

## Research Article

# Path Analysis and Correlations Among Yield and Related Traits in Different Genotypes of Soybean (*Glycine Max (L.) Merrill*) in the Benishangul Gumuz Region, Western Ethiopia

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## Abstract

Soybean is a warm-climate industrial crop, thrives in low- to medium-altitude legume crops. However, its production in Ethiopia lags behind global standards due to limited improved varieties and reliance on narrow genetic base materials, resulting in low productivity. Consequently, an experiment was undertaken to evaluate the genetic variability and associations among traits in various soybean genotypes concerning grain yield and related factors. Forty-nine soybean genotypes were assessed using a simple lattice design with two replications at Assosa Agricultural Research Center during the main cropping season of 2020. The majority of the characteristics displayed positive correlations both at phenotypic and genotypic levels. Seed yield had highly significant and positive correlations, genetically and phenotypically, with the total number of seeds/plant, number of pods/primary branch per plant, and the weight of a hundred seeds, indicating the potential for concurrent enhancement of grain yields and these associated traits. The total number of seeds/plant had the greatest genotypic (0.94) and phenotypic (0.51) direct influence on seed yield, followed by the number of pods/primary branch per plant and the weight of a hundred seeds, which showed higher genotypic direct effects on seed yield. This suggests that specific emphasis should be placed on these traits for direct selection aimed at improving yield. Moreover, through examinations of genetic diversity, it has been confirmed that there exists significant variability among the evaluated genotypes. This discovery offers valuable insights for future soybean breeding programs. The identification of such variability is crucial as it allows breeders to select and develop soybean varieties with desirable traits, ultimately contributing to the improvement and advancement of soybean varieties.

## Keywords

Correlation, Direct and Indirect Effect, Grain Yield

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## 1. Introduction

Soybean (*Glycine max (L.) Merrill*)  $2n = 2x = 40$ ) is one of the industrial crops of low- to medium-altitude legume crops that require a warm climate [1]. And it is known as a miracle crop as it is extra ordinary and second only to ground nut in terms of 85% unsaturated fatty acids and cholesterol-free among food legumes, so it is highly desirable in the human diet [2].

Soybean is the world's most widely grown leguminous crop and is an important food and feed source of protein and oil [3]. It has a highly nutritious diet that can play a major role in the human body, with positive health effects and disease prevention [4].

In Ethiopia, recently, the preference of soybean product is increasing as a result of increasing population growth, agro processing and urbanization [1]. Now days, the current national average production and productivity of soybean increased from 1.4 tons ha<sup>-1</sup> in 2011 [5] to 2.27 tons ha<sup>-1</sup> in 2017 [6]. But the production of soybean is low when compared with the world average productivity potential of 2.7 tons ha<sup>-1</sup> [6]. Production and productivity of soybean in Ethiopia is below the world average mainly because of use of narrow genetic base materials [7].

To address the challenges facing soybean production in Ethiopia, it is essential to identify the constraints and stable genotypes possessing favorable agronomic traits and yield-contributing characteristics. Thus, solely emphasizing yield may not lead to significant improvements unless other relevant traits influencing yield are also taken into account. Correlation studies enable researchers to investigate the extent and direction of a yield's relationship with its constituents, as well as with other components. As a result, the best option is to use correlated response selection, which includes numerous contributing elements that influence seed production both directly and indirectly. The association of features based on correlation analysis may not provide an accurate picture of the relative importance of each yield component's direct and indirect influence on yield. Path analysis has been used to uncover characteristics in soybean that have a major impact on grain production [8].

Hence, keeping this objective in view, the present study was conducted to assess the type and strength of genetic correlations among characteristics and to differentiate between

direct and indirect influences to determine their effects on seed yield.

## 2. Materials and Methods

### 2.1. Description of Experimental Site

The experiment was conducted at Assosa Agricultural Research Center (AsARC) in Benishangul Gumuz Region, Ethiopia. The study site is Assosa Agricultural Research Center on station located at latitude of 9°30' to 11°39' N and longitude of 34° 20' to 36° 30' E and It is 660 km from Addis Ababa to the west of the country and 1550 meters above sea level (m.a.s.l). It also has a unimodal pattern of rainfall beginning at the end of April and lasting until mid-November, with maximum rainfall occurring in June, July and August. The overall average annual Assosa rainfall is 1275 mm. The temperatures of minimum and maximum are 17°C and 28°C, respectively. The dominant soil types of Benishangul Gumuz Region are Nitosols while the experimental site also included under this type of soil with pH of 5.0 to 6.0 ranges.

