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Assessment of grain yield and simultaneous selection of soybean using the WAASB approach

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Abstract

Soybean is one of the major oilseed crops cultivated in India, with a large proportion of its production occurring under rainfed conditions. In this study, seven soybean genotypes were evaluated across three locations during the kharif 2024-25. Stability was assessed using the Weighted Average of Absolute Scores (WAASB), a mixed-model approach based on best linear unbiased predictions (BLUPs) that incorporates the effects of all Interaction Principal Component Axes (IPCA). Among the evaluated genotypes, ASb 169 recorded the lowest WAASB score (5.56), indicating superior stability; however, its mean grain yield (2,220 kg ha⁻¹) was lower than the overall trial mean (2,329 kg ha⁻¹). To simultaneously assess productivity and stability, the Weighted Average of Absolute Scores and Yield (WAASBY) index was employed. Genotype ASb 185 achieved the highest WAASBY score (73.41), reflecting its superior grain yield (2,669 kg ha⁻¹) together with broad adaptability across test environments. Multi-trait performance was further evaluated using the Multi-Trait Stability Index (MTSI), which identified ASb 169 as the most desirable genotype for early maturity and stable performance, making it a valuable parent for soybean improvement programmes. Correlation analysis revealed that 100-seed weight, number of pods per plant, and plant height were positively associated with grain yield, suggesting their usefulness as indirect selection criteria in breeding. Genotypic cluster analysis also identified ASb 169 as the most genetically divergent genotype, possessing the highest mean 100-seed weight (14.8 g), thereby highlighting its potential as a promising parental line for the development of high-yielding soybean cultivars.

Keywords: Soybean, WAASB, stability and MSTI

Introduction

Soybean (*Glycine max* (L.) Merr.) is an important oilseed crop in India and is predominantly cultivated under rainfed conditions, where productivity is strongly influenced by seasonal rainfall variability and other climatic uncertainties. In recent years, increasing climate variability has further intensified yield instability, making the development of resilient and high-yielding soybean cultivars a key priority in breeding programmes.

The success of soybean improvement programs depends not only on achieving higher productivity but also on ensuring stable performance across diverse environments. Traits such as early maturity, broad adaptability, and tolerance to environmental fluctuations are particularly important for integrating soybean into existing cropping systems and minimizing exposure to terminal drought stress (Nataraj *et al.*, 2020) [5]. Grain yield in soybean is a complex quantitative trait influenced by multiple genes and is highly sensitive to environmental variation. As a result, genotype performance often varies considerably across locations and seasons due to genotype × environment interaction (GEI). This interaction complicates selection decisions but also provides valuable information for identifying genotypes with either wide or specific adaptation.

Traditional approaches such as the Additive Main Effects and Multiplicative Interaction (AMMI) model have been widely used for interpreting GEI patterns. However, AMMI-based methods primarily rely on fixed-effect assumptions and may not fully capture the advantages of mixed-model frameworks. On the other hand, BLUP-based approaches offer more accurate prediction of genotypic performance by treating genotypic effects as random, though they lack intuitive graphical interpretation of GEI patterns. To address these limitations, recent advances

have introduced mixed-model-based stability statistics such as the Weighted Average of Absolute Scores from BLUPs (WAASB) (Olivoto and Lúcio (2020) [8]. This method integrates information from all significant interaction principal components, providing a more comprehensive representation of genotype stability. Unlike earlier stability measures that rely on limited interaction axes, WAASB incorporates the full structure of GEI while assigning proportional weights based on explained variance.

However, selecting genotypes based solely on stability may overlook yield potential. To overcome this limitation, the WAASBY index combines mean performance and stability into a single selection criterion, allowing breeders to adjust the importance of each component depending on breeding objectives. In multi-trait breeding scenarios, simultaneous selection becomes even more complex. The Multi-Trait Stability Index (MTSI), derived from the WAASBY framework, enables the identification of genotypes that perform closer to an ideal genotype across several traits simultaneously (Olivoto *et al.*, 2019, 2019b) [9, 10].

In this context, the present study was conducted to (i) evaluate yield stability in soybean genotypes using WAASB, (ii) identify high-yielding and stable genotypes through the WAASBY index, and (iii) perform simultaneous multi-trait selection using MTSI for grain yield and related agronomic traits.

