



RESEARCH ARTICLE

Kirkuk University Journal for Agricultural Sciences

ISSN:2958-6585

<https://kujas.uokirkuk.edu.iq><https://doi.org/10.58928/ku26.17203>

Correlations and Path Coefficient Analysis Between Yield and Related Traits for a Set of Soybean Genetic Compositions

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Received: 26/03/2026

Revised: 20/04/2026

Accepted: 23/05/2026

Published: 07/06/2026

ABSTRACT

Soybean (*Glycine max* L. Merrill) is one of the most important oilseed and grain-legume crops worldwide, and is represents a promising crop in Iraq. A field experiment was conducted in the field of the Technical College / Al-Mussaib Technical College during the 2025 growing season using a randomized complete block design with three replicates. The objective of this study was to evaluate genotypic, phenotypic, and environmental correlations among yield and related traits in five soybean genotypes and to determine their direct and indirect effects on seed yield using path coefficient analysis. The results revealed significant genetic variability among the studied genotypes. Environmental correlations were generally weak and non-significant, indicating limited environmental influence on trait relationships. In contrast, genotypic correlations were strong and significant, suggesting that genetic factors predominantly control these associations. Seed yield showed strong positive genotypic correlations with dry matter weight, Pod number, number of seeds per pod, harvest index and protein percentage. achieved highest positive genetic correlation coefficients with yield; the highest of them was the correlation of dry matter weight with total yield, amounting to 0.985, whereas the highest negative correlations were recorded with the number of pods and the number of seeds per pod. The values of phenotypic correlation coefficients were moderate to high but they were lower than the values of genetic correlations and in the same direction. Path coefficient analysis demonstrated that dry matter weight had the highest positive direct effect on yield, followed by protein percentage, Pod number contributed indirectly to yield mainly through its association with dry matter weight and protein percentage. Conversely, oil percentage exhibited an overall negative relationship with yield due to its adverse indirect effects. These findings indicate that dry matter weight and protein percentage can be considered reliable selection criteria for improving soybean yield in breeding programs.

Keywords: Soybean; genetic correlation; path coefficient analysis; yield components; plant breeding.

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INTRODUCTION

Soybean (*Glycine max* L. Merrill) is one of the oldest legume crops known to humans [1]. Due to its high nutritional value, it is among the most important grain legumes worldwide. Soybean seeds are characterized by a high protein content (approximately 40–42%), together with 18–22% oil, about 30% carbohydrates, and around 5% mineral substances, in addition to various vitamins, resulting from the high protein content of its seeds (40–42) % and (18–22) % fats, 30% carbohydrates, 5% mineral substances, and many vitamins [2]. Because of its industrial, nutritional, and feed importance, soybean has become one of the most economically important crops globally with a large economic return worldwide. Its nutritional importance comes from the high quality of its protein, which contains most of the essential and necessary amino acids required for human and animal nutrition and growth [3]. Soybean oil is characterized by a high proportion of 85% unsaturated fatty acids (approximately 85% and being free of cholesterol [4]. In addition to its use for human consumption and industrial products, soybean is widely utilized in animal production systems. It is used as green forage, hay, or silage for animals or its seed meal is incorporated as a primary ingredient in animal feeds [5].

The soybean plant is also considered a natural source of bioactive compounds including various phenolic compounds and antioxidants. In addition, soybean cultivation contributes to improving soil properties and increasing soil fertility through biological nitrogen fixation [6]. However, soybean cultivation in arid and semi-arid regions, including Iraq, faces several challenges [7]. Previous studies conducted on soybean have shown that grain yield and yield-related traits that affect yield differ depending on genetic factors and environmental conditions [8]. Therefore, identifying high-yielding cultivars with high

economic value is very important. Grain yield is a highly complex trait and very important for plant breeders, and detecting relationships among traits is necessary in breeding programs [9].

