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Research Article
Exploring the Genetic Variability, Heritability and Genetic Gain in Soybean (*Glycine max* L. Merrill) Genotypes

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Abstract

Background and Objective: The presence of variability in the existing germplasm is fundamental for successful crop improvement. Because of this, study was conducted at Uke, Western Ethiopia in the 2018 main cropping season to explore the genetic variability potentials of existing soybean genotypes for future breeding programs. **Materials and Methods:** Hundred soybean genotypes were tested in 10×10 simple lattice design and data were collected on several agronomic traits. **Results:** The study revealed highly significant differences among soybean genotypes tested for all characters except for primary branches per plant and the number of nodules per plant. The highest mean seed yield of 2897 kg ha^{-1} was about 83% yield advantage over the grand mean while 228% over the lowest yielding genotype. And, about 41% of the genotypes had seed yield above the grand mean. Moreover, high GCV coupled with high heritability and genetic advance as percent of mean characters was obtained for primary branches, several nodules per plant, biological yield and seed yield indicating the presence of more additive genes and high possibility of genetic improvement through selection and/or hybridization in these characters. **Conclusion:** The result suggests the existence of sufficient genetic variability among soybean genotypes tested for various desirable characters to achieve better genetic gain for seed yield.

Key words: Additive genes, broad-sense heritability, coefficient of variability, genetic gain

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Soybean (*Glycine max* L) is an economically important leguminous crop. Genetic improvements of soybeans have focused on the enhancement of seed and oil yield, the development of varieties suited to different cropping systems and breeding resistant/tolerant varieties for various biotic and abiotic stresses[1]. The consumer's demand for soybean remains strong and continues to grow because soybeans as food are very versatile and a rich source of essential nutrients. They are also an excellent source of good-quality protein, comparable to other protein foods and suitable for all ages[2]. Soybean is known for its wide adaptability coupled with its higher productivity per unit area compared to other grain legumes[3].

The world soybean production was projected at 311.1 MM t in 2020 and 371.3 MM t in 2030 with annual growth rates are 2.9% from 2005-07 to 2010 and were projected to be 2.5% from 2010-2020 and 1.8% from 2020-2030. Nevertheless, the quantity level in 2030 is estimated approximately to be 1.7 times greater than that of 2005-07[4]. The most important countries of the world with the highest rate of soybean production include the USA, Brazil, Argentina, China and India[5]. However, recently soybean productivity in Ethiopia is about 2.3 t ha^{-1} and the production trend of Soya Bean in Ethiopia shows up and down during the last ten years[6] which is challenging that needs to be tackled.

The research report shows that in the USA soybean [*Glycine max* (L.) Merr.] The mean yield of on-farm increased at a rate of 23.4 kg/ha/yr between 1924 and 2010 mainly as a result of genetic improvements and agronomic technologies. The finding showed soybean genetic yield potential has been a large contributor to the rate of on-farm yield improvement[7]. Thus, genetic improvement is among the basic requirement in increasing yield. Thus, assessment of the extent genetic variability existing in any crop species is essential for formulating effective breeding strategies to achieve high-yielding cultivars[8]. Heritability estimates provide an insight into the extent of genetic control to express a particular character and phenotypic reliability in predicting its breeding value[9]. Heritability provides information on the magnitude of the inheritance of characters from parent to offspring, while genetic advance helps find the actual gain expected under selection[10,11]. The existence of substantial variability among soybean genotypes was reported by different researchers[12-14] on different quantitative traits.

Genetic variation is a prerequisite in crop improvement to develop improved seed yield which is the ultimate goal of breeders. However, seed yield itself is influenced by the interaction of many components traits in different magnitude which requires frequent assessment of genetic parameters using standard procedures. Therefore, it is important to compare the relevance of each of the traits to give more attention to those having the highest influence on yield[13] for better achievement. In this regard, in this study, the extent of essential genetic components among the existing 100 soybean genotypes is important for future breeding. Thus, this study aimed to assess the potentials of genetic variability, broad-sense heritability and genetic gain among soybean genotypes for yield and yield-related traits for future breeding.