The experiment was conducted in 7x7 Lattice Design with two replications at Assosa Agricultural Research Center during main cropping season of 2020/21 under rain-fed conditions. Each plot consisted four rows per plot with inter and intra row distances of 60cm and 5cm, respectively with plot size of 7.2 meter square (2.4m\*3m). The amounts of seed and NPS fertilizer used were 60 kg h<sup>-1</sup> and 120 kg h<sup>-1</sup>, respectively. Management of the field was carried out manually following the production package of the crop in the area.

### 2.2. Experimental Materials

For the experiment, forty-nine genotypes of soybeans were used in the study. They were obtained from different sources, and 15 of genotypes with 1 released variety served as standard check, were obtained from Jima agriculture research center (JARC) while the rest 31 genotypes and 2 released varieties used as standard check, got from Pawe Agricultural Research Center (PARC) (Table 1).

**Table 1.** Description of soybean genotypes used in the experiment.

No	Genotypes Designation	Source	Year introduced	No	Genotypes Designation	Source	Year introduced
1	T44-15-T105-16-sc1	JARC	2016	26	PB-12-8	PARC	2012
2	PI417089A	JARC	2016	27	PM12-9	PARC	2012
3	PI471904	JARC	2016	28	PM12-10	PARC	2012
4	T47-15-T126-16-SF1	JARC	2014	29	PM12-11	PARC	2012

No	Genotypes Designation	Source	Year introduced	No	Genotypes Designation	Source	Year introduced
5	Tgx-2008-4F	PARC	2014	30	PM12-12	PAR	2012
6	SCS -1 (check)	JARC	2016	31	Tgx-1990-59p	PARC	2012
7	JM-CLK/CRFD-15-SD	JARC	2016	32	Gishama (Check)	PARC	
8	JM-ALM/H3-15-SG	JARC	2016	33	Belessa-95 (STCH)	PARC	
9	T34-15-T73-16-SD1	JARC	2016	34	Tgx-1990-55F	PARC	2014
10	Tgx-2004-13F	PARC	2014	35	Tgx-2011-3F	PARC	216
11	JM-ALM/H3-15-SE1	JARC	2016	36	Tgx-1990-57F	PARC	2014
12	JM-ALM/H3-15-SF-2	JARC	2016	37	Tgx-1987-10F	PARC	2014
13	5002 T	JARC	2014	38	Tgx-1935-10F	PARC	2014
14	JM-HAR/ALM-15-SB	JARC	2016	39	Tgx-2004-3F	PARC	2016
15	T34-15-T74-16-SE1	JARC	2014	40	Tgx-1448-2F	PARC	2016
16	T34-15-T72-16-Sc1	JARC	2014	41	Tgx-2010-3F	PARC	2016
17	JM-ALM/H3-15-SB-2	JARC	2016	42	Tgx-1990-78F	PARC	2013
18	JM-PR142/CLK-15-SE	JARC	2016	43	Tgx-1989-19F	PARC	2013
19	PB-12-1	PARC	2012	44	Tgx2008-2F	PARC	2016
20	PB-12-2	PARC	2012	45	Tgx-2007-11F	PARC	2016
21	PB-12-3	PARC	2012	46	TgX-19-87-68F	PARC	2014
22	PB-12-4	PARC	2012	47	Tgx-2006-3F	PARC	2016
23	PB-12-5	PARC	2012	48	Tgx-2010-12F	PARC	2014
24	PB-12-6	PARC	2012	49	Tgx-2010-11F	PARC	2014
25	PB-12-7	PARC	2012				

### 2.3. Data Collection and Measurements

Data were collected on plot basis and plant basis from the central two rows for all parameters. For on plant basis data were collected; ten plants were randomly taken and tagged from the net harvestable plots and the mean value of these ten plants was calculated by using Micro soft Excel. The yield and yield component data were collected on plant basis and plot basis on locations was described as follows.