Materials and Methods

Materials and Environments

In the present investigation, a total of seven soybean genotypes, namely ASb 153, ASb 169, ASb 185, Basara, AISb 50, JS 335, and JS 93-05, were studied. The experimental genotypes were developed at the Agricultural Research Station, Adilabad, Telangana, using diverse parental combinations. Multi-environment trials were conducted during the kharif 2024-25 at three representative locations across Telangana to assess genotype performance, stability, and adaptability under varying agro-climatic condition

Experimental method

The experiment was conducted in randomized block design with three replications in 8 rows of 5 m length with row to row spacing of 45 cm and accommodating 21 plants per meter. Data was recorded on nine quantitative traits *i.e.*, days to 50% flowering, plant height (cm), days to maturity, number of clusters per plant, number of pods per plant, first pod height (cm), number of branches per plant, 100 seed weight (g) and grain yield (kg ha⁻¹). The data for days to maturity was recorded on line basis at 90% pod maturity and each genotype was represented by a single value. Ten plants randomly selected from each replication were used to record data. The genotypes were harvested upon reaching the R8 growth stage according to the classification of Fehr *et al.* (1971) [4]. Grain yield was determined for each genotype and expressed as kg ha⁻¹. To estimate seed size, a randomly selected sample of 100 seeds from each genotype was weighed, and the results were recorded in grams. The broad-sense heritability (h^2_{BS}), selection differential (SD), selection differential percentage (SD%) and selection gain in percentage (SG%) were calculated as per standard formula (Olivoto and Nardino, 2020) [8].

The details have been given below

$$1. h^2_{BS} = (V_{gen}) / (V_{gen} + V_{res}),$$

Where V_{gen} = genotypic variance, V_{res} = residual variance.

$$2. SD = X_s - X_o \text{ where,}$$

X_s = mean of the selected genotypes, X_o = mean of the original population.

$$3. (SD\%) = (X_s - X_o) \times 100$$

$$4. (SG\%) = [(X_s - X_o) \times h^2_{BS} / X_o] \times 100$$

Statistical Analyses

A combined analysis across environments was carried out to partition variation into genotype, environment, and genotype $\times$ environment interaction (GEI) effects. Variance components were estimated using a mixed-model framework, where genotypic effects were treated as random to obtain best linear unbiased predictions (BLUPs). Stability of genotypes was evaluated using the Weighted Average of Absolute Scores from the BLUP-based GEI matrix (WAASB) (Olivoto *et al.* (2019a) [9]. This approach is derived from the singular value decomposition of the interaction matrix and considers all significant interaction principal components. Genotypes with lower WAASB values are interpreted as more stable due to reduced fluctuations across environments.

To jointly evaluate yield performance and stability, the WAASBY index was employed. This index integrates standardized mean performance and WAASB-based stability into a single superiority measure. Depending on breeding objectives, different weights can be assigned to yield and stability; in the present study, 65% weight was assigned to grain yield and 35% to stability. Higher WAASBY values indicate genotypes that combine superior productivity with consistent performance across environments.

For simultaneous selection of multiple traits, the Multi-Trait Stability Index (MTSI) was applied (Olivoto *et al.*, 2019b) [10]. This index is based on the distance of each genotype from an ideotype defined by optimal values of all traits considered. Genotypes with lower MTSI values are considered closer to this ideotype and are therefore preferred for selection in breeding programs targeting multiple traits simultaneously.

All statistical analyses were performed using the R package “metan” (Olivoto & Lúcio, 2020) [8], which facilitates mixed-model analysis, stability estimation, and multi-trait selection procedures.

Results

Mean performance of genotypes and environments

Mean performance of genotypes for different traits in different environments is shown in Table 1.1, 1.2 & 1.3. For days to flowering, grand mean was 39.1, with a range of 35.0 (genotype ASb 185 in E1 environment to 45.0 (Basara in E1). Environments E16 and E5 had the lowest (30) and highest (71.26) means. Genotype ASb 185 had the lowest (36.4) and Basara had the highest (42.0) mean for days to flowering. Similarly, for 100-seed weight, the grand mean was 13.0 g, with a range of 10.5 g (Basara in E3) to 15.0 g (ASb 169 in E2). Genotypes Basara (11.4 g) and ASb 169 (14.8 g) had the lowest and highest mean 100-seed weight. Similarly, grain yield ranged from 1450 kg ha⁻¹ (Basara in E3) to 3328 kg ha⁻¹ (G3ASb 185 in E1), with a grand mean of 2329 kg ha⁻¹. The genotypic mean for grain yield was lowest in Basara (2046 kg ha⁻¹) and highest in ASb 185 (2669 kg ha⁻¹).

