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RESEARCH ARTICLE

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE ESTIMATES IN SOYBEAN [*GLYCINE MAX* (L.) MERRILL] GENOTYPES FOR SEED YIELD AND OTHER AGRONOMIC TRAITS

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Abstract: Present investigation utilized 20 soybean genotypes, including 18 from diverse Nagaland regions and 2 reference checks. Using a Randomized Complete Block Design, genotypes were sown with 50 cm row-to-row and 10 cm plant-to-plant spacing in an upland setting. Assessment occurred over consecutive 2017 and 2018 kharif seasons at experimental farm of Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, Medziphema. ANOVA revealed significant trait variations. Yearly fluctuations and genetics played crucial roles in shaping soybean traits. Examining soybean traits, notable seed yield variation was observed. Genotypes T1, T8, T9, T10, T11, and T12 exhibited promising yields for cultivation and breeding. Highest values of GCV, PCV exhibited at NC/P with PCV at 51.79% and GCV at 41.64%. NPo/C has PCV 27.9%, GCV 17.71%. NPo/P features PCV at 33.99%, GCV at 28.37%. HSW exhibits PCV reaching 23.29%, GCV at 23%. BY/P stands at PCV 32.02%, GCV 22.63%. Finally, SY/P indicates PCV of 32.89%, GCV of 22.31%. High heritability observed at traits HSW: h^2 - 97.53% (High), DFF: h^2 - 95.39% (High), DM: h^2 - 95.97% (High), PH: h^2 - 84.34% (High), PoL: h^2 - 74.99% (High), NC/P: h^2 - 64.65% (High), NPo/P: h^2 - 69.67% (High), and Oil%: h^2 - 68.01% (High). In this study, high heritability coupled with high genetic advance per cent mean observed at Days to 50% flowering, plant height, number of clusters per plant, number of pods per plant and 100 seed weight appear to be governed by additive gene action, enabling breeders to selectively enhance these traits within soybean populations.

Keywords: Soybean, Genetic variability, Heritability, Genetic gain

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a widely cultivated leguminous plant of significant agricultural and nutritional importance. Soybean finds its place among other well-known legumes such as peas, lentils, and peanuts. Its scientific classification encompasses the kingdom Plantae, the order *Fabales*, and the family *Fabaceae*, also known as the Leguminosae family (Joshi et al. 2018). Chromosome studies have unveiled soybean's diploid chromosome number of 2n=40, underscoring its genetic diversity utilized through selective breeding for varied cultivars. Originating in East Asia, particularly China and Japan, soybean boasts a millennia-spanning history of domestication, serving as a nourishing staple for humans and livestock.

Soybean (*Glycine max* (L.) Merrill) is a crucial global oilseed crop, contributing significantly to both human and animal nutrition, as well as industrial applications. The worldwide production of soybeans had been steadily increasing. India produced around 13.5 million metric tons of soybeans, covering an area of about 11 million hectares. Nagaland, a northeastern state of India, is also engaged in soybean cultivation as a part of its agricultural activities. However, specific and recent production and area data for soybeans in Nagaland may not be readily available. Regional variations, climatic conditions, and local agricultural practices would contribute to the yield and area under soybean cultivation in Nagaland.

Soybean exhibits a rich array of biochemical aspects that underpin its diverse applications. It is recognized for its high protein content, boasting essential amino acids and contributing to its status as a significant plant-based protein source. With an oil content of around 18-22%, soybean is a vital contributor to cooking oil and industrial products. Isoflavones, bioactive compounds found in soybean, offer potential health benefits due to their antioxidant and hormone-modulating properties. Moreover, soybean is a source of vitamins such as vitamin E and minerals like magnesium, potassium, iron, and zinc. The carbohydrate composition includes dietary fibers and complex polysaccharides, with enzymes and antinutritional factors necessitating careful processing. This biochemical complexity not only enhances its nutritional profile but also underscores

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its importance in both nutrition and industrial sectors (Karnwal and Singh, 2009)

Genetic variability is a fundamental concept in soybean breeding that underscores the diversity present within the genetic makeup of soybean populations. This variability forms the basis for selecting and developing improved soybean cultivars with desirable traits. By tapping into the genetic variability inherent in soybean germplasm, breeders can identify and harness specific genes responsible for traits like yield, quality, disease resistance, and stress tolerance.