MATERIALS AND METHODS

Study area: The field experiment was conducted at Uke, East College, Western Ethiopia in the 2018 cropping season. The Uke site is located 365 km from Addis Ababa. The site is located at 8°11'52" and 10°94'44" North latitude and 36°97'51" and 37°11'52" East longitude and at the altitude of 1500-1700 masl, with a prevalence of lowlands. The place has a mean maximum and minimum temperature is 31 and 16°C with 1400 and 1200 mm rainfall, respectively. The pH of the soil is acidic with the red colour of Nitosol a dominant soil type in Western Ethiopia

Experimental material and design: A total of 100 genotypes (97 genotypes and 3 varieties) of soybean were obtained from Jimma Agricultural Research Center, Ethiopia and used for the study in Table 1. The experiment was laid out in a 10×10 simple lattice design. Each genotype in the plot was grown in two rows of 4 m in length. A spacing of 60 cm between rows and 5 cm between plants was used. The crop was sown 8th of July, 2018 and NPS fertilizer was applied at the rate of 120 kg ha^{-1} at sowing time and all other recommended agronomic management practices were applied uniformly to all plots.

Data collected: The following data were recorded on days to 50% flowering, days to 90% maturity, days to grain filling period, plant height, some primary branches per plant, nodules per plant, some pods per plant, seeds per pod, hundred seed weight, biological yield, seed yield and harvest index following standard procedures.

Statistical analysis: The data were subjected to analysis of variance using GLM procedures of the SAS[15] and variances were derived to calculate the genetic parameters following the standard procedures as follows.

Table 1: List of soybean genotypes used in the study

S/No	Accession	S/No	Accession	S/No	Accession
1	T29-15-T63-16-SA1	35	T47-15-T122-16-SA1	69	T6-15-T2-16-SA2
2	T23-15-T45-16-SA1	36	T46-15-T119-16-SA1	70	T27-15-T52-16-SB1
3	T73-15-T228-16-SC1	37	T70-15-T220-16-SG1	71	T27-15-T51-16-SA1
4	T73-15-T231-16-SF1	38	T27-15-T57-16-SG1	72	T55-15-T159-16-SA1
5	T45-15-T116-SC2	39	T24-15-T46-16-A2	73	T15-15-T20-16-SH1
6	T45-15-T155-16-SA2	40	T72-15-T225-16-SA1	74	Nyala
7	T15-15-T18-16-SF1	41	T50-15-T141-16-SC1	75	T35-15-T80-16-SE1
8	T35-15-T77-16-SB1	42	T35-15-T78-16-SC1	76	T48-15-T128-16-SA1
9	T74-15-T239-16-SE2	43	T27-15-T57-16-SG2	77	T44-15-T106-16-SD1
10	T63-15-T183-16-SB1	44	T54-15-T156-16-SB1	78	T25-15-T47-16-SA2
11	T16-15-T23-16-SC1	45	T49-15-T132-16-SA1	79	T45-15-T116-16-SA1
12	T6-15-T223-16-SB	46	T16-15-T27-16-SG3	80	T15-15-T16-16-SD1
13	T35-15-T79-16-SD1	47	T44-15-T107-16-SE1	81	T33-15-T68-16-SA1
14	T66-15-T193-16-SB1	48	T44-15-T111-16-SI1	82	Afgat
15	T53-15-T153-16-SC1	49	T52-15-T147-16-SA1	83	T28-15-T62-16-SD1
16	T52-15-T149-16-SC1	50	T70-15-T219-16-SF2	84	T34-15-T70-16-SA1
17	T55-15-T160-16-SB2	51	T25-15-T47-16-SA1	85	T19-15-T39-16-SD1
18	T74-15-T240-16-SF2	52	T49-15-T134-16-SC1	86	T56-15-T163-16-SA1
19	T56-15-T164-16-SB1	53	T25-15-T48-16-SB1	87	T26-15-T50-16-SB1
20	T50-15-T139-16-SB2	54	T52-15-T148-16-SB1	88	T27-15-T58-16-SH1
21	T42-15-T97-16-SA1	55	T33-15-T69-16-SB1	89	T24-15-T46-16-SA1
22	T44-15-T111-16-SI2	56	T29-15-T64-16-SB1	90	T56-15-T165-16-SC1
23	T54-15-T155-16SA1	57	T39-15-T92-16-SC2	91	T27-15-T51-16-SA2
24	T28-15-T61-16-SC1	58	T44-15-T108-16-SF1	92	T76-15-T241-16-SC1
25	T16-15-T28-16-SH1	59	T27-15-T51-16-SA3	93	T39-15-T96-16-SG1
26	T27-15-T58-16-SH2	60	T37-15-T81-16-SA1	94	T47-15-T124-16-SC1
27	T19-15-T38-16-SC1	61	T53-15-T152-16-SB1	95	T51-15-T142-16-SA1
28	T52-15-T147-16-SA2	62	T16-15-T-31-16-SK1	96	T47-15-T122-16-SA2
29	T73-15-T230-16-SE1	63	T71-15-T222-16-SA1	97	T51-15-T146-16-SE1
30	T74-15-T240-16-SF1	64	T27-15-T53-16-SC1	98	T57-15-T167-16-SB1
31	T71-15-T224-16-SC1	65	T62-15-T181-16-SA1	99	T55-15-T161-16-SC3
32	T75-15-T240-16-SA1	66	T74-15-T236-16-SB1	100	T50-15-T139-16-SA1
33	T54-15-T157-16-SC1	67	Clarck 63 K		
34	T74-15-T239-16-SE1	68	T67-15-T203-16-SG2		

