

ADVANCES IN SOYBEAN GENOTYPES ANALYSIS: UNRAVELING THE COMPLEXITIES OF PLANT GROWTH AND DEVELOPMENT

 Orkhan Bayramli*,  Zeynal Akparov

Institute of Genetic Resources, Ministry of Science and Education, Baku, Azerbaijan

Abstract. This study presents a comprehensive analysis of soybean genotypes, focusing on the intricate relationships between plant growth parameters and their impact on productivity. The research utilized a diverse set of 40 soybean genotypes, cultivated in 5 replicates, to investigate the correlations between days to emergence, days to flowering, number of root nodules, maturity days, plant height, pod per plant, seed per pod and 1000 seed grain weight. The findings revealed significant positive correlations between days to emergence and maturity days and between plant height and number of root nodules. Additionally, the study showed a strong link between nodulation and both vegetative and reproductive parameters, suggesting that nodulation could be a key target for agricultural interventions aimed at improving crop yields. The data provided a valuable foundation for future research, which should aim to elucidate the causal mechanisms behind these correlations. The study's conclusions highlight the importance of understanding the genetic and environmental factors that contribute to plant growth and development, emphasizing the potential for selecting desirable characteristics in plant breeding.

Keywords: Soybean, productivity, correlation, One-Way Anova.

***Corresponding Author:** Orkhan Bayramli, Institute of Genetic Resources, Ministry of Science and Education, Baku, Azerbaijan, Tel: +994513864453, e-mail: bayramliorxan98@gmail.com

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1. Introduction

Soybean (*Glycine max* (L.) Merrill), a crucial legume crop cultivated globally in tropical, subtropical and temperate climates, is often referred to as the “protein hope” for the future due to its high nutritional profile and protein content ranging between 42-45% (Sathe, 2009; Sarkar *et al.*, 2002). Soybeans (*Glycine max* (L.) Merr.), a legume crop with East Asian origins, are now grown all over the world because of their high protein and oil content (Bayramli, 2024). With its myriad applications, soybean is aptly described as the “Golden gift of nature to mankind”. Globally, soybean cultivation spans an average area of 121.53 million hectares, with a yield of 2.76 tons per hectare and a total production reaching 334.89 million tons. This extensive cultivation and high yield underscore soybean's significance as a staple crop that contributes substantially to meeting the nutritional needs of populations worldwide (Sarkar *et al.*, 2002). The most extensive soybean cultivation occurs in the Americas, which lead the world in terms of area dedicated to this crop. Asia comes next, followed by Europe and Africa in terms of cultivation size. In Nepal specifically, soybean is grown across 22,507 hectares,

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yielding a total production of 28,335 tons and an average productivity of 1.25 tons per hectare. This highlights the global importance of soybean as a versatile and vital agricultural commodity and its role in supporting the agricultural economy and food security in diverse regions, including Nepal (Dragan *et al.*, 2018). Soybean cultivation is on the rise in Nepal, particularly in the Terai and inner Terai regions, where it is grown either as a standalone crop or along the embankments of rice fields. This increase in popularity can be attributed to the soaring demand for soy meal in the poultry sector. Soy meal is a major player in the global market, representing over 60% of the total production of vegetable and animal meals. It holds a significant place in the protein feed industry, being a key ingredient in the manufacture of feed concentrates. Additionally, soybean oil, extracted from these beans, stands out as the most consumed vegetable oil, renowned for its array of health benefits, including its role in heart health and cholesterol management. The versatility and economic value of soybean, both as a food and an industrial crop, make it a golden resource for agriculture and nutrition (MOAD, 2018/19). Around the world, soybeans constitute a significant crop for food and a significant source of protein and oil (Wang, 2011). To increase soybean output, several researchers have focused on yield-related factors in recent years, such as the quantity of grains and pods per plant (Singh, 2010; Li, 2018; Du *et al.*, 2019). However, thus far, efforts haven't resulted in a significant improvement in yields (Song *et al.*, 2020). Therefore, in order to raise soybean yields, it is necessary to identify the primary elements influencing them. Throughout the growth and development of soybeans, soybean flower and pod drops are a frequent occurrence. It happens at every step of podding, from the appearance of flower buds until blooming. Even 30 to 80% of the flower and pod loss rates are possible (Zhang *et al.*, 2012). Thus, flowering and the flower and pod drop can greatly raise the yield of soybeans (Selvaraj *et al.*, 2019). Over the years, several scholars have examined various facets of soybean flower and pod patterns in the context of the study of flower and pod drop patterns (Wang *et al.*, 2010). First, the order of floral abscission in soybeans was studied. It was shown that early flower abscission is higher than late flower abscission and that this order is the same as the order of flowering (Gao *et al.*, 1958). Ma *et al.* (1960) noticed that, out of 163 soybean plants, the average rates of bloom loss, pod drop and bud drop were 56.5%, 28.4% and 13.1%, respectively. Song (2002) studied the flowering order in detail and came to the conclusion that, while the flowering order of both sub-limited and unlimited pod habit soybeans opens sequentially from the bottom upward, the limited pod habit soybeans flower in the middle and gradually open upward and downward. Su *et al.* (2004) found gene areas linked to flowering and pod setting and located the QTL for the amount of flowers and pods per plant attribute from a genetic standpoint (Wang *et al.*, 2010). Departing from the traditional method of collecting information on flower drops and blossoming in a static manner, Zhao (2013) and Bock (2010) examined flowering patterns from a temporal and geographical standpoint. They concluded that distinct soybean flowering phases, with varying blooming nodes and durations, differed greatly in the quantity of flowers produced each day. In the meanwhile, there were notable differences in the flower drop rates at various phases. Nevertheless, there is a deficiency in this field of study overseas and the aforementioned studies' manual indicator creation can be labor-intensive and time-consuming and their surveys are challenging, subjective and prone to mistake and these shortcomings make it problematic to physically conduct flower and pod phenotypic surveys for vast fields and challenging to apply on big samples, which inhibits the drawing of more broadly applicable results. However, many

