

Association of Traits in Soybean (*Glycine max* (L.) Merrill) Genotypes in Northwestern Ethiopia

Asmamaw Amogne¹, Mulugeta Atnaf², Muluken Bantayehu³

¹Ethiopian Institute of Agricultural Research, Pawe Agricultural Research Center, Pawe

²Ethiopian Institute of Agricultural Research, Fogera National Rice Research and Training Center, Fogera

³Bahir Dar University College of Agriculture and Environmental Science, Bahir Dar

Abstract— Eighty-one genotypes were tested in 9x9 simple lattice design to assess association of traits using quantitative, qualitative and quality traits at Pawe main station and Dibate substation during 2018/2019 cropping season. Highly significant and significant genotypic positive correlation with yield was showed by plant height (0.23*) at Dibate, number of pods per plant (0.35**) and number of seeds per pod (0.3*) at Pawe. Highly significant and positive phenotypic correlation with grain yield was recorded by number of branches (0.23**) and number of pods per plant (0.20**) at Pawe and number of branches (0.23**) and number of pods per plant (0.20**) at Dibate. Positive and high direct effect at genotypic level was observed by number of pods per plant and number of seeds per pod at both locations. Maximum phenotypic direct effect on grain yield was observed by number of pods (0.44) at Pawe and (0.48) at Dibate. Thus, genotypes with traits such as number of pods and number of seeds per plant having high and positive association with grain yield and with high direct effects on grain yield are important for grain yield improvement through direct selection and considered as a parental material for further breeding work.

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 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).

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 (Afework 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 numbers 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 Pawe Agricultural Research Center main station and Dibate sub-station during main cropping season of 2018/19. Pawe Agricultural Research Center is located at (11°18'49.6"N and 036°24'29.1"E) in Metekel Zone. It is located 570 km away from Addis Ababa, the capital city of Ethiopia.

The altitude of the area ranges from 1150 meters above sea level (m.a.s.l) and it receives 1586mm rainfall annually. The mean annual maximum and minimum temperatures are 32.6°C and 16.5°C, respectively. The soil type of the site is characterized by well drained clay soil with pH value 4.3-5.5. 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 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.

TABLE 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 (%), grain yield (kg) and disease 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

The data were checked for its normal distribution using Shapiro Wilk’s test (Shapiro and Wilk, 1965) before proceeding to analysis and all data were found normal. Test of homogeneity of error variance was done using Bartlett test (Snedecor and William, 1989) and the result showed heterogeneous error variances for all traits. Therefore, the results of the two locations were analyzed and interpreted separately. 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. Genotypes mean separation was tested for significance by Duncan multiple range test (DMRT) at 5% and 1% probability levels.

Correlation and path coefficient analysis

Phenotypic and genotypic correlations between yield, yield related and quality traits were estimated using SAS proc candisc procedure (SAS, 2011). Phenotypic correlation coefficient between character x and y; $r_{pxy} = \frac{COV_{pxy}}{\sqrt{\sigma^2_{px}\sigma^2_{py}}}$; where COV_{pxy} = phenotypic covariance between character x and y, σ^2_{px} = phenotypic variance for character x and σ^2_{py} = phenotypic variance for character y. Phenotypic correlation coefficient between character x and y was tested for their significance by the formulae $t = r/SE(r_p)$ where, r_p = phenotypic correlation; $SE(r_p)$ = standard error of phenotypic correlation. $SE(r_p) = (\sqrt{1 - r^2_p})/(n-2)$; where, n number of genotypes tested, r_p is phenotypic correlation coefficient. Genotypic correlation coefficient between character x and y; $rgxy = \frac{COV_{gxy}}{\sqrt{\sigma^2_{gx}\sigma^2_{gy}}}$; where, $rgxy$ = genotypic correlation coefficient between character x and y. COV_{gxy} = genotypic covariance between character x and y. σ^2_{gx} =

