

Correlation and Path Coefficient Analysis in Soybean (Glycine Max (L.) Merrill) Genotypes in Dibate, Northwestern Ethiopia

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Abstract— Eighty one soybean genotypes were tested in 9x9 simple lattice design to assess their association of traits using quantitative, qualitative and quality traits in Dibate substation during 2018/2019 cropping season. Based on analysis of variance, days to flowering, days to maturity, plant height, number of branches per plant, hundred seed weight, protein and oil contents and yield showed highly significant ($p < 0.01$) differences. Positive and significant associations of plant height (0.23*) and number of pods per plant (0.24*) with grain yield were observed. Highly significant and positive phenotypic correlation with grain yield was observed by number of pods per plant (0.31**). Positive and high direct effect at genotypic level was observed by number of pods per plant (0.38) and number of nodules per plant (0.21). High phenotypic and positive direct effect on grain yield was observed by number of pods per plant (0.48) and negative direct effect by number of branches (-0.28). About 0.88 and 0.90 residuals was observed from genotypic and phenotypic direct and indirect effects, respectively. Thus, genotypes with traits such as number of pods and number of nodules per plant having high and positive association and with high direct effects should be criteria for grain yield improvement through direct selection and considered as a parental material for further breeding programs.

Keywords— Correlation, Genotypes, Grain Yield, Soybean, Traits.

I. 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 Huysen, 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).

In soybean, grain yield, as in other crops, is a complex character, quantitative in nature and an integrated function of a number of component traits. Therefore, selection for yield per se may not be much rewarding unless other yield attributing traits are taken into consideration. Correlation study provides a measure of association between characters and helps to identify important characters to be considered while making selection. Understand the correlation between grain yield and other characters is helpful in selection of suitable plant type. Study of direct and indirect effects of yield components on yield provide the basis for its successful breeding program and thus improvement of yield can be more effective on the basis of yield components performance and selection for closely associated traits (Besufikad Endeg, 2019). Therefore, selection for yield may not be much rewarding unless other yield attributing traits are taken into consideration (Aditya *et al.*, 2011; Jain *et al.*, 2015).

The national average production and productivity of soybean increased from 15824.4 tons with productivity of 1.4 tons ha^{-1} in 2010 (CSA, 2012) to 86467.9 tons with productivity of 2.27 tons ha^{-1} in 2017 (CSA, 2018). However, it is low compared to the world average productivity potential of 2.7 tons ha^{-1} (CSA, 2018). In Ethiopia, currently, the demand for soybean product is increasing as a result of increasing population growth, agro processing and urbanization (Afewerk Hagos and Adam Bekele, 2018). Though, its production and productivity in Ethiopia remains low due to lack of diversified soybean materials and genetic potential reductions of released varieties (Mesfin Hailemariam and Abush Tesfaye, 2018). There are considerable number of introduced soybean materials, which are not systematically characterized under Ethiopian condition. As a result, genotypes that has been introduced from abroad by Pawe agricultural research center of the Ethiopian Institute of Agricultural Research need to be characterized and clustered, because quantitative traits are strongly influenced by environmental factors (Dudley, 1993), to use as a base material for further breeding programs such as breeding for higher yield, wider adaptation, desirable quality and disease resistant. Therefore, the present study was conducted to estimate the association among grain yield and yield related traits and to identify traits that are significantly correlated with grain yield to be used for plant selection in soybean breeding programs.

II. MATERIALS AND METHODS

Description of Experimental Sites

The experiment was conducted at Dibate substation of Pawe Agricultural Research Center during main cropping

season of 2018/19. Dibate substation is located at (10°30' 0" N, 36° 10' 0" E) and 543 km away from Addis Ababa with an altitude of 1572 m.a.s.l. The mean annual maximum and minimum temperatures are 29°C and 15°C, respectively and it receives 1650 to 1700 mm rainfall annually. The soil type of the substation is characterized by nitosol or loam type (PARC, 2017).

Plant Materials and Experimental Design

Eighty-one introduced soybean genotypes from IITA, USA and Brazil were used for the experiment (Table 3.1). The

experiment was laid out in 9x9 simple lattice design with plot size of 7.2-meter 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 m². 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 recommendation.