fine phenotypes are unavailable due to the complex structure of the soybean plant and the intense shading that occurs during the growing season. Even significant phenomena, like flower and pod abscission, have been impeded by the difficulty of conducting phenotypic investigations and the lack of reliable, accurate and large-scale phenotypic support for their patterns. (Singh *et al.*, 2021).

2. Material and Methods

The research was conducted at the Saray Support Point Institute of Genetic Resources of the Ministry of Science and Education of Azerbaijan during 2022 and 2023. A total of 40 varieties, namely Kanata, CHU-11, Геч-8, БК-98, Kyota, Л-1, Л-12, Krasnodar-68, Л-3, Alexa, CHU-10, Л-4, Л-7, Л-9, Opus, CHU-14, Л-8, Anjelica, Л-2, Кол-6, Л-11, БК-82, Л-10, Кол-27, Sinara, Asuka, Antonia, REGALE, Biyson, Umanskaya, Bravo, Kanada 4, Kanada 5, Kanada-6, Kanada 7, Л-5, БК-88, Л-6, БК-83 and БК-104, were utilized as the material for the study. The experimental material consisted of 40 genotypes cultivated in 5 replicates. Planting was conducted in 6 patches with 20 samples in each patch. The distance between rows was 0.7 meters, the length of the row was 10 meters and the distance between patches was 1 meter. Consequently, a total of 200 samples were obtained. These genotypes were also used in our previous analysis using polyacrylamide gel electrophoresis (A-PAGE) to analyze the storage globulin proteins (Bayramli, 2024).

Table 1. Comprehensive catalogue of forty soybean (*Glycine max*) genotypes utilized in AZGR experimentation: Nomenclature and provenance

Genotypes			Genotypes		
Genotypes	AZGR name	Origin	Genotypes	AZGR name	Origin
1 Kanata	13566	Canada	21 Л-11		Uzbekistan
2 CHU-11	13898	Türkiye	22 БК-82		Uzbekistan
3 Геч-8		Uzbekistan	23 Л-10		Uzbekistan
4 БК-98		Uzbekistan	24 Кол-27		Uzbekistan
5 Kyota	13565		25 Sinara	13904	Austria
6 Л-1		Uzbekistan	26 Asuka	13570	Japonia
7 Л-12		Uzbekistan	27 Antonia	13215	
8 Krasnodar-68	13902		28 REGALE	13216	
9 Л-3		Uzbekistan	29 Biyson	13878	
10 Alexa	13241		30 Umanskaya	13906	
11 CHU-10	13897	Türkiye	31 Bravo	13879	
12 Л-4		Uzbekistan	32 Kanada 4	13883	Canada
13 Л-7		Uzbekistan	33 Kanada 5	13884	Canada
14 Л-9		Uzbekistan	34 Kanada-6	13885	
15 Opus	13568		35 Kanada 7	13886	Canada
16 CHU-14	13901	Türkiye	36 Л-5		Uzbekistan
17 Л-8		Uzbekistan	37 БК-88		Uzbekistan
18 Anjelica	13214		38 Л-6		Uzbekistan
19 Л-2		Uzbekistan	39 БК-83		Uzbekistan
20 Кол-6		Uzbekistan	40 БК-104		Uzbekistan

