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Analysis of Heritability and Genetic advance in soybean [Glycine max (L.) Merrill] in Northwestern Ethiopia

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Abstract

Eighty-one genotypes were tested in a 9x9 simple lattice design to evaluate their genetic variability, heritability, and genetic advance for 11 contributing traits at Pawe (main research station) and Debate substation of Pawe Agricultural Research Center during 2018/2019 cropping season. Based on analysis of variance, most of the traits showed highly significant ($p<0.01$) differences except the number of nodules per plant, number of pods per plant, and number of seeds per pod. The estimates of phenotypic and genotypic coefficients of variations (PCV&GCV) showed that the values of PCV were higher than of GCV. This would be indicated the expression of traits was highly influenced by environmental factors. High GCV and PCV values were observed by the number of seeds per plant and grain yield at Pawe and only by grain yield at Dibate implied that the presence of genetic variability for selection in these traits. High heritability coupled with high genetic advance as per cent of mean was recorded by number of seed per plant(82.8% and 56.81%) and grain yield (89.9% and 45.2%) at Pawe and days to flowering (97.2% and 23.7%) and plant height (96.6% and 33.7%) at Debate implying selection could be effective for these traits per each location.

Keywords: Genetic advance, Heritability, Selection, Soybean, Trait, Variability

1. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a self-pollinated diploid and has a chromosome number of 2n = 4x = 40. Soybean is categorized in the legume family, Leguminosae (Hymowitz 2004; Smith and Huyser, 1987). Soybean is cross-compatible with the wild species *Glycine soja*, but undesirable growth characteristics of *Glycine soja*are apparent in the progeny. Soybean is the most widely grown leguminous crop in the world and is an important source of protein and oil for food and feed (Sharma *et al*., 2013; Hossain, and Komatsu, 2014). Soybean seeds are rich in proteins, unsaturated fatty acids, minerals (e.g. Ca and P) and vitamins (e.g. A, B, C, and D) which meet the nutritional needs of humans and other animals (He and Chen, 2013; Ghosh *et al*., 2014; Malik *et al*., 2014). Effective selection is dependent on the existence of genetic variability. The characterization ofthis variability in a population is pertinent since genetic diversity within the population and within species determines the rates of adaptive evolution and the extent of response in crop improvement. Dissimilarity will always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success in a crop improvement program (Poehlman 1979; Welsh, 1981). The extent of the genetic variability in a specific breeding population depends on the germ plasm included in it (Frey, 1981). Hence, genetic variability is of immense importance to plant breeders because it can be transmitted to the progeny and the proper management of the diversity can produce a permanent gain in the performance of the plant (Welsh, 1981).

Estimations of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance are useful genetic parameters for the determination of genetic variability. These parameters enable breeders to select the characteristics to be considered in the initial and advanced steps of the breeding program (Farias, 2008). Therefore, the present study was conducted to estimate the variability among genotypes and genetic parameters to be used for plant selection in soybean breeding programs.

1. MATERIALS AND METHODS

The experiment was conducted at Pawe Agricultural Research Center main station and Debate $(10^{o}30' 0''$ N, 36^{o} $10'$ $0''$ E) sub-station during the main cropping season of 2018/19. Pawe Agricultural Research Center (11^{0}18\`49.6\`\`N and $036^{0}$24\`29.1\`\`E) in Metekel Zone (PARC, 2017). Eighty-one introduced soybean genotypes from IITA, USA and Brazil were used for the experiment. The experiment was laid out in a 9x9 simple lattice design with a plot size of 7.2 meters square (2.4m*3m). Each plot consisted of four rows with 60cm inter-row and 5cm intra row spacing. The spacing between plots, blocks, and replications were 0.8m, 1m, and 2m, respectively. The total net harvestable experimental area for each location was 583.2 m^{2}. The amounts of seed and DAP fertilizer rate per plot were 54g and 72g, respectively. All the cultural practices were applied as per individual location recommendations.

Data were recorded during the cropping season and after harvesting. Observations that were were recorded both on plot and plant bases are listed below. Data on days to 50% flowering, days to 95% maturity, protein content (%), oil content (%), and grain yield (kg) were recorded on plot bases. The grain yield per plot was measured from the middle two rows and converted to hectare bases. All other parameters were recorded on a plant basis by taking ten plants randomly from each experimental plot according to Malik *et al*. (2014).