Data on days to 50% flower initiation, days to maturity, oil content (percentage), 100 seed weight (g) and grain yield (Kg ha<sup>-1</sup>) were recorded on plot bases. Plant height (cm), Branch per plant (cm), number of pod per plant, number of seed per pod, total number of seeds per plant, fresh weight of biomass (g), dry weight of the plant (g), number of primary braches per plant, number of pods per primary branches per plant, number of seeds per primary branches per plant, pod length (cm), number of nodules per plant, were recorded from plant basis according to the random sampling methods [9]. All the data were collected from the middle two harvestable rows.

The amount of oil content was determined in the laboratory of Oil Seeds Research at Holetta agricultural research center (HARC) using a non-destructive method utilizing nuclear magnetic resonance (NMR). A 25g sample of seeds was dried in an oven for 3 hours at 78 °C and cooled for 3 hours. The oil content of the seeds was then determined using a nuclear magnetic resonance machine on a 22g working sample.

### 2.4. Data Analyses

#### Analysis of Variance

All the data recorded were subjected to analysis of variance (ANOVA) and the mean separation was tested by using Least Significant Difference (LSD) at 5% probability levels as per the method of Gomez and Gomez [10] using SAS 9.3 software.

The model for lattice design

$$Y_{ij} = \mu + \alpha + \beta_j + p_j + y_l + \varepsilon_{ij}; \text{ where}$$

$\mu$  = grand mean  $r_i = i$  treatment effect,  $\beta_j$  block effect

(nested with in replication),  $p_j = j$  replication effect,  $y_l$  = effect of 1 level of intra block error and  $\varepsilon_{ij}$  = error term.

Association of Characters

Phenotypic and genotypic correlation

Both phenotypic and genotypic correlation coefficients, which is the inherent association between two variables were estimated using the standard procedure suggested by [11] using the corresponding variance components as shown in Equation below.

$$\text{Phenotypic correlation coefficient (r}_{pxy}) = \frac{\sigma_{pxy}}{\sqrt{\sigma^2_{px} \sigma^2_{py}}}$$

Where  $r_p$  = phenotypic correlation coefficient.  $\text{Cov}(x,y)$  = phenotype co-variance between variable x and y,  $\sigma^2_{px}$  = phenotype variance for variable,  $\sigma^2_{py}$  = phenotype variance for variable y.

$$\text{Genotypic correlation coefficient (r}_{gxy}) = \frac{\sigma_{gxy}}{\sqrt{\sigma^2_{gx} \sigma^2_{gy}}}$$

Where  $r_g$  = genotypic correlation coefficient,  $\text{Cov}(x,y)$  = genotype co-variance between variance x and y,  $\sigma^2_{gx}$

Correlation value ( $r = 1$ ) implies perfect (100%) correlation, where both traits vary hand in hand  $r = -1$  means there is 100 % correlation between two characters, but they vary in opposite direction, and  $r = 0$  implies that there is no correlation at all between the two characters.

## 2.5. Path Coefficient Analysis

Path coefficient analysis was done as suggested by Wright [12] and worked out following Dewey and Lu [13] using the phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of yield components on grain yield following relationship as follow.

$$R_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where,  $r_{ij}$  = mutual association between the independent character i (yield- related trait) and dependent character j (grain yield) as measured by the genotypic correlation coefficient;  $P_{ij}$  = components of direct effects of the independent character (i) on the path coefficient; and  $\sum r_{ik} P_{kj}$  = summation components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent.

The contribution of the remaining unknown factor was measured as the residual factor. This was calculated as: residual effect =  $\sqrt{1 - R^2}$ , where  $R^2 = \sum p_{xy} r_{xy}$ .

## 3. Results and Discussion

### 3.1. Genotypic Correlation Coefficient

The result shows that the genotypic correlation's magni-

tude surpasses that of the phenotypic correlation, suggesting a significant inherent association among different traits and a robust genetic linkage between them. In line with [14]. The majority of traits evaluated showed greater genotypic correlation coefficients [15]. The results reveal that the phenotypic correlation is inferior to the genotypic correlation, signifying a greater contribution of genetic factors compared to environmental factors to the variations among the studied materials.

