RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
58 (3) 1008-1018, 2026
http://doi.org/10.54910/sabrao2026.58.3.6
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

GENETIC VARIABILITY AND INHERITANCE OF AGRONOMIC TRAITS IN F_1 AND F_2 POPULATIONS OF SOYBEAN (*GLYCINE MAX* L.)

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SUMMARY

This study sought to investigate the genotypic variability in F_1 and F_2 populations and inheritance of key agronomic traits in soybeans (*Glycine max* L.) derived from diverse parental genotypes. The F_1 hybrids exhibited considerable heterosis and dominance deviations, especially in cross combinations involving parental genotypes Ehtiyoj and To'maris, which consistently cross several traits. In F_2 populations, transgressive segregation appeared frequently, indicating the presence of wide phenotypic diversity and polygenic inheritance. The highest heritability estimates ($h^2 \geq 0.91$) and trait stability in cross combinations like Ehtiyoj × To'maris and Nena × Ehtiyoj suggested their suitability as donor genotypes in soybean breeding programs. The coefficient of phenotypic variation (V%) ranged from 4.8% to 55.9%, observing the highest variability in the seed weight. The 1000-grain weight showed moderate to high genetic control. The results underline the importance of parental genotype selection in breeding and support the integration of high-performing hybrids into future improvement strategies of soybeans.

Keywords: Soybean (*G. max* L.), F_1 hybrids, F_2 populations, heritability, phenotypic variability, transgressive segregation, agronomic traits

Communicating Editor: Dr. Gwen Iris Descalsota-Empleo

Manuscript received: November 11, 2025; Accepted: March 15, 2026.

Citation: Kurbanbaev I, Abdushukirova S, Qulmamatova D, Sanayev N, G'ulomov G, Sobirov F, Yunusova L, Ismoilov I (2026). Genetic variability and inheritance of agronomic traits in f_1 and f_2 populations of soybean (*Glycine max* L.). *SABRAO J. Breed. Genet. 58 (3) 1008-1018. http://doi.org/10.54910/sabrao2026.58.3.6*.

Key findings: The soybean (*G. max* L.) F_2 populations showed wide phenotypic variation and high heritability for key agronomic traits. The populations Ehtiyoj × To'maris and Nena × Ehtiyoj exhibited considerable inheritance for the seed number and weight, indicating valuable potential for selection and high-yielding soybean breeding programs.

INTRODUCTION

The soybean (*Glycine max* L.) crop is one of the most widely cultivated and economically important leguminous crops worldwide (Kurbanbaev *et al.,* 2008; Abdurazakova *et al.,* 2020a). Soybean seeds contain approximately 20% oil and 40% protein, making the crop highly valuable for human and animal nutrition, as well as for various industrial applications (Hakimov *et al.,* 2023; Toshmatov *et al.,* 2024). Improving soybean cultivars to enhance grain yield and tolerance to various stress factors requires the implementation of breeding programs based on comprehensive assessments of genetic diversity (Abdurazakova *et al.,* 2020b; Azimov *et al.,* 2024).

Modern breeding techniques, particularly genetic analysis and hybridization-based studies, offer expanded opportunities to develop high-yielding, stable, and trait-integrated cultivars for considerable improvement in soybeans (Yunuskhanov *et al.,* 2007, 2021; Jabborova *et al.,* 2016; Xu *et al.,* 2022). In this regard, studying the inheritance of economically valuable traits in F_1 and F_2 populations and determining the degree of genetic control of these traits is critically important (Jaynaqov *et al.,* 2022; Khan *et al.,* 2024).

In soybean genotypes, traits such as plant height, the number of pods per plant, the number of seeds per plant, seed weight per plant, and a thousand-grain weight have emerged as key selection indicators. These traits represent major yield components and play a crucial role in assessing yield stability across diverse environmental conditions, as well as in establishing reliable selection criteria for soybean breeding programs (Matniyazova *et al.,* 2023).

F_1 populations enable breeders to evaluate heterotic effects, wherein specific hybrid combinations exhibit superior performance compared with their parental lines. In contrast, F_2 populations showed characteristics of segregation, revealing substantial phenotypic diversity that can have quantitative assessment through estimates of genetic variability, heritability (h^2), and phenotypic coefficient of variation (V%) (Wang *et al.,* 2023).

