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Genetic divergence among soybean (*Glycine max* (L) Merrill) introductions in Ethiopia based on agronomic traits

Agdew Bekele[1*], Getint Alemaw[2] and Habtamu Zeleke[3]

1. Hawasa Agricultural Research Center, P.O.Box 06, Hawasa, Ethiopia
2. Ethiopian Institute of Agricultural Research (EIAR) Melkasa Agricultural Research center, P.O.Box, 436, Nazareth, Ethiopia. E-Mail: alemawg@yahoo.com
3. Haramaya University, P.O.Box, 138, Diredawa, Ethiopia. E-Mail: habtaamu@yahoo.com

* E-mail of the corresponding author: agdew_bek@yahoo.com

Abstract

The experiment was conducted at two locations, Awassa and Gofa during 2006 main growing season. The objective of the experiment was to evaluate the genetic diversity among soybean germplasm introductions. Forty-nine soybean genotypes were sampled from the introduction populations and used for experimentation. Data were collected on plot basis for nine traits and from ten randomly sampled plants for the rest eight traits. Protein content was determined using micro Kjeldhal method whereas oil content was determined using Nuclear Magnetic Resonance Spectroscopy. Genetic parameters were estimated following the variance components. Genotypes were clustered following the Mahalanobis's D^2 distance between genotypes. Relatively high broad sense heritability was observed for plant height (0.42), days to flower (0.6), days to maturity (0.45), lodging (0.47) and shattering (0.4) indicating the existence of possibility for selection of varieties which are early, with short height to resist lodging. The clustering of genotypes based on 17 traits revealed the existence of variability among genotypes. The maximum inter cluster divergence was observed between genotypes under clusters IX and X hence, the genotypes grouped under these clusters could be used for crossing if yield superior varieties are planned in the hybrid development program.

Keywords: variance components, heritability, genetic advance, cluster

1. Introduction

The major areas of soybean production in the world were restricted to temperate regions until the mid 1940s, when the area started to expand to tropical and subtropical regions (Tukamuhawba *et al*. 2002). Soybean is a short-day plant usually flowers and matures earlier when introduced from temperate to the new tropical and subtropical regions (Zhihui 1999). The new production areas are characterized by warmer and more humid conditions, which impose different production problems such as pod shattering and poor seed viability that result in reduction of yield. However, plant breeding enhanced the adaptation of soybean to a broad range of temperate environments hence; varieties are now being grown as far north and south as 50º latitude (Gardner & Payne 2003).

The crop was not domesticated to Ethiopia in earlier times that research activities were stared with the introduction of germplasms. The introductions have been categorized based on their maturity group (broadly early, medium and late maturing type). There is also variation among germplasms in terms of morphological characters like plant height, pod number and size, seed size, inflorescence, seed coat color etc. Despite the probable narrow genetic base of those germplasm introductions, varieties were either recommended or released following selection procedures. Hence, the objective of this study was to evaluate the genetic diversity of soybean introductions using agronomic traits so as to characterize and cluster with in introduction populations for further breeding purposes.

2. Materials and Methods

The experiment was conducted at Hawassa and Gofa in Southern Nations, Nationalities and Peoples Regional State of Ethiopia. Hawassa is 275 km South of Addis Ababa, capital of Ethiopia, and located at 1700 meters above sea level at 07^0 05N' latitude and 38^0 29E' longitude. It receives average rainfall of 1110 mm annually with average maximum temperature of 27.42^0 C, and minimum of 12.38^0 C. The soil type is Andosole. Gofa is 520 Km South of

Addis Ababa at 1400 meters above sea level and lies at 06^0 19N' latitude and 36^0 53E' longitude. It receives 1338.95 mm average rainfall annually with average maximum and minimum temperatures of 29.4^0 C and 17.63^0 C, respectively. The soil type at Gofa is Acrisole.

Forty-nine genotypes of soybean, including six registered varieties, were grown in 7 x 7 simple lattice design (Allard, 1952) in 2005 main season. The plot size was four rows, 3 m long and 1.6 m wide. The spacing between plants, rows, plots and blocks was 10 cm, 40 cm, 80 cm and 1 m, respectively. Data were measured on plot basis as well as from 10 randomly selected plants of each experimental plot. Protein content was determined according to the methods of C.G. Youngs as described by Stringam *et al*. (1974). Fatty oil content was determined using Nuclear Magnetic Resonance Spectroscopy. Analysis of variance for all traits and locations were carried out using SAS (SAS, 2001) statistical package.

