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Multi-trait selection and genetic evaluation of soybean (*Glycine max* L.) advanced lines for enhanced yield performance

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Abstract

In the present study, eleven soybean genotypes along with two commercial checks (JS 335 and AISb 50) were evaluated for grain yield and its attributing traits over two seasons, *kharif,* 2023 and *kharif,* 2024, at the Agricultural Research Station, Adilabad, PJTAU, Telangana, India. The study aimed to identify superior lines for yield, assess the variability among advanced lines, and examine trait associations. Among the evaluated genotypes, ASb-101 recorded the highest mean grain yield (3665 kg/ha), followed by RSC-11-95 (3606 kg/ha), KSS-225 (3596 kg/ha), and MAUS 816 (3544 kg/ha), outperforming the best check variety AISb 50 (3110 kg/ha) across seasons. Using the MGIDI index, ASb-101 and MAUS-816 were identified as the best-performing genotypes when considering all measured traits. Cluster analysis indicated significant genetic diversity, particularly in Cluster III, suggesting potential for heterosis through crosses between genetically distant clusters. Correlation analysis showed that 100-seed weight was significantly and positively associated with grain yield over two seasons. The genotypes identified in this study represent valuable resources for direct varietal release or for further large-scale through adoptive trials in farmers' fields.

Keywords: Soybean, MGIDI, correlation and cluster analysis

Introduction

Soybean is a major oilseed crop in India, predominantly cultivated under rainfed conditions across an area of approximately 12.9 million hectares, with a total production of 15.10 million tonnes and an average productivity of 1170 kg ha^{-1} (DE & S, 2024). Despite being one of the leading soybean-producing countries, India remains heavily dependent on edible oil imports, currently importing about 16.5 million tonnes annually. The value of India's edible oil imports has increased sharply from USD 2.2 billion in 2006-07 to nearly USD 15 billion during 2023-2024. In contrast, India is a significant exporter of soybean meal, exporting soymeal worth approximately USD 1.11 billion to international markets.

Although India ranks fifth in global soybean production, its productivity is considerably lower than that of major soybean-producing countries such as Brazil, the USA, Argentina, and China. The predominance of rainfed cultivation, coupled with susceptibility to biotic stresses, is a major factor contributing to low soybean productivity in the country. Therefore, the identification and development of widely adapted, high-yielding, and disease-resistant soybean genotypes is a critical step toward enhancing productivity and ensuring sustainability of soybean cultivation in India.

Globally, soybean yield improvement is constrained by the narrow genetic variability within *G. max*, which restricts the development of cultivars with enhanced stress tolerance and resistance. Most released soybean varieties can be traced back to a limited number of ancestral genotypes (Delannay *et al*. 1983; Bisen *et al*. 2015; Kumawat *et al*. 2015) [2, 1, 4]. This genetic narrowing is largely a consequence of domestication and intensive breeding, although substantial gains in yield have been achieved through hybridization among elite genotypes (Thorne and Fehr 1970) [13]. Broadening the genetic base through the use of exotic germplasm, wild relatives, and multi-parent breeding populations is therefore critical for sustainable genetic improvement.

Improving soybean yield potential requires a comprehensive understanding of genetic variability and the interrelationships among yield and yield-attributing traits. The development of climate-resilient ideotypes demands an integrated breeding approach supported by detailed characterization of diverse germplasm for economically important agronomic and physiological traits. Germplasm resources play a vital role in cultivar development through trait introgression, and globally, more than 170,000 soybean germplasm accessions are conserved for this purpose. Systematic evaluation of promising and well-adapted breeding lines is thus essential to enhance soybean productivity and sustainability in India.

Precise estimation of genotypic values is a prerequisite for effective selection and varietal recommendation. Breeders often aim to improve multiple traits simultaneously rather than yield alone. Traditionally, multi-trait selection has been performed using linear selection indices such as the Smith-Hazel (SH) index. However, the effectiveness of the SH index is often limited by multi-collinearity among traits and subjective assignment of economic weights, which can reduce selection efficiency. To address these limitations, the multi-trait genotype-ideotype distance index (MGIDI) proposed by Olivoto and Nardino (2020) [9] has been developed. The MGIDI index effectively accounts for multi-collinearity and enables simultaneous optimization of multiple traits by integrating both favorable and unfavorable selection directions.