Correlation studies enable the breeder to know the strength of the relationship among different traits, in addition to estimating the magnitude and direction of the expected changes during the selection process. Correlation and path coefficient analyses [10; 11], also contribute to helping select traits whose direct selection leads to the improvement of complex traits such as yield. Correlation coefficients are used to study the interrelationships among plant traits and identify traits influencing production that can be utilized in breeding programs to improve production [12]. The path coefficient is the partial regression coefficient, splitting the correlation of a set of independent variables with the dependent variable into direct and indirect effects. Understanding the genetic basis of important traits in soybean and their interactions with diverse environments is of great importance for developing appropriate breeding strategies and effective agricultural practices to improve soybean and its cultivation [13]. Jawad et al. (2025) found that soybean genetic compositions differ in their performance and in their vegetative and productive traits in the middle Euphrates region [14]. This present study aims to evaluate the relationships among yield and its components in soybean genotypes and to identify the most important traits contributing to yield improvement under Babylon conditions.

Materials And Method

A field experiment was conducted during the 2025 growing season at Al-Mussaib Technical College in Babylon governorate. The experiment was arranged in a randomized complete block design (RCBD) with three replicates to evaluate the performance of five soybean genotypes: Warka, Andalus, Rami, Shima and Yamasawya.

The experimental field was prepared by plowing, soil pulverization, and leveling. Each experimental plot consisted of 4 m in length, with 75 cm spacing between rows and 25 cm between plants. Standard agronomic practices were applied uniformly, resulting in 64 plants per experimental unit, and a plant density of 53,333 plants per hectare [15]. The experimental field was fertilized with nitrogen in the form of urea (46% N) at a rate of 160 kg N ha⁻¹, applied in two splits: the first at planting and the second during flowering. Triple superphosphate fertilizer (46% P₂O₅) was added at once at a rate of 80 kg P₂O₅ ha⁻¹ before planting (Ali, 2012). All crop management practices were carried out according to recommended guidelines, and irrigation was applied based on plant needs. The following traits were investigated: dry matter (g plant⁻¹), number of pods per plant (pod plant⁻¹), number of seeds per pod (seed pod⁻¹), 100-seed weight (g), biological yield (t ha⁻¹), harvest index (%), protein percentage (%), oil percentage (%), and seed yield (t ha⁻¹).

Statistical and genetic analysis

Statistical analysis:

The data for the studied traits were statistically analyzed according to the procedures for a randomized complete block design. Arithmetic means were compared using the least significant difference (LSD) test at a 5% probability level to identify significant differences between the varieties.

Estimation of Correlation Coefficients: The genotypic and phenotypic correlation coefficients between grain yield and various yield-attributing traits was determined with the following formula:

Genetic and Phenotypic covariance are basis for estimation of genetic and phenotypic correlation coefficient [16].

$$r_{Pxy} = \frac{\text{cov.}P_{xy}}{\sqrt{(\sigma^2 P_x)(\sigma^2 P_y)}}$$

$$r_{Gxy} = \frac{\text{cov.}G_{xy}}{\sqrt{(\sigma^2 G_x)(\sigma^2 G_y)}}$$

Where: x and y = studied traits

$\sigma^2 P$ and $\sigma^2 G$ represent phenotypic and genotypic variance, respectively.

cov.P and cov.G represent phenotypic and genotypic covariance, respectively.

r_{Pxy} and r_{Gxy} represent phenotypic and genotypic correlations, respectively.

The significance of the correlation coefficients was determined according to the critical values of the r-table as provided in the OPSTAT software analysis.

