eye leaf spot, soybean rust, and number of seed 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, hundred seed weight and number of pod, 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 Masreshaw*et al* (2021) and Neelima*et al* (2018) who reported high GCV and PCV for number of pod, number of seed, plant height and hundred seed weight.

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 (87.85%), days to maturity (76.25%), hundred seed weight (75.29), number of pod (69.38%) and number of branch (60.08%) exhibited high heritability estimates. On the other hand, moderate broad sense heritability estimates were observed for number of branch (60.08%), number of seed (48.56%) and soybean rust (36.89%), while other traits were found low heritability estimates. Similar to the current finding high heritability

estimates on plant height, days to maturity, hundred seed weightand number of pod was reported by (Neelima*et al*.,2018; Abush*et al*., 2017; Aditya*et al*.,2011; Yechalew*et al*.,2019; Masreshaw*et al*.,2021).

Table 4.Estimates of variance components for 11triats of 100 soybean genotypes

Traits	Range		mean	(σ^2g)	(σ^2p)	H(%)	GCV (%)	PCV (%)	GA	GAM(%)
	Min	Max								
DTF	26.75	66.75	55.60	11.80	45.15	26.14	6.18	12.08	3.62	6.52
DTM	115.50	130.75	121.93	24.80	32.53	76.25	4.08	4.68	8.97	7.36
PH	33.35	67.30	48.53	144.80	164.83	87.85	24.80	26.45	23.27	47.95
NPP	15.70	37.70	27.62	49.00	70.63	69.38	25.34	30.43	12.03	43.55
NSP	30.15	118.65	53.00	225.03	463.40	48.56	28.30	40.62	21.57	40.69
NBP	2.90	5.30	3.88	0.42	0.70	60.00	16.70	21.56	1.04	26.69
LG	1.00	2.00	1.17	0.03	0.11	27.27	14.80	28.35	0.19	15.95
SR	2.00	5.00	3.20	0.83	2.25	36.89	28.47	46.88	1.14	35.67
FLS	1.50	4.00	2.53	0.29	1.24	23.43	21.29	43.97	0.54	21.26
HSW	8.78	17.53	14.06	8.50	11.29	75.29	20.74	23.90	5.22	37.12
YLD	0.85	2.50	1.28	0.10	0.26	39.22	17.38	27.75	0.41	22.45

(σ^2g)=genotypic variance, (σ^2P)=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, SP= NBP=number of branch per plant, LG=lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha-1

Johnson *et al*(1955) categorized the genetic advance as the percent of mean as low (0-10%), medium (10-20%) and high (≥20%). Based on these category the highest GAM was observed from the present study for plant height (87.85%) followed by number of pod (43.55%), number of seed (40.69%), hundred seed weight (37.12%), soybean rust severity (35.67%), number of branch(26.69), yield (22.45) and frogeye leaf spot severity(21.26%). In contrast, the remaining traits showed low estimates of GAM. Traits which showed low GCV and low GAM were under high environmental influence; hence selection based on such traits would be less effective. High heritability estimates accompanied by the high genetic advance is usually more helpful in predicting increase under selection than heritability estimates alone (Johnson *et al*., 1995).

Accordingly, combined high GCV, high heritability and high GAM were recorded for plant height (24.80%, 87.85% and 47.95%), number of pod (25.34%, 69.38% and 43.55%) and hundred seed weight (20.74%, 75.29% 37.12%). Hence, this trait can be improved through direct selection more easily than other traits. Masreshaw*et al* (2021) reported similar result with this investigation, high heritability combined with high GAM for plant height and hundred seed weight was reported by Abush*et al* (2017), while Aditya*et al* (2011) and Neelima*et al*

(2018) were reported combined High heritability with high GAM for plant height and number of pod .

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 (Abate *et al*., 2015), 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.

Cluster analysis

Cluster analysis categorized 100 soybean genotypes into five clusters (table 5). The grouping pattern showed; cluster-I contained highest number of genotypes (57%) followed by cluster-II (35%), cluster-III (5%), cluster-IV (2%) and cluster-V (1%). In cluster analysis, if the categorization is successful, individuals within (homogenous) shall be closer and different clusters (heterogeneous) shall be farther apart (Hair *et al*., 1995). The distribution pattern of genotypes in to different cluster might be difference in genetic background through their pedigree.