Genotypic correlation coefficients between soybean grain yield and its related traits are presented in (Table 2). In the present study, grain yield showed positive and highly significant ( $p < 0.01$ ) genotypic correlation coefficients with plant height (0.34), number of branches per plant (0.47), number of pods per plant (0.64), number of total seeds per plant (0.57), fresh weight (0.44), pod length (0.49), number of primary branches (0.47), number of pod per primary braches per plant (0.53) and 100 seed weight (0.50).

Similarly, positive and significant genotypic correlation coefficients ( $P < 0.05$ ) of grain yield with plant height (0.34), dry weight (0.24), and oil content (0.27) was recorded. It agreement with who reported grain yield correlated with oil content by [16]. In the same way, number of pods per plant, number of primary braches per plant (0.47), showed positive and significant genotyping correlation with yield in soybean has been reported by [17], total number of seed per plant, number of branch per plant and hundred seed weight by [18]. Days to flowering showed highly significant positive genotypic correlation with plant height (0.56) with grain yield and highly significant negative genotypic correlation with number of seed per pod (-0.52) and plant pod length (-0.37) with yield. Similarly negative correlations of days to flowering with grain yield in soybean have been reported by Akramet et al. [18] and Faisal et al. [19], Number of branch showed positive and highly significant associations with number of primary braches per plant (1.0) and correlation with number of pods per primary branches per plan (0.82), number of seeds per primary branches per plant (0.80), fresh weight of biomass (0.43), total number of seed per plant (0.66), number of pod per plant (0.6) and yield (0.47) and significant genotypic correlation with dry weight (0.35), pod length (0.30) and number of seeds per pod (0.27). Total number of seed per plant showed positive and highly significant genotypic correlation (0.57) with grain yield, and also highly significant genotypic correlation with highly significant genotypic correlation with number of seed per primary branches per plant (0.87), number of pods per primary branches per plant (0.79) and number of primary branch.

### 3.2. Phenotypic Correlation Coefficient

Phenotypic correlation coefficients among yield related component are presented in (Table 2). Traits such as plant height (0.34), number of branch per plant (0.41), number of

pod per plant (0.62), total number of seed per plant (0.57), fresh weight of biomass (0.44), pod length (0.42), number of primary braches per plant, (0.41), number of pods per primary branches per plant (0.52) and number of seeds per primary branches per plant, (0.51), hundred seed weight (0.45) showed positive and highly significant ( $P < 0.01$ ) phenotypic

correlation coefficient with soybean grain yield. On the other hand, dry weight (0.25) and oil content had positively significant phenotypic correlation coefficient ( $r_p$ ) with grain yield. In agreement with this result, positive and significant correlation of number of pods with grain yield has been reported [20, 17].

