Path analysis, Genetic variability and Correlation studies for Soybean (*Glycine max* (L.) Merrill) for grain yield and Secondary traits at Asosa, Western Ethiopia

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ABSTRACT

The aim of the study is assessing the nature and magnitude and revealing the genetic correlation among the traits and partition the genetic correlations into direct and indirect effects so that to estimate direct and indirect effects of various character on grain yield. Twenty-four soybean accessions, sown at Asosa agricultural research centre, Asosa (Ethiopia) were evaluated by using randomized completely block design with three replicates for the estimation of genetic variability, heritability, genetic advance, correlation, path analysis and genetic Divergence in twenty- four soybean genotypes obtained from introduction and some two local checks. Observation on 18 agronomic and morphological were observed. Analysis of variance a significant ($P \leq 0.05$) to highly significant difference ($P \leq 0.01$) among the genotypes among for all the characters, but for days to maturity, number of seed per pod, inter-node length and total nodules weights. The phenotypic coefficient of variance was found superior than the genotypic coefficient of variation for all traits studied, showing that the variation is not only genetic but also influenced by growing environments in the expression of the traits. The genotypic coefficient of variation was high for days to maturity, plant height, number of seed per plant, grain yield per plant and fresh biomass weight. High heritability coupled with high to moderate genetic advance was estimated for seed yield per plant was positively and significantly correlated with plant height, pods per plant, and days to 50 per cent flowering and days to maturity. Pod per plant recorded highest positive direct effect on seed yield per plant followed plant height. The information that generated from the study will be useful for grain yield and yield contributing traits, especially from the soil and root architecture and nutrient absorptions.

1. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) the 'golden bean', as it is an important crop in the world in terms of its uses in human food and animal feeds. It belongs to the family leguminosae and is self-pollinated crop having chromosome number of ($2n=2x=40$). It is considered to be a miracle crop as it is extraordinary rich in proteins (~40%) and is also second only to ground nut in terms of oil content (~20%). Comprising 85% unsaturated fatty acids and is free from cholesterol, among food legumes, so it is highly desirable in the human diet (Iqbal *et al.*, 2008). According to central statistics authority (CSA) 2016/17 in Ethiopia, 12,574,107.33 hectares is covered by the grain production among this about 804,752 hectares are oil seeds, which is 6.40%. It is grown globally producing 329.40 million tone year in the world food basket. Ethiopia is experiencing the rise in the soybean production due to its widespread use in food and feed industry.

In Ethiopia, so far around twenty-five soybean varieties were released. According central statistics authority (CSA) of Ethiopia 2015/16 pulse grown covered 13.24% (1,652,844.19 hectares) of the grain crop area and 10.38 (about 27,692,743.11 quintals) of the grain production to oil seeds added 6.88 % (about 859,110.39 hectares) of the grain crop area and 2.94% (about 7,848,093.10 quintals) of the production to the national grain total. Sesame, Neug and linseed covered 3.11% (about 388,245.50 hectares), 2.25% (about 281,036.36 hectares) and 0.68% (about 85,415.67 hectares) of the grain crop area and 1.03% (about 2,742,174.27 quintals), 0.96% (about 2,563,271.66 quintals) and 0.33% (about 885,511.44 quintals) of the grain production, respectively (CSA, 2015/16). Due to the narrow genetic base of soybean in the country, the production and productivity is very low.

The importance of genetic diversity in the improvement of soybean is a paramount importance. In this study was designed to estimate the genetic parameters GCV, PCV, heritability, expected genetic advance (GA), genetic advance as percent of mean (GAM) for yield and morphological traits of soybean that may be used for the selection tools for the future breeding programs and also useful biometrical tools for measuring genetic parameters (Aditya *et al.*, 2011).

Keeping it in view, the present investigation was carried out to assess the nature and magnitude and revealing the genetic correlation among the traits and partition the genetic correlations into direct and indirect effects so that to estimate direct and indirect effects of various character on seed yield.

2. MATERIALS AND METHODS

2.1. Experimental site - The experiment was carried out at experimental fields Asosa agricultural research

centre (AsARC), Asosa, Ethiopia, during June to November 2015. Geographically, the place is located 10°02'N 34°34'E. Agro-ecology's of the area is characterized as hot-warm moist lowland plain tepid to cool humid sub humid lowland plain tepid to cool sub humid mountain. The annual Rain fall 1130mm and that of 15.9-29 °c. The area soil type is characterized as dystic nitisols (EIAR,)

2.2. Plant Materials - The experiment was conducted with twenty-four soybean genotypes laid out in randomized complete block design with three replications used as the experimental materials. The name of the twenty-four soybean genotypes was described in table 1.

2.3. The experimental design and setting the experiments - The experiments is laid out in randomized complete design with three replications.