genotypic variance for character x. σ^2_{gy} = genotypic variance for character y. Genotypic correlation coefficient was tested with the formulae $t = rgxy/SErgxy$; where $SErgxy = (\sqrt{1 - r^2_{gxy}})/2H_x * H_y$. $SErgxy$ = Standard error of genotypic correlation coefficient between character X and Y. H_x = heritability for character x and H_y = heritability for character y. Both phenotypic and genotypic correlation coefficients split into direct and indirect effects on grain yield. Path coefficient analysis was done using proc IML SAS procedure (SAS, 2011). $r_{ij} = P_{ij} + \sum r_{ik} P_{kj}$ where, r_{ij} = mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients. P_{ij} = components of direct effects of the independent character (i) as measured by the path coefficients and $\sum r_{ik} P_{kj}$ = summation of components of indirect of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The contribution of the remaining unknown factor was measured as the residual factor (P_R), which was calculated as; $P_R = \sqrt{(1 - \sum r_{ij}P_{ij})}$; the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999). If P_R value is small (for instance, nearly zero) the dependent character (grain yield) considered is fully explained by the variability in the independent characters, whereas higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (grain yield). Traits showed significant genotypic correlation coefficients with yield were considered for path analysis.

III. RESULTS AND DISCUSSION

Analysis of Variance

The results of analysis of variance (ANOVA) for eight traits analyzed using lattice design and three traits analyzed by using RCBD are given in Table 2 and 3 at Pawe and Tables 4 and 5 at Dibate. 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, oil content and seed yield at both locations.

TABLE 2. Mean squares of eight traits in lattice design

Trait	Rep (1)	Geno. adjusted (80)	Block with in rep	Error		
			Adjusted (16)	Intra block (64)	RCBD (80)	RE over RCBD
DF	9.38ns	65.7**	14.11	10.7	17.03	109.9
DM	207ns	79.12**	21.9	11.3	24.2	108.4
PHT	299ns	321.8**	119.2	80.29	93.7	107
BrP ⁻¹	7.86ns	1.75**	1.15	0.92	0.98	105.8
PdP ⁻¹	3571*	191.3ns	146.9	47.1	138.2	105.4
SdP ⁻¹	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
Protn cont	3.64ns	12.13**	5.2	3.9	4.20	105.1

“*”, “**” = significant at 1% and 5% levels, respectively. Rep= replication, Geno=genotypes, RCBD= randomized complete block design, DF = days to 50% flowering, DM = days to 95% maturity, PHT= plant height, BrP⁻¹ = number of branch per plant, PdP⁻¹ = number of pod per plant, SdP⁻¹= number of seeds per pod, HSW=hundred seed weight & Protn cont= protein content in percentage.

TABLE 3. Mean squares for three traits of soybean genotypes in RCBD

Trait	Rep (1)	Genotypes (80)
Number of nodules per plant	1ns	6.06 ns
Oil content (%)	0.04ns	2.34**
Yield	618192**	1252523.9**

TABLE 4. 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)	Intra block (64)	RCBD (80)	
DF	26.9ns	131.1**	5.98	1.88	2.7	126.3	
NN	25.5ns	15.1ns	79.3	29.3	72.4	108	
DM	0.62ns	153.6**	202	140.7	153	110.4	
PHT	20.9*	185.33**	5.9	3.5	4	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 5. 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.

Association of Traits

Genotypic correlation coefficient

The genotypic correlation coefficients of traits are given under Table 6 for both locations. At Pawe, days to flowering showed non-significant and negative genotypic correlation (-0.2) with grain yield and highly significant negative genotypic correlation with number of seed (-0.34**) and oil content (-0.71**). Days to maturity showed also non-significant and negative (-0.1) association with yield. In agreement with this result, negative correlations of days to flowering and days to maturity with grain yield in soybean have been reported by various workers (Ramteke *et al.*, 2010; Aditya *et al.*, 2011; Faisal *et al.*, 2014; Akram *et al.*, 2016). Though such an inverse association is not expected at potential environments like Pawe, the reason would be that there was rainfall gap and minimum average, below the minimum requirement, rainfall (4.4mm day⁻¹) was recorded on September at flowering stage (Appendix Table.1). The need for moisture in soybean increases with plant development, peaking during the flowering and seed setting stages (8 mm day⁻¹) (Souza *et al.*, 2013). It requires a minimum of 400mm of well distributed rainfall during the vegetative growth period which lasts 3-4 months (<http://ishaba.com>). Branch number showed positive and highly significant associations with oil content (0.3**) and non-significant association with yield (0.14ns). Number of pods and number of seeds showed highly significant (0.4**) and significant (0.20*) positive genotypic correlation with yield, respectively. Similarly, number of pods showed positive and significant genotypic correlation with yield in soybean has been reported by Siahisar and Rezai (1999). Oil and protein contents had negative and significant association (-0.6**). In agreement to this result, negative and significant association between oil and protein in soybean has been reported by Varnica *et al.* (2018).