2.1. Eighty one soybean genotypes used in the experiment

S no.	Genotype Designation	Source	Year of Introduction	S no.	Genotype Designation	Source	Year of introduction
1	Tgx-1448-2e	IITA	2016	45	Tgx-1989-42f	IITA	2014
2	Tgx-2010-11f	IITA	2015	46	Tgx-1989-45f	IITA	2014
3	Tgx-1989-19f	IITA	2015	47	Tgx-1989-75f	IITA	2014
4	Tgx-2006-3f	IITA	2015	48	Tgx-1990-106fn	IITA	2014
5	Tgx-2008-4f	IITA	2016	49	Tgx-1990-107fn	IITA	2014
6	Tgx-2010-12f	IITA	2016	50	Tgx-1990-110fn	IITA	2014
7	Tgx-2004-10f	IITA	2016	51	Tgx-1990-111fn	IITA	2014
8	Tgx-1485-1d	IITA	2016	52	Tgx-1990-114fn	IITA	2014
9	Tgx-2007-8f	IITA	2016	53	Tgx-1990-87f	IITA	2014
10	Tgx-2008-2f	IITA	2016	54	Tgx-1990-8f	IITA	2014
11	Tgx-2004-13f	IITA	2016	55	Tgx-1990-95f	IITA	2014
12	Tgx-2007-11f	IITA	2016	56	Tgx-1993-4fn	IITA	2014
13	Tgx-2010-15f	IITA	2016	57	Tgx-1989-48fn	IITA	2014
14	Tgx-2011-3f	IITA	2016	58	Tgx-1989-68f	IITA	2014
15	Tgx-2010-3f	IITA	2016	59	Tgx-1990-78f	IITA	2015
16	Tgx-2004-3f	IITA	2016	60	Tgx-1990-57f	IITA	2014
17	Tgx-2011-7f	IITA	2016	61	Tgx-1835-10f	IITA	2014
18	Tgx-1987-10f	IITA	2016	62	Tgx-1995-5f	IITA	2014
19	Tgx-1987-42f	IITA	2016	63	Tgx-1987-20f	Malawi	2009
20	Tgx-1987-45f	IITA	2013	64	Tgx-1987-23f	Malawi	2009
21	Tgx-1990-101f	IITA	2013	65	Tgx-1987-64f	Malawi	2009
22	Tgx-1990-47f	IITA	2013	66	Tgx-1987-65f	Malawi	2009
23	Tgx-1990-70f	IITA	2013	67	Tgx-1987-6f	Malawi	2009
24	Tgx-1990-73f	IITA	2013	68	Tgx-1987-37f	Malawi	2009
25	pr142-15-SG	USA	2016	69	Tgx-1987-35f	Malawi	2009
26	H3-15-SG	USA	2016	70	Tgx-1987-38f	Malawi	2009
27	H3-15-SE-1	USA	2016	71	Tgx-1987-15f	Malawi	2009
28	CLK-15-sb-1	USA	2016	72	Tgx-1987-19f	Malawi	2009
29	ALM-15-SB	USA	2016	73	Tgx-1986-3f	Malawi	2009
30	CRFD-15-SC	USA	2016	74	Tgx-1987-40f	Malawi	2009
31	PR142-1-SE	USA	2016	75	Tgx-1740-2f	Malawi	2009
32	G99-15-SE-2	USA	2016	76	pb12-1	Brazil	2012
33	CLK-15-SA-1	USA	2016	77	pb12-6	Brazil	2012
34	CRFD-15-SB	USA	2016	78	pb12-7	Brazil	2012
35	CLK-15-SA-1	USA	2016	79	pb12-8	Brazil	2012
36	H3-15-SB-2	USA	2016	80	pb12-4	Brazil	2012
37	G99-15-SA	USA	2016	81	pun11-4	Brazil	2012
38	SCS-1	USA	2016				
39	Tgx-1990-78f	IITA	2013				
40	Tgx-1990-80f	IITA	2013				
41	Tgx-1990-95f	IITA	2013				
42	Tgx-1991-10f	IITA	2013				
43	Tgx-1904-6f	IITA	2013				
44	Tgx-1989-11f	IITA	2014				

Data Collected

Data were recorded during the cropping season and after harvesting. Observations which 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 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 grinded using grinder at 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) monochromator 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).