For determination of the quantity of oil and protein, one hundred fifty grams of dried seed samples from each genotype were ground using a grinder in the laboratory room. Then, two to three grams of seed flour was taken using small cups (internal diameter of 35 mm and depth of 8 mm) and scanned by Near-infrared spectroscopy (NIRS) mono chromator model FOSS 6500 (FOSS NIR Systems, Inc., Silver Spring, Denmark) to estimate the percentage of oil and protein contents. Proximate compositions (list of the parameter) were predicted using plant-based global calibration (infra soft international) from the collected spectra (Osborne and Vogt, 1978).

2.RESULTS AND DISCUSSION

3.1. Variability of Genotypes

The analysis of variance (ANOVA) for traits with effective relative efficiency was done based on simple lattice design and RCBD was considered for traits that had non-effective relative efficiency at both locations. Mean squares for eight traits were analyzed based on lattice design and three traits based on RCBD at Pawe Tables 1 & 2, respectively. Mean squares for eight traits were analyzed based on lattice design and three traits based on RCBD at Debate Tables 3 & 4, respectively. There was highly significant difference (P<0.01) among genotypes in days to flowering, days to maturity, plant height, number of branches per plant, hundred seed weight, protein content, protein content and seed yield at Pawe and Debate indicate the existence of variability among genotypes for these traits.

Similarly, significantly different (p<0.01) results have been reported in soybean for days to 50% flowering, days to maturity, plant height, number of branches per plant, and hundred seed weight (Akram *et al*., 2016; Nutan and Gabrial, 2016). Where as, the number of nodules per plant and the number of pods per plant were showed non-significant difference at both locations. Mean square of the number of seeds per pod showed a significant difference at Pawe and non-significant difference Debate.

Table 1. Mean squares for eight traits of soybean genotypes tested at Pawe in a lattice design

Trait	Rep (1)	Geno. adjusted (80)	Block within rep adjusted (16)	Error		
				Intra block (64)	RCBD (80)	RE
DF	9.38ns	65.7**	14.11	10.7	17.03	109.9
DM	206.72ns	79.12**	21.9	11.3	24.2	108.4
PHT	299.3ns	321.8**	119.2	80.29	93.7	107
BraP	7.86ns	1.75**	1.15	0.92	0.98	105.8

PdP	3571.1	191.3ns	146.9	47.1	138.2	105.4
SdP	0.29*	0.07ns	0.07	0.03	0.06	106.3
HSW	4.37ns	5.3**	1.6	1.23	2.12	119.7
Protein	3.64ns	12.13**	5.2	3.9	4.20	105.1

Table 2. Mean squares for three traits of soybean genotypes tested at Pawe in RCBD

Trait	Rep (1)	Geno (80)	CV (%)
NN	1ns	6.06 ns	12.7
Oil	0.04ns	2.34**	0.9
Yield	618192**	1252523.9**	7.8

NN= number of nodules per plant & CV= Coefficient of variation.

Table 3. Mean squares for eight traits of soybean genotypes tested at Dibate in lattice design

Traits	Rep (1)	Geno. adjusted (80)	Block within rep adjusted (16)	Error		RE over RCBD
				Intra block (64)	RCBD (80)	
DF	26.9ns	131.1**	5.98	1.88	2.70	126.3
NN	25.5ns	15.1ns	79.30	29.3	72.4	108
DM	0.62ns	153.6**	202	140.70	153.0	110.4
PHT	20.9*	185.33**	5.9	3.50	4.0	105.4
BrP	7.5ns	1.33**	0.8	0.51	0.58	108.6
PdP	323.9ns	74.31ns	48.6	48	48.6	109.1
Oil	0.02ns	2.41**	0.01	0.01	0.01	108.3
Protein	0.01ns	9.23**	0.02	0.02	0.02	110.1

DE= Days to 50% flowering, NN= number of nodules per plant, DM= Days to 95% maturity, PHT= Plant height, BrP = number of branches per pod, PdP=Number of pods per plant, and RE= Relative Efficiency

Table 4. Mean squares for three traits of soybean genotypes tested at Debate in RCBD

Trait	Rep (1)	Geno (80)	CV (%)
SdP	0.29*	0.06ns	13.2
HSW	17.3**	3.9**	8.2
Yield	16265.5ns	245526**	13

"*", **"= significant at 1% and 5% levels, respectively. DF=days to flowering, NN= number of nodules, DM= days to maturity, PH=plant height, BrP= number of branches per plant, PdP= number of pods per plant, SdP= number of seeds per pod, HSW=hundred seed weight, Geno= Genotype and Rep = number of replication.