In soybean hybrid populations, the traits of segregation and variability study enable the identification of promising genotypes for future selection, the evaluation of genetic advantages, and the determination of traits transmissibility across generations. These insights serve as a foundation for developing stable, high-yielding, and environmentally resilient cultivars (Li *et al.,* 2020). Research findings suggested certain traits, such as 1000-grain weight, exhibited relatively stable inheritance and can be favorable as a reliable indicator for early-stage selection. Conversely, the traits, such as pod number and seed weight, tend to exhibit higher phenotypic variability, necessitating intensive selection pressure (Kholikova *et al.,* 2024).

Previous studies have shown the integration of genetically diverse sources can facilitate the development of cultivars with superior genetic potential and stable yield performance (Li *et al.,* 2020). Moreover, early identification of key yield-related traits with high heritability improves selection efficiency and shortens the overall breeding cycle (Wang *et al.,* 2023; Shavkiev *et al.,* 2025). In Uzbekistan, where the soybean cultivation area is expanding each year, the demand for high-yielding, climate-adapted, and agronomically stable soybean genotypes is steadily increasing.

The objectives of this study were to investigate the inheritance patterns, phenotypic variability, segregation behavior, heterosis effects, and heritability coefficients of important agronomic traits in F_1 and F_2 populations derived from crosses among genetically diverse soybean parental lines. Additionally, the study sought to identify promising hybrid combinations for use in future soybean breeding programs. The results will provide a solid scientific basis for national soybean breeding initiatives and have significant practical relevance.

MATERIALS AND METHODS

Experimental site and growing conditions

The soybean field experiments commenced during the growing season of 2024–2025 at the Dormon Scientific Experimental Station, Institute of Genetics and Plant Experimental Biology, Academy of Sciences, Tashkent Region, Uzbekistan (41.32°N, 69.43°E; altitude 498 m). The said region has a sharply continental climate characterized by hot and dry summers and moderately cold winters. The soil type is meadow–alluvial, medium loamy, with 1.2%–1.4% humus, a pH of 7.2–7.4, and moderate nutrient contents.

Plant materials

The study utilized two groups of plant material comprising a) parental lines, viz., Sochilmas, Genetik-1, Selekta-302, Ehtiyoj, Nena, and To'maris, and b) F_1 hybrids and their corresponding F_2 populations obtained through controlled crosses conducted during 2023.

Hybridization procedure

The crossing proceeded manually according to classical soybean emasculation and hybridization methods. Flower buds of the female parents entailed emasculation in the evening before anthesis. The following morning, the application of viable pollens from the designated male parents took place to the female parent's stigma. Each cross group created 25–30 crosses.

Experimental design

The study established a field experiment comprising parental genotypes and F_1 and F_2 populations using a randomized complete block design with three replications. The subplot size was 10 m² with plant spacing of 45 cm × 10 cm. Each F_1 hybrid and F_2 population has 20 plants and 150–200 plants per replication, respectively.

Phenotypic data collection

In F_1 and F_2 populations, the morphological and agronomic traits' measurement followed the UPOV (2015) and FAO (2018) descriptors. The data recorded were on plant height (cm), pods per plant, seeds per plant, seed weight per plant (g), and 1000-grain weight (g).

Statistical and genetic analyses

Heterosis and degree of dominance (hp) had the following formula:
$hp = (F1 - MP) / (HP - LP)$, where MP is ???, HP is ????, and LP is ????
Phenotypic variability (V%):

$$V\% = (\sigma / \bar{X}) \times 100$$

Broad-sense heritability (h2):

$$h2 = \sigma2\_G / \sigma2\_P$$

Transgressive segregation evaluation was according to F_2 populations exceeding parental genotypes.

The analysis of variance (ANOVA) proceeded using Excel, R v4.2.2, and SPSS 26 with significance levels of $p < 0.05$, 0.01, and 0.001. For graphical analyses, the study used bar plots and boxplots for visualization of the variability and heritability in F_1 and F_2 populations for various agronomic traits.