2.4. Intercultural operations - Plots were made up of four rows 4m long and with 0.6 m inter row and 0.05m intra -row spacing. Fertilizer DAP was applied at the rate of 100 kg ha⁻¹ at planting for all experiments. Sowing was conducted under rain-fed condition. The fields were kept free of weeds by hand weeding and other management practices were followed according to the recommendations of the specific area was followed for raising the crop.

2.5. Data Collections - Descriptor of soybean (*Glycine max* (L.) Merrill) developed by International Plant Genetic Resources Institutes (IPGRI)/International Institutes for Tropical Agriculture (IITA) (1986) were used for data collection. (Table 2).

Among the descriptor developed in (IPGRI)/1986 the following eighteen quantitative data were measured. Data on days to flower, days to maturity, plant height(cm), 100 seed weight(g), branch per plant(cm), number of seeds per plant, number of pod per plant, harvest index, seed yield (Kg ha⁻¹), fresh biomass weight(g), root fresh weight (g), root volume (ml), tap root length(cm), plant dry weight (g), pod length (cm), internode length(cm), number of nodules(number), effective nodule weight(g), total nodule weight(g) were taken from ten competitive plants from each plot.

Measurements were done according to the IPGRI descriptors lists of *G.max* L.

2.6. Statistical Analysis

Analysis of variance (ANOVA) using the generalized linear model (GLM) procedures of the SAS 9.3 Software for windows (SAS institute's, 2011). Comparison among means were made using Least Significance Difference (LSD) at $\alpha = 0.05$ or less when ANOVA indicated that model and treatments were significant. Genetic parameters were estimated by the formula given by

Burton, DeVane (1953) and Johanson using equation (1) - (5).

$$\text{Environmental variance } (\sigma^2_E) = \text{Ms}_e \text{----- (1)}$$

$$\text{Phenotypic variance } (\sigma^2_P) = \sigma^2_g + \sigma^2_e \text{----- (2)}$$

$$\text{Genotypic variance } (\sigma^2_g) = (\text{Ms}_e - \text{Ms}_t)/r \text{----- (3)}$$

Where, Ms_e is the mean square error, Ms_t is the mean square treatment and r is the number of replications.

$$\text{PCV} = \frac{\sigma^2_P}{\bar{X}} \text{----- (4)}$$

$$\text{GCV} = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \text{----- (5)}$$

Estimation of heritability in broad sense: Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (g) to the phenotypic variance (p) and was estimated on genotype mean basis as described by Robinson *et al.* (1949) as equation (6):

$$h^2_b = \frac{\sigma^2_g}{\sigma^2_P} \times 100. \text{----- (6)}$$

Where, h^2_b is the heritability in a broad sense, σ^2_P is the phenotypic variance and σ^2_g is the genotypic variance.

Heritability values are categorized as low, moderate and high (Robinson *et al.*, 1949) and are given below,
0-30% - Low
30-60% - Moderate
60% and above - High

Genetic Advance (GA) and the percentage of the mean (GAM) assuming selection of the superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955) and equations (7) and (8):

$$\text{GA} = \frac{K \times \sqrt{(\sigma^2_P + \sigma^2_g)}}{\sigma^2_P} \text{----- (7)}$$

Where, GA is the expected genetic advance, K is the standardized selection differential at 5% selection intensity ($K \frac{1}{4} = 2.063$), σ^2_P is the phenotypic variance and σ^2_g is the genotypic variance.

$$\text{GAM (\%)} = \frac{\text{GA}}{\bar{X}} \times 100 \text{----- (8)}$$

Where, GAM is the genetic advance as a percentage of the mean, GA is the expected genetic advance and $\bar{X}$ is the grand mean of a character. Genetic advance as

percent of mean was classified as low, moderate and high (Johnson *et al.*, 1955) and values are given below:

0-10% - Low
10-20% - Moderate and
20% and above - High

Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Miller *et al.* (1958) using the corresponding variance and covariance components as shown in equations (9) and (10):

$$r_g = \frac{P_{\text{covx.y}}}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}} \text{----- (9)}$$

and

$$r_p = \frac{G_{\text{covx.y}}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}} \text{----- (10)}$$

Where, r_p is the phenotypic correlation coefficient, r_g is the genotypic correlation coefficient between the characters x and y , $P_{\text{covx.y}}$ is the phenotypic covariance and $G_{\text{covx.y}}$ is the genotypic covariance between the character's x and y .

Path coefficient analysis was conducted as suggested by Dewey and Lu (1959) using the phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of the yield component on the fruit yield based on equation (11):

$$r_{ij} = p_{ij} + \sum r_{ik} \times p_{kj} \text{----- (11)}$$

where, r_{ij} is the mutual association between the independent trait (i) and the dependent trait (j) as measured by the correlation coefficient, p_{ij} is the component of direct effects of the independent trait (i) on the dependent variable (j) and $r_{ik}p_{kj}$ is the assumption of components of the indirect effect of a given independent trait via all other independent traits.