Estimation of variance components: The phenotypic and genotypic coefficients of variation were estimated from variances and classified[16].

While heritability in a broad sense (H_2) which is expressed as the proportion of the genotypic variance to the phenotypic variance was calculated according to Marwede *et al.*[17]. And genetic advance (GA) and genetic advance as percentage of the mean (GAM) was estimated by assuming selection of superior 5% of the genotypes per Marwede *et al.*[17].

RESULTS

Mean, range, genotypic and phenotypic variances of soybean genotypes: The analysis of variance showed that genotypes were significantly ($p<0.01$) in Table 2 different for all traits except several primary branches per plant and the number of nodules per plant. Soybean genotypes tested showed a notable range of variation especially in some desirable characters. For instance, days to maturity ranged from 95-125 days whereas the number of pods per plant varied from 23-78. And, genotypes also showed a high range of variation (11-43) for the number of nodules per plant. The number of primary branches per plant and hundred seed weight also varied from 2-8 and 12-19, respectively. In addition to this, biomass yield also had a high range of variation (2109-5743 Kg ha^{-1}) among the soybean genotypes tested. Seed yield ranged from 883-2897 kg ha^{-1} and this result is significantly higher than the grand mean (1579 kg ha^{-1}). And, the mean values of the harvest index for the genotypes varied from 28-51% in Table 3. Besides this, high genotypic variances were observed days to maturity, grain filling period, plant height, number of nodules per plant, biomass yield and seed yield. GCV values were between 10 and 20% for grain filling period, plant height, number of primary branches, number of pods per plant and number of nodules per plant while GCV values were greater than 20% for biological yield and seed yield (Table 3). On other hand, the PCV (%) values were between 10 and 20% for grain filling period, plant height and harvest index and the values were greater than 20% for the number of primary branches, number

Table 2: Mean squares values for 13 characters of soybean genotypes tested at Uke in 2018

Characters	Rep (Df = 1)	MSG (Df = 99)	MSE (Df = 90)	Mean
Days to 50% flowering	3.41	33.36**	2.13	54.0
Days to 95% maturity	0.126	122.20**	0.42	107.9
Grain filling period	4.24	93.70**	2.49	52.00
Plant height (cm)	4.13	185.10**	65.49	63.14
Number of primary branches	20.30	2.78^{ns}	1.70	4.846
Number of pods per plant	60.2	234.16**	74.55	49.991
Number of seeds per pod	0.64	0.225**	0.175	5.16
Number of nodules per plant	752.7	65.10 ns	36.67	25.82
Hundred seed weight (g)	1.125	3.148**	0.251	15.146
Biological yield (kg ha^{-1})	141180	1193218**	58574	3532.2
Seed yield (kg ha^{-1})	124440	235875**	29187	1579.29
Harvest index	0.0025	0.0037**	0.0013	0.4432

ns : Non-significant and ** : Highly significant

Table 3: Range, mean, variances, coefficient of variation, heritability and genetic gain for agronomic characters of soybean genotypes