Table 1. Inheritance and variability in F_1 populations for agronomic traits in soybeans.

Parental genotypes	Plant height (cm)		Pods plant^{-1}		Seeds plant^{-1}		Seed weight plant^{-1} (g)		1000-grain weight (g)	
Sochilmas	85.5±0.66		60.0±1.31		149.7±2.95		23.04±0.45		154.0±0.01	
Genetik 1	60.5±0.24		34.8±0.98		89.4±2.45		11.65±0.34		129.7±0.02	
Selekta-302	138.0±0.39		60.0±0.66		96.5±1.0		13.48±0.14		139.7±0.01	
Ehtiyoj	178.0±0.95		74.3±1.84		183.2±4.5		31.75±2.94		130.7±0.14	
Nena	102.5±0.64		56.9±0.56		142.2±2.02		15.02±0.21		100.5±0.06	
To‘maris	95.0±0.71		60.2±0.95		131.9±1.39		21.17±0.45		160.7±0.01	
F_1 hybrids	F_1	hp	F_1	hp	F_1	hp	F_1	hp	F_1	hp
Sochilmas x Genetik-1	90.4±0.25	1.4	144.4±1.15	7.7	308.2±5.39	6.3	35.82±0.46	3.2	118.4±0.11	-1.7
Sochilmas x Selekta-302	108.75±1.55	-0.1	79.5±2.19	19.5	257.75±16.38	5.1	30.76±2.03	2.6	117.4±0.13	-4.1
Ehtiyoj x To‘maris	151.11±3.55	0.4	209.33±25.09	20.2	482.56±59.43	12.7	75.36±10.05	9.2	157.7±0.17	-6.1
Ehtiyoj x Nena	142.0±0.67	0.0	191.6±2.5	14.5	448.±1.97	13.9	73.83±1.62	6.0	157.1±0.11	2.3
Genetik-1 x Sochilmas	92.60±0.77	1.6	142.8±1.42	7.6	331.4±3.29	7.0	39.24±0.20	3.8	118.6±0.61	-1.9
Selekta-302 x Sochilmas	122.4±0.55	0.4	105.4±1.75	45.4	241.6±4.07	4.5	30.51±0.41	2.6	126.7±0.93	-2.8
To‘maris x Ehtiyoj	139.0±1.12	10.7	155.4±1.57	12.5	349.8±2.72	41.3	50.87±0.33	4.6	145.5±0.72	-0.4
Nena x Ehtiyoj	121.0±0.41	0.5	134.4±1.29	7.9	308.6±2.92	7.1	33.71±0.27	1.2	109.5±1.15	-0.8

RESULTS

Plant height

In the soybean F_1 hybrids, plant height ranged from 90.4 to 151.1 cm, which fell within the range of the shortest parental genotype, Genetik-1 (60.5 cm), and the tallest parent, Ehtiyoj (178.0 cm) (Table 1). The F_1 hybrid Ehtiyoj × To‘maris exhibited the tallest average plant height (151.1 ± 3.55 cm). The dominance degree (h_p) for this trait varied between −0.1 and 10.7 across the F_1 populations, indicating the combined influence of additive and dominance gene effects. From a breeding standpoint, these cross combinations represent promising genotypes with strong vegetative growth potential in soybeans.

Analysis of the variability and heritability of plant height in the F_2 populations revealed significant differences among the soybean parental genotypes (Figure 1). The shortest plant height resulted in Genetik-1 (56.33 ± 0.63 cm), while the tallest was in Ehtiyoj (145.8 ± 1.23 cm), representing a nearly 89-cm difference that signifies substantial genetic contrast for selection. However, intermediate plant height appeared in parental genotypes To‘maris (94.05 cm), Nena (100.33 cm), and Selekta-302 (109.67 cm). The coefficient of phenotypic variation (V%) ranged from 3.46% to 6.92% in parental genotypes, indicating low variability and a stable phenotypic expression during selection.