3.2 Mean and Range values of Soybean Traits

Range and mean values of eleven quantitative and three qualitative traits are presented in Table 5 at both locations. Genotypes showed a wide range of variability for all traits. The highest and lowest range values showed that genotypes had different performances in yield, yield-related traits, and quality traits. The lowest (1586.9g) and highest (2822g) yield per plot were recorded at Pawe. The lowest (844.4g) and highest (2445.2g) yield per plot were recorded at Debate. Variation for flower color, stem pubescence color, and pod pubescence color as qualitative descriptors were recorded. More than half (85.2%) of the genotypes had a purple flower color, while 14.8% of the genotypes had white flower color. The genotypes showed two different pubescence colors, brown and white, which accounts for 64.2% and 35.8 %, respectively. All genotypes showed 100% stem and pubescence color.

Table 5. Descriptive statistics for eleven quantitative and four qualitative traits

	Pawe				Debate			
Traits	Range	Mean ± S.E	CV(%)	R^2(%)	Range	Mean± S.E	CV(%)	R^2(%)
DF	43-78	57.4±0.23	7.1	88	60-102	69.4± 0.14	2	97
NN	10.8-28.2	17.3 ±3.8	12.7	85.5	2.4-27	13.9± 0.7	15.8	78
DM	98-141	112.6 ±0.25	2.2	85.6	110-150	124.6± 0.2	1.6	96
PHt	41.9-156.6	78.3 ±2.5	9.7	83.7	42-108.6	62.01± 0.59	3	91
BrP	1.5-8.1	4.22 ±0.25	18.4	75.8	2.2-7.6	4.1± 0.22	17.4	77.8
PdP	26.7-118.8	55.2 ±2.2	12.7	71.9	14-65.4	31.1± 1.7	18	67
SdP	1-3.7	1.93 ±0.1	13.4	60	0.9-3.48	1.9± 0.1	13	79
HSW	8.5-18	13 ±0.1	6.8	77.4	8.5-15.5	13± 0.1	7.2	90.9
Oil	19.5-24.2	21.2±0.02	0.9	98.5	18.6-23.9	21.3±0.01	0.3	98
Protein	8.6-41.4	35.6±0.2	5.6	76.8	30.2-40.8	36.2 ±0.01	0.3	76.8
Yield	1587-2822	2147 ±166	7.8	83	844-2445	1543± 20.6	14	87.5

Flower color	Purple (85.2%) followed by white (14.8%)
pubescence	Present (100% present)
Stem pubescence color Pod pubescence color	Brown (64.2%) followed by white (35.8%)

SE = Standard Error and DF = days to flowering, NN = number of nodules, DM= days to maturity, PHt = Plant height, BrP= number of branches per plant, PdP = number of pods per plant, SdP = number of seeds per pod, HSW=hundred seed weight, Coefficient of Variation and R^2=efficiency of the model.

3.3 Estimates of Genetic Parameters

An estimate of phenotypic (σ^2p), genotypic (σ^2g), and environmental (σ^2e) variances and phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are provided in Tables 6 and 7 at Pawe and Debate, respectively. High δ^2g and δ^2p were recorded for grain yield, plant height, number of pods per plant, days to maturity, and days to flowering at Pawe, whereas grain yield, plant height, days to maturity, and days to flowering showed the highest δ^2g and δ^2p at Debate. Similarly, high genotypic and phenotypic variances have been reported in soybean for grain yield, days to flowering, and days to maturity (Basavaraj *et al*., 2015; Besufikad Enideg, 2018).

At Pawe, genotypic coefficients of variation (GCV) values ranged from 0.05% for the number of nodule per plant to 29.2% for the number of seeds per pod, whereas the phenotypic coefficients of variation (PCV) values ranged from 5.1% for oil content to 32.1% for the number seeds per pod. The highest GCV value was recorded by the number of seeds followed by grain yield. Moderate (10%-20%) GCV values were recorded by the number of pods, the number of branches, plant height, and hundred seed weight. Similarly, moderate GCV values have been reported in soybean for the number of pods, the number of branches, plant height, and hundred seed weight (Akram*et al*., 2011; Santosh*et al*., 2018).