Pooled ANOVA

A pooled analysis of variance (ANOVA) was performed for all the traits evaluated. The results revealed that the genotypic effects were highly significant ($p < 0.01$) for all traits.

WAASB-based stability analysis

Based on WAASB-based stability scores for the different

genotypes under study, ASb 169 (5.56) was found to be highly stable, whereas ASb 153 (12.78) was found to be highly unstable, followed by Basara (11.79), JS 93-05 (11.35) and ASb 185 (11.04) (Table 2). Simultaneous interpretation of productivity, stability, and environments is done using WAASB biplot, with quadrants containing four different classes of genotypes and environments (Fig. 1). In the first quadrant, highly unstable genotypes and highly discriminating environments are included. Genotype, JS 93-05 being most unstable (*i.e.*, having its mean below the grand mean), is included in this quadrant. Unstable genotype ASb 153 having its mean greater than grand means is included in the second quadrant. Environments Adilabad and Rudrur were discriminative (*i.e.*, their environmental means were found to be greater than the grand mean). The third quadrant included stable, widely adapted, and low yielding genotypes having their mean lower than the grand mean. A lower value of WAASB indicates a higher magnitude of stability. Stable genotypes included in this quadrant are Basara, AISb 50 and ASb 169. Environment, Mudhole can be considered low productive with lesser discriminating ability. Similarly, in the fourth quadrant, widely adapted, high-yielding (genotypic means greater than grand mean) genotypes with low WAASB scores are included. They are JS 335 and ASb 185. This quadrant was found to be less discriminative but more productive.

WAASBY Index-Ranking of genotypes

Simultaneous selection for grain yield and stability was performed using the WAASBY index, assigning weights of 65% to grain yield and 35% to WAASB (Table 2). Among the genotypes evaluated, ASb 185 recorded the highest WAASBY score (73.41). In the biplot (Fig. 1), this genotype was positioned in the fourth quadrant. The lowest WAASBY value was observed for Basara (4.79), followed by AISb 50 (24.01) and JS 93-05 (33.60). Basara and AISb 50 were grouped in the third quadrant, whereas JS 93-05 was located in the first quadrant.

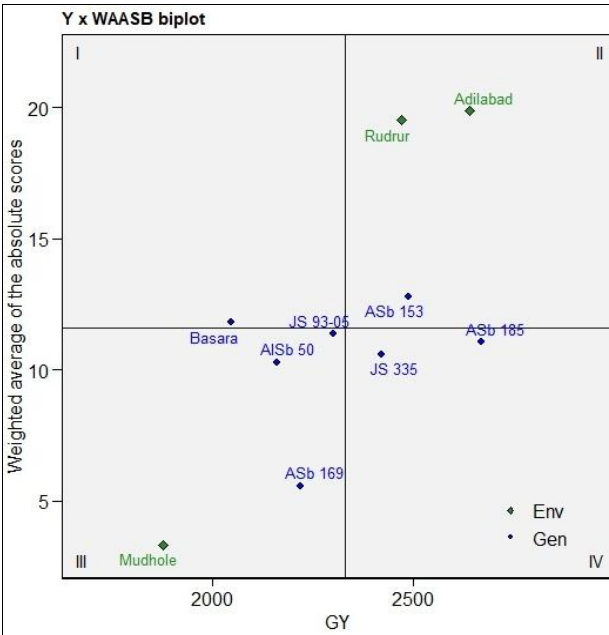


Fig 1: Biplot of grain yield (kg ha⁻¹) vs. weighted average of the absolute scores

MTSI analysis

Multi-trait stability analysis was conducted with the objective of identifying genotypes combining high grain yield and early

maturity. Based on MTSI at 15% selection intensity, ASb 169 was selected (Fig. 2). Mean grain yield of selected genotypes (2220 kg ha⁻¹) was less than the grand mean (2329 kg ha⁻¹), and mean 100 seed weight of selected genotypes (14.8g) was greater than the grand mean (13.0g). Selection differentials for the trait means were -109.0 and -0.206 for grain yield and days to maturity, respectively. The broad-sense heritability (*h*²) ranged from 0.125-0.90. Very high value of heritability was recorded for number of clusters per plant suggesting a strong likelihood of genetic gains.