Cluster analysis, correlation and One-Way ANOVA were employed to analyze this extensive dataset, comprising 40 treatments and to categorize them into similar cluster groups. The objective of cluster analysis was to organize the data into groups based on measured characteristics that exhibit identical or similar values. In this study,

the complete linkage method of cluster analysis was utilized. This method determines the distance between two clusters by the farthest-neighbor distance, specifically the distance between the two farthest inter-cluster observations or units. This approach tends to yield compact clusters, allowing relatively similar observations to remain in separate clusters until the analysis is completed. The varieties taken as research material were obtained from the National Genbank (AZGR) operating under the Institute of Genetic Resources of the Ministry of Science and Education of the Republic of Azerbaijan.

2. Result and Discussion

The morphological correlation analysis conducted on various plant growth parameters has yielded insightful findings. The days to emergence (DE) displayed a positive correlation with maturity days (MD), with a coefficient of 0.229, which is significant at the 0.01 level. This suggests that plants which take longer to emerge also require a longer period to reach maturity, potentially indicating a genetic or environmental influence that extends across the plant's lifecycle.

Conversely, a significant negative correlation was observed between the number of root nodules (NN) and days to flowering (DF), with a coefficient of -0.424. This implies that a greater number of nodules may contribute to earlier flowering, possibly due to enhanced nitrogen fixation capabilities provided by the nodules.

Plant height (PH) showed a strong positive correlation with the number of root nodules (NN), evidenced by a coefficient of 0.763. This relationship underscores the importance of nodulation in supporting not only the plant's vertical growth but also its overall health and productivity.

Furthermore, pod per plant (PP) correlated positively with the number of root nodules (NN) at 0.653, reinforcing the critical role of nodules in the plant's reproductive success. The 100 seed grain weight (SW) also exhibited a moderate positive correlation with pod per plant (PP) at 0.292, indicating that plants with a higher pod count tend to produce heavier seeds, which is significant for yield quality.

These correlations highlight the intricate network of interactions that govern plant growth and development. The strong link between nodulation and both vegetative and reproductive parameters suggests that nodulation could be a key target for agricultural interventions aimed at improving crop yields. Additionally, the correlation between seed weight and pod count may inform breeding strategies focused on enhancing both the quantity and quality of the harvest.

The data presented in this study provide a valuable foundation for future research, which should aim to elucidate the causal mechanisms behind these correlations. Such understanding could lead to the development of more robust plant varieties that are better equipped to thrive in their respective environments, ultimately contributing to more sustainable agricultural practices.

The height of the plant, the length of the pod, the pod per plant, the pod per seeds and the weight of 100 seeds grain have a negative correlation with the days of flowering. The length of the pod, the pod per plant, the pod per seeds and the weight of 100 seeds grain have a negative correlation with the maturity days. The height of the plant, the length of the pod, the pod per plant, the pod per seeds and the weight of 100 seeds grain have a positive correlation with the number of root nodules.

Table 2. Correlation analysis of soybean genotypes among productivity elements

	DE	DF	NN	MD	PH	PL	PP	SPP	SW
DE	1								
DF	0.209**	1							
NN	-0.070	-0.424**	1						
MD	0.229**	0.346**	-0.183**	1					
PH	-0.138	-0.397**	0.763**	0.006	1				
PL	-0.046	-0.414**	0.484**	-0.057	0.546**	1			
PP	-0.179*	-0.462**	0.653**	-0.209**	0.704**	0.438**	1		
SPP	-0.223**	-0.262**	0.062	-0.229**	0.052	0.010	0.093	1	
SW	-0.011	-0.237**	0.106	-0.025	0.135	0.270**	0.292**	0.151*	1

** . Correlation is significant at the 0.01 level (2-tailed).

* . Correlation is significant at the 0.05 level (2-tailed).