The residual effect was obtained as per the formula given below:

$$R = \sqrt{1 - E_{di} r_{ji}} \text{----- (12)}$$

Where, d_i = Direct effect of the character
 r_{ij} = correlation coefficient of i^{th} character with j^{th} character.

Path coefficient analysis was calculated using the SAS software package (Cosme, 2013). Genotypic and phenotypic coefficient variations are for the different character were calculated in all possible combinations following the formula.

Table 1. Details of genotypes used for the experiment

Strain Sub-Designation	Cultivar Name	Seed Source*	Strain Sub-Designation	Cultivar Name	Seed Source*
PI634193	5002T	AON	PI559932	Ks3496	AON
PI570668	Ciaric	AON	-	Clarck-63k	Released
PI633970	Ozark	AON	PI533050	Choska	AON
PI 603953	Motte	AON	PI594669	Liu yue mang	AON
PI595081	Ks4895	AON	PI594675	Huang dou No-1	AON
PI	UA4805	AON	PI594675	Hs93-4118	AON
PI 560207	Delsoy 4710	AON	PI614153	Croton 3.9	AON
PI 553051	Spry	AON	-	SCS-1	Released
PI561702	Harbar	AON	PI639740	LDOO-3309	AON
TGX-1892-10F	AFGAT	released	PI612157	Prichard	AON
PI594675	Graham	AON	PI633610	Desha	AON
PI559932	Manokin	AON	Hawassa-04	AGS-7-1	Released

Source: EIAR/JARC* **AON** =Advanced Observation Nursery**Table 2. List of different traits and their description measurement**

S. N	Traits	Methods of measurements
1.	Days to maturity	Number of days from sowing till 95% pod turned in to yellow was recorded
2.	Plant height(cm)	Actual measurement in cm as a mean of ten randomly selected plants
3.	100 Seed Weight(g)	Weight in gram of 100 randomly selected seeds from dried, cleaned grain
4.	Branch per plant(cm)	Total number of pod bearing branches in a plant
5.	Number of seeds per plant	Total number of seeds in a plant
6.	Number of pod per plant	Mean number of pod per plant estimated from ten plants
7.	Harvest index	The ratio of grain yield per biological yield
8.	Grain Yield (Kg ha ⁻¹)	Weighing the seeds produced in a plot and then converted in to kg ha ⁻¹ adjusted to 13% moisture
9.	Fresh biomass weight(g)	Fresh plants from each plot were uprooted at full flowering and weight was recorded removing the root part and average was calculated
10.	Root fresh weight(g)	The fresh weight that measured by the sensitive balance
11.	Root Volume (ml)	The volume of the root the measured by the gauged cylinder
12.	Tap root length(cm)	The tap root length that measured up to tip bottom of the root
13.	Plant dry weight(g)	The total plant dry weight after the crop dry out in an oven for 70 ⁰ c for 24 hours
14.	Pod length (cm)	The length of the od that measured in centimeters
15.	Inter node length(cm)	The distance between two nodes that taken with three samples at bottom, middle and tip pars of the crop
16.	Number of nodules	Number of nodules per plant is counted by taking out randomly selected 10 plants at 45 days after sowing
17.	Effective nodule weight(g)	The active nodule that identified by color
18.	Total nodule weight(g)	The weight of nodules on the roots of ten plants at the time when the first flowers appear and again the three weeks after first flowering

3. RESULTS AND DISCUSSION

3.1. Variance Components and Coefficient of Variations

ANOVA showed that mean squares among genotypes were ranges from significant ($P \geq 0.05$) to very highly significant for significant ($P \geq 0.001$) for the traits, but non-significant difference for the traits like days to maturity, number of seed per pod, inter-node length and total nodules weights (Table 3). These results indicate that, there is a genotypic variation for among the genotypes for all the studied traits, except the four. This implied that the population of soybean genotypes would respond positively to selections. This indicates that substantial variability has been created and genetic base is broadened for most of the important characters among different genotypes developed through hybridization involving diverse parents. The exploitation of the present variability may lead to develop potential and suitable genotypes in future.

Similar results have been reported by Aditya *et al.* (2011), for plant height, pods per plant, branches per plant and 100 seed weight, Gupta and Punetha (2007) for pods per plant, Reni and Rao (2013) for pods per plant, branches per plant, biological yield, harvest index, yield per plant and Suresh Rao *et al.* (2014) for number of pods per plant and seed yield per plant.