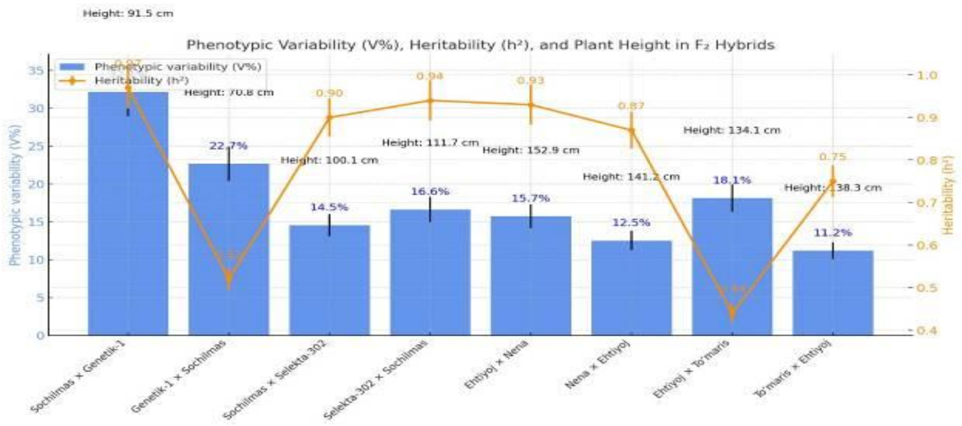

Figure 1. Genotypic variability and heritability ranges in F₂ populations as compared with parental genotypes for plant height in soybeans.

In the F_2 populations, average plant height varied from 70.78 to 152.94 cm, and some F_2 populations exceeded the parental limits, confirming transgressive recombination. The lowest average values occurred in Genetik-1 × Sochilmas (70.78 ± 1.83 cm, V% = 22.69%, $h^2 = 0.52$), while the highest were in Ehtiyoj × Nena (152.94 ± 4.39 cm, V% = 15.72%, $h^2 = 0.93$). Some F_2 populations exhibited a broad distribution range of 50 to 172 cm, reflecting the involvement of multiple alleles in trait expression and a high level of genetic polymorphism.

Pods per plant

In F_1 hybrids, the most pods per plant was in the cross combination To'maris × Ehtiyoj (155.4 ± 1.57 pods; hp = 12.5), while the lowest was evident in Sochilmas × Selekta-302 (79.5 pods; hp = 19.5), indicating a considerable dominance effect in soybeans (Table 1). Although the latter cross combination produced fewer pods, however, they demonstrated notable stability (V% < 8%). Among parental genotypes, pod number varied significantly, from Genetik-1 (57.9 ± 1.59 pods; V% = 15.05%) to To'maris (158.27 ± 4.07 pods; V% = 14.09%), revealing the highest genetic polymorphism. Mid-range values for the said trait were notable in the parental genotypes Sochilmas, Ehtiyoj, and Selekta-302; however, the genotypes To'maris and Ehtiyoj stood out as potential donors due to their higher pod production.

In F_2 populations, pod number ranged from 56.69 to 136.38, with several cross combinations exceeding or falling below the parental-genotype limits, thus confirming transgressive recombination (Figure 2). Top-performing F_2 populations included To'maris × Ehtiyoj (136.38 ± 4.05 pods, V% = 27.21%), Ehtiyoj × To'maris (121.33 ± 4.17 pods, V% = 34.38%), and Nena × Ehtiyoj (122.31 ± 2.44 pods, V% = 22.36%). These combinations exhibited considerable heterosis and phenotypic variation. The greater variability was noteworthy in the F_2 population of Ehtiyoj × Nena (V% = 54.61%), indicating substantial genetic diversity in soybeans.

From a breeding perspective, F_2 population Nena × Ehtiyoj (122.31 pods, V% = 22.36%) offered stability and performance; To'maris × Ehtiyoj (136.38 pods) was evidently valuable for selecting productive lines; and Ehtiyoj × Nena was suitable for expanding genetic diversity. The results highlighted the importance of pod number as a yield-contributing trait governed by both genetic regulation and environmental responsiveness in soybeans.