The variance components were estimated with mixed model procedure in which location effect is considered as fixed and genotype, replications with in location, blocks in replication, and the interaction of genotype with location were considered effects as random. Heritability in Broad sense (h^2_B) and Genetic advance as percent of means were calculated for all characters according to the method described by Johnson *et al.* (1955a). Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were estimated according to Burton (1951) while the Mahalanobis's generalized distance (D^2) statistics (Bhatt, 1970) was used for clustering of genotypes by assessing the divergence between genotypes for the traits measured.

3. Result and Discussion

3.1 Genetic Variability

The estimates of genotypic variance, phenotypic variance, broad sense heritability, genetic advance, genetic advance in percentage of means, and phenotypic and genotypic coefficients of variation are indicated in Table 1. The magnitude of phenotypic variance was higher than genotypic variance as the latter is a component of the former. The phenotypic variance (σ^2_p) is the sum of environmental variance (σ^2_e), genetic variance (σ^2_g) and their interaction (σ^2_{ge}). However, the phenotypic and genotypic variance values cannot be used for comparing degrees of variability since different traits have different means across environments. For this reason the genotypic and phenotypic coefficient of variations were used. Relatively wider differences between genotypic and phenotypic coefficients were observed for traits branches/plant, harvest index an grain filling period while relatively narrow differences were observed for traits days to flowering, shattering and lodging. This implies that traits showed narrow differences between genotypic coefficient of variation and the respective phenotypic coefficient of variation had relatively low sensitivity to environmental effects while those with wider differences were affected by environmental factors.

3.2 *Heritability*

Heritability estimates ranged from 0.00% for harvest index to 59.59% for days to flowering (Table 1). Iqbal *et al*. (2003) reported the magnitude of heritability ranging from -3.2% for seed/pod to 99.4% for 100 seed weight. Heritability estimates for days to flowering, lodging, shattering, days to maturity, and plant height were relatively higher than for other traits. This is in agreement with the findings of Anand and Torrie (1963) and Weber and Moorthy (1952) who reported high heritability for days to flower, grain filling period, lodging and plant height. In this study, the heritability of oil content was 39 %. Weber and Moorthy (1952) reported the heritability of 54.7% for oil content and Johnson *et al* (1955) also found 67.5 % and 77.6 % in two soybean populations. The heritability of protein content in this study was very low (8.4%) while Johnson *et al* (1955) reported heritability estimate of 38.9%. Heritability indicates the ease in which a trait can be improved through selection and could vary with materials studied and the environment. Therefore, varieties that are early, short in height with shattering resistance can be developed through selection. Heritability estimates of branches/plant, grain filling period, harvest index, protein content and seed yield were low (<10%). Low estimates of heritability for seed yield/plant, seed weight, protein content was reported in previous studies (Kown and Torrie 1964, Anand and Torrie 1963).

Relatively high heritability (>40%) with high genetic advance (>10%) and genetic advance in percentage of mean (>20%) was exhibited for only plant height, reflecting the chance that this trait could be further improved through selection. In line to this Iqbal *et al*. (2003) reported high heritability with high genetic advance as percentage of mean for plant height. Days to flowering, days to maturity, lodging index, pod shattering and oil content revealed high heritability (>40) with low genetic advance (<10) indicating delayed for further improvement of these traits through selection.

3.3 Genotype Clustering

The square of the distance (D^2) between any two genotypes was calculated as sum of the squares of the distance between the mean values of all transformed variables. Totally 1176 D^2 values were obtained and these values were tested for their significance using Wilks's criterion (Bhath, 1970). The test showed the existence significant differences between genotypes in the mean values for the aggregate of 17 traits assessed. The relative contribution of each trait to the total D^2 between each pair of genotypes was given in Table 2. The percent of each trait contribution varied between 0.085 for grain filling period to 20.66 for grain yield/plant. Based on this seed yield/plant, oil content, days to maturity, and shattering, stood the first, second, third, and fourth, respectively while grain filling period contributed the least.

The smallest D^2 value (2.94) was obtained by combining genotypes IPB-849-285D-2 and SR-4-2 while the maximum D^2 value (101.84) of the most distantly related combination was between Clark-63k and Moya-80. By using the criterion of smaller D^2 for determining constellations, 49 genotypes were grouped into 16 clusters (Table 3). The clustering pattern of genotypes did not follow mostly their growth habit. The varieties under production fall in three different clusters showing the existence of divergence among them.