Cluster characterization using quantitative traits

Mean performance of clusters (table 6) for the 11 traits reflected that the genotypes in cluster-III exhibited the highest mean yield, days to flowering, soybean rust, number of pod and branch. Even though, the genotypes in this cluster had relatively highest soybean rust severity level, the score value lays in moderately resistant level, Genotypes in cluster I were characterized by medium mean values for all the traits except for highest in crop lodging. Genotypes in Cluster-II were characterized by shortest plant height, early maturity date, minimum number of pod, number of seed, number of branch and highest hundred seed weight. Cluster-IV possessed accessions with short days to flowering, lowest score in frogeye leaf spot disease, and lowest in crop yield. Conversely, cluster-V which comprised of only one genotype was mainly characterized late physiological maturity, tallest plant height, highest score for frog eye leaf spot, lowest for crop lodging and hundred seed weight.

Table 5.The distribution of 100soybean genotypes in to five clusters tested at Jimma and Mettu (2019).

Cluster No.	No. geno.	(%)	genotypes
I	57	57	T1-EL-OS-JM17-A13, T1-EL-OS-JM17-A15, T1-EL-OS-JM17-B11, T1-EL-OS-JM17-B14,T1-EL-OS-JM17-C2,T1-EL-OS-JM17-D4, T1-EL-OS-JM17-D6, T1-EL-OS-JM17-D14, T1-EL-OS-JM17-E2,T1-EL-OS-JM17-E3, T1-EL-OS-JM17-E5,T1-EL-OS-JM17-E13,T1-EL-OS-JM17-E15,T1-EL-OS-JM17-E18,T1-EL-OS-JM17-E27,T1-EL-OS-JM17-E28,T1-EL-OS-JM17-G13,T1-EL-OS-JM17-H6,T2-EL-LG-90-JM17-I12,T2-EL-LG-90-JM17-I15, T2-EL-LG-90-JM17-I22,T3-EL-LG-63-JM17-A1,T3-EL-LG-63-JM17-A8,T3-EL-LG-63-JM17-A10,T3-EL-LG-63-JM17-A22,T3-EL-LG-63-JM17-A28,T3-EL-LG-63-JM17-B4,T3-EL-LG-63-JM17-B6,T3-EL-LG-63-JM17-C1,T3-EL-LG-63-JM17-E8, T3-EL-LG-63-JM17-E31,T3-EL-LG-63-JM17-FI1,T3-EL-LG-63-JM17-F29,T3-EL-LG-63-JM17-I31,T3-EL-LG-63-JM17-I36,T4-EL-LG-65-JM17-A11,T4-EL-LG-65-JM17-A13,T4-EL-LG-65-JM17-B8,T4-EL-LG-65-JM17-C15,T4-EL-LG-65-JM17-C18,T4-EL-LG-65-JM17-C20,T4-EL-LG-65-JM17-F2,T4-EL-LG-65-JM17-G1,T4-EL-LG-65-JM17-G9,T4-EL-LG-65-JM17-G27, T5-EL-LD-77-JM17-A5,T5-EL-LD-77-JM17-A7,T5-EL-LD-77-JM17-A11,T5-EL-LD-77-JM17-A14,T5-EL-LD-77-JM17-A15, T5-EL-LD-77-JM17-H3,T5-EL-LD-77-JM17-H43,T5-EL-LD-77-JM17-I3,T5-EL-LD-77-JM17-I22,T5-EL-LD-77-JM17-I24, Nyala, Clarck 63K
II	35	35	T3-EL-LG-63-JM17-A3,T3-EL-LG-63-JM17-B1,T3-EL-LG-63-JM17-E14,T3-EL-LG-63-JM17-E17,T3-EL-LG-63-JM17-E30,T4-EL-LG-65-JM17-E24,T4-EL-LG-65-JM17-I14,T5-EL-LD-77-JM17-A2B,T5-EL-LD-77-JM17-A9,T5-EL-LD-77-JM17-A17,T5-EL-LD-77-JM17-E10,T5-EL-LD-77-JM17-C1,T5-EL-LD-77-JM17-C3,T5-EL-LD-77-JM17-C4,T5-EL-LD-77-JM17-C6,T5-EL-LD-77-JM17C7,T5-EL-LD-77-JM17-C25,T5-EL-LD-77-JM17-D4,T5-EL-LD-77-JM17-B16, T5-EL-LD-77-JM17-E25,T5-EL-LD-77-JM17-E27,T5-EL-LD-77-JM17-F3,T5-EL-LD-77-JM17-F4,T5-EL-LD-77-JM17-F11,T5-EL-LD-77-JM17-F15,T5-EL-LD-77-JM17-G7,T5-EL-LD-77-JM17-G18,T5-EL-LD-77-JM17-G29,T5-EL-LD-77-JM17-H1,T5-EL-LD-77-JM17-F28,T5-EL-LD-77-JM17-H31,T5-EL-LD-77-JM17-H44,T5-EL-LD-77-JM17-I34,T5-EL-LD-77-JM17-I35T5-EL-LD-77-JM17-H30
III	5	5	T1-EL-OS-JM17-E1,T1-EL-OS-JM17-E23,T1-EL-OS-JM17-H9,T4-EL-LG-65-JM17-A8,T1-EL-OS-JM17-H12
IV	2	2	T1-EL-OS-JM17-E6,T5-EL-LD-77-JM17-F27
V	1	1	T3-EL-LG-63-JM17-A17