3.2. Genotypic and Phenotypic Coefficients of Variations (GCV and PCV)

Broad sense heritability (Hb), genetic advance (GA) and genetic advance as percent of mean were calculated for all traits (Table 4). In the present investigation, PCV was found higher than GCV for all traits under study. The highest observed for effective nodule weight recorded the highest PCV and GCV (94 and 43%, resp.) followed by total nodule weight (93 and 28%, resp.), plant height, branch per plant and the lowest PCV and GCV recorded for days to maturity (8 and 5%, resp.). In agreement with the present findings Chandda *et al.* (2013), Ghodrati (2013), Dilnesaw *et al.* (2013), Mahbub *et al.* (2015) and Pawae *et al.* (2014), Hakim *et al.* (2014), Pawar *et al.* (2014) and Malek *et al.* (2014) for days to maturity, Reni and Rao *et al.* (2013) and Chandel *et al.* (2013) for biological weight, Reni and Rao (2013), Chandel *et al.* (2013) and Pawar *et al.* (2014) for harvest index, Ghodrati (2013), Reni and Rao (2013), Chandel *et al.* (2013), Dilnesaw *et al.* (2013), Pawar *et al.* (2014), Malek *et al.* (2014) and Mahbub *et al.* (2014) for number of branches per plant, Aditya *et al.* (2011), Reni and Rao (2013), Chandel *et al.* (2013), Dilnesaw *et al.* (2013), Hakim *et al.* (2014), Pawar *et al.* (2014) and Suresh Rao *et al.* (2014) for number of pods per plant, Chandel *et al.* (2013) for number of pod clusters per plant, Osekita and Ajayi (2013) for number of seeds per plant, Pawar *et al.* (2014) for 100 seed weight, Aditya *et al.* (2011), Reni and Rao (2013), Osekita and Ajayi

(2013), Chandel *et al.* (2013), Pawar *et al.* (2014), Suresh Rao *et al.* (2014) and Mahbub *et al.* (2015) for seed yield per plant reported similar findings.

3.3. Heritability and Genetic Advance

Heritability in broad sense estimated for all the traits under study and presented in Table 4. The result indicates that estimate of heritability was high for plant height, grain yield and that of fresh weight. This result indicates that the preponderance of additive gene action. High heritability coupled with high genetic advance was recorded plant height, grain yield, and fresh biomass weight. In conformity of the results high heritability coupled with high genetic advance been reported plant height Hakim *et al.* (2014), Badkul *et al.* (2014) and Ghodrati (2013) for plant height, Mehta *et al.* (2016) for fresh biomass weight. So, the result suggests that selection may be effective because these traits may have governed by additive gene action.

3.4. Associations among Traits

The phenotypic and genotypic correlation of yield with yield components characters are indicated in table 6. Most of the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficient indicating the masking of the efficiency of the environment which modified the expression of a character thereby reducing the phenotypic expression (Saha *et al.*, 1992; Islam *et al.*, 1993). All characters observed for quantitative data showed positive genotypic and phenotypic correlations with the fruit yield, except genotypic coefficient of variation for days to maturity (Table 6). The grain yield had a highly significant, positive, genotypic and phenotypic correlation with the days to maturity, plant height, number of seed per plant, harvest index, fresh biomass weight, root fresh weight, tap root length, pod dry weight, number of nodules, effective nodule weight, and total nodule weight, days to flower showed a negative correlation with the grain yield (Table 3).

3.5. Path Coefficient Analysis

Path coefficient analysis is known as standard partial regression coefficient analysis which is unitless. It is carried out using genotypic and phenotypic and taking the yield as the dependent variable in order to see the casual factor and to identify the best components, which is responsible for increasing the yield per plant. The genotypic path coefficient analysis of different morphological traits on seed yield per plant revealed that pod dry weight recorded very high estimates of positive direct effect. The high estimate of positive direct effect was recorded for days to maturity followed plant height, hundred seed weight, number of seed per plant, number of pod per plant, fresh biomass weight, and nodule number, while effective nodule weight recorded

low value of positive direct effect on seed yield per plant. The very high negative direct effect on seed yield per plant was exhibited by tap root length and inter-node length.

Similar finding has also been obtained by Salimi and Moradi (2012) for fresh weight at full flowering, Badkul *et al.* (2014), Chandel *et al.* (2014) and Jain *et al.* (2015) for biological weight, Abady *et al.* (2013), Badkul *et al.* (2014) and Chandel *et al.* (2014) for harvest index, Salimi and Moradi (2012), Badkul *et al.* (2014) and Silva *et al.* (2014) for number of seeds per plant, Salimi and Moradi (2012), Malek *et al.* (2014) and Jain *et al.* (2015) for 100 seed weight. However, Chandel *et al.* (2014) recorded low direct positive effect on seed yield per plant.

3.6. Diversity Analysis

3.6.1. Cluster Analysis

Cluster analysis is based on 18 morphological traits group twenty-four soybean genotypes grouped into seven different clusters and indicated twenty-four soybean genotypes exhibited notable genetic divergence in terms of morphological traits (Figure 1). Formation of different number of clusters using morphological characters in diverse soybean genotypes was also reported. Reni *et al.* (2013) obtained 6 and 7 clusters by Mahalanobis' D^2 statistic and cluster analyses.