**Table 2.** Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients at Assosa in 2020/2021.

Variable	DF	DM	PH	NBPP	NSPP	NPPP	TNSPP	NDN	FWT
DF	1.00	0.69**	0.52**	-0.07ns	-0.45**	-0.07ns	-0.04ns	-0.13	0.17*
DM	0.70**	1.00	0.68**	0.02ns	-0.43**	0.05ns	0.07ns	-0.04ns	0.24*
PH	0.56**	0.71**	1.00	0.21*	-0.34	0.23*	0.17ns	0.06ns	0.39**
NBPP	-0.06	0.07ns	0.16	1.00	0.26*	0.68**	0.62**	0.17ns	0.37**
NSPP	-0.51**	-0.48**	-0.40**	0.27*	1.00	0.13ns	0.13ns	-0.01ns	-0.05
NPPP	-0.06ns	0.07ns	0.20ns	0.6**	0.11ns	1.00	0.88**	0.23*	0.38**
TNSPP	-0.03ns	0.08ns	0.15ns	0.66**	0.12ns	0.89**	1.00	0.35**	0.24*
NDPP	-0.15ns	-0.03ns	0.05ns	0.18ns	-0.02ns	0.22ns	0.35*	1.00	0.09ns
FWT	0.18ns	0.25	0.39*	0.43**	-0.08ns	0.39**	0.23ns	0.08ns	1.00
DWT	-0.02ns	-0.02ns	-0.04ns	0.35*	0.17ns	0.24ns	0.2ns	-0.02	0.55**
PLTH	-0.37**	-0.17ns	0.06ns	0.30*	0.33*	0.12ns	0.13ns	0.01ns	0.24ns
NPB	-0.06ns	0.07ns	0.16ns	1**	0.27*	0.70**	0.66**	0.18ns	0.43**
NPPBR	-0.09ns	0.03ns	0.01ns	0.82**	0.20ns	0.87**	0.79**	0.17ns	0.41**
NSPPBP	-0.11ns	-0.01ns	-0.04ns	0.80**	0.25*	0.86**	0.87**	0.25*	0.33*
OILC	-0.41**	-0.22ns	-0.09ns	0.21ns	0.37*	0.14ns	0.08ns	-0.08ns	0.13ns
HSWT	-0.20ns	0.01ns	0.14ns	0.03ns	0.14ns	0.17ns	-0.09ns	-0.22ns	0.36*
SYtph	-0.06ns	0.11ns	0.34*	0.47**	0.12ns	0.64**	0.57**	0.15ns	0.44**

  

Variable	DWT	PLTH	NPB	NPPBR	NSPPBP	OILC	HSWT	SYtph
DF	-0.02ns	-0.34**	-0.07ns	-0.09ns	-0.11ns	-0.36**	-0.15ns	-0.06ns
DM	-0.02ns	-0.17	0.02ns	0.01ns	-0.01ns	-0.21	0.04ns	0.11ns
PH	-0.02ns	0.09ns	0.21ns	0.05ns	-0.01ns	-0.06ns	0.15ns	0.34**
NBPP	0.31**	0.29**	1**	0.77**	0.72**	0.27*	0.07ns	0.41**
NSPP	0.15ns	0.26*	0.2*	0.20*	0.23*	0.34**	0.07ns	0.11ns
NPPP	0.24*	0.16ns	0.68**	0.87**	0.85**	0.17ns	0.18ns	0.62**
TNSPP	0.20*	0.14ns	0.62**	0.79**	0.86**	0.10ns	0.01ns	0.57**
NDPP	-0.01ns	0.03ns	0.17ns	0.18ns	0.25	(-0.0ns	-0.19*	0.15ns
FWT	0.55**	0.22*	0.37**	0.40**	0.33**	0.12ns	0.32**	0.44**
DWT	1.00	0.27*	0.31**	0.35**	0.29**	0.23*	0.41**	0.25*
PLTH	0.29*	1.00	0.29**	0.18*	0.18*	0.30**	0.35**	0.42**
NPB	0.35*	0.30*	1.00	0.77**	0.72**	0.2*	0.07ns	0.41**

Variable	DWT	PLTH	NPB	NPPBR	NSPPBP	OILC	HSWT	SYtph
NPPBR	0.35*	0.17ns	0.82**	1.00	0.94**	0.20*	0.15ns	0.52**
NSPPBP	0.30*	0.17ns	0.80**	0.96**	1,00	0.19*	0.07ns	0.51**
OILC	0.27ns	0.44**	0.21ns	0.18ns	0.19ns	1,00	0.21*	0.25*
HSWT	0.46**	0.44**	-0.03ns	0.14ns	0.06ns	0.24*	1,,00	0.45**
SYtph	0.24*	0.49**	0.47**	0.53**	0.52**	0.27*	0.50**	1,00

DF=days to flower, DM=days to maturity, PH=plant height, NBPP = number of branch per plant, NSPP=number of seeds per pod, NPPP=number of pod per plant, TNSPP=.total number of seed per plant, NDPP= number of nodule per plant, FWT= fresh weight of biomass, DWT=dry weight, PLTH= pod length, NPB=number of primary braches per plant, NPPBR=number of pods per primary branches per plant, NSPPBP=number of seeds per primary branches per plant, OILC=oil content, HSWT= hundred seed weight, SYTPH=seed yield tone per hecta

### 3.3. Path Coefficient Analysis

Path Coefficient Analysis was used to determine the inter-relationship between grain yield and other yield attributes. It was used to investigate both direct and indirect effects. This technique provides knowledge that aids in indirect selection for genetic yield improvement and tests the relative value of each trait. Eleven traits were chosen as casual (independent) variables in this experiment, and genotypic and phenotypic associations were partitioned into direct and indirect effects using grain yield as a dependent variable. The direct and indirect impact of traits under consideration on grain yield, both phenotypic and genotypic levels.