Estimate for Genotypic Path Coefficient Analysis

Once the genotypic correlation among the traits studied was confirmed, genotypic path coefficient analyses were performed [17; 18]. The causal model for the relationships between the variables is shown in Fig. 1 (Figure 1)

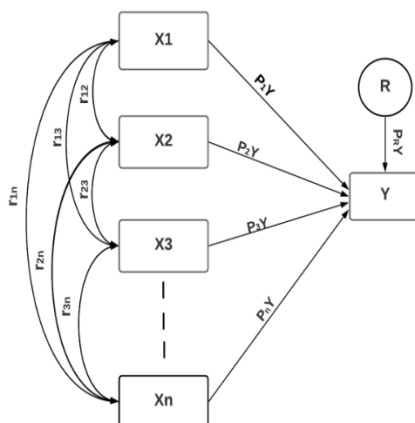


Figure1. Path coefficient diagram depicting interrelationships among traits.

Calculating the matrix first led to calculating the values of the path coefficient:

$$\begin{bmatrix} p_{x1y} \\ p_{x2y} \\ \cdot \\ \cdot \\ \cdot \\ p_{x10y} \end{bmatrix} = \begin{bmatrix} 1 & r_{x1x2} & \dots & r_{x1x10} \\ r_{x2x1} & 1 & \dots & r_{x2x10} \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ r_{x10x1} & r_{x10x2} & \dots & 1 \end{bmatrix} \times \begin{bmatrix} r_{x1y} \\ r_{x2y} \\ \cdot \\ \cdot \\ \cdot \\ r_{x10y} \end{bmatrix}$$

Using a computer to solve the matrix, the path coefficient estimates were computed by means of the method proposed by [19]. Furthermore, in order to test the significance of both direct and indirect effects, we also used the scale developed by [20].

Results

1- Correlation coefficients

1-1 Environmental correlation

The environmental correlation matrix presented in Table 1 showed that most correlation coefficients among the studied traits were non-significant (NS), ranging from weak positive to negative values. This suggest that environmental factors did not exert a strong common influence on the expression of these traits. Dry matter weight showed a positive, non-significant environmental correlation with most traits, with the highest coefficients recorded for pod number and harvest index ($r=0.440$ and 0.419 , respectively). This trait also showed a negative, non-significant environmental correlation for 100-seed weight, reaching -0.425 , indicating that environmental changes affecting dry matter weight did not necessarily influence the other traits simultaneously. The characteristic of the number of pods was positively correlated with the number of seeds in the pod (0.557), which indicates that there is a limited common environmental impact between these two traits, whereas the remaining environmental correlations were weak and non-significant. The number of pods trait recorded the highest highly significant positive environmental correlation with oil percentage, reaching 0.661 ; nevertheless, its correlations with the other traits remained non-significant, which indicates that this environmental effect is specific to these two traits only. The characteristic of the weight of 100-seed showed a non-significant positive environmental correlation with oil percentage and biological yield, and the same trait showed a non-significant negative environmental correlation with plant yield, harvest index, and protein percentage. The characteristic of the plant yield recorded a negative high-significance environmental correlation with the oil percentage ($r=-0.678$), and the characteristic was also associated with a positive high-significance environmental correlation with the biological yield of 0.670 . It also showed a highly significant positive environmental correlation with biological yield, reaching 0.670 . The harvest index was found to have a significant positive environmental correlation with protein percentage at 0.547 . Oil percentage correlated positively, but non-significantly, with protein percentage and negatively, but non-significantly, with biological yield. Protein percentage also showed a positive, non-significant environmental correlation with biological yield ($r=0.299$). Environmental correlations were generally low, suggesting limited environmental influence on trait associations.

Table 1. Values of environmental correlations coefficients of nine agronomic characters of soybean genotypes

Traits	X1	X2	X3	X4	X5	X6	X7	X8
X1								
X2	0.440NS							
X3	0.218NS	0.557*						
X4	-0.425NS	0.345NS	0.418NS					
X5	0.348NS	0.094NS	-0.402NS	-0.128NS				
X6	0.419NS	-0.065NS	0.416NS	-0.279NS	-0.385NS			
X7	-0.166NS	0.300NS	0.661**	0.404NS	-0.678**	0.073NS		
X8	0.334NS	0.005NS	0.306NS	-0.315NS	-0.247NS	0.547*	0.479NS	
X9	0.265NS	0.211NS	0.126NS	0.224NS	0.670**	-0.025NS	-0.121NS	0.299NS

X1= Dry matter weight, X2=Number of pods, X3= Number of seeds per pod, X4= Weight of 100 seeds, X5= Plant yield, X6= Harvest index, X7= Oil percentage, X8= Protein percentage, X9= Biological yield.