Table 3. Mean square value for eighteen different phonological and morphological characters

Source of variations	DF	Agronomic traits																	
		DM	PH	HSW	BPP	NSPP	NPPP	HI	GYLD	FBW	RFW	RV	TRL	PDW	PODL	IL	NN	ENW	TNW
Replications	2	83.87	24.68	2.04	3.04	953.50	96.53	0.000	417934.09	2588.94	0.51	19.88	73.87	94.83	2.89	1.04	116.24	0.07	0.04
		83.87n				437.39	125.70						27.50			0.66			0.13n
Genotypes	23	s	396.81*	11.89*	2.83*	ns	*	0.004	977905.16*	618.98*	2.52*	3.72*	*	47.33*	0.24*	ns	53.51*	0.06*	s
Error	46	48.18	22.19	3.72	0.67	288.06	25.35	0.001	155096.18	100.07	0.79	1.97	10.87	17.48	0.12	0.59	26.14	0.04	0.10
S. Ed±		5.67	3.85	1.57	0.67	13.86	4.11	0.03	321.55	8.17	0.73	1.15	2.69	3.41	0.28	0.63	4.17	0.16	0.26
CD (P≥0.05)		11.41	7.74	3.17	1.35	27.89	8.27	0.06	647.26	16.44	1.46	2.31	5.42	6.87	0.56	1.26	8.40	0.31	0.52
CD (P≥0.01)		15.23	10.33	4.23	1.80	37.24	11.05	0.08	864.02	21.95	1.95	3.08	7.23	9.17	0.75	1.69	11.22	0.42	0.70

NB:DM=Days to maturity, PH=Plant height, HSW=Hundred seed weight(g), NSPP=Number of seed per plant, BPP=Branch per plant, NPPP=Number of pod per plant, HI=Harvest index, GYLD=Grain yield, FBW=Fresh Biomass weight, RFW=Root fresh weight, RV=Root volume(ml), TRL=Tap root length(cm), PDW=pod dry weight, PODL=Pod length(cm), IL=Inter-node length, NN=Number of nodule, ENW=Effective nodule weight, TNW=Total nodule weight(gm), ** Significantly at 1% , * Significantly at 5%

Table 4. Parameters of genetic variability for physiological and economic traits of soybean genotypes

Sr.	Characters	Mean ± SD	Range		Genotypic variance(σ^2_g)	Phenotypic variance(σ^2_p)	PCV (%)	GCV (%)	H_b	GA	GA as % of Mean 5%
			Min.	Max.							
1	DM(Days)	104.72 ±5.67	90.00	120.00	27.96	76.14	8	5	37	6.60	6.30
2	PH(cm)	53.93±3.85	35.20	90.00	124.87	147.06	22	21	85	21.21	39.33
3	HSW(g)	17.63±1.57	11.00	25.00	2.72	6.44	14	9	42	2.21	12.54
4	BPP	2.76±0.67	0.80	8.20	0.72	1.39	43	31	52	1.26	45.63
5	NSPP	63.80±13.86	23.00	164.80	49.78	337.84	29	11	15	5.58	8.74
6	NPPP	31.64±4.11	12.00	57.60	33.45	58.80	24	18	57	8.99	28.40
7	HI (%)	0.15±0.03	0.07	0.26	0.00	0.00	32	20	40	0.04	26.10
8	GYLD (Kg ha ⁻¹)	2972.51±321.55	1814.41	4426.13	274269.66	429365.84	22	18	64	862.25	29.01
9	FBW (g)	39.84±8.17	8.50	90.05	172.97	273.04	41	33	63	21.56	54.13
10	RFW(g)	2.71±0.73	0.92	9.42	0.58	1.37	43	28	42	1.02	37.48
11	RV(ml)	5.04±1.15	2.40	14.00	0.59	2.56	32	15	23	0.76	15.01
12	TRL(cm)	18.13±2.69	7.00	30.80	5.54	16.41	22	13	34	2.82	15.55
13	PDW(g)	15.21±3.41	5.40	31.14	9.95	27.43	34	21	36	3.91	25.74
14	PODL(cm)	3.48±0.28	2.00	4.50	0.04	0.16	11	6	26	0.21	6.03
15	IL(cm)	2.84±0.63	1.80	8.06	0.02	0.61	28	5	4	0.06	2.07
16	NN	7.48±4.17	0.60	31.00	9.12	35.26	79	40	26	3.17	42.31
17	ENW(g)	0.23±0.16	0.00	1.12	0.01	0.05	94	43	21	0.09	41.38
18	TNW(g)	0.36±0.26	0.04	2.20	0.01	0.11	93	28	9	0.06	17.01