### 3.4. Genotypic Direct and Indirect Effects

The genotypic direct and indirect effects of various traits on soybean grain yield were analyzed (Table 3). Among the traits studied, such as total number of seeds per plant (0.94), number of pods per primary branches per plant (0.85), and hundred seed weight (0.37), showed strong positive impacts and high correlation coefficients with grain yield. This sug-

gests that directly selecting for these traits would be advantageous for improving soybean yields. On the other hand, traits like fresh weight of biomass, pod length, and oil content had secondary importance direct effects on grain yield, with coefficients of 0.32, 0.26, and 0.1, respectively.

Previous research by scholars including [21-23] has also reported positive and direct effects of the number of pods on soybean grain yield. Similarly, [7] found high and positive direct effects of the number of seeds, fresh weight of biomass, and hundred seed weight on soybean grain yield. In addition, some traits showed negative direct effects on grain yield, such as the number of seeds per primary branches per plant (-0.89), dry weight (-0.36), number of pods per plant (-0.16), and number of primary branches per plant (-0.12).

The indirect effect of plant height characters through total number of seed per plant, dry weight, pod length and number of primary branch was less effect on seed yield. The maximum positive indirect effect was exerted by total number of seeds per plant, through number of primary branches per plant, number of pod per primary braches per plant and Number of seeds per primary branches per plant had positive and highly significant genotypic correlation with seed yield.

**Table 3.** Direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of traits on seed yield of 49 soybean genotypes.

Traits	PH	NPPP	TNSPP	FW	DWT	PL	NPB	NPPBR	NSPPBP	OILC	HSW
PH	0.07	-0.01	0.03	0.11	0.03	-0.01	0.00	-0.11	0.17	-0.01	0.00
NPPP	0.00	-0.16	0.82	0.11	-0.08	-0.01	-0.08	0.73	-0.75	0.02	0.00
TNSPP	0.00	-0.14	0.94	0.06	-0.06	-0.01	-0.07	0.64	-0.75	0.01	-0.06
FW	0.02	-0.06	0.19	0.32	-0.19	0.04	-0.04	0.34	-0.29	0.01	0.09
DWT	0.00	-0.04	0.16	0.17	-0.36	0.07	-0.04	0.3	-0.24	0.03	0.17
PL	0.00	0.01	-0.04	0.04	-0.09	0.26	-0.03	0.04	-0.05	0.04	0.11
NPB	0.00	-0.11	0.57	0.11	-0.11	0.06	-0.12	0.68	-0.7	0.02	-0.07
NPPBR	-0.01	-0.14	0.71	0.13	-0.13	0.01	-0.09	0.85	-0.85	0.02	0

Traits	PH	NPPP	TNSPP	FW	DWT	PL	NPB	NPPBR	NSPPBP	OILC	HSW
NSPPBP	-0.01	-0.14	0.79	0.1	-0.1	0.02	-0.09	0.81	-0.89	0.02	-0.04
OILC	-0.01	-0.03	0.1	0.04	-0.09	0.1	-0.02	0.19	-0.18	0.1	0.08
HSW	0.00	0.00	-0.16	0.08	-0.17	0.08	0.02	-0.01	0.09	0.02	0.37
Residual	0.26										

### 3.5. Phenotypic Direct and Indirect Effects

The phenotypic direct and indirect effects of traits on grain yield are presented in (Table 4) Traits viz total number of seed per plant (0.51), hundred seed weight (0.33), pod length (0.22) - fresh weight of biomass (0.21) number of pods per primary branches per plant (0.12), plant height (0.10) and oil content (0.10) showed higher phenotypic direct effects on soybean grain yield [24]. Reported the highest phenotypic direct effect of hundred seed weight on seed yield per hectare which is in agreement with our study. The authors also reported high direct effect of seed yield per plant on seed yield per hectare in line with this study. The indirect effect of plant height characters through dry weight, and number of seed per primary branch per plant was less effect on seed yield.