At Dibate, 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 and significant association with yield (0.31**). Oil and protein contents had negative and significant association (-0.8**) like at Pawe. 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 6 for both locations. At Pawe, days to flowering showed positive and highly significant phenotypic correlation coefficients with days to maturity (0.6**), plant height (0.4**) and non-significant positive association with yield (0.11). The positive and highly significant association of days to flowering with days to maturity and plant height would indicate that these traits can be improved simultaneously based on phenotypic selection. Similarly, positive and significant phenotypic association of days to flowering with days to maturity in soybean has been reported (Devvart *et al.*, 2005; Manasa, 2008). Number of pods showed positive and highly significant phenotypic association with yield (0.36**) and number of branch (0.6**). In agreement with this result, positive and significant association of number of pods with grain yield has been reported (Bekele and Getnet, 2011).

At Dibate, days to flowering showed positive and highly significant phenotypic association 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 pods showed significant phenotypic association with yield (0.23*) and (0.24*), respectively. 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. Generally, positive and significant associations of pairs of characters at phenotypic and genotypic level justify the possibility of simultaneous response to selection. But, negative correlations make difficult the simultaneous improvement of those traits.

TABLE 6. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients at both locations

Location	Traits	DF	NN	DM	PHT	BrP	PdP	SdP	HSW	Oil	Protein	Yield
Pawe	DF		-0.1ns	0.60**	0.42**	-0.1ns	0.20ns	-0.3**	-0.2ns	-0.0ns	-0.06ns	0.10ns
Dibate			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}
Pawe	NN	0.12ns		-0.0ns	0.1ns	0.2ns	0.01ns	0.02ns	-0.0ns	-0.1ns	-0.1ns	0.2ns
Dibate		0.4**		0.17 ^{ns}	0.13 ^{ns}	-0.0 ^{ns}	0.24*	0.25*	0.25*	-0.3*	-0.13 ^{ns}	0.10 ^{ns}
Pawe	DM	0.70**	0.16ns		0.35**	0.02ns	0.34**	-0.4**	-0.0ns	-0.4**	-0.34**	0.1ns
Dibate		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}
Pawe	PHT	0.6**	0.2ns	0.6**		-0.2ns	0.1ns	-0.2ns	-0.1ns	-0.1ns	-0.1ns	0.2ns
Dibate		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*
Pawe	BrP	-0.3*	0.1ns	-0.1ns	0.05ns		0.6**	-0.2ns	0.01ns	-0.1ns	-0.2ns	0.23**
Dibate		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}
Pawe	PdP	-0.20ns	0.03ns	-0.3*	-0ns	0.5**		-0.4**	-0.1ns	-0.1ns	-0.08ns	0.2**
Dibate		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*
Pawe	Sdp	-0.34**	0.09ns	-0.3*	-0.2ns	0.07ns	0.08ns		0.05ns	0.14ns	0.1ns	0.00ns
Dibate		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}
Pawe	HSW	0.05ns	-0.1ns	0.2ns	-0ns	-0.2*	-0.3*	-0.1ns		-0.1ns	-0.1ns	0.19ns
Dibate		-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}
Pawe	Oil	-0.71**	-0.2ns	-0.5**	-0.3*	0.3**	0.2ns	0.2ns	-0.1ns		0.6**	-0.2ns
Dibate		-0.3*	-0.36**	-0.5**	-0.5**	0.21 ^{ns}	-0.18 ^{ns}	0.14 ^{ns}	0.28*		0.42**	0.07 ^{ns}
Pawe	Protein	0.47**	-0.1ns	0.4**	0.23*	-0.2ns	-0.1ns	-0.2ns	0.2ns	-0.6**		-0.11ns
Dibate		0.24*	0.44**	0.43**	0.37**	-0.3*	0.14 ^{ns}	-0.06 ^{ns}	-0.22 ^{ns}	-0.8**		-0.01 ^{ns}
Pawe	Yield	-0.2ns	0.2ns	-0.1ns	-0.01ns	0.14ns	0.35**	0.20*	0.2ns	0.2ns	-0.2ns	
Dibate		0.08 ^{ns}	0.30*	0.11 ^{ns}	0.12 ^{ns}	0.10 ^{ns}	0.15 ^{ns}	0.31**	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= number of branches per plant, PdP= number of pods per plant, SdP = 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 presented in Table 7 for both locations. At Pawe, number of pods per plant showed positive and high direct effect (0.47) followed by hundred seed weight (0.32), number of nodules per plant (0.20) and number of seeds (0.13) on grain yield. Similarly, positive and direct effect of number of pods on grain yield of soybean has been reported by various workers (Patil *et al.*, 2011; Chavan *et al.*, 2016; Yechalew Sileshi, 2018). Positive and high direct effect of number of seeds on grain yield of soybean has also been reported by various workers (Badkul *et al.* 2014; Mesfin Hailemariam, 2018). Negative and high direct effects were observed by protein content (-0.15) followed by number of branches per plant (-0.13) and days to 50% flowering (-0.04).

