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Genetic variability, genetic advance and heritability of black and brown seeded soybean [*Glycine max* (L.) Merrill] lines in Jimma and Bonga Southwest Ethiopia

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ABSTRACT

An experiment was conducted with a simple lattice design with two replications to estimate the genetic variability in 62 soybean genotypes and 2 standard check varieties. The variability parameters such as mean, range of variation, genotypic and phenotypic coefficient of variation, heritability in the broad sense, genetic advance, and genetic advance as percentage of mean were estimated for 11 different traits. The values of the phenotypic coefficient of variation (PCV) were greater than the genotypic coefficient of variation (GCV) for all the traits, revealing the influence of environmental factors. The value of heritability was determined to be high for the traits such as grain yield, harvest index, number of seeds per pod, number of primary branches per plant, number of pods per plant and hundred seed weight. Indicating that the larger portion of total variation would be under genetic control and selection based on phenotypic levels would be useful for the improvement of these traits in soybean. High estimates of heritability together with high genetic advance as percentage of mean were recorded for grain yield, harvest index, number of seeds per pod, number of primary branches per plant, number of pods per plant and hundred seed weight, which may be attributed to the presence of additive gene action and had high selective value. Thus, selection pressure could successfully be applied to these traits for soybean improvement programs.

Keywords: Black, Brown, Genetic variability, Heritability

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Introduction

Soybean [*Glycine max* (L.) Merrill] is a self-pollinated diploid and has a chromosome number of 2n = 4x = 40. Soybean was categorized in the legume family, Leguminosae (Hymowitz and Newell, 1981). Soybean is a highly nutritive food, which can play an important functional role in the human body, with beneficial effects on health and the prevention of diseases (Hea and Chen, 2017). According to FAOstat (2018), world soybean production is 337 million tons per year. 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). The land dedicated to soybean cultivation in Africa in 2016 exceeded 1.5 million hectares. About 6.8 million households in SSA, representing about 28.6 million people grow soybean (Scheinfeldt *et al.*, 2012). The productivity of soybean on smallholder farmer fields in Ethiopia is estimated to be 2217 kg ha^{-1} in the 2016 cropping season (CSA, 2017), which was low relative to the global average (2791 kg ha^{-1}). (Tadesse and Alamerew, 2015; FAOstat, 2020). About 209,000 small-scale farmers are soybean producers from the western part of the country in Oromia, Benishangul-Gumuz and Amhara (CSA, 2021). Lack of improved varieties, low response to nutrients, diseases problem etc. are the most identified problems for low productivity (Tesfaye, 2012). In Southwestern Ethiopia, the Jimma zone is one of the high potential soybean production areas in the country, whereas soybean is a new crop for Modio in Kaffa, zone. However, soybean production is still very low in these high potential areas, particularly, in the Jimma Zone, whereas there were no soybean trials conducted, and soybean production had not started in Modio before. There has been growing interest in assessing the importance of black and brown seeded soybean varieties in the country for its economic importance. There is no research activity conducted, particularly on black and brown seeded soybean genotypes. Therefore, this study was initiated with the objective of assessing genetic variability and estimating the magnitude of heritability of yield and yield-contributing traits in black and brown seeded soybean genotypes.

Materials and Methods

An experiment was conducted at Jimma and Bonga by using simple lattice design with two replication. For the aim of estimating the variability parameters such as mean, range of variation, genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percentage of mean using 62 genotypes with two standard checks of soybean on main rainy season in 2019. The data were recorded for 11 different traits such as plant height, number of pods per plant, number of primary branches per plant, number of seeds per pod, pod length, hundred seeds weight, days to 50% flowering, days to 95% physiological maturity, biological yield, harvest index and grain yield. The genotypic and phenotypic coefficients of variation were computed as per the formula suggested by Burton (1952), Johnson and Wichern (1955). Heritability in broad sense will be calculated as per the formula suggested by Allard (1999). The formula given by Allard (1999), Johnson and Wichern (1955) calculated the expected genetic advance.