The maximum positive indirect effect was exerted by total number of seeds per plant, through number of pod per plant,

number of pod per primary braches per plant and Number of seeds per primary branches per plant had positive and highly significant phenotypic correlation with seed yield. Other scholars also reported indirect effects of number of branch per plant on seed yield [25, 24].

In essence, the traits directly impacting grain yield are crucial for seed production in soybean breeding programs. These traits should be considered as selection criteria due to their significant influence on seed yield. Specifically, traits like plant height, pod numbers, fresh weight, pod length, number of pod per primary branch per plant, oil content and hundred seed weight are positively correlate with seed yield and should be prioritized for improvement through selection methods. Analysis of genotypic and path coefficients helps identify these influential traits, guiding selection pressure towards enhancing seed yield. The residual factors of genotypic and phenotypic path coefficient analysis were found to be 0.26 and 0.36, respectively.

**Table 4.** Direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of 49 soybean genotypes.

Traits	PH	NPPP	TNSPP	FW	DWT	PL	NPB	NPPBR	NSPPBP	OILC	HSW
PH	0.10	0.02	0.09	0.08	0.00	0.02	-0.03	0.01	0.00	-0.01	0.05
NPPP	0.02	0.09	0.45	0.08	-0.04	0.03	-0.09	0.11	-0.11	0.02	0.06
TNSPP	0.02	0.08	0.51	0.05	-0.03	0.03	-0.08	0.10	-0.11	0.01	0.00
FW	0.04	0.03	0.12	0.21	-0.09	0.05	-0.05	0.05	-0.04	0.01	0.11
DWT	0.00	0.02	0.10	0.12	-0.17	0.06	-0.04	0.04	-0.04	0.02	0.13
PL	0.01	0.01	0.07	0.05	-0.05	0.22	-0.04	0.02	-0.02	0.03	0.11
NPB	0.02	0.06	0.31	0.08	-0.05	0.06	-0.13	0.09	-0.09	0.03	0.02
NPPBR	0.01	0.08	0.40	0.09	-0.06	0.04	-0.10	0.12	-0.12	0.02	0.05
NSPPBP	0.00	0.08	0.44	0.07	-0.05	0.04	-0.09	0.12	-0.13	0.02	0.03
OILC	-0.01	0.02	0.05	0.03	-0.04	0.06	-0.03	0.02	-0.02	0.10	0.07
HSW	0.02	0.02	0.01	0.07	-0.07	0.08	-0.01	0.02	-0.01	0.02	0.33

Residual 0.36

DF=days to flower, PH=plant height (cm), NBPP =. number of branch per plant, NSPP=number of seeds per pod, NPPP= number of pod per plant, TNSPP=.total number of seed per plant, NDPP=number of nodule per plant, FWT= fresh weight of biomass, DWT (gm) =dry weight (gm), PLTH=pod length (cm), NPB=number of primary braches per plant, NPPBR= number of pods per primary branches per plant, NSPPBP= numberof seeds per primary branches per plant, OILC=oil content, HSWT= hundred seed weight (gm), SYTPH=seed yield tone per hectare.

## 4. Conclusions

In this study, it was found that there is notable genetic variability among the examined genotypes across various traits. Consequently, to enhance soybean grain yield and related characteristics effectively, a greater focus should be placed on traits like as total number of seeds per plant, number of pods per primary branch per plant and hundred seed weight. These traits exhibited favorable correlations, both phenotypically and genotypically, and demonstrated significant direct and indirect impacts on grain yield. Therefore, prioritizing these traits in breeding efforts could lead to substantial improvements in soybean yield.

## Author Contributions

**Wakjira Getachew Fufa:** Conceptualization, Data curation, Formal Analysis, Methodology, Software, Writing – original draft, Writing – review & editing

**Bulcha Weyessa:** Supervision, Visualization

## Conflicts of Interest

The authors declare no conflicts of interest.

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