At Dibate, number of pods per plant showed positive and high 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, positive and high direct effect of number of nodules on grain yield of soybean has also been reported by Mesfin Hailemariam (2018). Negative and high 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.

TABLE 7. Direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of traits on yield of soybean genotypes at both locations

Location	Traits	DF	NN	DM	PHT	BrP	PdP	SdP	HSW	Oil	Protein	gr
Pawe	DF	-0.04	0.02	0.02	0.04	0.04	-0.1	-0.04	0.02	-0.08	-0.07	-0.2 ^{ns}
Dibate		-0.03	0.08	0.05	-0.02	-0.03	0.05	0	-0.01	-0.03	0.02	0.08 ^{ns}
Pawe	NN	-0.01	0.2	0	0.02	-0.01	0.01	0.01	-0.03	-0.02	0.01	0.2 ^{ns}
Dibate		-0.01	0.21	0.02	-0.01	-0.01	0.07	0.03	-0.02	-0.05	0.03	0.30*
Pawe	DM	-0.03	0.03	0.03	0.05	0.01	-0.13	-0.04	0.06	-0.06	-0.05	-0.1 ^{ns}
Dibate		-0.02	0.07	0.07	-0.02	0	0.14	-0.06	-0.04	-0.06	0.03	0.11 ^{ns}
Pawe	PHT	-0.02	0.04	0.02	0.08	-0.01	-0.02	-0.02	0	-0.03	-0.03	0.0 ^{ns}
Dibate		-0.02	0.05	0.05	-0.03	-0.01	0.17	-0.03	-0.03	-0.06	0.03	0.12 ^{ns}
Pawe	BrP	0.01	0.02	0	0	-0.13	0.23	0.01	-0.07	0.04	0.03	0.1 ^{ns}
Dibate		-0.01	0.03	0	0	-0.11	0.16	0.02	0	0.03	-0.02	0.01 ^{ns}
Pawe	PdP	0.01	0.01	-0.01	0	-0.06	0.47	0.01	-0.1	0.02	0.01	0.35*
Dibate		0	0.04	0.03	-0.01	-0.04	0.38	-0.05	-0.01	-0.02	0.01	0.31**
Pawe	SdP	0.01	0.02	-0.01	-0.02	-0.01	0.04	0.13	-0.03	0.02	0.02	0.20*
Dibate		0	0.04	-0.02	0.01	-0.01	-0.1	0.2	0.02	0.02	0	0.14 ^{ns}
Pawe	HSW	0	-0.02	0.01	0	0.03	-0.14	-0.01	0.32	-0.01	-0.02	0.2 ^{ns}
Dibate		0	-0.02	-0.02	0.01	0	-0.02	0.02	0.18	0.04	-0.01	0.18 ^{ns}
Pawe	Oil	0.03	-0.03	-0.01	-0.02	-0.04	0.08	0.03	-0.03	0.11	0.09	0.2 ^{ns}
Dibate		0.01	-0.08	-0.04	0.01	-0.02	-0.07	0.03	0.05	0.13	-0.05	-0.03 ^{ns}