Table 6. Cluster mean values for 11 traits of 100 soybean genotypes tested at Jimma and Mettu (2019).

	Traits										
Cluster	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	FLP	HSW	YLD
I	56.69	123.11	51.98	29.80	56.66	4.01	1.23**	3.37	2.33	13.75	1.96
II	54.96	119.86*	42.96*	22.76*	42.22*	3.62*	1.10	2.90	2.86	14.90**	1.58
III	56.80**	122.50	48.98	35.86**	72.87	4.15**	1.20	3.40**	2.40	12.44	2.16**
IV	32.88*	121.00	43.25	27.63	54.79	3.68	1.01	3.25	2.25*	13.59	1.55*
V	56.00	125.75**	55.23**	31.95	118.65**	4.00	1.00*	2.50*	3.00**	11.83*	1.85

**,* represents maximum and minimum values respectively, 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, SP= NBP=number of branch per plant, LG=lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot ,HSW=hundred seed weight, YLD= yield ton per ha-1

Genetic divergence (D2)

Multivariate analysis by means of Mahalanobis' D^2 statistics is a useful tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence at intra and inter-cluster levels (Das and Gupta, 1984).The values of pair wise average intra and inter-cluster divergence ($D^{2)}$ among 100soybean genotypes in five clusters based on 11 quantitative traits are presented in table 7. Thus, the inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider diversity among the genotypes of the distant clusters. The intra-cluster degree of diversity was maximum in cluster-IV (7.82), indicating that the genotypes in cluster IV were a little bit heterogeneous as compared to those in other clusters. Generally, the range of intra-cluster values indicated homogeneous nature of the genotypes within the clusters.

The chi-square test revealed the existence of highly significant differences among the paired inter cluster distance except cluster I with II and III. The maximum inter-cluster distance was found between cluster-IV and V (760.20) followed by cluster-II and V (605.30), cluster-I and V (538.10), and cluster- III and V (427.70).The highest value of inter-cluster distance indicated that the genotypes belonging to these cluster were far diverged. The lowest inter-cluster distance was recorded between clusters-I and II (10.68) followed by cluster-I and III (13.83), which means a close relationship between the genotypes. Cluster-V was found divergent from other clusters chiefly due to days to maturity, plant height number of pods per plant and frog eye leaf spot, indicating maximum contribution of these traits towards the divergence. Similarly, cluster-III was found diverged from cluster I, II and IV due to the highest in grain yield, days to flowering, soybean rust, and number of pod and branch. On the other hand cluster I and II were diverged from cluster IV due to their highest crop lodging and hundred seed weight, respectively.

Table 7 .Pair wise average intra (bold) and inter cluster divergence values (D^2)among 100soybean genotypes in five clusters based on 11 traits tested at Jimma and Metu (2019).

Cluster	I	II	III	IV	V
I	**(1.12)**	10.68	13.83	243.50**	538.10**
II		**(2.10)**	39.66*	245.50**	605.30**
III			**(5.99)**	267.60**	427.70**
IV				**(7.82)**	760.20**
V					**(0.00)**

*, **= significant, ($p<0.01$) χ**2**=24.72, and ($p<0.05$) χ**2**=19.67, respectively