Traits	Range	Mean±S.E	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
DF	48-63	54.00±0.40	15.60	2.13	17.70	7.29	7.77	88.00	7.60	14.00
DM	95-125	107.90±0.78	60.80	0.42	61.30	7.21	7.23	97.00	15.58	14.43
GFP	41-69	52.20±0.68	45.57	2.5	48.10	12.80	13.20	93.00	13.28	25.40
PH	34-92	63.10±0.96	59.80	65.5	125.30	12.50	17.700	48.0	11.00	17.50
NBP	2-8	4.80±0.12	0.55	1.68	2.23	15.30	30.00	24.0	0.73	15.00
NNP	11-43	25.00±0.75	14.20	36.6	50.80	14.60	27.60	27.9	3.96	15.30
NPP	23-78	49.90±1.08	79.80	74.5	154.3	17.90	24.80	51.0	13.00	26.00
NSP	2-3	5.16±0.01	0.025	0.175	0.20	3.06	8.60	12.5	0.14	1.90
HSW	12-19	15.10±0.127	1.44	0.25	1.70	7.90	8.60	84.7	2.24	14.80
BY	2109-5743	3532±57.2	567322.0	58574	625896.0	21.30	22.03	88.0	1466.0	41.50
SY	883-2897	1579±34.30	103344.0	29187	132531.0	20.80	23.00	78.0	577.00	36.50
HI	0.28-0.51	44±0.40	0.0012	0.0013	0.0025	7.80	11.36	48.0	4.94	11.22

DF: Days to 50% flowering, DM: Days to 95% maturity, GFP: Grain filling period, PH: Plant height, NBP: Number of primary branches per plant, NPP: Number of pods per plant, NSP: Number of seeds per pod, NNP: Number of nodules per plant, HSW: Hundred seed weight, HI: Harvest index, BY: Biomass yield, SY: Seed yield. S.E. Mean: Standard error of the mean, σ^2g: Genotypic variance, σ^2e: Environmental variance, σ^2p: Phenotypic variance, H^2 (%): Heritability, GCV (%): Genotypic coefficient of variation, PCV (%): Phenotypic coefficient of variation, (%), GA: Genetic advance and GA (%): Genetic advance as percent of mean

of pods per plant, number of nodules per plant, biological yield and seed yield. Generally, the result showed that for most of the characters, the estimates of the phenotypic coefficient of variation (PCV) were greater than the genotypic coefficient of variation (GCV) (Table 3).

Broad sense heritability and genetic advance: Broad sense heritability values were greater than 60% for characters such as days to 50% flowering, days to 95% maturity, grain filling period, hundred seed weight, seed yield and biological yield (Table 3). Moreover, the greater genetic advance was recorded for biological yield, seed yield, number of nodules per plant, days to maturity, grain filling period and plant height. And, relatively high genetic advance as percent of the mean (greater than 20 %) was recorded for grain filling period, several nodules per plant, biological yield and seed yield. Relatively higher heritability combined genetic advance as percent of mean was recorded for grain filling period, some pods per plant, biomass and yield seed yield (Table 3).

DISCUSSION

The soybean genotypes studied showed highly significant variation for all characters except some primary branches per plant and some nodules per plant (Table 2) indicating the presence of substantial variability for genetic improvement. Therefore, this provides the importance of doing further statistical analysis to differentiate the genetic potential existing among the populations. Similarly, Aditya *et al.*[14] reported significant differences among genotypes for the number of pods per plant, days to flowering, days to maturity and seed yield, plant height, harvest index and seed yield on soybean. Mean value, range of mean, variances and other genetic parameters revealed variability for most of the parameters studied which would be useful to design and execute effective future breeding programs in the short term and long term. The soybean genotypes evaluated had highly varied for days to maturity (95-125), number of pods per plant (23-78), number of nodules per plant (11-43), number of primary branches per plant (2-8), hundred seed weight (12-19), biomass yield (2109-5743 kg ha^{-1}), seed yield (883-2897 kg ha^{-1}) and harvest index (28-51%) (Table 3). And the maximum seed yield (2897 Kg ha^{-1}) recorded was about 83% advantage over the grand meanwhile 228% over the lowest yielding genotype indicating the extent of variation among the genotype population. Therefore, this revealed remarkable variability among soybean genotypes tested for desirable traits for genetic improvement in this highly valued crop.

PCV (%) and GCV (%) values greater than 20% can be regarded as high whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. Thus, GCV values were between 10 and 20% for grain filling period, plant height, number of primary branches, number of pods per plant and number of nodules per plant while the GCV values were greater than 20% for biological yield and seed yield (Table 3). On other hand, the PCV (%) values were between 10 and 20% for grain filling period, plant height and harvest index whereas the PCV values were greater than 20% for the number of primary branches, number of pods per plant, number of nodules per plant, biological yield and seed yield (Table 3). This assessment shows the presence of genotypic and phenotypic variability among genotypes for most quantitative traits for selection. And, the selection of traits with high GCV would be more promising for genetic improvement. This result coincides with Aditya *et al.*[14] and Ibrahim *et al.*[12] findings who reported the presence of substantial variability among soybean varieties for GCV and PCV. Moreover, high to moderate genotypic coefficients of variation were also reported by Aditya *et al.*[14] for several pods/plant, plant height and grain yield.