Data Analyses

Analysis of variance

The data were checked for its normal distribution using Shapiro Wilk’s test (Shapiro and Wilk, 1965) before proceeding to analysis. All data were found normal. Analysis of variance (ANOVA) was done using proc GLM for the traits analyzed based on RCBD and proc lattice procedures of SAS version 9.3 (SAS, 2011) for the traits analyzed based on lattice. Relative efficiency of using lattice over RCBD was checked and found that effective for traits days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod and protein content. But, relative efficiency of using lattice over RCBD was ineffective for traits number of nodules per plant, oil content and grain yield; hence ANOVA was carried out based on RCBD design.

The model for simple lattice design employed was:

$Y_{ij} = \mu + \alpha_i + \beta_j + \rho_j + \gamma_l + \epsilon_{ij}$; where μ = grand mean, $\alpha_i = i^{th}$ treatment effect, $\beta_j = j^{th}$ block effect (nested with in replication), $\rho_j = j^{th}$ replication effect, γ_l =effect of l^{th} level of intra block error and $\epsilon_{ij} =$ error term. The model for RCBD employed was $\mu + \alpha_i + \beta_j + \epsilon_{ij}$; where μ = grand mean, $\alpha_i = i^{th}$ treatment effect, $\beta_j = j^{th}$ replication effect and $\epsilon_{ij} =$ error term.

III. RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance (ANOVA) for eight traits analyzed using lattice design is given in Table 3.1 and three traits analyzed using RCBD is given in Table 3.2. There was highly significant different ($P < 0.01$) 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. Whereas, number of nodules per plant and number of pods per plant were showed non-significant differences.

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 Gabriel, 2016).

Table 3.1. Mean squares of eight traits 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 ⁻¹	7.5ns	1.33**	0.8	0.51	0.58	108.6
PdP ⁻¹	323.9ns	74.31ns	48.6	48	48.6	109.1
Oil content (%)	0.02ns	2.41**	0.01	0.01	0.01	108.3
Protein content (%)	0.01ns	9.23**	0.02	0.02	0.02	110.1

Table 3.2. Mean squares for three traits in RCBD

Trait	Rep (1)	Geno (80)	CV (%)
SdP ⁻¹	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, PHT=plant height, BrP⁻¹= number of branches per plant, PdP⁻¹= number of pods per plant, SdP⁻¹= number of seeds per pod, HSW=hundred seed weight, Geno= Genotype, Rep = number of replication, RE= Relative Efficiency and CV=coefficient of Variation.

Associations of Traits

Genotypic correlation coefficient

The genotypic correlation coefficients of traits are given under Tables 3.3. Number of nodules showed positive and significant association with yield (0.3*). Days to maturity showed positive and highly significant genotypic correlation with plant height (0.73**) and pod number (0.38**). This would indicate that late maturing genotypes have high plant

height and more number of pods. Number of pods showed positive associations with yield (0.31**). Days to flowering, number of nodules, days to maturity and plant height showed negative and highly significant correlation with oil content with r values of -0.3*, -0.36**, -0.5** and -0.5*, respectively. On the other hand, these traits showed positive and highly significant correlation with protein content. Oil and protein contents had negative and significant association (-0.8**). Oil and protein contents showed negative non-significant (-0.01) and positive non-significant (0.1) association with yield, respectively. Similarly, negative and non-significant association of oil content with yield of soybean has been reported by Ali *et al.* (2015).

Phenotypic correlation coefficient

The phenotypic correlation coefficients of traits are given in Table 3.3. Days to flowering showed positive and highly significant phenotypic correlation with days to maturity (0.72**), significant and negative association with hundred

seed weight (-0.26*) and non-significant positive association with grain yield (0.09). Plant height and number of pod showed significant phenotypic association with yield (0.23*) and (0.24*), respectively. The positive association of days to flowering with days to maturity, plant height and number of pod with yield would indicate that these traits could be

improved simultaneously based on phenotypic selection. Aditya *et al.* (2011) and Mahbub *et al.* (2015) reported significant and positive association among yield related traits and that would indicate an increase in the value of one of these traits would increase the value of another trait.