Pawe	Protein	-0.02	-0.01	0.01	0.02	0.03	-0.04	-0.02	0.05	-0.06	-0.15	-0.2
Dibate		-0.01	0.09	0.03	-0.01	0.03	0.05	-0.01	-0.04	-0.1	0.07	0.10 ^{ns}

Phenotypic direct and indirect effects

The phenotypic direct and indirect effects of traits on grain yield are presented in Table 8 for both locations. At Pawe, positive and high direct effects were observed by number of pods per plant (0.44) followed by hundred seed weight (0.25), days to 50% flowering (0.20) and number of seeds (0.17) on grain yield of soybean. Days to 95% maturity (-0.25), days to 50% flowering (0.20) and oil content (-0.22) showed negative and direct effects on grain yield of soybean. At Dibate, positive and high 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.

TABLE 8. Direct (bold diagonal) and indirect effects (off diagonal) at phenotypic level of traits on yield of soybean genotypes at both locations

Location	Traits	DF	NN	DM	PHT	BrP	PdP	SdP	HSW	Oil	Protein	pr
Pawe	DF	0.2	-0.01	-0.15	0.07	0.00	0.09	-0.04	-0.05	0.01	0.00	0.10 ^{ns}
Dibate		0.01	0.01	-0.11	-0.02	-0.01	0.06	0.00	-0.03	0.01	0.00	0.09 ^{ns}
Pawe	NN	-0.01	0.13	0.01	0.01	0.00	0.00	0.00	-0.01	0.03	0.00	0.16 ^{ns}
Dibate		0.00	0.09	-0.03	0.02	0.01	-0.04	0.05	0.03	-0.04	0.00	0.01 ^{ns}
Pawe	DM	0.12	-0.01	-0.25	0.06	0.00	0.15	-0.06	-0.01	0.08	-0.01	0.07 ^{ns}
Dibate		0.01	0.02	-0.16	0.00	0.03	0.00	0.00	-0.02	0.00	0.00	-0.12 ^{ns}
Pawe	PHT	0.08	0.01	-0.09	0.16	-0.01	0.03	-0.03	-0.02	0.01	0.00	0.15 ^{ns}
Dibate		0.00	0.01	0.00	0.14	-0.01	0.09	-0.01	0.02	-0.01	0.00	0.23*
Pawe	BrP	-0.01	0.01	0.00	-0.03	0.04	0.25	-0.03	0.00	0.02	0.00	0.23*
Dibate		0.00	0.00	0.01	0	-0.28	0.3	0.03	-0.01	0.01	0.00	0.05 ^{ns}
Pawe	PdP	0.04	0.00	-0.08	0.01	0.02	0.44	-0.06	-0.03	0.02	0.00	0.36 ^{**}
Dibate		0.00	-0.01	0.00	0.03	-0.17	0.48	-0.09	-0.01	0.01	0.00	0.24*
Pawe	SdP	-0.05	0.00	0.09	-0.03	-0.01	-0.16	0.17	0.01	-0.03	0.00	0.00 ^{ns}
Dibate		0.00	0.02	0.00	0.00	-0.03	-0.21	0.23	0.01	-0.02	0.00	0.00 ^{ns}
Pawe	HSW	-0.04	-0.01	0.01	-0.01	0.00	-0.04	0.01	0.25	0.02	0.00	0.19 ^{ns}
Dibate		0.00	0.02	0.03	0.03	0.03	-0.04	0.03	0.11	-0.01	0.00	0.19 ^{ns}
Pawe	Oil	-0.01	-0.02	0.09	-0.01	0.00	-0.04	0.02	-0.03	-0.22	0.01	-0.19 ^{ns}
Dibate		0.00	-0.03	0.00	-0.01	-0.01	0.03	-0.04	0.00	0.14	-0.01	0.07 ^{ns}
Pawe	Protein	-0.01	-0.01	0.08	-0.01	-0.01	-0.04	0.02	-0.02	-0.13	0.02	-0.11 ^{ns}
Dibate		0.00	-0.01	0.01	0.00	-0.01	-0.01	-0.01	0.01	0.06	-0.03	-0.01 ^{ns}