Multivariate analytical tools such as principal component analysis (PCA) and linear discriminant analysis have been widely employed to study trait relationships in field experiments. Although these methods effectively explain trait associations, they offer limited support for ranking genotypes based on multiple traits simultaneously. The MGIDI approach provides a robust framework for multi-trait genotype ranking and has been successfully applied in several crop improvement studies to identify superior genotypes.

With this background, the present investigation was undertaken with the following objectives:

1. To develop and evaluate advanced soybean breeding lines for yield and yield-attributing traits.
2. To assess the genetic variability among advanced breeding lines.
3. To determine the association among yield and related traits using correlation and multivariate approaches.

Materials and Methods

Experimental site

The experiments were conducted over two seasons at Agricultural Research Station, Adilabad (ARS. Adilabad) PJTAU during *kharif*, 2023 and *kharif*, 2024. In the present study, the advanced lines were evaluated and handled in accordance with relevant guidelines and regulations of the PJTAU & ICAR-NSRI, Indore.

Experimental details

Evaluation of for eleven soybean advanced breeding lines along with two commercial check varieties (JS 335 and AISb 50) were evaluated in three replicates with 8 rows of 5 metres length for each genotype for grain yield and attributing traits. The eleven lines were evaluated for two seasons 2023 and 2024 (June-October) at experimental fields of Agricultural Research Station, Adilabad, PJTAU, Telangana, India to select the best genotypes. The data on days to 50% flowering, plant height (cm), days to maturity, number of branches per plant, number of pods per plant, number of clusters per plant, first pod height (cm), number of seeds per pod and 100-seed weight (g) were recorded on five randomly selected plants on each genotype in all the three replicates using standard procedure (IBPGR, 1984) [3]. Grain yield was recorded in kg on plot basis for each genotype in all replications. Then converted to kg/ha using conversion factor. 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) [9].

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=Xs−Xo where,

Xs =mean of the selected genotypes, Xo = mean of the original population.

3. (SD%) = (Xs -Xo) ×100

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

Data analysis

Pooled Analysis of Variance (ANOVA) was performed to compare thirteen genotypes including advanced breeding lines and check varieties. All the analyses have were carried out using R software version 4.2.1 (R Core Team 2022) [11]. Pooled Analysis of Variance (ANOVA) and MGIDI index were calculated using R package ‘metan’ (Olivoto and Lucio 2020) [8]. A least significant difference (l.s.d.) test was carried out using R package ‘agricolae’ (Mendiburu, 2021) [7]. Correlation analysis has been carried out using R package “Performance-Analytics” (Peterson & Carl, 2018) [10].

Results

In the present investigation, quantitative data of 13 soybean genotypes were subjected to ANOVA for 10 characters which are presented in Table 1. The mean sum of square was observed significant for all the characters studied except seeds per pods indicating that there is sufficient variation among the treatments. Two checks *viz*, JS 335 and AISb 50 were used for the comparison among 11 advanced breeding lines. The l.s.d. ($P = 0.05$) indicated variation for various traits studied for both the years (Table 2). For grain yield, the advanced lines performed better than the best checks over two years (Table 2). For instance, genotype, ASb-101 produced the highest mean grain yield (3665 kg/ha) followed by RSC-11-95 (3606 kg/ha), KSS-225 (3596 kg/ ha), MAUS 816 (3544 kg/ha) compared to the best check variety, AISb 50 (3110 kg/plot) over the two seasons (Tabe 2). Similarly, 100-seed weight was the highest in the entry, MACS 1810 (15.88 g) followed by MAUS 816 (15.74 g), RSC -11-95 (14.67 g), KSS- 225 (14.31 g), whereas the best check variety recorded only 13.76 g for 100-seed weight. The details of year-wise performance of the 13 genotypes are presented in Table 2.