NB:DM=Days to maturity, PH=Plant height, HSW=Hundred seed weight(g), NSPP=Number of seed per plant, BPP=Branch per plant, NPPP=Number of pod per plant, HI=Harvest index (%), GYLD=Grain yield, FBW=Fresh Biomass weight, RFW=Root fresh weight, RV=Root volume(ml), TRL=Tap root length(cm), PDW=pod dry weight, PODL=Pod length(cm), IL=Inter-node length, NN=Number of nodule, ENW=Effective nodule weight, TNW=Total nodule weight(gm), PCV=Phenotypic coefficient of variation; GCV=Genotypic coefficient of variation; h_b = broad sense heritability; GA=Genetic advance

Table 5. Path analysis showing direct (bold-diagonal) and indirect effects (Off-diagonal) effect at genotypic (G) and phenotypic (P) on yield component trait on yield in soybean genotypes (genotypic and phenotypic residual effect was 33.3 and 76.4% respectively).

Traits		DM	PH	HSW	BPP	NSPI	NPP	HI	FBW	RFW	RV	TRL	PDW	PODL	IL	NN	ENW	TNW
DTM	G	0.452	0.027	0.017	0.033	-0.086	-0.018	-0.080	0.113	-0.017	-0.034	-0.167	0.306	-0.075	0.020	0.081	0.002	-0.046
	P	0.050	0.094	0.019	0.008	-0.022	-0.005	-0.004	0.019	0.002	0.014	0.000	0.073	0.011	0.006	0.005	-0.004	0.003
PHT	G	0.198	0.062	-0.025	-0.038	0.134	0.030	-0.060	0.154	-0.019	-0.030	-0.357	0.368	0.059	0.026	0.147	0.010	-0.036
	P	0.014	0.337	-0.030	-0.021	0.025	0.021	-0.003	0.035	0.006	0.032	-0.001	0.093	-0.013	0.006	0.007	0.025	0.005
HSW	G	0.055	-0.011	0.139	0.008	-0.061	-0.026	-0.103	0.052	-0.008	-0.015	0.145	0.262	-0.162	-0.021	0.146	0.003	-0.039
	P	0.004	-0.048	0.207	0.007	-0.025	-0.018	-0.005	0.012	0.002	0.012	0.001	0.029	0.017	-0.007	0.008	0.018	0.004
BPP	G	-0.105	0.017	-0.008	-0.139	0.321	0.074	-0.018	0.073	-0.006	-0.014	-0.199	0.230	0.094	-0.067	0.063	0.007	-0.002
	P	-0.005	0.095	-0.018	-0.074	0.074	0.048	0.001	0.016	0.001	0.008	0.000	0.072	-0.007	-0.009	0.004	-0.001	0.000
NSPI	G	-0.077	0.016	-0.017	-0.088	0.508	0.068	-0.018	0.049	-0.006	-0.015	-0.185	0.145	0.063	-0.086	-0.046	-0.001	0.024
	P	-0.006	0.049	-0.030	-0.032	0.170	0.046	0.000	0.014	0.001	0.012	-0.001	0.065	-0.012	-0.014	0.000	-0.012	-0.002
NPP	G	-0.076	0.018	-0.034	-0.097	0.327	0.106	0.003	0.019	-0.002	-0.010	-0.138	0.000	0.101	0.000	-0.087	-0.001	0.036
	P	0.010	0.086	-0.045	-0.043	0.095	0.083	0.002	0.014	0.000	0.003	-0.001	0.015	-0.022	-0.014	-0.002	-0.004	-0.003
HI	G	0.138	0.014	0.055	-0.010	0.035	-0.001	-0.262	0.087	-0.028	-0.040	0.129	0.270	-0.086	-0.048	0.154	0.005	-0.039