DF=days to 50% flowering, NN = number of nodules per plant, DM = days to 95% 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, rg= genotypic correlation coefficient and rp = phenotypic correlation coefficient.

IV. CONCLUSIONS AND RECOMMENDATION

At Pawe, number of branches and number of pods per plant showed highly significant and positive phenotypic correlation with grain yield. Number of pods per plant and number of seeds per pod showed positive and highly significant and significant genotypic associations with grain yield. Number of pods per plant and hundred seed weight showed positive and high direct effects on grain yield at both genotypic and phenotypic levels. Whereas at Dibate, plant height and number of pods per plant showed significant and positive phenotypic correlation with grain yield. Number of nodules and number of pods per plant showed positive significant and highly significant genotypic associations with grain yield. Number of pods and seeds per plant showed positive and high direct effects on grain yield at genotypic level. Number of pods and number of branches per plant showed positive and negative high direct effects on grain yield, respectively.

Therefore, this study has clearly indicated the need for focusing on traits such as number of branches per plant, number of pods per plant, plant height and number of nodules per plant showed positive and significant association with seed yield and traits with high direct effect on seed yield such as number of pods per plant and hundred seed weight towards improving seed yield of soybean through direct selection.

REFERENCES

- [1] Aditya J., Pushpendra B.P. and Anuradha B. 2011. Genetic variability, heritability and character association for yield and component characters in soybean (*G. max* (L.) Merrill). Journal of Central European Agriculture. 12(1): 27-34.
- [2] Afework Hagos and Adam Bekele. 2018. Cost and returns of soybean production in Assosa Zone of Benishangul Gumuz Region of Ethiopia. Journal of Development and Agricultural Economics. Vol. 10(11), pp 377-383.
- [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] Ali A., Khan S.A., Khan E., Ali N., Hussain I., Ahmad F. 2015. Genetic studies among diverse soybean (*Glycine max* L. Merrill) genotypes for variability and correlation at Swat. International Journal of Biosciences. 6 (4):165-169.
- [5] Badkul A., Bisen R. and Mishra S. 2014. Study of principal components analyses for yield contributing traits in fixed advanced generations of soybean (*Glycine max* L. Merrill). Soybean Research. Vol. 2: 44-50.
- [6] Bekele and Getnet. 2011. Desirable Traits Influencing Grain Yield in Soybean (*Glycine max* (L.) Merrill). Innovative Systems Design and Engineering. 2(3), 14-23.
- [7] Besufikad Enideg. 2019. Soybean (*Glycine max* L. merill) genetic improvement in Ethiopia. International Journal of Research Granthaalayah. Vol.7, 2394-3629.

[8] Central Statistical Agency of Federal Democratic Republic of Ethiopia 2000-2012. Annual report.

[9] Central Statistical Authority (CSA). 2018. *Agricultural sample survey*, statistical volume 1 Bulletin no 586. Addis Ababa, Ethiopia. P14.

[10] Chavan B. H., Dahat D. V., Rajput H. J. Deshmukh M. P. and Diwane S. L. 2016. Correlation and Path Analysis in Soybean. *International Research Journal of Multidisciplinary*. Vol(2): p2454-8499.