At Dibate, genotypic coefficients of variation (GCV) values ranged from 4.4 % for the number of nodules per plant to 20.7% for grain yield, whereas the phenotypic coefficients of variation (PCV) values ranged from 5.4% for oil content to 43.4% for number of nodules per plant. Number of nodules, the number of branches, the number of pods, and grain yield showed the highest phenotypic coefficients of variation (PCV) values. Similarly, the highest phenotypic coefficients of variation values have been reported in soybean for grain yield, number of pods, number of nodules, and number of branches (Besufikad Enideg, 2018; Mesfin Hailemariam 2018).

3.4 Estimation of heritability and genetic advance

Heritability estimate for traits studied at Pawe and Debate are given in Tables 6and 7, respectively. At Pawe, broad-sense heritability values were ranged from 12% for the number of nodules to96.1 % for oil content (Table 4.4). Oil content, grain yield, days to flowering, days to maturity, and number of seeds at Pawe had the highest broad sense heritability values. At Debate, broad-sense heritability values were ranged from 1% for the number of a nodule to 97.2% for days to flowering (Table 6). Days to flowering, plant height, oil content, days to maturity, and protein content had the highest broad-sense heritability. In agreement with this result, high heritability for days to flowering and plant height in soybean has been reported by Weber and Moorthy, (1952). Conversely, low heritability for protein content in soybean has been reported (Alexandra *et al*., 2017;

Agdew Bekele *et al*., 2012). Characters with low heritability may be difficult or impractical for selection, due to the masking effect of the environment.

At Pawe, genetic advance as percent of mean ranged from 0.57% for the number of a nodule to56.8% for the number of seeds per pods (Table 6). At this location, the highest genetic advance as percent of mean was recorded by the number of seeds per pod followed by the number of branches, grain yield, number of pods, and plant height. At Debate, genetic advance as percent of mean ranged from 0.9% for number of the nodule to 36% for grain yield (Table 6). Within this range, the highest genetic advance as percent of mean was recorded from grain yield followed by plant height, days to flowering, and number of branches. In agreement with this result, high genetic advance as percent of mean in soybean for plant height has been reported (Parameshwar, 2006; Besufikad Endeg, 2012; Yechalew Sileshi, 2018).

High heritability estimates along with the high GAM are usually more helpful in predicting gain under selection than heritability estimates alone (Johnson *et al*., 1955). The present study showed high heritability coupled with high genetic advance as a percent of the mean for the number of seeds (82.8% and 56.8%) and grain yield (89.9% and 45.2%) at Pawe. High genetic advance coupled with high heritability offers the most effective condition for selection because of variability (Larik *et al*., 2000) and indicates the presence of additive genes in the inheritance of the trait. Similarly, high heritability coupled with high genetic advance as percent of mean has been reported for plant height, grain yield, number of seeds, and number of pods in soybean by various workers (Besufikad Endeg, 2012; Ghodrati, 2013; Badkul *et al*., 2014; Hakim *et al*., 2014; Mesfin Hailemariam, 2018; Santosh*et al*., 2018).

At Debate, high heritability coupled with relatively high genetic advance as percent of mean was recorded for days to flowering (97.2% and 23.7%), plant height (96.6% and 33.7%), and grain yield (71.1% and 36%) (Table 6). Similarly, high heritability with high GAM has been reported for plant height and grain yield in soybean (Iqbal*et al*., 2003; Besufikad Endeg, 2012; Yechalew Sileshi, 2018). So, high values of heritability along with high GAMfor characters such as days to flowering, plant height, and grain yield can be effective for predicting gain under selection. Besides, effective phenotypic selection and high genetic gain from such characters can be achieved (Ghodrati, 2013; Nassar, 2013; Mahbub*et al*.,2015).

Table 6. Variances and Genetic parameters of soybean traits studied at Pawe.

Traits	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
DF	32.39	5.23	37.6	9.91	10.7	86.14	10.87	18.93

NN	0.65	4.8	5.5	0.05	13.5	12	0.57	3.3
DM	34.6	6.2	40.8	5.2	5.7	84.8	11.2	10.1
PHT	154.6	60.8	215.4	15.6	18.7	71.8	26	33.21
BrP	0.48	0.8	1.28	16.3	26.8	37.3	2	47.4
PdP	114.4	48.9	163.3	19.4	24.6	70.1	22.6	43.62
SdP	0.32	0.07	0.39	29.2	32.1	82.8	1.1	56.81
HSW	1.9	0.8	2.7	10.6	13.1	70.3	2.9	23.29
Oil	1.13	0.04	1.2	4.9	5.1	96.1	2.2	10.2
Protein	4.11	3.92	8.03	5.7	7.9	51.2	5.02	14.1
Yield	246470	27702	274172	23.1	24.4	89.9	969.7	45.2

Table 7. Variances and Genetic parameters of soybean traits studiedat Dibate.