Table 3.3. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients

Traits	DF	NN	DM	PHT	BrP ⁻¹	PdP ⁻¹	SdP ⁻¹	HSW	Oil	Protein	Yield
DF		0.12 ^{ns}	0.72**	-0.1 ^{ns}	0.03 ^{ns}	0.12 ^{ns}	-0.02 ^{ns}	-0.26 ^{ns}	0.04 ^{ns}	0.01 ^{ns}	0.09 ^{ns}
NN	0.4**		0.17 ^{ns}	0.13 ^{ns}	-0.0 ^{ns}	-0.09 ^{ns}	0.24*	0.25*	-0.3*	-0.13 ^{ns}	0.10 ^{ns}
DM	0.67**	0.33**		0.01 ^{ns}	-0.1 ^{ns}	0.01 ^{ns}	0.01 ^{ns}	-0.16 ^{ns}	-0.0 ^{ns}	-0.05 ^{ns}	0.12 ^{ns}
PHT	0.5**	0.25*	0.73**		0.03 ^{ns}	0.18 ^{ns}	-0.03 ^{ns}	0.21 ^{ns}	-0.1 ^{ns}	-0.03 ^{ns}	0.23*
BrP ⁻¹	0.27*	0.14 ^{ns}	0.03 ^{ns}	0.12 ^{ns}		0.62**	0.11 ^{ns}	-0.10 ^{ns}	0.05 ^{ns}	0.05 ^{ns}	0.05 ^{ns}
PdP ⁻¹	0.14 ^{ns}	0.17 ^{ns}	0.38**	0.44**	0.41**		-0.43**	-0.09 ^{ns}	0.06 ^{ns}	-0.02 ^{ns}	0.24*
SdP ⁻¹	0.00 ^{ns}	0.17 ^{ns}	-0.3*	-0.2 ^{ns}	0.11 ^{ns}	0.25 ^{ns}		0.11 ^{ns}	-0.2 ^{ns}	-0.06 ^{ns}	0.00 ^{ns}
HSW	-0.1 ^{ns}	-0.09 ^{ns}	-0.2 ^{ns}	-0.2 ^{ns}	-0.0 ^{ns}	-0.04 ^{ns}	0.11 ^{ns}		-0.0 ^{ns}	0.07 ^{ns}	0.19 ^{ns}
Oil	-0.3*	-0.36**	-0.5**	-0.5**	0.21 ^{ns}	-0.18 ^{ns}	0.14 ^{ns}	0.28*		0.42**	0.07 ^{ns}
Protein	0.24*	0.44**	0.43**	0.37**	-0.3*	0.14 ^{ns}	-0.06 ^{ns}	-0.22 ^{ns}	-0.8**		-0.01 ^{ns}
Yield	0.08 ^{ns}	0.30*	0.11 ^{ns}	0.12 ^{ns}	0.10 ^{ns}	0.31**	0.15 ^{ns}	0.18 ^{ns}	-0.0 ^{ns}	0.10 ^{ns}	

* ** = significant at 1 % and 5% levels, respectively. DF=days to 50% flowering, NN = number of nodules per plant, DM = days to 95% maturity, PH=plant height, BrP⁻¹= number of branches per plant, PdP⁻¹= number of pods per plant, SdP⁻¹ = number of seeds per pod, HSW = hundred seed weight.

Path Coefficient Analysis

Genotypic direct and indirect effects

The genotypic direct and indirect effects of traits on grain yield are given in Table 3.4. Number of pods per plant showed higher positive direct effect (0.38) followed by number of nodules per plant (0.21) and number of seeds per pod (0.20) on grain yield. Similarly, high and positive direct effect of number of nodule on grain yield of soybean has also been reported by Mesfin Hailemariam (2018). High and negative direct effect was observed by number of branches per plant (-0.11) followed by days to 50% flowering (-0.03) and plant

height (-0.03) on grain yield. About 0.88 residual was observed and that would be explained by other traits which has not been considered here.

Phenotypic direct and indirect effects

The phenotypic direct and indirect effects of traits on grain yield are presented in Tables3.5. High and positive direct effect was observed number of pods (0.48) followed by number of seeds (0.23) and highest negative direct effect observed by number of branches (-0.28) followed by days to maturity (-0.16) on grain yield. About 0.90 residual was observed.