	P	0.010	0.058	0.049	0.002	0.003	-0.010	-0.020	0.021	0.010	0.055	0.001	0.081	0.022	0.003	0.006	0.021	0.004
FBW	G	0.217	0.041	0.031	-0.043	0.106	0.008	-0.097	0.235	-0.028	-0.041	-0.404	0.661	-0.055	-0.075	0.274	0.014	-0.049
	P	0.015	0.183	0.039	-0.019	0.036	0.009	-0.006	0.064	0.008	0.057	-0.001	0.182	-0.005	-0.016	0.015	0.028	0.006
RFW	G	0.192	0.030	0.029	-0.020	0.080	0.004	-0.182	0.161	-0.040	-0.042	-0.197	0.450	-0.050	-0.105	0.247	0.014	-0.058
	P	0.006	0.116	0.024	-0.004	0.014	0.000	-0.011	0.030	0.018	0.048	-0.001	0.115	0.012	-0.008	0.010	0.035	0.007
RV	G	0.261	0.031	0.034	-0.033	0.131	0.018	-0.176	0.164	-0.029	-0.059	-0.189	0.479	-0.051	-0.077	0.155	0.005	-0.026
	P	0.007	0.099	0.024	-0.005	0.014	0.002	-0.010	0.034	0.008	0.107	-0.001	0.072	-0.010	-0.010	0.003	0.004	0.001
TRL	G	0.130	0.038	-0.035	-0.048	0.162	0.025	0.058	0.164	-0.014	-0.019	-0.579	0.423	0.076	-0.072	0.155	0.010	-0.027
	P	0.001	0.134	-0.047	-0.011	0.030	0.013	0.007	0.027	0.005	0.027	-0.003	0.071	0.029	-0.019	0.004	0.011	0.003
PDW	G	0.194	0.032	0.051	-0.045	0.103	0.000	-0.099	0.218	-0.025	-0.040	-0.344	0.713	-0.065	-0.131	0.243	0.015	-0.053
	P	0.014	0.125	0.024	-0.021	0.044	0.005	-0.006	0.047	0.008	0.031	-0.001	0.250	0.029	-0.006	0.012	0.027	0.006
PODL	G	0.135	-0.015	0.090	0.052	-0.127	-0.043	-0.089	0.036	-0.008	-0.012	0.175	0.185	-0.251	-0.014	0.112	0.000	-0.029
	P	0.005	-0.041	0.033	0.005	-0.021	-0.018	-0.004	-0.003	0.002	-0.010	0.001	0.034	0.103	0.002	0.001	0.005	0.001
IL	G	-0.029	-0.005	0.010	-0.031	0.144	0.000	-0.042	0.041	-0.014	-0.015	-0.137	0.307	-0.011	-0.304	0.158	0.012	-0.024
	P	-0.003	-0.007	0.017	-0.008	0.027	0.001	0.001	0.012	0.002	0.012	-0.001	0.018	-0.003	-0.090	0.003	0.014	0.001
NN	G	0.082	0.020	0.045	-0.020	-0.052	-0.020	-0.090	0.100	-0.022	-0.020	-0.200	0.386	-0.062	-0.107	0.449	0.018	-0.082
	P	0.008	0.082	0.057	-0.010	-0.001	-0.004	-0.004	0.033	0.006	0.009	0.000	0.102	0.004	-0.008	0.029	0.049	0.010
ENW	G	0.034	0.019	0.015	-0.028	-0.014	-0.002	-0.038	0.072	-0.017	-0.020	-0.187	0.325	0.003	-0.117	0.256	0.032	-0.063
	P	-0.002	0.078	0.028	-0.017	-0.007	-0.003	-0.002	0.021	0.006	0.004	0.000	0.077	0.001	-0.012	0.014	0.106	0.011
TNW	G	0.171	0.019	0.045	-0.003	-0.100	-0.032	-0.084	0.066	-0.020	-0.013	-0.131	0.313	-0.060	-0.061	0.306	0.017	-0.120
	P	0.006	0.078	0.036	0.001	-0.019	-0.012	-0.004	0.017	0.006	0.004	0.000	0.064	0.005	-0.002	0.014	0.051	0.022