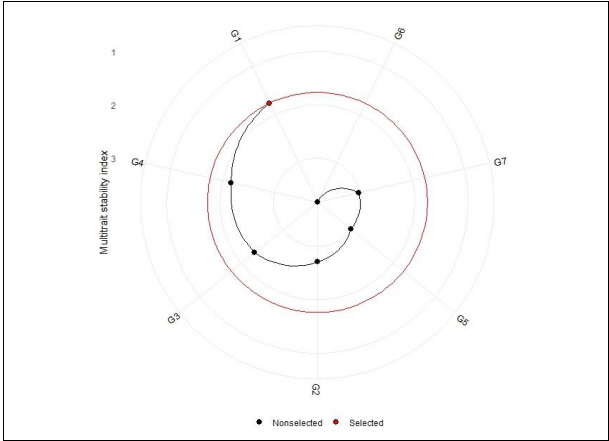


Fig 2: MGIDI index analysis for the genotypes under study for selection of ideal genotypes

Note: G1- ASb 169; G2 -AISb 50, G3-JS 335, G4- ASb 185, G5-JS 93-05, G6-Basara and G7-ASb 153

Correlation

For correlation analysis, grain yield (GY) was considered as dependent parameter and other parameters, namely, days to 50% flowering (DTF), days to maturity (DTM), number of pods per plant (POD), number of clusters per plant (CLS), number of branches per plant (BRN), plant height (PH), first pod height (FPH) and 100-seed weight (HSW) were counted as independent parameters. Through correlation, it was found that HSW, PHA and POD were significantly and positively correlated with grain yield (Fig.3).

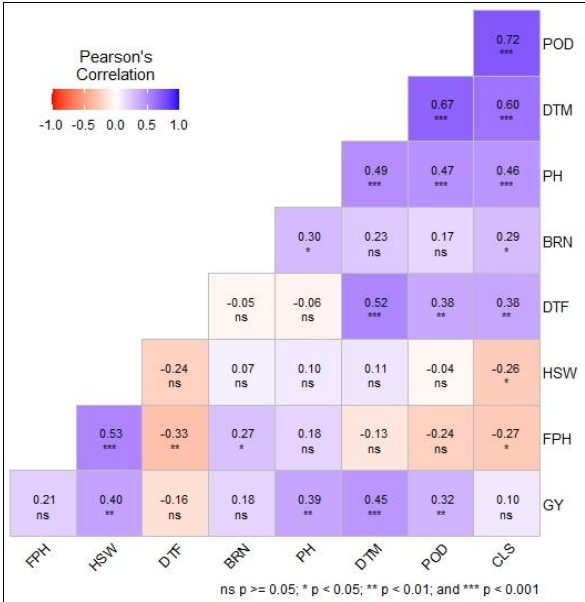


Fig 3: Association of the yield and its attributing traits

Cluster analysis

Two groups were discovered from the dendrogram that resulted from the combined data of the growth and yield metrics among 07 genotypes (Fig. 4). According to this cluster analysis, four genotypes, AISb 50, Basara, ASb 169, JS 335 were grouped in one cluster and three genotypes ASb 185, ASb 153, JS 93-05 were grouped into another cluster. Based on the genetic diversity, the genotypes of cluster I and cluster II can be crossed to obtain high yielding varieties.

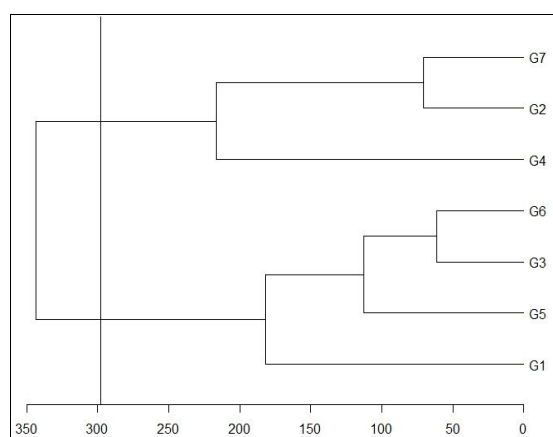


Fig 4: Cluster diagram of soybean genotypes

Discussion

Genotype $\times$ environment interaction plays a decisive role in determining the performance of soybean genotypes across multi-environment trials. In the present study, the significant contribution of environmental variation to total phenotypic expression of grain yield highlights the strong influence of external conditions on crop performance under rain fed agro-ecosystems variability (Bhartiya *et al.*, 2018; Nataraj *et al.*, 2021) ^[2, 6]. Similar patterns have been widely reported in soybean, where environmental heterogeneity tends to outweigh genetic effects in determining yield stability, particularly under variable rainfall regimes.