Intra cluster and inter-cluster divergence value among 16 clusters and their statistical distance were computed (Table 4). Cluster number V showed the least intra cluster D^2 value (5.53) while the maximum intra cluster D^2 value (27.75) was from cluster number XII. This indicates that genotypes under cluster V are with least divergence and genotypes cluster under XII are with maximum divergence. Since it contained the solitary genotype, cluster number XVI had zero intra cluster D^2 value. The inter cluster D^2 values varied from 12.16 (between clusters V and VI) to 66.56 (between clusters IX and X). It is true that the larger the divergence between the genotypes, the higher will be the heterosis when hybrid program is planned to develop yield superior variety. Therefore, genotypes could be selected from clusters IX and X for crossing purpose.

The mean values of assessed traits for 16 clusters were shown in Table 5. Genotypes grouped under cluster II are averagely with least branches/plant, seeds/plant, and seeds/pod. Those genotypes of cluster V took shortest time to fill grain and ended up with least seed yield/plant. The genotypes grouped under cluster IX showed longer plant height, high nodes/plant, and high seeds/plant finally yielded best of all clusters. The genotypes under cluster X were characterized by shortest height and inter node length, with lowest pods/plant, matured earlier, and were resistant to lodging. Cluster XII genotypes took longer time to mature but with least mean harvest index. More branchy types of cluster XIV genotypes produced average maximum seed/pod and finally ended up with lowest seed weight. Those genotypes of cluster XV took longer time to grain filling and hence with maximum seed weight and protein content. The long grain filling period probably associated with suitable nutritional conditions for protein since protein is influenced by environmental conditions until late maturity. Based on the cluster mean one can see that if the objective of plant breeding is to develop short and lodging resistant and early maturing variety, then genotypes under cluster X can be used as parent material for crossing.

The clustering of genotypes into groups based on 17 traits assessed revealed the existence of divergence among genotypes. The magnitude of divergence (measured in terms of D^2 value) varies with different clusters, which can be an indication of different hetrosis level that can be attained during crossing. Generally, largest heterosis can be achieved from the cross of genotypes with highest divergence. This study indicated that, from the genotypes studied, genotypes grouped under cluster IX and X could be used for crossing if the aim is to develop a hybrid with high yield.

4. Conclusion

In this study plant height showed moderately higher heritability associated with higher genetic advance and higher genetic advance as means of percentage indicates the better chance of selection for shorter varieties that can with stand lodging than those traits with moderate heritability but having low genetic advance such as days to maturity, lodging resistance, pod shattering and oil content. The higher genetic divergence observed in this study indicates the potential of improving yield of soybean by crossing those parents shows highest divergence which can yield heterosis.

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Table 1. Estimates of means, variance components, PCV, GCV, heritability in broad sense (h^2_B), genetic advance (GA), and genetic advance as percentage of mean (GA%) for the combined data

No	Traits	Mean ± SE	σ^2_g	σ^2_{ge}	σ^2_e	σ^2_p	PCV	GCV	h^2_B	GA	GA%
1	Plant height	59.3 ± 1.59	120.00	42.89	123.61	286.5	28.54	18.47	41.88	14.64	24.69
2	Inter node length	5.88 ± 0.04	0.02	0.002	0.0648	0.0867	12.37	5.94	23.07	0.14	5.89
3	Branches/plant	4.16 ± 0.03	0.003	0.02	0.0568	0.0798	14.12	2.74	3.759	0.022	1.10
4	Nods/plant	10.12 ± 0.01	0.001	0.004	0.0027	0.0084	9.18	3.17	11.9	0.023	2.26
5	Pods/plant	30.1 ± 0.01	0.0045	0.01	0.0099	0.024	10.68	4.63	18.75	0.06	4.14
6	Days to flower	47.17 ± 0.03	29.65	15.62	4.49	49.76	14.95	11.54	59.59	8.68	18.40
7	Days to maturity	92.73 ± 0.80	30.41	6.09	31.65	68.15	8.90	5.95	44.62	7.607	8.20
8	Grain filling period	45.56 ± 0.82	5.41	19.12	33.04	57.57	16.65	5.11	9.397	1.472	3.23
9	Lodging	1.68 ± 0.03	0.048	0.021	0.034	0.103	25.47	17.39	46.6	0.309	24.51
10	Shattering	2.03 ± 0.03	0.05	0.009	0.0427	0.102	23.31	16.32	49.02	0.323	23.60
11	Seeds/plant	69.68 ± 0.02	0.009	0.003	0.0164	0.029	9.41	5.24	31.03	0.109	6.03
12	Seeds/pod	2.42 ± 0.03	0.011	0.011	0.038	0.0599	15.89	6.81	18.36	0.093	6.03
13	100 seed weight	14.62 ± 0.27	3.02	3.52	3.46	10.00	21.63	11.89	30.2	1.972	13.49
14	Harvest Index	40.01 ± 0.81	0.00	34.27	31.91	66.18	19.72	0.00	0.00	0.00	0.00
15	Crude protein (%)	35.06 ± 0.87	3.89	0.00	36.76	40.65	17.83	5.63	9.959	1.285	3.67
16	Oil content (%)	18.1 ± 0.11	0.847	0.53	0.76	2.13	8.07	5.09	39.77	1.198	6.63
17	Seed yield/plant	9.22 ± 0.07	0.048	0.287	0.236	0.571	25.53	7.40	8.406	0.131	4.43