Traits	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
DF	65.6	1.9	67.5	11.67	11.83	97.2	16.44	23.70
NN	0.5	49	49.5	4.4	43.43	1.0	0.15	0.90
DM	75.7	4.1	79.8	6.98	7.16	94.9	17.46	14.00
PHT	99.6	3.5	103.1	16.1	16.91	96.6	20.21	33.70
BrP	0.42	0.5	0.92	15.71	23.33	45.4	0.89	21.80
PdP	14.95	48.5	63.45	12.43	26.01	23.5	3.87	12.63
SdP	0.03	0.09	0.12	9.9	19.8	25	17.8	19.8
HSW	1.49	0.9	2.5	10.2	13.2	59.6	1.9	16.2
Oil	1.2	0.06	1.26	5.23	5.41	95.2	2.20	10.61
Protein	4.6	0.95	5.6	5.64	6.53	83.0	4.04	11.17
Yield	102006.6	41513.5	143520	20.7	24.6	71.1	554.9	36

DF=days to 50% flowering, NN= number of nodules per plant, DM=days to 95% maturity, PH=plant height, BrP= number of branch per plant, PdP= number of pod per plant, SdP= number of seeds per pod, HSW=hundred seed weight, Pro=protein content, σ^2g= genotypic variance, σ^2e=environmental variance, σ^2p=phenotypic variance, GCV= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, GA= genetic advance and GAM= genetic advance as percent of the mean.

CONCLUSIONS

The analysis of variance showed highly significant ($p<0.01$) differences among the tested genotypes for days to 50% flowering, days to 95% maturity, plant height, number of branches, hundred seed weight, oil and protein contents, and seed yield at both locations. High heritability coupled with high genetic advance as percent of mean was observed by the number of seeds and grain yield at Pawe and days to flowering and plant height at Debate.

RECOMMENDATIONS

Therefore, genotypes with traits that had high heritability coupled with high genetic advance as percent of means such as a number of seeds and grain yield at Pawe and days to flowering and plant height at Debate would be considered as a selection criterion for further trait improvements in soybean.

REFERENCES

1. Agdew Bekele, Getinet Alemaw, and Habtamu Zeleke. 2012. Genetic divergence among soybean (Glycine max (L) Merrill) introductions in Ethiopia based on agronomic traits. Journal of Biology, Agriculture, and Healthcare. Vol 2, No.6.

2. Akram R. M., Fares W. M., Fateh H. S. A. and Rizk A. M. A. 2011. Genetic variability, correlation, and pathanalysis in soybean. Egypt. J. Plant Breed. 15 (1): 89–102.

3. Akram S., Hussain B.N., Bari M.A., Burritt D.J., and Hossain M.A. 2016. Genetic variability and association analysis of soybean (Glycine max (L.) Merrill) for yield and yield attributing traits. Journal of Plant Gene and Trait. 7(13):1-13.

4. Alexandra D., Amandine G., Simon T., Jean D., and Brigitte M. 2017. Genomic Selection for Yield and Seed Protein Content in Soybean. Crop Science Society of America. vol. 57 1325-1337.

5. Basavaraj B.L., Vilas G.D., and Vijayakumar R. 2015. Study on genetic variability and character inter-relation of quality and yield components in tomato (SolanumLycopersicum L.). Hort. Flora Research Spectrum. 4(2): 108-115.

6. Besufikad Endeg. 2012. Genetic variability and character association in soybean (Glycine max L. Merrill) genotypes. MSc thesis, Jimma University, Ethiopia, pp105.

7. BesufikadEnideg. 2018. Genetic variability, heritability and expected genetic advance in Soybean (Glycine max L. Merrill) Genotypes.

Agriculture, Forestry and Fisheries, Vol. 7, No. 5, 2018, pp. 108-112.