Mean, selection differential and genetic gain

Overall mean of the genotypes was higher for grain yield (3320 kg/ha) for the 2023 season than in 2024 (3233 kg/ha). Similarly, means for other traits like branches per plant, 100-seed weight and first pod height were also higher in 2023 than 2024 season. The selection differential and selection gain were found to be higher for number of pods per plant, 100-seed weight, grain yield and seed per pod in 2024 season compared to 2023 season. The heritability was found to be high for all the traits for both years except clusters per plant in 2023 and seeds per pod in 2024 season (Table 3). Based on the genetic gain, ASb-101 and MAUS 816 were selected in both the seasons

Selection of genotypes based on MGIDI

The MGIDI index was applied within each crop season to select genotypes that perform well in specific conditions thus exploiting narrow adaptations. The multi-trait genotype-ideotype distance index (MGIDI) was calculated to identify best genotypes when considering all measured traits. The broad-sense heritability (h^2) ranged from 0.36-0.99 and 0.79-0.99 for the 2023 and 2024 seasons, respectively. Very high values of heritability were estimated for all traits except number of clusters per plant in 2023 and seeds per pod in 2024 under consideration, suggesting a strong likelihood of genetic gains.

ASb- 101 and MAUS 816 were selected as the best genotypes in both the seasons using the MGIDI index (Fig. 1 & Fig.2)

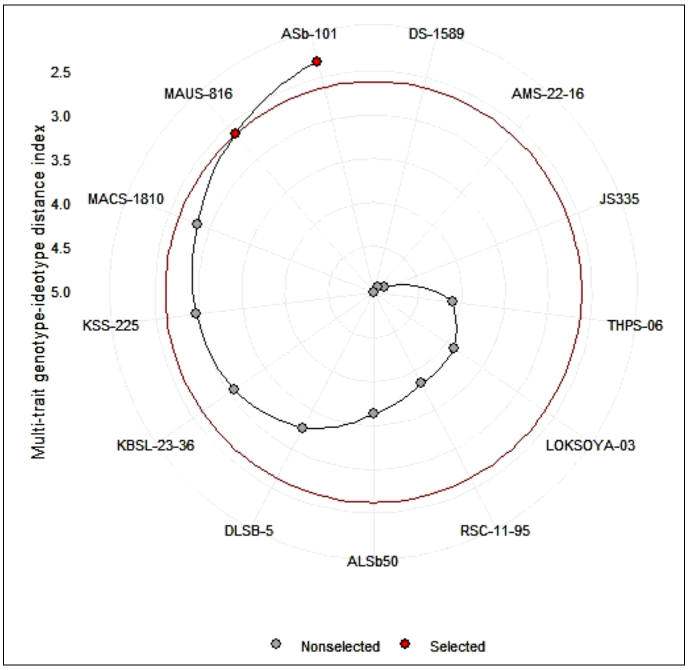

Fig 1: MGIDI index analysis for the 13 genotypes under study for selection of ideal genotypes during 2023

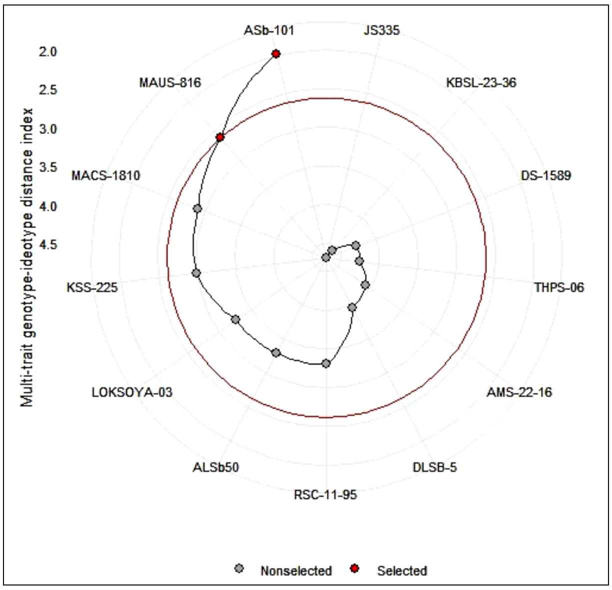

Fig 2: MGIDI index analysis for the 13 genotypes under study for selection of ideal genotypes during 2024

Cluster analysis

Three groups were discovered from the dendrogram that resulted from the combined data of the growth and yield metrics among 13 genotypes (Fig. 3). According to this cluster analysis, Group 1had highest number (07) of genotypes, while Group 2 had 2 and Group 3 had 4 genotypes. These findings demonstrated that there was a considerable amount of diversity among 3 groups that were examined in this group.