The relatively low proportion of genotypic variance compared to environmental and GEI components indicates that direct selection based solely on mean performance may not be sufficient for reliable cultivar recommendation. This also explains the reduced heritability observed for grain yield, emphasizing the importance of multi-environment evaluation for effective selection in soybean breeding programmes.

Traditional stability approaches such as AMMI provide useful visualization of GEI; however, they rely heavily on a limited number of interaction principal components, which may not fully capture the complexity of genotype responses across environments (Bocianowski *et al.*, 2019) ^[3]. In contrast, the WAASB approach (Olivoto *et al.*, 2019a) ^[9] integrates information from all significant interaction axes, thereby offering a more comprehensive and balanced measure of

stability. This improves the discrimination of genotypes based on their overall interaction pattern rather than relying on a single dominant component.

In the present study, WAASB analysis identified ASb 169 as the most stable genotype across environments. However, its relatively moderate grain yield indicates that stability alone does not necessarily translate into superior agronomic performance. This observation reinforces the need to combine stability with productivity when making selection decisions in breeding programmes. To address this limitation, the WAASBY index was used to integrate yield and stability into a single selection framework (Olivoto *et al.*, 2019a) ^[9]. The results showed that genotypes with high yield potential but moderate stability, such as ASb 185, achieved superior WAASBY scores, indicating their suitability for broader adaptation. This confirms that selection based on combined indices is more effective than independent evaluation of yield or stability alone, particularly in multi-environment testing scenarios. These results are in accordance with Nataraj *et al.* (2021b) ^[7].

The Multi-Trait Stability Index (MTSI) further extended the selection framework by allowing simultaneous consideration of multiple agronomic traits. In this study, MTSI identified ASb 169 as the closest genotype to the ideotype defined by yield, maturity, and related traits. Although its grain yield was slightly below the trial mean, its superiority in early maturity and favorable trait combination makes it a valuable genetic resource for breeding programs targeting crop duration optimization and adaptation to short-season environments. Similar results were found with Nataraj *et al.* (2021b) ^[7].

Correlation analysis revealed that grain yield was positively associated with 100-seed weight, plant height, and number of pods per plant, indicating that these traits contribute significantly to yield formation. These relationships suggest that indirect selection through component traits may enhance selection efficiency in soybean improvement programs, especially when direct selection for yield is constrained by strong environmental influence consistent with Similar results were observed with Bhartiya & Aditya, 2016 ^[1]; Wang *et al.*, 2012 ^[13].

Cluster analysis demonstrated considerable genetic divergence among the evaluated genotypes, indicating the presence of useful variability for breeding. The grouping pattern suggests that crosses between genetically distinct clusters may generate greater variability in segregating populations. Among the tested genotypes, ASb 169 exhibited notable divergence and desirable seed weight characteristics, making it a promising parental line for future hybridization programmes aimed at improving yield and adaptation.

Overall, the integration of WAASB, WAASBY, and MTSI approaches provided a comprehensive framework for evaluating genotype performance across environments and traits. This multi-criteria strategy improves selection accuracy and enhances the identification of genotypes combining yield potential, stability, and adaptability under variable environmental conditions.

Table 1.1: Mean performance of genotypes and environments (E1- Adilabad; E2-Rudrur; E3: Mudhole)

Entry name	Plant height (cm)				Days to 50% flowering				Days to maturity			
	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM
Basara	79.5	81.7	41.5	67.6	45.0	40.3	40.7	42.0	114.3	105.0	90.0	103.1
ASb 153	49.7	63.4	46.0	53.0	37.7	36.7	38.0	37.5	98.7	95.3	85.3	93.1
AISb 50	60.0	69.0	51.4	60.1	44.3	38.0	39.0	40.4	112.3	102.0	88.0	100.8
ASb 185	79.5	74.8	64.7	73.0	35.0	36.3	38.0	36.4	96.3	97.7	86.7	93.6
JS 93-05	47.8	62.9	45.5	52.1	37.7	36.7	38.7	37.7	96.0	96.7	86.0	92.9
ASb 169	55.0	69.9	57.9	60.9	42.0	37.0	37.7	38.9	97.7	95.3	85.0	92.7
JS 335	55.6	68.4	49.5	57.8	41.7	38.7	42.0	40.8	108.0	103.3	90.7	100.7

Table. 1.2: Mean performance of genotypes and environments (E1- Adilabad; E2-Rudrur; E3: Mudhole