Seeds per plant

The maximum seeds per plant emerged in the soybean F_1 hybrids Ehtiyoj × To'maris (482.56

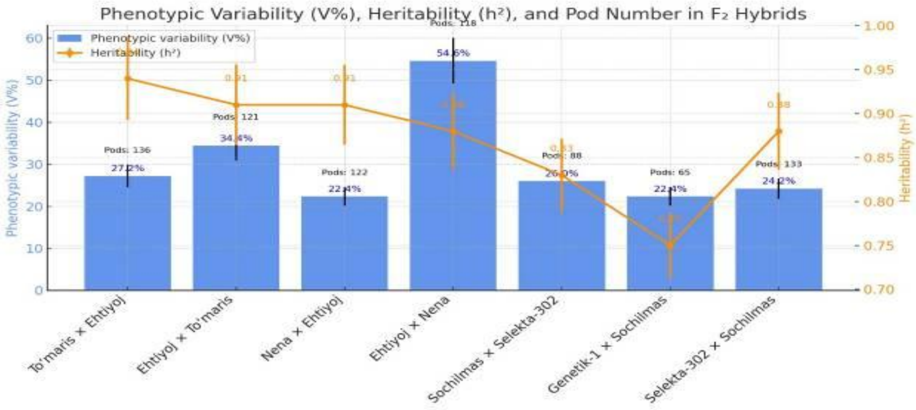

Figure 2. Genotypic variability and heritability ranges in F_2 populations as compared with parental genotypes for pods per plant in soybeans.

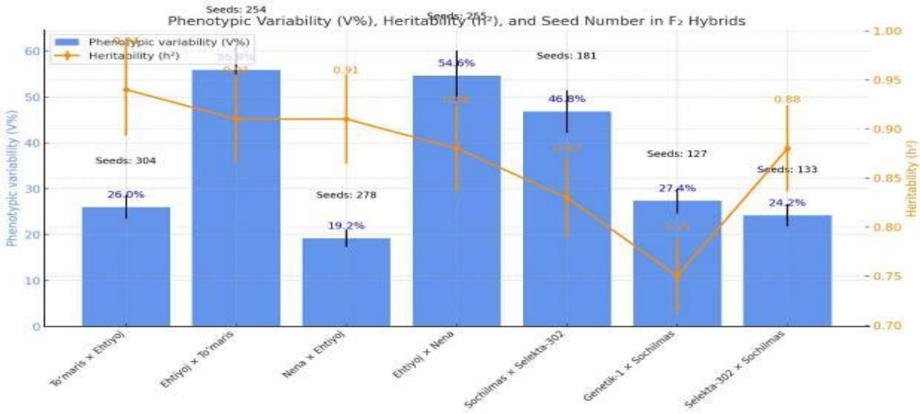

Figure 3. Genotypic variability and heritability ranges in F_2 populations as compared with parental genotypes for seeds per plant in soybeans.

± 59.43 seeds; hp = 12.7) and Ehtiyoj × Nena (448.0 ± 1.97 seeds; hp = 13.9) (Table 1). These cross combinations showed better performance by surpassing both parental values, suggesting their potential as valuable donors in breeding programs. The F_1 hybrid To'maris × Ehtiyoj also displayed a higher average (349.8 seeds), indicating robust yield potential in soybeans.

Among the soybean parent lines, To'maris and Ehtiyoj stood out as valuable genetic resources. The parental genotype To'maris showed greater variability, also producing the most seed number (347 ± 8.14). In the F_2 populations, seed number ranged from 127.18 to 303.57, confirming the presence of transgressive recombination beyond the parental limits (Figure 3). The F_2 cross combinations To'maris × Ehtiyoj and Nena × Ehtiyoj exhibited the highest expression of yield traits. Notably, the F_2 population Nena × Ehtiyoj showed relatively low variability (V% = 19.19%), indicating its stability and suitability for selection.

In contrast, the F_2 hybrid Ehtiyoj × To'maris gave the highest phenotypic variability (V% = 55.9%), signifying considerable genetic segregation and the potential to identify extreme phenotypes in the F_2 population. A V% > 50 reflects the presence of genetically diverse and potentially elite segregants. Conversely, a V% < 20, as seen in

Nena × Ehtiyoj, reveals faster stabilization of the genotypes through selection.