A significant research gap in soybean plant breeding revolves around the exploration of genetic resources for enhanced stress tolerance and adaptability. While substantial efforts have been directed towards improving yield and quality traits in soybean, there remains a crucial need to identify and exploit genetic variants that confer resilience to various environmental stresses, such as drought, salinity, pests, and diseases. Integrating stress-tolerant traits into high-yielding cultivars is paramount for sustainable agriculture, especially considering the changing climate and evolving pest pressures. Thus, a key research gap lies in systematically characterizing and harnessing genetic diversity to develop soybean varieties that can thrive under diverse and challenging growing conditions, ultimately ensuring food security and agricultural sustainability.

This study aims to address a research gap pertaining to the genetic variability, heritability, and genetic advance estimates in different genotypes of Soybean (*Glycine max* (L.) Merrill) specifically within the context of Nagaland. While soybean's genetic traits and heritability have been explored in various regions, there exists a scarcity of information specifically focused on the Nagaland region. Consequently, this research gap necessitates an investigation into the genetic variability, heritability, and genetic advance estimates within this specific geographical context. By conducting this study, we aim to contribute valuable insights into the extent of genetic diversity, the degree of heritability, and the potential for genetic progress in soybean genotypes related to seed yield and other agronomic traits in the unique agro-climatic conditions of Nagaland.

MATERIALS AND METHODS

The experimental material employed in the present study comprised 20 (Table- 1) soybean genotypes, a combination of 18 distinct genotypes sourced from diverse regions within Nagaland, alongside the inclusion of 2 established reference checks. The chosen genotypes were directly sown in well-moistened soil, meticulously arranged using a Randomized Complete Block Design (RCBD) approach. This experimental layout encompassed three replications, with row-to-row spacing set at 50 cm and plant-to-plant distance maintained at 10 cm within the context of an upland ecosystem. The evaluation of these genotypes spanned two consecutive kharif seasons, specifically those of 2017 and 2018, within the research facilities of the School of Agricultural Sciences (SAS), Medziphema Campus, Nagaland. This evaluation took place on the dedicated experimental farm focused on Genetics and Plant Breeding, facilitating a comprehensive assessment of both yield and grain quality traits. Data recorded for yield traits such as days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), hundred seed weight, biological yield per plant (g), harvest index and seed yield per plant (g) and oil content. The mean values were subjected to statistical analysis to work out analysis of variance for all the characters as suggested Panse and Sukhatme (1967). The phenotypic, genotypic and environmental coefficient of variation was calculated according to Burton and De Vane (1953). Heritability estimate was calculated according to Allard (1960) and genetic gain was estimated using the method of Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance

The ANOVA conducted on soybean traits revealed significant variations attributed to different sources. The characters under examination were subjected to meticulous analysis, revealing their mean sum of squares and offering insights into their inherent variability. Yearly fluctuations exhibited a notable impact on the traits under study, evident in mean sum of squares for attributes like DFF, DM, PH, NPB/P, NC/P, NPo/C, NPo/P, NS/Po, PoL, HSW, Oil%, BY/P, HI, and SY/P.

The interaction between year and replication (rep) exerted a significant influence on specific traits. Traits such as DFF, NPB/P, and Oil% displayed variability influenced by both the year and replication factors. The genetic composition (Gen) of the 19 soybean genotypes emerged as a substantial contributor to the variability observed in traits, particularly in DFF, DM, PH, NPB/P, NC/P, NPo/C, NPo/P, NS/Po, PoL, HSW, Oil%, BY/P, HI, and SY/P.

The interaction between year and genotype also contributed significantly to observed variability in traits like DM, PH, NPB/P, NC/P, NPo/C, NPo/P, NS/Po, PoL, HSW, BY/P, HI, and SY/P, exhibiting distinctive patterns influenced by the interplay of both the year and genotype.

Lastly, residual variations within the pooled data, known as Pooled Error, also contributed to overall trait variability. This comprehensive ANOVA analysis illuminated the intricate dynamics of year-to-year variations, genetic influences, and their complex interactions, collectively shaping diverse soybean traits. Varying degrees of susceptibility to these influences provided valuable insights into potential tailored plant breeding strategies aimed at enhancing specific traits in soybean cultivation. ANOVA results represented at Table 2. Baraskar *et al.* (2014) also presented analogous outcomes, emphasizing significant diversity within the soybean crop, which harmonizes with the aforementioned observations. Corresponding conclusions were affirmed by Painkra *et al.* (2018), and Chandrawat *et al.* (2017) for attributes such as days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, 100-seed weight (g), oil percentage, and seed yield per plant (g).