DE: days to emergence, DF: days to flowering, PL - pod length, RNN - node number, PH: plant height, NN: number of root nodules, MD: maturity days, PP: pod per plant, SPP: seed per pod, SW: 100 seed grain weight.

The ANOVA analysis conducted on various plant growth parameters has revealed significant differences across the groups studied. The Days to Emergence (DE), with a p-value of .000, indicates a significant variability in the time required for the plants to emerge. This could be attributed to genetic differences or environmental influences affecting germination rates.

Similarly, the Days to Flowering (DF) and Number of Root Nodules (NN) also show significant differences (p-values: .000), suggesting that the flowering time and root nodule formation are influenced by the treatments or conditions applied to the different groups. The substantial variation in Plant Height (PH), with a p-value of .000, could have implications for light interception and photosynthetic efficiency, which are critical for plant growth and yield.

The Maturity Days (MD) and Pod per Plant (PP), both with p-values of .000, demonstrate significant group differences, indicating that the time to reach maturity and the number of pods produced per plant are highly variable traits. These findings are essential for understanding the growth cycle and potential yield of the plants.

Interestingly, the Seed per Pod (SPP) did not show a significant difference (p-value: .066), which suggests that this trait is relatively stable across the groups and may be under stronger genetic control. In contrast, the 100 Seed Grain Weight (SW) showed a highly significant difference (p-value: .000), pointing to the potential for selecting for seed size in breeding programs.

Overall, the results highlight the importance of understanding the genetic and environmental factors that contribute to plant growth and development. The significant differences observed in most traits suggest that there is potential for selecting desirable characteristics in plant breeding. The stability of seed per pod across groups is reassuring for consistency in yield. However, the variability in other traits like plant height and pod number underscores the complexity of plant growth and the need for careful management and selection to achieve optimal production.

Table 3. One-Way ANOVA analysis of soybean genotypes among productivity elements

		Sum of Squares	df	Mean Square	F
DE	Between Groups	75.020	39	1.924	2.829*
	Total	183.820	199		
DF	Between Groups	844.555	39	21.655	8.812*
	Total	1237.755	199		
NN	Between Groups	927.995	39	23.795	11.750*
	Total	1251.995	199		
MD	Between Groups	31472.475	39	806.987	8.758*
	Total	46214.875	199		
PH	Between Groups	59235.900	39	1518.869	33.783*
	Total	66429.500	199		
PL	Between Groups	45.760	39	1.173	5.153*
	Total	82.192	199		
PP	Between Groups	271491.200	39	6961.313	33.745*
	Total	304498.000	199		
SPP	Between Groups	.622	39	.016	1.427*
	Total	2.412	199		
SW	Between Groups	1252.574	39	32.117	40.170*
	Total	1380.498	199		

*.One-Way Annova is significant

DE: days to emergence, DF: days to flowering, RNN - node number, PH: plant height, NN: number of root nodules, MD: maturity days, PP: pod per plant, SPP: seed per pod, SW: 100 seed grainweight

Figure 1, showed that the morphological traits of soybean using cluster analysis procedure defined 3 clusters in Groups (5 sub-clusters). Cluster I consisted of 14 accessions, cluster II of 5 and cluster III of 21 accessions.

The analysis was able to identify related groups of accessions and many of the soybean plant introductions included in the study were found to be genetically distinct from the accessions of Uzbekistan origin. For example, Clusters II was composed mainly of plant introductions of Canada and Turkiye origin, while clusters I consisted of most of the Uzbekistan accessions. However, one Turkiye accession formed the cluster II (b) independently while rest of the accessions of Turkiye origin were spread in III cluster. The genotypes in cluster II are grouped separately according to the pod per plant, maturity day and the highest indicators are also listed according to this characteristic for pod per plant. CHUKUROVA 10 genotype from Turkey, located in cluster II, subcluster b, was the only one in this group according to the pod per plant and among all genotypes, it was distinguished from the others by having the highest indicator according to the pod per plant. Uzbekistan genotypes were recorded in all 3 clusters, the most Uzbekistan genotypes were located in cluster I, but the 100 seeds

grain weight was recorded in genotypes located in subcluster a cluster III, the highest indicator.