SE= standard error, σ^2_{ge} = variance of G x E interaction, σ^2_g = genotypic variance, σ^2_e = environmental variance, and σ^2_p = phenotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, h^2_B = heritability in broad sense, GA= genetic Advance, and GA (%) = genetic advance as percent of mean.

Table 2. Relative contribution of individual trait to population divergence

No	Trait	Number of first rank	Percent of contribution
1	Plant height	29	2.47
2	Inter node length	6	0.51
3	Branches/plant	5	0.43
4	Nodes/plant	2	0.17
5	Pods/plant	22	1.87
6	Days to flowering	189	16.07
7	Days to maturity	5	0.43
8	Grain filling period	1	0.09
9	Lodging	99	8.42
10	Shattering	145	12.33
11	Seeds/plant	69	5.87
12	Seeds/pod	9	0.77
13	Seed weight	71	6.04
14	Harvest index	23	1.96
15	Protein content (%)	17	1.45
16	Oil content (%)	241	20.49
17	Seed yield/plant	243	20.66
	Total	1176	100.00

Table 3. Clustering pattern of 49 soybean genotypes based on genetic divergence test

Cluster	Genotypes	Cluster	Genotypes
I	Awassa -95, Cocker-240*, IPB-849-285D-2, SR-4-2	IX	Bossier-2, TGX-1892-10F
II	Crow ford, Williams-82-1, SR-4-1	X	PR-157-47-2, TGX-1895-33F
III	Clark-63k, Davis, Williams, Protona, Tgx-536-100c, V1	XI	PR-118 (2780), AGS-234, F82-7629-3
IV	Pr-41- (339-1), IPB-350-8D-1, PR-157-47-1, SS79168-79-9-1	XII	Moya-80, AGS-162, AGS-208-1, GAIL-2
V	Duicker-3, TGX-1893-10F	XIII	GAIL-1, ST-5-1, Impala (18), EPPS-2
VI	UFV1-1, AGS-65	XIV	Hardee-1, FB-82-7629-1
VII	IPB-400-34 (P), AGS-3-1, SR-4-3	XV	Braxton, ESSEX-1
VIII	Forest -2, D75-92-07-1, Monkey hair-2, TGM-58-4192-1, TAB 144-81(p)	XVI	TGX-1185-10

* Light shaded are released varieties of soybean included in the experiment.

Table 4. Inter cluster D-square values (above diagonal), intra cluster D-square values (diagonal and bold), and inter cluster distance values (below diagonal) with in 16 clusters of soybean genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**13.23**	47.92	20.12	17.1	12.65	29.46	53.73	32.42	60.53	12.32	33.65	57.7	34.49	35.49	21.92	40.34
II	6.92	**12.04**	53.66	44.98	33.33	25.33	14.92	27.06	31.67	60.32	28.13	39.05	29.56	35.35	36.08	46.43
III	4.486	7.325	**17.59**	24.4	16.63	35	54.99	42	51.58	17.75	28.19	57.75	40.33	29.51	25.17	35.8
IV	4.135	6.707	4.94	**21.25**	13.9	21.98	49.96	32.06	54.57	17.51	30.88	49.8	30	34.6	17.91	42.84
V	3.557	5.773	4.078	3.728	**5.53**	12.16	37.66	22.64	36.56	14.65	18.6	36.27	21.48	20.74	15.14	30.07
VI	5.428	5.033	5.916	4.688	3.487	**6.05**	29.28	19.28	25.41	33.71	19.78	22.37	15.7	26.07	17.51	36.22
VII	7.33	3.863	7.416	7.068	6.137	5.411	**17.8**	30.61	25.72	65	20.26	40.66	34.92	37.26	40.52	44.73
VIII	5.694	5.202	6.481	5.662	4.758	4.391	5.533	**23.06**	36.95	41.8	27.93	42.31	21.91	35.03	29.82	53.35
IX	7.78	5.628	7.182	7.387	6.046	5.041	5.071	6.079	**8.49**	66.56	27.71	22.53	37.6	23.15	39.66	29.12
X	3.51	7.767	4.213	4.184	3.828	5.806	8.062	6.465	8.158	**10.2**	37.16	60.3	39.17	40.55	20.32	38.82
XI	5.801	5.304	5.309	5.557	4.313	4.447	4.501	5.285	5.264	6.096	**24.26**	36.69	26.14	22.18	26.75	36.28
XII	7.596	6.249	7.599	7.057	6.022	4.73	6.377	6.505	4.747	7.765	6.057	**27.75**	39.25	33.62	37.9	33.61
XIII	5.873	5.437	6.351	5.477	4.635	3.962	5.909	4.681	6.132	6.259	5.113	6.265	**23.65**	35.12	25.32	54.52
XIV	5.957	5.946	5.432	5.882	4.554	5.106	6.104	5.919	4.811	6.368	4.71	5.798	5.926	**17.17**	31.72	32.17
XV	4.682	6.007	5.017	4.232	3.891	4.184	6.366	5.461	6.298	4.508	5.172	6.156	5.032	5.632	**18.43**	32.6
XVI	6.351	6.814	5.983	6.545	5.484	6.018	6.688	7.304	5.396	6.231	6.023	5.797	7.384	5.672	5.71	**0**