Mean performance

Analyzing the mean performance of various soybean traits across multiple genotypes, specific attention is drawn to seed yield per plant. Notably, the seed yield ranged from 2.98 g (T13) to 16.33 g (T1), with an overall mean of 7.33 ± 1.02 g. Among these genotypes, T1 showcased the highest seed yield, while T13 and T16 exhibited lower yields compared to the mean and other genotypes. A closer examination of the data reveals that six genotypes—T1 (16.33), T8 (8.48), T9 (8.80), T10 (12.24), T11 (9.12), and T12 (9.02)—outperformed the rest by yielding above 8.41 g per plant, surpassing the reference variety T19 (check variety, yielding 6.37 g). About half of the evaluated genotypes (eleven) showed seed yields similar to the reference, while T13 and T16 demonstrated the lowest yields compared to the reference (<4.33 g). Therefore, based on seed yield performance, genotypes T1, T8, T9, T10, T11, and T12 emerge as promising candidates for potential soybean cultivation and breeding efforts. Mean performance of 14 traits represented at Table 3.

Estimation of genetic parameters

Genetic parameters play a pivotal role in understanding the inheritance and variability of traits within plant populations. The study of these parameters provides valuable insights into the genetic architecture of a crop species, shedding light on the potential for targeted improvement through breeding programs. This is particularly relevant in the context of soybean (*Glycine max*) breeding, where a comprehensive understanding of genetic parameters can facilitate the development of improved soybean varieties with desirable traits. The analysis of genotypic and phenotypic variances, along with heritability, genotypic and phenotypic coefficient of variation (PCV), genetic advance (GA), and genetic advance as a percentage of the mean (GA%), for all yield-contributing traits are presented in Table 4.

This investigation focuses on the genotypic and phenotypic coefficient of variation (PCV) in soybean, providing insights into the variability of various traits. PCV reflects the extent of diversity among genotypes, encompassing both genetic and environmental influences. The classification system suggested by Sivasubramanian and Menon (1973) guides the interpretation, categorizing genetic coefficient of variation (GCV) and PCV values as low (<10%), moderate (10-20%), and high (>20%).

Lowest GCV and PCV values observed from DM: PCV - 9.32% (Low), GCV - 9.13% (Low), NC/P: PCV - 51.79% (Low), GCV - 41.64% (Low)), NS/Po: PCV - 8.74% (Low), GCV - 5.07% (Low), PoL: PCV - 7.61% (Low), GCV - 6.59% (Low), and Oil%: PCV - 8.71% (Low), GCV - 7.18% (Low).moderate values observed from DFF: PCV - 15.6% (Moderate), GCV - 15.23% (Moderate), PH: PCV - 19.05% (Moderate), GCV - 17.5% (Moderate), NPB/P: PCV - 19.26% (Moderate), GCV - 12.65% (Moderate), NPo/C: PCV - 27.9% (High), GCV - 17.71% (Moderate), and HI: PCV - 13.21% (Moderate), GCV - 9.49% (Low). Highest GCV and PCV values obtained by NC/P: PCV - 51.79% (High), GCV - 41.64% (High), NPo/C: PCV - 27.9% (Moderate), GCV - 17.71% (Moderate), NPo/P: PCV - 33.99% (High), GCV - 28.37% (High), HSW: PCV - 23.29% (High), GCV - 23% (High), BY/P: PCV - 32.02% (High), GCV - 22.63% (High), and SY/P: PCV - 32.89% (High), GCV - 22.31% (High). Through this interpretation, we observe varying levels of genetic and environmental influence on these traits. These insights are crucial for devising targeted breeding strategies aimed at improving specific soybean attributes.

This study explores the heritability of diverse soybean traits, shedding light on genetic influences. The interpretation framework, following Robinson *et al.* (1949), categorizes heritability values into high (>60%), moderate (40% to 60%), and low (<40%). High heritability observed for HSW: h^2 - 97.53% (High), DFF: h^2 - 95.39% (High), DM: h^2 - 95.97% (High), PH: h^2 - 84.34% (High), PoL: h^2 - 74.99% (High), NC/P: h^2 - 64.65% (High), NPo/P: h^2 - 69.67% (High), and Oil%: h^2 - 68.01% (High). Moderate values obtained by NPB/P: h^2 - 43.15% (Moderate), NPo/C: h^2 - 40.31% (Moderate), BY/P: h^2 - 49.94% (Moderate), HI: h^2 - 51.59% (Moderate), SY/P: h^2 - 46% (Moderate) and low heritability observed on NS/Po: h^2 - 33.72% (Low). These insights inform the genetic component of trait variation, guiding effective breeding strategies for soybean enhancement.