Jgadev*et al*. (1991) stated that the traits contributing maximum towards the divergence should be given greater emphasis for deciding the type of

cluster for the purpose of further selection and choice of the parents for hybridization. In this perspective, intra cluster mean performance for days to physiological maturity, plant height, and frog eye leaf spot in cluster-V was maximum and greater than the mean of other clusters, suggesting that the role of those traits towards the divergence between cluster-V with other clusters. Generally, maximum genetic segregation and recombination will be expected from cross that involve parents from the significant inter cluster distance. In the present investigation, superior hybrids or recombinants can be exploited by crossing genotypes from cluster-V with other clusters. Moreover, the heterosis could also be exploited by crossing between genotypes with moderate diversity like cluster-III and V followed by cluster- II and IV, I and VI, and II and III.The current result is in support the previous findings (Tadesse and Sentayehu, 2015; Abush *et al.*, 2017)

Principal component analysis (PCA)

Principal component analysis was done using 11 quantitative traits with the intention of minimizing the dimensionality of large number of interrelated traits in a given data set and retaining maximum information about the genetic variation (table 8). Accordingly, the first four principal components with Eigen values exceeding one were responsible for about 72.62 % of the total variation among the genotypes. Maximum variation was accounted from the first principal component (39.31%) followed by the second (13.82%) principal components, which means, out of the entire variations, the first and the second principal components accounted for more than two third of the total variations (53.13%).

The first principal component that accounted maximum variation (39.31%) was due to the principal contribution of positive discriminatory traits like number of pod per plant, number of seed per plant, grain yield, plant height and days to maturity. The considerable variation observed in the second principal component (13.82%) was attributed to hundred seed weight, days to maturity and plant height. Traits which had substantial contribution to the third principal component (10.26%) were days to flowering, crop lodging and frog eye leaf spot. On the other hand, hundred seed weight, grain yield and soybean rust predominantly influenced the variation in the fourth principal component. Consistent with this finding earlier investigators also found comparable result from different soybean genotypes (Tadesse and Sentayehu, 2015; Abush *et al.*, 2017; Yechalew*et al*., 2019).

Chahal and Goal (2002) inferred that characters with the largest absolute values closer to unit within the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in the current investigation

discrimination of the accessions in to different cluster was mainly due to number of pod per plant, number of seed per plant, grain yield, plant height, days to flowering, days to maturity and hundred seed weight.

Table 8. Eigenvectors and Eigen values of the first four principal components for 11 traits of 100 soybean genotypes testedatJimma and Metu (2019).

	Principal component			
Traits	Prin1	Prin2	Prin3	Prin4
DTF	0.19	0.14	**0.64**	-0.14
DTM	**0.31**	**0.43**	0.03	-0.24
PH	**0.34**	**0.40**	0.18	0.07
NPP	**0.43**	-0.10	-0.23	-0.12
NSP	**0.38**	-0.13	-0.28	-0.23
NBP	0.29	-0.18	0.17	-0.27
LG	0.24	-0.15	**0.48**	0.28
SR	0.21	-0.35	0.03	**0.58**
FLP	-0.26	-0.34	**0.39**	-0.13
HSW	-0.21	**0.56**	0.02	**0.40**
YLD	**0.36**	-0.03	-0.15	**0.43**
Eigen values	4.32	1.52	1.13	1.02
Total variance (%)	39.31	13.82	10.26	9.25
Cumulative variance (%)	39.31	53.13	63.39	72.62

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, SP= NBP=number of branch per plant, LG=lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha-1

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Association among Quantitative Traits

Phenotypic (rph) and genotypic (rg) correlation of yield and component traits

The result revealed that, genotypic correlation coefficients were generally higher in magnitude than phenotypic correlation coefficients values (table 9) for most of the paired traits, indicating the strong inherent association among these traits. Accordingly, grain yield exhibited significant and positive phenotypic and genotypic association with days to maturity (r_{ph}=0.38; r_g=0.26), plant height(r_{ph}=0.50; r_g=0.50), number of pod per plant(r_{ph}=0.49; r_g=0.65), number of seed per plant(r_{ph}=0.20; r_g=0.54), and number of branch per plant(r_{ph}=0.19; r_g=0.33), indicating genotypes characterized by lately matured, tallest plant height, maximum number of pod, seed and branch per plant were high yielder. Alternatively, days to flowering showed positive and significant phenotypic and genotypic correlations with days to maturity (r_{ph}=0.16;rg=0.31), plant height (r_{ph}=0.19; r_g=0.33)and number of pod per plant (r_{ph}=0.12; r_g=0.22),hence, indirect selection in favor of these traits can improve gain yield in soybean.