Results and Discussion

Combined ANOVA revealed that the mean squares due to genotypes were found significant for all the traits under study, which showed the presence of genetic variability among tested genotypes. The mean square due to the genotype x location interaction was significant only for biomass yield, harvest index and grain yield indicating the differential response of genotypes for these traits at each location.

Table 1. ANOVA for yield and yield related traits.

SV	DF	Plant height	Pods plant^{-1}	Primary branches plant^{-1}	Seeds pods	Pod length^{-1}	Days to 5% followering	Days to 95% maturity	Biological yield	Harvest index	Hundred seed weight	Grain yield
Lo	1	78.58	3.04	0.75	54.57	2.30	2.56	1378.26	1147.51	6180693.21	0.00024	3024285.65
Re	1	18.12	2.82	0.000039	0.16	0.0009	0.36	0.56	268.14	3143.00	0.00072	12713.79
Bl	14	7.64	46.95	2.93	6.30	0.20	1.30	5.53	86.11	3945.19	0.00039	8033.81
Ge	63	60.09	84.98	89.23	254.87	0.34	12.25	42.80	94.17	63325.89	0.02	843206.71
Lo*ge	63	7.58	2.67	2.75	3.00	0.08	0.15	2.02	6.36	53337.78	0.001	11169.97
Er	113	7.03	13.64	18.33	8.44	0.13	0.50	3.23	14.89	3464.00	0.00026	7239.18

*Where, SV= source of variance, DF=degree of freedom, Lo=location, Re=rep, Bl=block, Ge=genotype, Lo*ge=location by genotype *, ** significant at 5% and 1%, respectively.*

Estimation of broad-sense heritability

In this study, broad-sense heritability ranged from 15.77% to 98.82% (Table 2). Broad sense heritability estimates greater than 80% are considered very high, whereas values in the range of 60 and 80%, 40 to 59% are considered high, and medium, respectively, while values less than 40% are regarded as low (Singh, 2001). Accordingly, Robinson and Wilcox (1988), the heritability estimates in this study might be considered very high for all the traits, except for pod length (68.96%) and biological yield (15.77%) (Table 2). Traits whose heritability is higher, allow greater success in the selection so that the chance of obtaining superior progenies with selected individuals is higher. For this reason, breeders may adopt the use of indirect selection for quantitative traits with low heritability, a selection through correlated characters. Similar results were reported by Ghodrati (2013) for plant height and Karnwal and Singh (2009) and Sirohi *et al.* (2006) for the number of seeds per plant and number of pods per plant for soybean genotypes. Also, Aditya *et al.* (2011) estimated heritability for 31 soybean genotypes and reported high heritability for days to 50% flowering, plant height, number of primary branches per plant, and number of pods per plant, harvest index, hundred seed weight, and grain yield.

Genetic advance as percent of mean

The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented in Table 2. According to Johnson and Wichern (1955), genetic advances as a percent of the mean can be categorized as low (0-10%), moderate (10-20%) and high (20% and above). The genetic advance as percent of mean (GAM) value in the present study ranged from 1.79% for biological yield to 60.78% for grain yield. The genetic advance as percent of mean estimates was high for grain yield (60.78%), harvest index (57.32%), number of seeds per plant (33.1%), number of branches per plant (31.34%), number of pods per plant (30.88%) and hundred seed weight (26.68%).

Selection based on those traits with a relatively high genetic advance as a percent means will result in the improvement of the performance of the genotypes for the traits. It was moderate for plant height (11.48%) and days to 50% flowering (10.87%). However, the estimates of low GAM were low for pod length (8.3%), biological yield (1.79), days to 95% physiological maturity (7.14%) and pod length (8.3%). This low estimate of genetic advance as a percent means arises from a low estimate of phenotypic variance and heritability. Similar results had reported for the number of pods per plant, number of seeds per plant, seed yield, number of branches per plant, hundred seed weight, and biological yield by Jain *et al.* (2017), Major and Singh (1996), Koraddi and Basavaraja (2019).