In the realm of soybean genetics, this study offers insights into the concept of genetic advance, shedding light on the potential for trait improvement through breeding strategies. Genetic advance indicates the extent by which traits can be enhanced through selection and breeding. The classification framework, with divisions of high genetic advance (>20%), moderate genetic advance (10% to 20%), and low genetic advance (<10%), provides a valuable tool for assessing the practical significance of observed changes (Johnson *et al*. 1955).

High genetic advance per cent mean observed from DFF: - 30.65% (High), PH: - 33.1% (High), NC/P - 68.98% (High), NPo/C: - 23.16% (High), NPo/P: - 48.78% (High), HSW: - 46.78% (High), BY/P: - 32.94% (High), and SY/P: - 31.16% (High). Moderate values obtained from DM: - 18.41% (Moderate), NPB/P: - 17.12% (Moderate), PoL: - 11.76% (Moderate), Oil%: - 12.21% (Moderate), and HI: - 14.04% (Moderate). Low values observed at NS/Po: - 6.07% (Low) only.

The integration of heritability and genetic advance per cent of mean serves as a powerful framework in the realm of agricultural genetics, particularly in crops like soybean. Heritability, a measure of the proportion of trait variation attributed to genetic factors, provides insights into the potential of traits to respond to selective breeding. On the other hand, genetic advance per cent of mean highlights the magnitude of improvement that can be achieved through selective breeding strategies. By combining these two concepts, we gain a comprehensive understanding of the inherent genetic potential of traits and the extent to which they can be enhanced through purposeful breeding efforts.

In this study, high heritability coupled with high genetic advance per cent mean observed at Days to 50% flowering, plant height, number of clusters per plant, number of pods per plant and 100 seed weight appear to be governed by additive gene action, enabling breeders to selectively enhance these traits within soybean populations. High heritability coupled with moderate GAM was recorded for days to maturity, pod length and oil content appeared too governed by non additive gene action. Moderate heritability coupled with high genetic advance per cent mean were obtained for traits such number of pods per cluster, biological yield per plant and seed yield per plant. Moderate heritability coupled with moderate genetic advance per cent mean resulted for as number of primary branches per plant and harvest index. Moderate heritability coupled with low genetic advance per cent mean was observed for number of seeds per pod, these all are indicates those traits governed by additive gene action. High heritability coupled with high genetic advance indicates additive gene action in enhancing traits like flowering time, height, clusters, pods, and seed weight in soybean. Moderate heritability and moderate-to-high genetic advance reflect controlled progress in primary branches and yield. Moderate heritability with low genetic advance signifies limited improvement in seed number, possibly due to additive gene action.

In recent studies, congruent results have emerged among researchers. Goonde and Ayana (2021) found consistent outcomes for traits like pod number, biological yield, and seed yield. Kumar et al. (2020) confirmed these trends for most traits except cluster number, paralleling Baraskar *et al.* (2014) findings. Baraskar *et al.* (2014) supported this for primary branch count, while Jandong *et al.* (2020) affirmed consistency for flowering time. Baraskar et al. (2014), while largely in agreement, diverged on pod number per cluster due to low heritability and GAM considerations.

Table 1. Details of the soybean genotypes and their place of collection with source

S.No.	Genotypes	Place of collection			Source
		State	District	Institute	
1	T1	Assam	Cachar	Jirighat	Farmer
2	T2 (small)	Manipur	Imphal	CAU	CAU
3	T3 (large)	Manipur	Imphal	CAU	CAU
4	T4	Arunachal Pradesh	Lower Dibang valley	Jiali	Farmer
5	T5	Mizoram	Lawngtlai	Lawngtlai	Farmer
6	T6	Arunachal Pradesh	Lower Siang	Basar	Farmer
7	T7	Mizoram	Serchip	East Lungdar	Farmer
8	T8	Mizoram	Lunglei	Hnahthial	Farmer
9	T9	Nagaland	Dimapur	Dimapur	Farmer
10	T10	Nagaland	Kohima	Chiephobozu	Farmer
11	T11	Nagaland	Kiphere	Mimi	Farmer
12	T12	Nagaland	Tuensang	Tuensang	Farmer
13	T13 (JS-9305)	MP	Jabalpur	JNKVV	JNKVV
14	T14	Nagaland	Peren	Samjuiram	Farmer
15	T15	Nagaland	Tuensang	Tuensang	Farmer
16	T16 (JS-9560)	MP	Jabalpur	JNKVV	JNKVV
17	T17	Nagaland	Wokha	Yimkha	Farmer