Table 5. Mean values of 17 traits in16 clusters of 49 soybean genotypes grown at Awassa and Gofa

Cluster	Plant height*	Internode length*	Branches /plant	Nodes/ plant	Pods/ plant	DF (days)	DM (days)	GFP (days)	Lodging index	Pod shattering	Seeds /plant	Seeds /pod	100 SW (gm)	HI (%)	Oil (%)	Protein (%)	Seed yield/ plant (gm)
I	43.11	4.73	3.69	8.85	19.4	39.88	86.94	47.06	1.27	2.01	62.81	2.73	14.72	44.13	18.84	33.41	8.80
II	68.75	6.92	1.25	9.97	20.6	51.1	93.5	42.42	3.02	1.50	49.66	2.38	14.69	36.00	18.33	33.60	7.20
III	52.04	4.95	3.36	9.86	21.1	41.1	86.35	45.25	1.42	3.07	61.8	2.68	14.84	41.58	17.42	34.72	9.00
IV	48.86	5.35	4.29	8.92	20.8	42.94	91.19	48.25	1.05	2.13	61.24	2.66	15.80	44.23	18.65	38.00	8.60
V	50.50	4.85	4.07	10.08	19.9	44.88	86.88	42.00	1.21	2.05	57.41	2.60	13.67	39.55	18.64	33.48	6.67
VI	58.59	5.75	4.15	10.04	20.1	51.5	96.38	44.88	1.00	1.45	57.81	2.62	13.96	39.56	18.63	36.96	7.54
VII	77.84	7.18	3.86	10.89	19.7	52.1	94.25	42.17	3.07	1.35	56	2.55	17.11	39.75	17.15	36.58	8.15
VIII	66.48	6.10	3.83	10.86	22.6	48.3	94.4	46.10	1.58	1.26	78.51	2.87	14.88	42.1	19.15	32.60	11.40
IX	81.87	6.45	4.33	12.62	22.7	54.63	97.88	43.25	2.07	1.45	97.27	3.29	13.42	38.97	16.11	39.54	12.33
X	39.03	4.52	4.02	7.97	20.3	40.63	86.25	45.63	1.00	2.37	58.34	2.61	16.20	40.26	18.30	32.91	7.39
XI	66.50	5.97	3.39	10.92	21.1	48.75	94.33	45.58	1.86	2.44	54.7	2.48	14.22	37.81	17.65	33.16	6.97
XII	59.30	5.94	4.67	9.63	20.4	55.56	100.31	44.75	1.36	1.42	78.16	3.02	12.47	35.00	17.19	37.37	8.36
XIII	63.1	5.79	3.88	10.68	22.2	50.13	97.69	47.56	1.44	1.59	66.10	2.77	14.94	38.12	19.37	32.78	9.03
XIV	72.29	6.44	5.05	11.00	22.3	48.13	92.63	44.50	2.07	2.99	90.36	3.15	10.55	38.84	17.93	35.10	8.96
XV	57.14	5.68	4.67	9.87	20.7	44.25	95.5	51.25	1.10	1.81	57.94	2.62	17.20	37.40	17.76	39.67	8.76
XVI	47.00	4.75	4.34	9.08	20.9	45.5	92.00	46.50	1.65	1.45	70.2	2.82	14.19	44.80	14.53	34.86	9.62

* Measured in centimetre