The highest broad sense heritability values for days to 50% flowering, days to 95% maturity, grain filling period, hundred seed weight, seed yield and biological yield (Table 3) indicated the presence of suitable conditions for effective selection in these traits. The magnitudes of heritability for most of the quantitative characters were moderate to high, except for some primary branches per plant and the number of seeds per pod indicating less environmental influence. Broad-sense heritability (H^2) only indicates whether or not there is sufficient genetic variation in a population, which implies whether or not a population will respond to selection pressure[18]. High heritability has been reported on days to flowering by Barh *et al.*[19] in soybean. Moreover, according to Aditya *et al.*[14] moderate heritability was observed for pods $plant^{-1}$ which is in line with the present findings a d except for the number of branches, this result coincides with the report of Sulistyo *et al.*[20] who stated that high heritability values were obtained for days to flowering, days to maturing, plant height, the weight of 100 seeds and yield in soybean implying the additive type of gene action.

Moreover, the higher genetic advance for biological yield, seed yield, number of nodules per plant, days to maturity, grain filling period and plant height implies more than 10% increment could be achieved after one cycle of selection in these traits. Besides this, the heritability value alone may not help in identifying characters for effective selection, however, heritability estimates are reliable when considered together with genetic advance[14]. Moreover, in this study, relatively high heritability coupled with high genetic advance was obtained for biomass, seed yield, grain filling period and days to maturity (Table 3) showing effective improvement in these traits. High GCV coupled with high heritability and genetic advance as percent of mean was obtained for some primary branches, some nodules per plant, biological yield and seed yield (Table 3). High GCV and heritability for quantitative traits show that the traits are governed by additive gene action which can be fixed through selection[9]. The knowledge of heritability provides information on the magnitude of the inheritance of characters from parent to offspring, while genetic advance is useful in predicting the actual gain expected under selection[10-11]. This study is against the Hakima and Suyamto[21] which had obtained high heritability value coupled with high genetic advance as percent of the mean for harvest index. And, high values of heritability and genetic advance with high GCV for branch number, plant height, pod number and seed weight was reported by Malik *et al.*[13] can be considered as favourable attributes for soybean improvement through phenotypic selection.

Furthermore, high heritability estimates coupled with high genetic advances were recorded for plant height and number of pods/plant[14]. The correlated response of multiple traits is used mainly for improving traits that have low heritability. Hence, breeders must determine the most important traits, keeping in mind the breeding populations and resources. Three basic strategies including tandem selection, independent culling and selection index can be utilized to simultaneously breed or select for multiple traits[22]. In this study, there is a chance to improve multiple traits simultaneously for indirect selection.

CONCLUSION

The result revealed that genotypes exhibited considerable variation for most of the desirable characters studied which is an important foundation for future improvement. Higher harvest index greater than the mean (45%) were recorded for most of the genotypes indicating the greater potential for productivity. And, the highest mean seed yield of 2897 kg ha^{-1} was while the lowest was 1579 kg ha^{-1} indicating the highest yielding genotype had about 83% advantage over the grand meanwhile 228% over the lowest yielding genotype. And, about 41% of the genotypes gave seed yield above the grand mean. Furthermore, the high heritability coupled with high genetic advance obtained for biomass, seed yield and grain filling period and days to maturity suggests that an initial selection of 5% of the top populations would result in an increase by 1466 kg, 577 kg, 13.28 and 15.58%, respectively, in these characters after one cycle of selection. Relatively higher heritability combined with genetic advance as percent of the mean for grain filling period, number of pods per plant, biomass and yield seed yield indicated the presence of more additive genes which makes suitable for effective selection in these characters.

SIGNIFICANCE STATEMENT

The study explored the genetic potential of soybean genotypes for yield and yield component characters which will be useful in future breeding. Soybean genotypes tested had shown a high range of variation for some important desirable characters and the characters with high GCV coupled with high heritability and genetic advance as percent of mean conditioned by additive genes were identified which have a high possibility for genetic improvement through selection and hybridization programs.

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