18	T18	Nagaland	Zunhebuto	Mishilimi	Farmer
19	T19 (JS-9752)	MP	Betul	Sirkhed	Farmer
20	T20 (JS-335)	MP	Jabalpur	Jabalpur	JNKVV

Table 2. Analysis of variance data for traits in soybean genotypes that contribute to seed yield

Sl. No.→		**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**
Source of variation	**d.f**	**Mean sum of squares for the characters under study**													
		DFF	**DM**	**PH**	**NPB/P**	**NC/P**	**NPo/C**	**NPo/P**	**NS/Po**	**PoL**	**HSW**	**Oil%**	**BY/P**	**HI**	**SY/P**
Year	1	2.41	72.07	336.51	18.93	230.56	31.22	15262.59	0.02	0.08	6.96	3.25	14209.93	6858.70	197.39
Rep(Year)	4	41.13	28.17	9.25	2.71	0.52	0.45	48.69	0.02	0.02	0.05	1.21	65.98	13.02	4.80
Gen	19	1402.90**	2216.85**	1257.53**	3.74**	85.60**	3.52**	4701.34**	0.25**	0.92**	69.70**	40.37**	761.95**	159.00**	53.98**
Year * Gen	19	8.43**	7.74^{NS}	88.96**	1.73**	11.83**	0.51*	802.82**	0.04 NS	0.04**	2.59**	0.67^{NS}	219.60**	113.35**	15.61**
Pooled Error	76	3.56	4.89	12.17	0.24	2.39	0.25	105.32	0.02	0.02	0.09	0.98	38.19	7.48	3.14

*** Significant at 5 % probability level and ** Significant at 1% probability level**

Abbreviations:- DFF: Days to 50% flowering, **DM:** Days to maturity, **PH**: Plant height (cm), **NPB/P**: Number of primary branches per plant, **NC/P**: Number of clusters per plant, **NPo/C**: Number of pods per cluster, **NPo/P**: Number of pods per plant, **NS/Po**: Number of seeds per pod, **PoL**: Pod length (cm), **HSW**: Hundred seed weight, **BY/P**: Biological yield per plant (g), **HI**: Harvest index and **SY/P**: Seed yield per plant (g)

Table 3. Mean performance for fourteen characters of soybean genotypes

S.N.	**Genotypes**	**DFF**	**DM**	**PH**	**NPB/P**	**NC/P**	**NPo/C**	**NPo/P**	**NS/Po**	**PoL**	**HSW**	**Oil %**	**BY/P**	**HI**	**SY/P**
1	**T1**	78.83	137.33	61.97	4.64	12.22	3.24	115.00	2.30	3.47	6.38	17.73	63.09	28.38	16.33
2	**T2**	79.50	148.00	77.46	3.64	2.56	2.24	73.64	2.32	2.81	3.10	14.90	20.85	24.79	4.86
3	**T3**	48.83	107.17	30.53	2.42	1.42	1.15	22.33	1.64	4.05	13.47	22.76	24.08	26.06	5.76
4	**T4**	75.50	136.83	44.86	3.53	9.69	2.83	68.47	2.30	3.34	5.53	20.52	32.79	23.17	7.28
5	**T5**	48.67	114.50	52.75	3.69	5.97	2.19	57.00	2.00	3.17	7.03	18.93	27.78	25.71	6.84
6	**T6**	39.00	98.50	28.27	2.97	4.44	3.14	36.78	2.08	3.34	12.00	22.73	23.90	38.90	7.99
7	**T7**	52.17	113.67	39.67	3.92	4.97	2.49	64.08	2.07	2.86	6.20	19.20	23.18	31.67	7.02
8	**T8**	71.17	143.33	58.90	4.28	15.72	3.12	111.44	2.17	2.94	3.79	14.17	34.94	24.03	8.48
9	**T9**	49.50	106.00	55.11	3.28	5.17	2.79	55.22	2.03	3.30	8.80	20.80	31.74	29.28	8.80
10	**T10**	49.83	108.00	48.94	3.61	5.97	2.79	51.03	1.85	3.26	13.39	21.70	37.54	35.48	12.24
11	**T11**	49.83	109.17	44.62	3.89	4.03	2.39	60.33	2.32	3.41	7.30	20.50	33.38	28.59	9.12
12	**T12**	72.00	133.50	56.62	4.11	6.11	2.92	69.47	2.25	3.20	6.87	20.80	32.02	28.84	9.02
13	**T13**	32.83	91.33	29.90	2.42	0.31	0.58	10.92	2.52	4.09	12.21	21.47	9.60	33.30	2.98
14	**T14**	77.83	148.00	71.99	3.50	3.92	2.05	82.33	2.34	2.85	2.82	15.50	21.86	24.29	5.12
15	**T15**	64.67	133.00	45.73	3.97	4.69	2.59	47.94	2.17	3.13	7.66	20.33	25.30	26.00	6.55
16	**T16**	34.50	89.33	26.71	1.06	0.56	0.82	11.03	2.33	3.98	13.04	22.25	10.06	38.19	3.05
17	**T17**	49.67	113.33	39.79	3.17	3.72	2.35	50.06	1.96	2.89	7.00	22.10	22.69	32.36	6.44
18	**T18**	63.83	135.00	47.13	3.53	1.83	1.63	42.22	2.34	3.54	8.40	20.47	30.39	24.06	6.37
19	**T19 (check)**	49.50	100.00	32.91	2.89	3.72	3.12	38.47	2.08	2.97	9.24	21.28	19.03	36.71	6.37
20	**T20**	39.17	98.83	31.60	3.28	3.47	2.40	28.56	2.21	3.51	12.23	22.70	21.36	35.48	6.06