The results suggested that traits with high V% values may be under polygenic control. The cross combinations, such as To‘maris × Ehtiyoj, Ehtiyoj × Nena, and Nena × Ehtiyoj, which combine high seed number with stability, surfaced as the most promising genotypes. Although the cross combinations, such as Genetik-1 × Sochilmas and Selekta-302 × Sochilmas, had lower seed numbers, their stability suggests that these combinations can be effective as genetic reserves for future breeding. The cross combinations with the highest V% emerged to be ideal for intensive selection in the F_3 generation.

Seed weight per plant

For seed weight per plant, the most productive values resulted in the F_1 hybrids Ehtiyoj × To‘maris (75.36 ± 10.05 g; hp = 9.2) and Ehtiyoj × Nena (73.83 ± 1.62 g; hp = 6.0) (Table 1). These high seed-weight hybrids were notably crucial for enhancing overall seed yield in soybeans.

Among soybean parental lines, the seed weight per plant ranged from 16.55 to 50.33 g, indicating considerable genetic contrast. In the F_2 generation, the said trait ranged from 17.08 to 45.02 g, displaying broad phenotypic distribution and confirming robust genetic segregation. The F_2 populations Ehtiyoj × To‘maris and Selekta-302 × Sochilmas exhibited the highest heritability ($h^2 \geq 0.99$), suggesting robust genetic control and potential for selecting stable lines in the early breeding process.

Based on phenotypic variability (V%) and heritability (h^2) analysis, the highest V% resulted in F_2 population Ehtiyoj × To‘maris (55.98%), reflecting intense genetic segregation and the possibility of isolating extreme phenotypes (Figure 4). The topmost heritability ($h^2 = 0.99$) was evident in two F_2 populations, Ehtiyoj × To‘maris and Selekta-302 × Sochilmas, indicating robust selection advantage. The most stable F_2 hybrids combining high seed weight and heritability (V% < 30; $h^2 > 0.9$) included the F_2 cross combinations To‘maris × Ehtiyoj (28.03%; $h^2 = 0.91$), Nena × Ehtiyoj (28.97%; $h^2 = 0.91$), and Ehtiyoj × Nena (22.36%; $h^2 = 0.89$).

The results suggested F_2 populations To‘maris × Ehtiyoj, Nena × Ehtiyoj, and Ehtiyoj × To‘maris were remarkably promising due to their highest seed weight and stable inheritance, making them valuable for yield-based selection. Although the F_2 cross Sochilmas × Genetik-1 combination had a lower seed weight, its high heritability ($h^2 = 0.97$) implies that improvement through selection is possible. The seed weight trait appears to be polygenic and partially controlled by additive genes, identified as a reliable indicator for selection across the F_2 to F_4 generations.

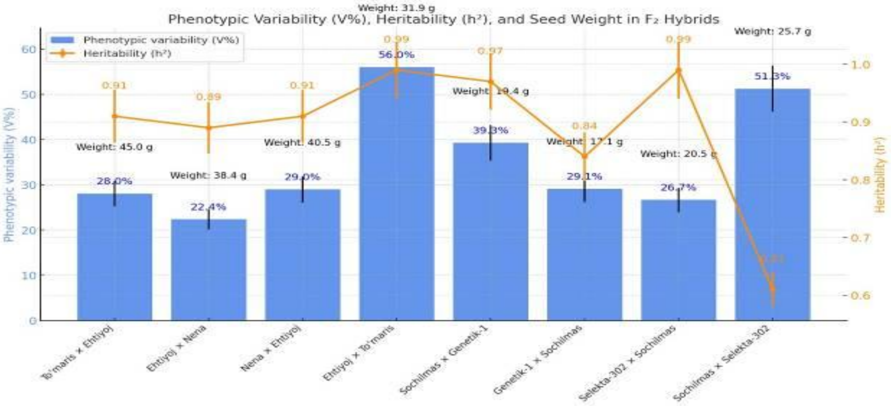

Figure 4. Genetic variability and heritability ranges in F_2 populations as compared with parental genotypes for seed weight per plant in soybeans.