Table 3.4. Direct (bold diagonal) and indirect effects (off diagonal) of traits on yield of soybean genotypes at genotypic level

Traits	DF	NN	DM	PHT	BrP ⁻¹	PdP ⁻¹	SdP ⁻¹	HSW	Oil	Protein	rg
DF	-0.03	0.08	0.05	-0.02	-0.03	0.05	0	-0.01	-0.03	0.02	0.08 ^{ns}
NN	-0.01	0.21	0.02	-0.01	-0.01	0.07	0.03	-0.02	-0.05	0.03	0.30*
DM	-0.02	0.07	0.07	-0.02	0	0.14	-0.06	-0.04	-0.06	0.03	0.11 ^{ns}
PHT	-0.02	0.05	0.05	-0.03	-0.01	0.17	-0.03	-0.03	-0.06	0.03	0.12 ^{ns}
BrP ⁻¹	-0.01	0.03	0	0	-0.11	0.16	0.02	0	0.03	-0.02	0.01 ^{ns}
PdP ⁻¹	0	0.04	0.03	-0.01	-0.04	0.38	-0.05	-0.01	-0.02	0.01	0.31**
SdP ⁻¹	0	0.04	-0.02	0.01	-0.01	-0.1	0.20	0.02	0.02	0	0.14 ^{ns}
HSW	0	-0.02	-0.02	0.01	0	-0.02	0.02	0.18	0.04	-0.01	0.18 ^{ns}
Oil cont (%)	0.01	-0.08	-0.04	0.01	-0.02	-0.07	0.03	0.05	0.13	-0.05	-0.03 ^{ns}
Protein cont (%)	-0.01	0.09	0.03	-0.01	0.03	0.05	-0.01	-0.04	-0.1	0.07	0.10 ^{ns}

Residual= 0.88. rg = genotypic correlation coefficient

Table 3.5. Direct (bold diagonal) and indirect effects (off diagonal) of traits on yield of soybean genotypes at phenotypic level

Trait	DF	NN	DM	PHT	BrP ⁻¹	PdP ⁻¹	SdP ⁻¹	HSW	Oil	Protein	pr
DF	0.01	0.01	-0.11	-0.02	-0.01	0.06	0	-0.03	0.01	0	0.09 ^{ns}
NN	0	0.09	-0.03	0.02	0.01	-0.04	0.05	0.03	-0.04	0	0.01 ^{ns}
DM	0.01	0.02	-0.16	0	0.03	0	0	-0.02	0	0	-0.12 ^{ns}
PHT	0	0.01	0	0.14	-0.01	0.09	-0.01	0.02	-0.01	0	0.23*
BrP ⁻¹	0	0	0.01	0	-0.28	0.3	0.03	-0.01	0.01	0	0.05 ^{ns}
PdP ⁻¹	0	-0.01	0	0.03	-0.17	0.48	-0.09	-0.01	0.01	0	0.24*
SdP ⁻¹	0	0.02	0	0	-0.03	-0.21	0.23	0.01	-0.02	0	0.00 ^{ns}
HSW	0	0.02	0.03	0.03	0.03	-0.04	0.03	0.11	-0.01	0	0.19 ^{ns}
Oil cont (%)	0	-0.03	0	-0.01	-0.01	0.03	-0.04	0	0.14	-0.01	0.07 ^{ns}
Prot cont (%)	0	-0.01	0.01	0	-0.01	-0.01	-0.01	0.01	0.06	-0.03	-0.01 ^{ns}

Residual=0.90

DF=days to 50% flowering, NN = number of nodules per plant, DM = days to 95% maturity, PHT=plant height, BrP⁻¹ = number of branches per plant, PdP⁻¹= number of pods per plant, SdP⁻¹= number of seeds per pod, HSW = hundred seed weight, rg= genotypic correlation coefficient and rp = phenotypic correlation coefficient.

IV. RECOMMENDATION

Positive and significant associations of pairs of characters at phenotypic and genotypic levels justify the possibility of simultaneous response to selection. But, negative correlations make difficult the simultaneous improvement of those traits.

Traits showed positive and significant association with seed yield such as plant height, number of pods per plant and number of nodules and traits with high direct effect on grain yield such as number of pods per plant and hundred seed weight can be used for trait improvement through direct selection.

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