Table 9.Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients among 11 traits of 100 soybean genotypes testedat Jimma and Metu (2019).

Trait	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	FLS	HSW	YLD
DTF		0.31**	0.33**	0.22*	0.15ns	0.21*	0.29**	0.08ns	-0.10ns	-0.13ns	0.18ns
DTM	0.16**		0.68**	0.48**	0.42**	0.31**	0.17ns	0.07ns	-0.46**	-0.06ns	0.26*
PH	0.19**	0.71**		0.50**	0.43**	0.37**	0.37**	0.14ns	-0.37**	0.06ns	0.50**
NPP	0.12*	0.38*	0.47**		0.83**	0.50**	0.34**	0.33**	-0.48**	-0.48**	0.65**
NSP	0.05ns	0.04ns	0.14**	0.64**		0.39**	0.26*	0.23**	-0.34**	-0.47**	0.54**
NBP	0.09ns	0.17**	0.28**	0.44**	0.34**		0.26**	0.25*	-0.11ns	-0.37**	0.33**
LG	0.16**	0.39**	0.4**	0.21**	0.01ns	0.16**		0.31**	-0.11ns	-0.26**	0.34**
SR	0.07ns	0.41**	0.37**	0.28**	-0.03ns	0.15**	0.29**		-0.13ns	-0.28**	0.46**
fls	-0.11*	-0.66**	-0.52**	-0.23**	0.13*	-0.05ns	-0.37**	-0.52**		0.01ns	-0.41**
HSW	0.01ns	0.25**	0.28**	-0.0ns	-0.21**	-0.09ns	0.06ns	0.11*	-0.30**		-0.14ns
YLD	0.09ns	0.38**	0.50**	0.49**	0.20**	0.19**	0.32**	0.36**	-0.40**	0.17**	

* *, *= significant at probability level of (p<0.01) and (p< 0.05), respectively. 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, SP= NBP=number of branch per plant, LG=crop lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha-1

On the other hand, grain yield also showed significant positive phenotypic and genotypic correlation with soybean rust reaction (r_{ph}=0.36; r_g=0.46) and lodging (r_{ph}=0.32; r_g=0.34), suggesting that high crop load aggravates soybean rust severity and crop lodging, which pose a challenge for breeders to improve these traits simultaneously. While, grain yield found negative phenotypic and genotypic correlation with frog eye leaf spot reaction (r_{ph}=-0.40; r_g=-0.41), which has important implication in the improvement of this trait during disease resistant soybean variety development. In the same manner, yield displayed positive phenotypic and negative genotypic correlation with hundred seed weight (r_{ph}=0.17; r_g=-0.14). The other yield related traits also had either positive or negative phenotypic and genotypic linear relationship with each other as indicated in the table 9above.

The current phenotypic and genotypic correlations of traits were in agreement with the previous report for most of the traits. Similar to these result, Mesfin (2018) found that days to maturity, plant height and number of seed per plant showed significant positive genotypic and phenotypic correlation with grain yield. Positive and strong phenotypic and genotypic correlation of pod with grain yield was also confirmed by Chamundeswari*et al* (2003) and Aditya *et al.* (2011).

Generally, the association could be either genetic or environment or else the contribution of both factors. Therefore, positive correlation among paired traits might allow improving both traits simultaneously, whereas for a negative correlation, selection for improving one trait will likely cause decreases the other trait (Rangaswamny, 1995). Kearsey and Pooni1 (996) also suggested that the positive and significant association of traits due to the effect of genes can be the existence of strong coupling linkage between genes or the traits might be the result of pleiotropic genes that could control the traits in the same direction, while the negative correlation might be because of different genes or pleiotropic genes that have dominance on the traits which would control in different direction.

Path coefficient analysis

Correlation coefficient among paired traits may not give a complete picture for a parameter like yield which is either directly or indirectly controlled by several other traits. In these circumstances, path analysis provides a means of partitioning the correlation coefficients into the measures of direct and indirect effects of independent variables on the dependent variable. Path analysis also effectively measure the relative importance of causal factors (Ali and Shakor, 2012), which helps to build an effective selection program. In the current research, path-coefficient analysis was carried out at genotypic level using grain yield as dependent variable and other traits as independent variables (Table10).