Entry name	Number of branches per plant				Number of clusters per plant				Number of pods per plant			
	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM
Basara	1.2	4.5	2.7	2.8	17.5	18.5	15.3	17.1	77.1	60.2	54.0	63.8
ASb 153	2.6	2.2	2.0	2.3	13.7	9.9	7.8	10.5	59.3	38.1	42.0	46.5
AISb 50	2.7	4.0	1.8	2.8	15.1	16.2	15.2	15.5	59.1	63.8	50.3	57.7
ASb 185	1.5	3.9	2.4	2.6	13.9	11.9	12.0	12.6	56.7	58.0	45.0	53.2
JS 93-05	2.3	3.1	1.6	2.3	9.9	9.4	9.9	9.7	43.9	43.3	43.0	43.4
ASb 169	2.9	1.9	2.3	2.4	12.8	11.4	10.1	11.4	53.7	51.8	41.0	48.8
JS 335	2.3	2.7	1.8	2.3	13.3	15.2	9.7	12.7	50.1	76.7	48.0	58.3

Table. 1.3: Mean performance of genotypes and environments (E1- Adilabad; E2-Rudrur; E3: Mudhole

Entry name	First pod height (cm)				100 seed weight (g)				Seed yield (kg ha ⁻¹)			
	E1	E2	E3	GM	E1	E2	E3	GM	E1	E2	E3	GM
Basara	6.0	10.7	5.4	7.4	12.2	11.5	10.5	11.4	2114	2573	1450	2046
ASb 153	8.3	10.5	6.5	8.4	13.8	12.7	13.1	13.2	3118	2223	2120	2487
AISb 50	5.7	8.5	6.6	6.9	14.1	14.0	11.1	13.1	2787	2113	1579	2160
ASb 185	8.1	8.7	9.0	8.6	13.2	13.6	12.8	13.2	3328	2633	2044	2669
JS 93-05	8.9	15.0	7.2	10.4	13.8	13.3	12.7	13.3	2244	2767	1892	2301
ASb 169	15.3	13.0	12.4	13.6	14.9	15.0	14.6	14.8	2509	2125	2024	2220
JS 335	5.8	7.5	6.5	6.6	12.9	12.9	11.1	12.3	2374	2852	2029	2419

Table 2: Mean grain yield and WAASB and WAASBY scores of genotypes under study

Code	Grain yield	rRESP	WAASB	rWAASB	WAASBY	rWAASBY
AISb 50	2160	6	10.28	2	24.01	6
ASb 153	2487	2	12.78	7	46.08	4
ASb 169	2220	5	5.56	1	53.11	2
ASb 185	2669	1	11.04	4	73.41	1
Basara	2046	7	11.79	6	4.79	7
JS 335	2419	3	10.57	3	49.6	3
JS 93-05	2301	4	11.35	5	33.6	5

Note: rRESP, genotype ranking based on grain yield; rWAASB, genotype ranking based WAASB; rWAASBY, genotype ranking based WAASBY.

Table 3: Estimates of selection differential, selection gain and heritability based on MGIDI for eight quantitative traits

Trait	Xo	Xs	SD	h ²	SG	SG percentage
Number of pods per plant	53.1	48.8	-4.27	0.567	-2.42	-4.56
Days to 50% flowering	39.1	38.9	-0.206	0.746	-0.154	-0.394
Days to maturity	96.7	92.7	-4.03	0.836	-3.37	-3.49
Number of clusters per plant	12.8	11.4	-1.36	0.900	-1.22	-9.54
First pod height (cm)	8.84	13.6	4.72	0.827	3.91	44.2
100 seed weight (g)	13.0	14.8	1.8	0.883	1.59	12.2
Grain yield (kg ha ⁻¹)	2329	2220	-109	0.125	13.7	-0.588
Plant height (cm)	60.8	60.9	0.098	0.738	0.0726	0.119

Conclusion

In the current study, for grain yield, variation was predominantly contributed by environment, indicating its importance in soybean multi-environmental trials. With the lowest WAASB score, ASb 169 was found to be highly stable. The WAASBY was highest for the genotype ASb 185, indicating its potential as a high-yielding and more widely adaptable genotype. Genotype ASb 169 was found to have the lowest MTSI score for early maturity and high grain yield and therefore can be used as a potential parent in breeding for higher yield and early maturity. Direct selection for grain yield can be done through 100-seed weight, plant height and number of pods per plant. The divergent genotype ASb 169 with highest 100-seed weight can be used as a parent aiming exclusively for higher yield.

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Competing Interests

Authors have declared that no competing interests exist.

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