1-2 Genotypic Correlations

The results of the genotypic correlation in Table 2 showed very high and significant genotypic correlations at the 1% level between most traits, reflecting strong common genetic control. It is evident that dry matter weight recorded very high positive genotypic correlations with pod number, number of seeds in the pod, the plant yield, the harvest index, and protein (%), the highest being with plant yield, reaching 0.985. The trait also recorded highly significant negative genotypic correlations with oil percentage and biological yield, reaching -0.887 and -0.880, respectively.

A high significant positive genotypic correlation was observed between pod number and a number of important traits such as, number of seeds in pod, the plant yield, the harvest index and protein %. The maximum value was in pod number at 0.951. The trait showed a perfect negative correlation with oil percentage, with correlation coefficient of -0.935. It also showed a very strong negative genotypic correlation with biological yield, with a coefficient of -0.993.

The number of seeds per pod showed a highly significant positive genotypic correlation with seed yield per plant, harvest index, and protein percentage, with the strongest correlation observed for protein percentage ($r = 0.996$). In contrast, it showed a highly significant negative genotypic correlation with oil percentage and biological yield per plant, with the correlation coefficient reaching -0.996. The genotypic correlation analysis indicated that 100-seed weight was only weakly correlated with the other studied, and all of these correlations were statistically non-significant. It showed weak, non-significant positive genotypic correlation with biological yield, oil percentage, and total yield, and weak non-significant negative genotypic correlation with harvest index and protein percentage. These results suggest that 100-seed weight is relatively independent of the other traits studied. Therefore, its value in indirect selection appears limited as genetic improvement in this trait may not necessarily lead to corresponding changes in the other traits.

The Table 2 indicates that plant yield showed a highly significant positive genotypic correlation with harvest index and protein percentage, with correlation coefficients of 0.868 and 0.933, respectively. The same trait also showed a highly significant negative genotypic correlation with oil percentage and biological yield, with coefficients of -0.924 and -0.913, respectively. Harvest index exhibited a significant positive genetic correlation with protein percentage ($r=0.979$), and highly significant negative genetic correlations with oil percentage and biological yield, with coefficients of -0.927 and -0.977, respectively. Oil percentage showed a very strong positive genotypic correlation with the biological yield of the plant ($r=0.988$ and a highly significant negative genotypic correlation with protein percentage ($r=-0.934$). Genotypic correlation of protein percent was found to be significant and negatively associated with biological yield ($r=-0.977$). In general, genotypic correlations were higher than phenotypic correlations, indicating that genetic factors played a major role in determining relationships among the studied traits.

Table 2. Values of genotypic correlations coefficients of nine agronomic characters of soybean genotypes

Traits	X1	X2	X3	X4	X5	X6	X7	X8
X1								
X2	0.884**							
X3	0.926**	0.951**						
X4	-0.030NS	-0.152NS	-0.043NS					
X5	0.985**	0.934**	0.988**	0.060NS				
X6	0.861**	0.881**	0.957**	-0.383NS	0.868**			
X7	-0.887**	-0.985**	-0.979**	0.152NS	-0.924**	-0.927**		
X8	0.911**	0.863**	0.996**	-0.188NS	0.933**	0.979**	-0.934**	
X9	-0.880**	-0.993**	-0.996**	0.232NS	-0.913**	-0.977**	0.988**	-0.977**

X1= Dry matter weight, X2=Number of pods, X3= Number of seeds per pod, X4= Weight of 100 seeds, X5= Plant yield, X6= Harvest index, X7= Oil percentage, X8= Protein percentage, X9= Biological yield.