[11] Devvart, Hooda J. S. and Malik B. P. 2005. Variability and association studies in soybean. *Crop Res. Hissar*. 29 (2): 247-251.

[12] Dudley J.W. 1993. Molecular markers in plant improvements manipulation of genes affecting quantitative traits. *Crop Sci*. 33:660-668.

[13] Faisal AM., Afsari s., Muhammad A. and Abdul G. 2014. Genetic Variability of the Main Yield Related Characters in Soybean. *International journal of agriculture and Biology*. Quaid-I-Azam University, Islamabad Pakistan. Pp815-819.

[14] Hossain Z. and Komatsu S. 2014. Potentiality of soybean proteomics in untying the mechanism of flood and drought stress tolerance. *Proteomes*. 2(1):10 127.

[15] 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.

[16] Jain S., Srivastava S.C., Singh K.S. and Singh B.K. 2015. Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean (*Glycine max* L. Merrill). *Agricultural Research Communication Center. Legume Research*. 38(2): 182-184.

[17] 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.

[18] 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.

[19] Manasa S. 2008. *Breeding investigations in segregating populations of narrow leaf let genotypes in (Glycine max (L.) Merrill)*. Msc. Thesis, University of Agricultural Sciences, Dharwad.

[20] Mesfin Hailemariam and Abush Tesfaye. 2018. Progress of Soybean [*Glycine max* (L.) Merrill] Breeding and Genetics Research in Ethiopia. *Journal of Natural Sciences Research*. vol.8, P70.

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

[22] Patil S.S., Naik M.R., Patil P.P. And Shinde D.A. 2011. Genetic variability, correlation and path analysis in soybean. *Navsari Agril. Uni*. 34(1): 36-40.

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

[24] Ramteke R., Kumar V., Murlidharan P. and Dinesh K. Agarwal. 2010. Study on genetic variability and traits interrelationship among released soybean varieties of India. *Electronic Journ. Plan. Breeding*. 1(6): 1483-1487.

[25] Shapiro S. S. and Wilk M. B. 1965. *An analysis of variance test for normality (complete samples)*, *Biometrika*, 52, 591-611.

[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] Siahsar B. and Rezaei A. 1999. Correlation and path coefficient analysis of morphological and phenological traits associated with yield in soybean (*Glycine max* (L.) Merr.). *Iranian J. Agri. Sci*. 30: 685- 696.

[28] Singh R.K. and Chaudhary B.D. 1999. *Biometrical Methods in Quantitative Genetics Analysis*. Kalyani Publishers. New Delhi, India. P318.

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

[30] Snedecor W. and William G. 1989. *Statistical methods*. Eighth Edition, Iowa State University Press.

[31] Souza M., Tiago A., Catuchi, Suzana C. Bertolli and Rogerio P. Soratto. 2013. *Soybean under Water Deficit, Physiological and Yield Responses*. PP274-298.

[32] Statistical Analysis System (SAS). 2011. *System Analysis Software*. Version 9.3. SAS Institute INC. Cary, North Carolina, USA.

[33] Varnica I., Petrović S., Rebekić A., Guberac S., Jukić K. and Jukić G. 2018. Characterization and Interrelationships of soybean (*Glycine max* (L.) Merrill) yield components during dry and humid seasons. *The Bc Institute, Dugo Selo, Croatia. Journal of Central European Agriculture*. 19(2): p466-481.

[34] Yechalew Sileshi. 2018. *Genetic variability and association of traits in soybean genotypes (Glycine max L. Merr.) Tested in western Ethiopia*. MSc. Thesis, Hawassa University, Ethiopia, 103pp.

Appendix Table 1. Rainfall distribution at Pawe main station for 2018/19 cropping season

Month	June	July	August	Sept	October
Total monthly rf (mm)	315.7	338.2	352.973	131	155.6
Average rf (mm)	10.5	11.3	11.8	4.4	5.2

Source: Pawe Agricultural Research Center Meteorology data.
RF and mm = rainfall and millimeter, respectively.