The path coefficient analysis revealed that number of pods per plant (0.295)

observed the maximum positive direct effect on grain yield followed by plant height (0.294). High and positive direct effect on yield was also found from soybean rust, which means high crop load makes a crop susceptible to soybean rust. Moderate positive direct effects were recorded from hundred seed weight (0.195) and number of seed per plant (0.133), while Number of branches per plant (0.015), days to flowering (0.038) and crop lodging (0.0.028) had low degree of positive direct effects on grain yield. Conversely, negative direct effects on grain yield was exhibited from physiological maturity (-0.304) and frog-eye leaf spot disease (-0.134).Comparable to this finding, Mesfin (2018) reported as number of pods per plant, number of seeds and hundred seed weight showed positive direct effect on grain yield. Moreover, according to Malik *et al* (2006), days to physiological maturity had negative direct effect on grain yield.

Table 10. Estimate of direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of 11 traits on yield in100 soybean genotypes

Trait	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	FLS	HSW	**rg**$_{(xy)}$
DTF	**0.038**	-0.094	0.098	0.098	0.020	0.003	0.008	0.023	0.014	-0.025	0.184
DTM	0.012	**-0.304**	0.199	0.217	0.056	0.005	0.005	0.019	0.062	-0.011	0.257
PH	0.013	-0.205	**0.294**	0.223	0.057	0.005	0.010	0.039	0.050	0.012	0.499
NPP	0.008	-0.146	0.146	**0.449**	0.111	0.007	0.010	0.093	0.064	-0.093	0.650
NSP	0.006	-0.127	0.126	0.375	**0.133**	0.006	0.007	0.065	0.046	-0.092	0.545
NBP	0.008	-0.093	0.108	0.224	0.052	**0.015**	0.007	0.069	0.014	-0.072	0.333
LG	0.011	-0.052	0.108	0.152	0.034	0.004	**0.028**	0.086	0.014	-0.051	0.335
SR	0.003	-0.020	0.041	0.149	0.031	0.004	0.009	**0.282**	0.017	-0.054	0.460
FLS	-0.004	0.141	-0.110	-0.215	-0.045	-0.002	-0.003	-0.035	**-0.134**	0.003	-0.405
HSW	-0.005	0.018	0.018	-0.214	-0.063	-0.005	-0.007	-0.078	-0.002	**0.195**	-0.144

Residual effects (*U*) =0.42

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, SP= NBP=number of branch per plant, LG=crop lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha-1, rg(xy)= genotypic correlation coefficient between yield per tree and other traits.

Traits which showed positive direct effect on yield had less magnitude of path coefficient values than their correlation values, implying less indirect influence of these traits by means of other component traits. The correlation coefficient of hundred seed weight with yield was negative, but the direct effect was positive, indicating the importance of indirect effect of this trait via other traits.

Generally, number of pod per plant and plant height not only found high and positive direct effect (p=0.449 and 0.294) but also showed strong and positive genotypic correlation coefficient (r_g=0.65 and 0.499) with grain yield, respectively. Therefore, these traits should be considered as important selection indices for yield improvement program. Residual effect in path analysis determines how best the component (independent) variables account for the variability of the dependent variable, yield (Singh and Chaudhary, 1985). To this end, the residual effect in the present study was 0.42 (table 10), showing that 58% of the variability in grain yield was explained by the component factors. Therefore the remaining unexplained variability will either due to non-studied traits or the influence of environment on the traits.

Conclusions

Presence of genetic variability is one of the pre-request to perform selection in any breeding program. Form the current investigation the tested soybean genotypes were found genetically diverse in terms of different morphological traits. 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 (24.80%, 87.85% and 47.95%), number of pod per plant (25.34%, 69.38% and 43.55%) and hundred seed weight (20.74%, 75.29% 37.12%). Hence, this trait can be improved through direct selection more easily than other traits. A total 100 soybean genotypes were grouped into five clusters. The maximum inter cluster distance was found between clusters-IV and V, suggesting superior hybrids or recombinants can be realized by crossing genotypes in these clusters. Principal component analysis (PCA) revealed that, the 1st four PCA with Eigen values exceeding one were responsible for about 72.62 % of the total variation. Out of the entire variations, 1stPCA and the 2ndPCA accounted for more than two third of the total variations (53.13%). On other hand, number of pod per plant and plant height were found maximum positive direct effect on grain yield, also showed strong and positive genotypic correlation coefficient with grain yield, thus, selection pressure could profitably be applied on these traits. Finally this research will enhance the utilization of variation present with in soybean genotypes for selection program. In the future, such a study should include other quality parameters with biochemical and molecular marker assisted techniques.

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