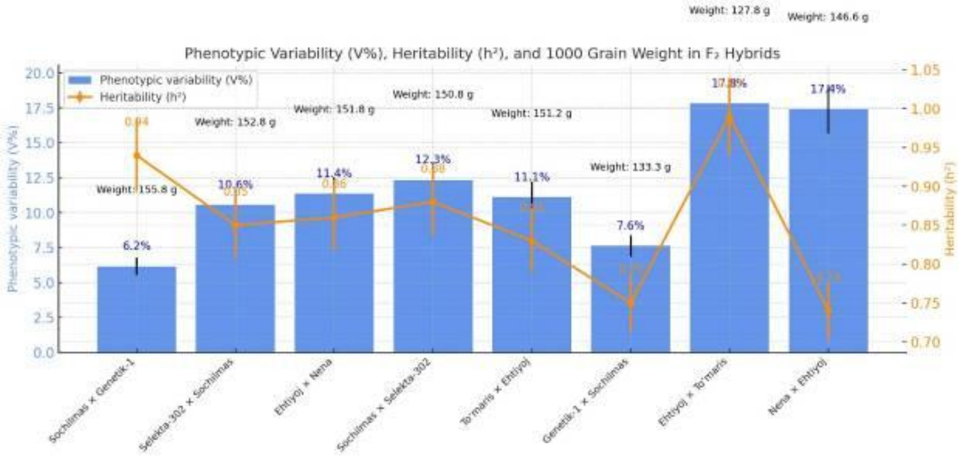

Figure 5. Genotypic variability and heritability ranges in F_2 populations as compared with parental genotypes for 1000-grain weight in soybeans.

1000-grain weight

For 1000-grain weight, the soybean parental genotype To'maris reached a recording of the highest value (160.7 g), while the genotype Nena had the lowest (100.5 g). Among F_1 hybrids, Ehtiyoj × Nena performed well with a 1000-grain weight of 157.1 g (hp = 2.3) (Table 1). In other F_1 populations, negative dominance values occurred (< -6.1), indicating that grain weight is polygenic and was critically under genetic control. Most of the cross combinations showed negative hp values, and the F_1 hybrids Sochilmas × Selekta-302 (117.4 g) and To'maris × Ehtiyoj (145.5 g) revealed moderately high values but weak dominance effects.

Parental genotypes Ehtiyoj (130.7 g) and To'maris (160.7 g) came out with the maximum genetic potential for 1000-seed weight. Hybrids derived from these parental genotypes showed considerable combining ability for multiple traits. Notably, the F_1 hybrid Ehtiyoj × To'maris displayed consistent superiority in plant height, seed number, and seed weight. Although the hybrid Sochilmas × Selekta-302 provided a lower plant height, it had a relatively stable 1000-grain weight in soybeans.

In F_1 hybrids, the dominance was the highest for yield-related traits, such as seed number and weight, particularly in cross combinations involving parental genotype Ehtiyoj, proving them highly promising for breeding purposes. Despite a negative dominance observed for 1000-grain weight, it remains a useful trait for intensive selection. The cross combinations like Ehtiyoj × To'maris and Ehtiyoj × Nena showed the best performance across all the agronomic traits, enhancing their values as donor genotypes.

Among parental lines, 1000-grain weight ranged from 117.8 g (Nena; V% = 19.41%) to 172.92 g (Selekta-302; V% = 4.8%). This wide range revealed better differentiation among the parental genotypes and provided scope for selecting both high and low extremes. The average grain weight ranged from 130 to 150 g, allowing selection of high-yielding and better-quality genotypes.

The heritability coefficient (h^2) was greater than 0.8 in most hybrids, which confirms this trait's genetic regulation and amenability to selection (Figure 5). Phenotypic variability (V%) ranged from 4.8% to 17.8%, with the lowest in Selekta-302 (V% = 4.8%) and the highest in Ehtiyoj × To'maris (V% = 17.8%). These values reflect considerable genetic segregation typical of polygenic traits and confirm the genetic diversity within the selection material.