8. Farias G.J.2008. Evaluation of progenies F2:4 deumapopulação of sojae improvement perspective. M.Sc. Thesis, University of São Paulo, Piracicaba, Brazil.
9. Frey K.J.1981. Breeding multilines. Plant improvement and somatic cell genetics. New York, Academic pres. 43-46.

10. Ghodrati G. 2013. Study of genetic variation and broad-sense heritability for some qualitative and quantitative traits in soybean (Glycine maxL.) genotypes.Journal of Current Opinion in Agriculture.Vol. 2: 31-35.

11. Ghosh J., Ghosh P.D. and Choudhury P.R. 2014. An assessment of genetic relatedness between soybeans cultivars using SSR markers. American Journal of Plant Sciences. 05: 3089-3096.

12. He F.J and Chen J.Q. 2013. Consumption of soybean, soy foods, soy is flavones, and breast cancer incidence. Differences between Chinese women and women in Western countries and possible mechanisms, Food Science, and Human Wellness. 2: 35-38.

13. Hossain Z. and Komatsu S. 2014. The potentiality of soybean proteomics in untying the mechanism of flood and drought stress tolerance. Proteomes. 2(1):10 127.

14. Hymowitz T. 2004. Speciation and cytogenetic Soybeans Improvement, Production, and Uses. American Society of Agronomy, Crop Science Society of America, Soil Science Society of America, Madison, Wis., pp. 97–136.

15. Iqbal S., Mahmood T., Tahira M., Ali M., Anwar, and Sarwar M. 2003. Path coefficient analysis in different genotypes of soybean (Glycine max (L) Merril). Pakistan Journal of Biological Science. 6 (12): 1085-1087.

16. Mahbub M., Rahman M., Hossain M.S., and Mahmud F. 2015. Genetic variability, correlation, and path analysis for yield and yield components in soybean. American Eurasian Journal of Agriculture and Environmental Science. 15: 231-236.

17. Malik M.A., Raffi M.Y., and Mondol M.A. 2014. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. The Scientific World Journal. 1-12.

18. MesfinHailemariam. 2018. Path analysis, genetic variability, and correlation studies for soybean (Glycine max (L.)Merill) grain yield and secondary traits. Greener Journal of Plant.

19. Nassar M.A. 2013. Heterosis and combining ability for yield and its components in some crosses of soybean. Australian Journal of Basic and AppliedSciences. 7: 566-572.

20. Nutan P. and Gabrial M. 2016.Study on Genetic variability and Character association in Soybean [Glycine max (L.) Merrill] germplasm. Sam Higginbottom Institute of Agriculture, Technology, and Sciences. Allahabad, U.P. India,Agric. Sci. Digest. 36 (1): 69-71.

21. Osborne D.R. and Voogt P. 1978. The Analysis of Nutrients in Foods.6thEdn. Academic Press, London. pp. 239-245.

22. Paramesh war MG. 2006. Genetic investigations insoybean (Glycine max (L.) Merrill). M. Sc. Thesis, University of Agricultural Sciences, Dharwad.

23. Pawe Agricultural Research Center. 2017. Laboratory and meteorology data.https: //en.wikipedia.org /wiki/ Dibateworeda, assessed on January 16, 2018.

24. Poehlman J M. 1979. Breeding field crops. Avi Pub. Co. (Westport, Conn.), USA.

25. Santosh K., Vedna K. and Vinod K.2018.Genetic variability and character association studies for seed yield andcomponent characters in soybean under Northwestern Himalayas. Legume research an International journal. Palampur. 176: 062.

26. Sharma S., Kaur M., Goyal R., and Gill B.S. 2013. Physical characteristics and nutritional composition of some new soybean (Glycine max L. Merrill) genotypes. Journal of Food Science and Technology. 51: 551-557.

27. Smith K. J. and Huyser W.1987. World Distribution and Significance of Soybean. American Society of Agronomy, Inc. Madison, WI.1-22.

28. Weber C.R. and Moorthy B.R. 1952. Heritable and non-heritable relationships and variability of oil content and agronomic characters in the F2 generation of soybean crosses. Agron. J. 44: 202-209.

29. Welsh J.R. 1981. Fundamentals of Plant Genetics and Breeding. John Willey and Sons, 290p.

30. YechalewSileshi. 2018. Genetic variability and association of traits in soybeangenotypes (Glycine max L. Merr.) Tested in western Ethiopia. MSc. Thesis, Hawassa University, Ethiopia, 103pp.