NB:DM=Days to maturity, PH=Plant height, HSW=Hundred seed weight(g), BPP=Branch per plant, NSPP=Number of seed per plant, NPPP=Number of pod per plant, HI=Harvest index, GYLD=Grain yield, FBW=Fresh Biomass weight, RFW=Root fresh weight, RV=Root volume(ml), TRL=Tap root length(cm), PDW= pod dry weight, PODL= Pod length(cm), IL=Inter-node length, NN=Number of nodule, ENW=Effective nodule weight, TNW=Total nodule weight(gm),

Table 6. Genotypic (G) and Phenotypic (P) correlation coefficient among important quantitative traits in soybean genotypes

Traits		DF	DM	PH	HSW	BBP	NSPI	NPP	HI	Yield	FBW	RFW	RV	TRL	PDW	PODL	IL	NN	ENW	TNW
DF	G	1	0.222	0.229	-0.097	-0.057	-0.075	0.032	-0.059	-0.119	0.011	-0.033	0.109	0.127	-0.154	-0.023	-0.378	-0.077	-0.111	-0.093
	P		0.249*	0.148	0.000	-0.107	-0.120	-0.018	0.075	0.053	0.187	0.041	0.044	-0.002	0.013	-0.144	-0.122	0.069	-0.052	0.003
DM	G		1	0.438*	0.122	-0.233	-0.170	-0.167	0.309	0.526**	0.480*	0.426*	0.577**	0.288	0.430*	0.299	-0.065	0.181	0.075	0.379
	P			0.278*	0.089	-0.105	-0.131	-0.063	0.197	0.267*	0.293*	0.131	0.132	0.011	0.292*	0.102	-0.070	0.168	-0.035	0.127
PH	G			1	-0.182	0.276	0.264	0.285	0.223	0.623**	0.656***	0.481*	0.505*	0.616**	0.517**	-0.237	-0.085	0.328	0.311	0.299
	P				-0.143	0.283*	0.146	0.256*	0.165	0.534***	0.542***	0.345*	0.2937*	0.398***	0.372**	-0.122	-0.020	0.242*	0.232	0.231
HSW	G				1	-0.054	-0.120	-0.243	0.395	0.365	0.219	0.209	0.247	-0.250	0.368	0.646***	0.069	0.326	0.104	0.320
	P					-0.089	-0.146	-0.217	0.247*	0.213	0.186	0.117	0.115	-0.229	0.115	0.161	0.081	0.274*	0.134	0.173
BBP	G					1	0.631***	0.700***	0.057	0.321	0.312	0.141	0.238	0.344	0.323	-0.375	0.220	0.141	0.203	0.018
	P						0.435***	0.581***	-0.039	0.228	0.250*	0.051	0.073	0.143	0.287*	-0.072	0.106	0.137	0.224	-0.014
NSPI	G						1	0.643***	0.059	0.334	0.209	0.157	0.259	0.319	0.203	-0.250	0.284	-0.103	-0.027	-0.197
	P							0.555***	0.016	0.255*	0.211	0.079	0.115	0.175	0.260*	-0.121	0.159	-0.007	-0.039	-0.113
NPP	G							1	-0.025	0.167	0.080	0.037	0.170	0.238	0.001	-0.404	-0.001	-0.193	-0.019	-0.300
	P								-0.133	0.168	0.109	0.000	0.023	0.162	0.061	-0.211	0.014	-0.052	-0.035	-0.139
HI	G								1	0.378	0.371	0.693**	0.666***	-0.233	0.378	0.362	0.156	0.348	0.146	0.325
	P									0.308**	0.327**	0.542***	0.507***	-0.349**	0.319**	0.213	-0.042	0.206	0.104	0.198
Yield	G									1	0.794***	0.512*	0.639**	0.448*	0.766***	0.213	0.077	0.468*	0.312	0.340
	P										0.600***	0.413***	0.343**	0.226	0.578***	0.091	-0.005	0.362**	0.302**	0.266*
FBW	G										1	0.685***	0.699***	0.698***	0.927***	0.218	0.248	0.610**	0.440*	0.403
	P											0.460***	0.532***	0.417***	0.728***	-0.053	0.180	0.518***	0.324**	0.261*
RFW	G											1	0.713***	0.341	0.631**	0.199	0.346	0.550**	0.425*	0.484*
	P												0.446***	0.252*	0.460***	0.119	0.093	0.348**	0.332**	0.330**
RV	G												1	0.326	0.672***	0.204	0.253	0.345	0.149	0.213
	P													0.252*	0.287*	-0.096	0.111	0.086	0.035	0.036
TRL	G													1	0.594**	-0.302	0.237	0.345	0.323	0.227
	P														0.283*	-0.254*	0.215	0.128	0.107	0.143
PDW	G														1	0.260	0.431*	0.542**	0.456*	0.439*
	P															0.135	0.071	0.407***	0.306**	0.25605*
PODL	G															1	0.045	0.249	-0.012	0.239
	P																-0.027	0.037	0.007	0.050
IL	G																1	0.351	0.386	0.201
	P																	0.092	0.128	0.026
NN	G																	1	0.571**	0.681***
	P																		0.464***	0.476***
ENW	G																		1	0.524**
	P																			0.477***
TNW	G																			1
	P																			

NB:DM=Days to maturity, PH=Plant height, HSW=Hundred seed weight(g), NSPP=Number of seed per plant, BPP=Branch per plant, NPPP=Number of pod per plant, HI=Harvest index, GYLD=Grain yield, FBW=Fresh Biomass weight, RFW=Root fresh weight, RV=Root volume(ml), TRL=Tap root length(cm), PDW=, PODL=, Pod length(cm), IL=Inter-node length, NN=Number of nodule, ENW=Effective nodule weight, TNW=Total nodule weight(gm), *, ** are significant at 1 % and 5% level of probability, respectively.

Figure 1. Dendrogram shows relation among the of 24 genotypes of soybean based on average linkage and Euclidean distance using the mean of 18 quantitative traits

5. CONCLUSION

From this study, it can be concluded that considerable genetic diversity was found at the genetic materials. Estimates of variance, genotypic and phenotypic coefficient of variation and range revealed large variability for seed yield per plant, number of pods per plant, biological yield per plant and number of nodules per plant over environments suggested that direct selection exercised for these traits can improve the seed yield.

- High estimates of heritability accompanied by high genetic advance were recorded for number of nodules per plant, number of pods per plant, days to
- maturity over environments suggested that direct selection on these traits can improve the seed yield
- The traits viz. number of primary branches per plant, plant height, number of nodules per plant, seed yield per plant and days to maturity have been identified as major yield contributing traits through association analysis.
- Therefore, there need to consider effort in making heterotic in hybridization, that may result good recombinant for improvement of quality traits.

Conflicting interests

The authors declare that they have no conflict of interests.

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