The soybean F_2 hybrids, such as Sochilmas × Genetik-1, Selekta-302 × Sochilmas, and Ehtiyoj × Nena, exhibited the highest 1000-grain weight and heritability, recognizing them as suitable for improvement in seed yield with better quality. The F_2 population Ehtiyoj × To‘maris showed the topmost heritability ($h^2 = 0.99$), indicating its potential for developing stable lines through genetic selection. The cross combinations like Nena × Ehtiyoj and Genetik-1 × Sochilmas expressed wide phenotypic spread and emerged as ideal for isolating extreme types. The results confirmed and identified the 1000-grain weight as a reliable indicator of seed quality and breeding efficiency.

In many sources, the high genetic superiority index (hp) correlates with the presence of favorable dominant genes. From a breeding perspective, the cross combinations Ehtiyoj × To‘maris, To‘maris × Ehtiyoj, and Ehtiyoj × Nena were considerably the most promising genotypes for obtaining superior F_2 and F_3 populations.

DISCUSSION

The results reinforced the importance of evaluating genetic variability in hybrid populations in comparison with parental genotypes and agronomic traits inheritance in soybeans. The observed transgressive segregation in traits, such as plant height, seed number, and seed weight, confirmed the potential of selected F_1 and F_2 hybrids to produce superior phenotypes beyond parental limits. In past studies, the said phenomenon has reached wide reporting as a key mechanism in broadening genetic diversity and enabling the expression of novel trait combinations (Wang *et al*., 2021; Kurbanbaev *et al.,* 2024).

The considerable heterotic responses observed in cross combinations, such as Ehtiyoj × To‘maris and Ehtiyoj × Nena across multiple traits, indicate the presence of strong non-additive gene effects, which can be effectively exploited in hybrid development. These findings are consistent with those of Yormatova (1987), who highlighted the importance of F_1 hybrids in expressing dominance and overdominance for yield-related traits. Heritability estimates of $h^2 \geq 0.90$ for seed number, seed weight, and 1000-grain weight suggested these traits were largely under genetic control, making them ideal targets for early selection. Wang *et al*. (2023) also reported the highest heritability was critical for effective trait improvement through conventional and molecular breeding approaches.

In F_2 populations, the phenotypic variation (V%) ranged broadly, and some cross combinations showed over 50% variability, particularly in seed weight and seed number. The results reflect the polygenic nature of these traits, with supported findings of Xu *et al.* (2022), who reported a strong association between high phenotypic coefficient of variation (V%) and the presence of multiple segregating alleles. In contrast, low V% values observed in cross combinations, such as Nena × Ehtiyoj, suggest early stabilization of the studied traits and high selection efficiency.

The study further confirmed the 1000-grain weight as a reliable and stable trait with high heritability, with the same also reported by Zhao *et al*. (2015) in breeding of high-yield, widespread, and high-quality soybeans. Stable expression of this trait in soybean hybrids, such as Selekta-302 × Sochilmas and Ehtiyoj × Nena, provides opportunities for improving seed quality. Consistent performance of the parental genotype Ehtiyoj across the traits, especially when crossed with other parental genotypes To‘maris and Nena, revealed its considerable general combining ability (GCA). These results were greatly analogous to the findings of Kholikova *et al*. (2024), who emphasized the role of parental line selection in enhancing hybrid vigor in soybeans.

In summary, this study confirms that integrating diverse parental lines and evaluating their hybrid combinations enables the identification of elite genotypes with superior agronomic performance. The results supported the strategic breeding decisions in soybean improvement programs and offer a valuable framework for selecting donor lines and early-generation material in soybeans.

CONCLUSIONS

The results demonstrated that F_1 and F_2 populations exhibited significant phenotypic variability and high heritability for agronomic traits, providing valuable opportunities for selection. In particular, the cross combinations involving parental genotype Ehtiyoj (Ehtiyoj × To'maris and Ehtiyoj × Nena) displayed the highest performance and trait stability across the yield-related traits, making them promising genotypes for breeding. The traits, such as 1000-grain weight, seed number, and plant height, showed the stable inheritance under genetic control, indicating their suitability for early selection. These results provide a scientific basis for identifying high-yielding and stable soybean lines in breeding programs.

ACKNOWLEDGMENTS

This article's preparation relied on scientific research conducted within the framework of state scientific programs funded by the state budget of the Republic of Uzbekistan and supported by the Uzbekistan Academy of Sciences.

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