Grand mean	**56.34**	**118.24**	**46.27**	**3.39**	**5.03**	**2.34**	**54.82**	**2.16**	**3.30**	**8.32**	**20.04**	**27.28**	**29.76**	**7.33**
CD at 5%	**2.17**	**2.54**	**4.01**	**0.57**	**1.78**	**0.58**	**11.80**	**0.18**	**0.14**	**0.35**	**1.14**	**7.11**	**3.15**	**2.04**

Table 4. Fourteen morphological traits in soybean with estimated genetic parameters

Sl.No	**Character**	**Coefficient of variation**			**h² (%) (broadsense)**	**Genetic Advance**	**Genetic Advance as percent of mean**
		PCV%	**GCV%**	**ECV%**			
1	**DFF**	15.60	15.23	3.35	95.39	17.27	30.65
2	**DM**	9.32	9.13	1.87	95.97	21.77	18.41
3	**PH**	19.05	17.50	7.54	84.34	15.32	33.10
4	**NPB/P**	19.26	12.65	14.53	43.15	0.58	17.12
5	**NC/P**	51.79	41.64	30.80	64.65	3.47	68.98
6	**NPo/C**	27.90	17.71	21.55	40.31	0.54	23.16
7	**NPo/P**	33.99	28.37	18.72	69.67	26.74	48.78
8	**NS/Po**	8.74	5.07	7.11	33.72	0.13	6.07
9	**PoL**	7.61	6.59	3.81	74.99	0.39	11.76
10	**HSW**	23.29	23.00	3.66	97.53	3.89	46.78
11	**Oil%**	8.71	7.18	4.93	68.01	2.45	12.21
12	**BY/P**	32.02	22.63	22.65	49.94	8.98	32.94
13	**HI**	13.21	9.49	9.19	51.59	4.18	14.04
14	**HSW**	32.89	22.31	24.17	46.00	2.29	31.16

Abbreviations: DFF: Days to 50% flowering, **DM:** Days to maturity, **PH**: Plant height (cm), **NPB/P**: Number of primary branches per plant, **NC/P**: Number of clusters per plant, **NPo/C**: Number of pods per cluster, **NPo/P**: Number of pods per plant, **NS/Po**: Number of seeds per pod, **PoL**: Pod length (cm), **HSW**: Hundred seed weight, **BY/P**: Biological yield per plant (g), **HI**: Harvest index and **SY/P**: Seed yield per plant (g).

CONCLUSION

Among the evaluated genotypes, specifically T1, T8, T9, T10, T11, and T12, emerged as standout performers with yields exceeding 8.41 per plant, effectively surpassing the check variety JS-9752's yield of 6.37. This observation holds promise for advancing cultivar quality. Traits such as the number of clusters per plant, number of pods per plant, and 100 seed weight, boasting high heritability and GA%, emerge as focal points for optimizing yield. The study's outcomes underscore substantial genetic variability, offering a platform to harness additive gene effects, transgressive segregation, and heterosis to amplify yield production potential.

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