1-3 Phenotypic Correlations

Phenotypic correlation coefficients ranged from moderate to high and were in the same direction as the genotypic correlations, although their magnitudes were generally lower, likely due to environmental effects. Table 3 shows that dry matter weight had highly significant positive phenotypic correlation with pod number, number of seeds per pod, biological yield, harvest index, and protein percentage, with the highest correlation observed for plant yield ($r=0.983$). In contrast, the dry matter weight was negatively correlated with oil percentage and plant biological yield.

Pod number exhibited strong positive phenotypic correlation with number of seeds per pod, plant yield, harvest index, and protein percentage, with the strongest association observed for number of seeds per pod ($r=0.778$). In contrast, also it was negatively correlated with oil percentage and biological yield. The results clarified that the number of seeds per pod was significantly positively correlated with plant yield, harvest index, and protein percentage, with the highest correlation recorded for protein percentage ($r=0.894$). It was also significantly negatively correlated with oil percentage and biological yield, with coefficients of -0.828 and -0.907 , respectively.

The phenotypic correlation analysis revealed that 100-seed weight was weakly and non-significantly correlated with most of the studied traits, suggesting that its phenotypic contribution under the experimental conditions was limited and that it may not be a reliable direct or indirect selection criterion.

In contrast, plant yield exhibited highly significant positive phenotypic correlation with harvest index and protein percentage ($r=0.865$ and 0.928 , respectively), and significant negative phenotypic correlation with oil percentage and biological yield ($r=-0.865$ and -0.911 , respectively).

Harvest index exhibited a highly significant positive phenotypic correlation with protein percentage ($r=0.976$), whereas it showed a highly significant negative phenotypic correlation with oil percentage and biological yield ($r=-0.891$ and -0.975 , respectively). The table further indicates that oil percentage was positively correlated with biological yield ($r=0.951$), and highly significantly negatively correlated with protein percentage. In addition, protein percentage was negatively correlated with biological yield at the phenotypic level ($r=-0.973$).

Table 3. Values of Phenotypic correlations coefficients of nine agronomic characters of soybean genotypes

Traits	X1	X2	X3	X4	X5	X6	X7	X8
X1								
X2	0.647**							
X3	0.828**	0.778**						
X4	-0.033 ^{NS}	-0.081 ^{NS}	-0.018 ^{NS}					
X5	0.983**	0.663**	0.870**	0.059 ^{NS}				
X6	0.859**	0.619**	0.860**	-0.382 ^{NS}	0.865**			
X7	-0.855**	-0.718**	-0.828**	0.157 ^{NS}	-0.896**	-0.891**		
X8	0.907**	0.608**	0.894**	-0.189 ^{NS}	0.928**	0.976**	-0.885**	
X9	-0.877**	-0.699**	-0.907**	0.231 ^{NS}	-0.911**	-0.975**	0.951**	-0.973**

X1= Dry matter weight, X2=Number of pods, X3= Number of seeds per pod, X4= Weight of 100 seeds, X5= Plant yield, X6= Harvest index, X7= Oil percentage, X8= Protein percentage, X9= Biological yield

2- Path analysis

Path coefficient analysis is considered one of the advanced statistical tools that enable the researcher to estimate both direct and indirect effects of the studied traits and to identify causal relationships. It aims to partition the genotypic correlation coefficients into direct effects and an indirect effect, which allows the identification and selection of the traits that are most efficient in their true effect on total yield. The path coefficient analysis presented in Table 4 showed that dry matter weight had the highest positive direct effect on yield (0.679), highlighting its importance as a selection criterion. The trait also had substantial indirect effects through harvest index, oil percentage, and protein percentage. Among these, protein percentage showed the highest positive indirect effect (0.3283), which contributed to the strong genotypic correlation observed between the trait and yield (0.985).