High heritability coupled with high genetic advance as percent of mean estimates were found for grain yield, harvest index, number of seeds per plant, number of primary branches per plant, number of pods per plant, and hundred seed weight. High heritability estimates, along with, the high GAM is usually more helpful in predicting grain yield under selection than heritability estimates alone (Johnson and Wichern, 1955). It indicates the predominance of additive gene action in the expression of these traits, which also indicates that these traits might be considered favorable attributes for improvement through selection. On other hand, low heritability and low GAM were noted for biological yield. This indicates that advancement in this trait through the usual selection may not be effective. The presence of higher environmental factors along with non-additive gene action might be the possible causes for the low values of heritability and genetic advance as a percentage of the mean for biological yield. In agreement with this result, former investigators viz., Malek *et al.* (2014) for 100 seed weight. Reni and Rao (2013); Bangar *et al.* (2003), and Basavaraja (2002) for several primary branches per plant. Denton and Nwangburuka (2011) found high heritability and genetic advance as percent mean for grain yield and harvest index.

Table 2. Estimates of mean, range, variance components and coefficients of variability, heritability and genetic advance of the 11 traits.

Trait	Range	Mean ±SD	σ^2p	σ^2g	σ^2gl	PCV (%)	GCV (%)	H^2b %	EGA k=5%	AM (%)
PH	47.68-71.80	60.69±4.82	15.02	13.12	7.58	6.38	5.96	87.33	6.97	11.48
PPP	14.20- 42.40	29.76 ±5.93	21.24	20.57	2.67	15.48	15.24	96.81	9.19	30.88
PBPP	1.20-6.40	3.75±0.70	0.35	0.34	0.04	15.84	15.60	96.04	1.17	31.34
SPP	24.00-84.80	49.00± 9.23	63.71	62.96	3.00	16.26	16.16	98.81	16.24	33.10
PL	4.10-5.90	5.04±0.43	0.08	0.06	0.08	5.86	5.08	68.96	0.41	8.30
HSW	7.40-20.70	13.32±1.99	3.06	3.02	0.15	13.13	13.05	98.59	3.55	26.68
DF	26.00-78.00	59.00±4.36	10.70	10.19	2.02	5.54	5.40	95.21	6.41	10.87
DM	119.00-168.00	130.00±6.94	23.54	21.95	6.44	3.72	3.59	93.23	9.31	7.14
BY	1640.30-2971.20	2279.48±237.60	15831.47	2497.02	3464	11.03	10.13	15.77	40.88	1.79
HI	0.10-0.45	0.24±0.07	0.00	0.00	0.00	29.04	28.44	95.91	0.13	57.32
GYD	435.12 - 2412.81	1530.28±517.50	210801.67	2980.91	11169.97	30.00	29.80	99.33	9.36	60.70

SD = standard deviation, σ2g = Genotypic variance, σ2p = Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, H2b = Broad sense heritability, EGA= Expected Genetic Advance, GAM= Genetic advance as percent of mean and K = Selection intensity. PH= plant height, PBPP= number of primary branches per plant, SPP= number of seeds per plant, PL=pod length, HSW=hundred seed weight, DF=days to 50% flowering, DM= days to 95% physiological maturity, BY=biological yield, HI= harvest index and GYD=grain yield.

Conclusion

Combined ANOVA revealed the presence of phenotypic variability among the studied genotypes. The magnitude of the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the traits showing the influence of environmental factors. High estimates of heritability together with high genetic advance as percentage of mean were observed for traits such as grain yield, harvest index, number of seeds per pod, number of primary branches per plant, number of pods per plant and hundred seed weight, which may be resulted from the presence of additive gene action and resulted in high selection response. Therefore, selection pressure based on these characters could result in improvement in their descendants.

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