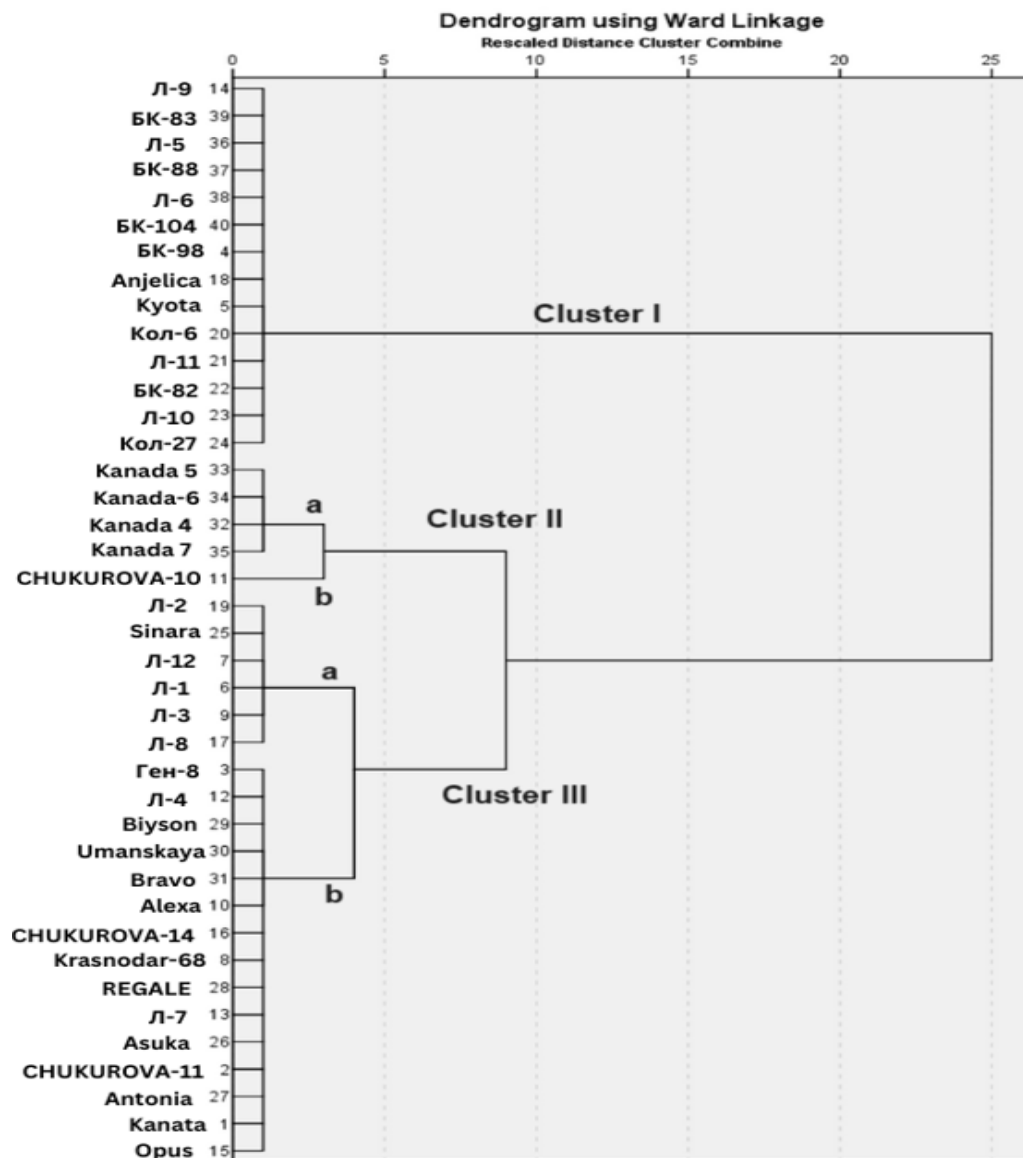


Figure 1. Classification of soybean genotypes into different clusters and subclusters by statistical analysis

3. Conclusion

The study analyzed 40 soybean genotypes to identify the primary elements influencing soybean yields. The results showed that days to emergence and maturity days were positively correlated, indicating that plants that take longer to emerge also require a longer period to reach maturity. The number of root nodules was negatively correlated with days to flowering, suggesting that a greater number of nodules may contribute to earlier flowering. Plant height was positively correlated with the number of root nodules, highlighting the importance of nodulation in supporting plant growth and productivity. The study concluded that nodulation could be a key target for agricultural interventions aimed at improving crop yields and that the correlation

between seed weight and pod count may inform breeding strategies focused on enhancing both the quantity and quality of the harvest.

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