Pod number contributed indirectly through its association with the other traits. In contrast, the 100-seed weight had a limited negative direct effect on total yield (-0.1360). Its indirect effects through the other traits were weak and inconsistent, resulting in a low and non-significant total genotypic correlation (0.060).

Harvest index showed a slight negative direct effect that is not of importance on total plant yield ($r=-0.0439$). However, the trait had indirect effects on total plant yield through dry matter weight, oil percentage, and protein percentage, and the highest was the effect via dry matter weight, reaching (0.5845). The combination of direct and indirect effects contributed to increase in the genotypic correlation coefficient, which reached 0.868.

Oil percentage showed a negative relationship with yield due to its indirect effects, suggesting that selection for higher oil content may negatively affect yield. Protein percentage recorded a high direct effect on total yield (0.328).

These findings are consistent with previous studies and emphasize the importance of selecting traits with strong direct effects on yield.

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on yield of soybean genotypes

Direct effects							
X1	X2	X3	X4	X5	X6	X7	X8
0.679	-0.011	-0.031	0.136	-0.149	-0.047	0.111	0.328
Indirect effects							
Character 5 vs 1							
X1	X2	X3	X4	X5	X6	X7	X8
0.6786	-0.0099	-0.0287	-0.0040	-0.1283	0.0420	0.1011	0.3283
Character 5 vs 2							
0.5998	-0.0112	-0.0295	-0.0206	-0.1313	0.0538	0.0958	0.7853
Character 5 vs 3							
0.6286	-0.010	-0.0310	-0.0058	-0.1426	0.0503	0.1106	0.0083
Character 5 vs 4							
-0.0201	0.0017	0.0013	0.1360	0.0571	-0.0072	-0.0209	-0.3658
Character 5 vs 6							
0.5845	-0.0099	-0.0297	-0.0521	-0.1490	0.0439	0.1087	0.1032
Character 5 vs 7							
-0.6017	0.0128	0.0330	0.0207	0.1382	-0.0473	-0.1037	0.5832
Character 5 vs 8							
0.6179	-0.0097	-0.0309	-0.0256	-0.1458	0.0442	0.1111	0.6844

Residual: -0.051

Discussion

Environmental correlations were generally weak and of limited significance, indicating that environmental conditions did not exert a strong common influence on the expression of the studied traits and were not the main determinant of the relationships among them. The higher genotypic correlation coefficients compared with the environmental correlation coefficients indicate that genetic factors had a stronger influence on the relationships among the studied traits. This study agrees with what [21], found, as seed yield recorded positive and significant genotypic and phenotypic correlations with pod number and number of seeds per pod. The results show that the phenotypic correlations are lower than the genotypic ones while maintaining the same direction, indicating that the phenotypic expression of the traits highly reflects the genetic makeup, with a limited environmental effect. This reinforces the possibility of relying on phenotypic traits as selection indicators in applied field settings. The results are consistent with those of [22], as the value of phenotypic correlation values were lower than the genotypic correlation values. The extremely low residual value (-0.00051) indicates that the studied traits account for nearly 100% of the genetic variance in yield, reflecting the high efficiency of the path analysis model used. These findings are consistent with the results reported by [23].

Conclusion

The estimates showed genetic factors were predominant in controlling the associations between studied traits, with genotypic correlations higher than phenotypic and environmental ones in most of the cases. Seed yield was significantly and more positively associated with dry matter weight, number of pods, protein (percent), and harvest index, whereas 100-seed weight showed weak and non-significant associations, indicating limited value for selection. Path coefficient analysis indicated that dry matter weight had the highest positive direct effect on yield, followed by protein percentage, but pod number made a great contribution too through strong indirect effects via dry matter weight and protein. In contrast, oil percentage showed overall unfavorable effects on yield due to negative indirect influences, suggesting that selection for higher oil content may reduce yield under these conditions. Accordingly, dry matter weight and pod number, supported by protein percentage, are the most efficient selection criteria for improving soybean yield

Supplementary Materials:

No Supplementary Materials.

Funding:

This research received no external funding.

Institutional Review Board Statement:

The study was conducted following the protocol authorized by the Head of the Ethics Committee, University of Anbar, Iraq Republic.

Informed Consent Statement:

Not applicable.

Data Availability Statement:

Data available upon request.

Conflicts of Interest:

The authors declare no conflict of interest.

Acknowledgments:

The authors are thankful to and the Head of the Plant Production Department, the College of Al-Musayyib Technical , Al-Furat Al-Awsat Technical University , Iraq.

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Conflict Of Interest

The authors declare no conflicts of interest associated with this manuscript.

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تحليل الارتباطات ومعاملات المسار بين المحصول والصفات المرتبطة به في مجموعة من التركيبات الجينية للقول السوداني

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الخلاصة

يُعد فول الصويا (*Glycine max* L. Merrill) من أهم المحاصيل الزيتية والبقولية في العالم، ويُعتبر من المحاصيل الواعدة في العراق. أُجريت تجربة حقلية في حقل الكلية التقنية/المسيب خلال موسم النمو 2025 باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات. هدفت الدراسة إلى تقييم الارتباطات ومعاملات المسار بين عدد من الصفات المورفولوجية والفسولوجية لستة تراكيب وراثية من أنماط فول الصويا، وذلك لتحديد أهم الصفات التي تؤثر بشكل مباشر أو غير مباشر على زيادة إجمالي إنتاجية النبات. أظهرت النتائج تبايناً واضحاً بين التراكيب الوراثية للأنماط المدروسة في صفات إنتاجيتها الخضريّة وإنتاجيتها، مما يعكس اختلافات في استجابتها للظروف البيئية. أشارت النتائج إلى أن معاملات الارتباط البيئي كانت ضعيفة وغير دالة إحصائياً لمعظم الصفات المُقيّمة. في المقابل، أظهرت نتائج الارتباط الوراثي أن صفات وزن المادة الجافة، وعدد القرون، وعدد البذور في القرن الواحد، ونسبة البروتين، ومؤشر الحصاد، حققت أعلى معاملات ارتباط وراثي إيجابي مع المحصول؛ وكان أعلى هذه المعاملات هو ارتباط وزن المادة الجافة بالمحصول الكلي، حيث بلغ (0.985)، بينما سُجلت أعلى معاملات الارتباط السلبي مع عدد القرون وعدد البذور في القرن الواحد. أما بالنسبة لصفة وزن 100 بذرة، فقد كانت الأقل ارتباطاً، حيث أظهرت معاملات ضعيفة وغير دالة إحصائياً. تراوحت قيم معاملات الارتباط الظاهري بين المتوسط والعالية، لكنها كانت أقل من قيم الارتباط الوراثي وفي نفس الاتجاه. أشارت نتائج معامل المسار إلى أن وزن المادة الجافة سجل أعلى تأثير مباشر إيجابي، بلغ (0.679)، يليه تأثير مباشر متوسط لنسبة البروتين (0.328). في المقابل، كان التأثير المباشر لعدد القرون سلبيًا وغير دال إحصائياً، حيث بلغ (-0.011)، ولكنه أظهر تأثيرات غير مباشرة عالية من خلال الصفات الأخرى. على النقيض من ذلك، سجلت صفة نسبة الزيت تأثيرات مباشرة وغير مباشرة سلبية، وبالتالي فهي من بين أقل الصفات ملائمة للاختيار. بناءً على ذلك، نستنتج أن أكثر الصفات فعالية لتحسين المحصول هي نسبة وزن المادة الجافة إلى عدد القرون، ونسبة الزيت.

الكلمات المفتاحية: فول الصويا؛ الارتباط الوراثي؛ تحليل معامل المسار؛ مكونات المحصول؛ تربية النبات.