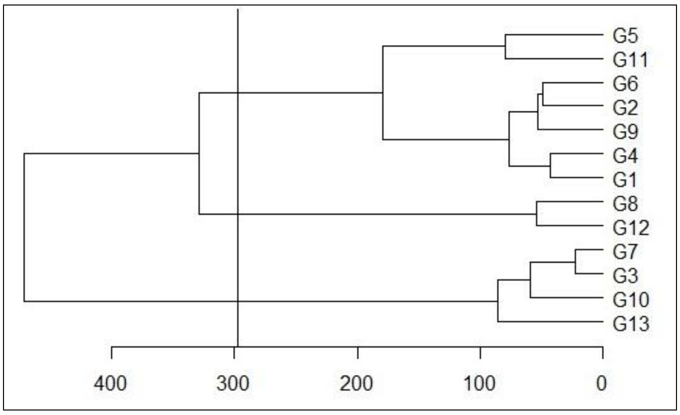

Fig 3: Cluster diagram of 13 soybean genotypes

Correlation analysis

For correlation analysis, grain yield (GY) was considered as dependent parameter and other parameters, namely, days to 50% flowering (DFT), days to maturity (DTM), number of pods per plant (POD), number of clusters per plant (CLS), number of branches per plant (BRC), number of seeds per pod (SPP), first pod height (FPH) and 100-seed weight (HSW) were counted as independent parameters. Through correlation, it was found that across the two seasons HSW were significantly and positively correlated with grain yield. Further, DTF had significant negative correlation with DTM, PHT, FPH and POD. The details of association among the yield and attributing traits are presented in Fig.4.

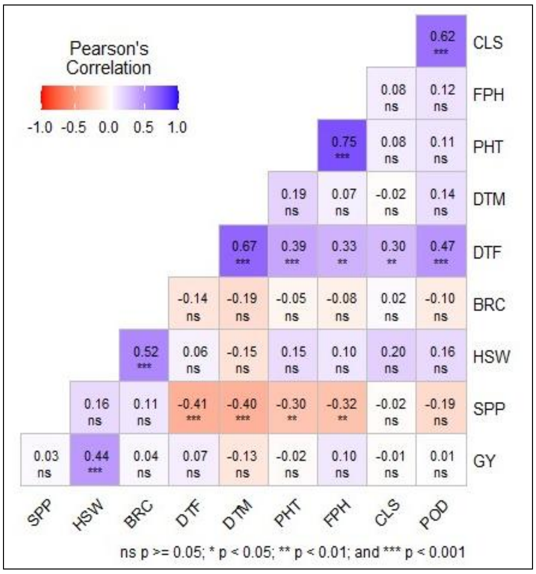

Fig 4: Association among the yield and attributing traits

Discussion

The utility of the MGIDI index for identifying ideal genotypes based on multiple traits has been well demonstrated for yield and yield-attributing traits in soybean (Maranna *et al*., 2023; Maranna *et al*., 2021) [5, 6]. In the present study, several genotypes were identified as superior based on MGIDI analysis across two seasons. An effort was made to dissect the performance of genotypes for yield and yield component traits under small field trial conditions. However, evaluation in larger plot sizes is essential to obtain a more realistic estimate of actual performance by minimizing experimental error. Accordingly, the superior genotypes identified in this study will be further evaluated in larger plots to confirm their superiority over the best check varieties.

MGIDI revealed clear differences among genotypes in their overall distance from the ideotype. Lower MGIDI values indicate closer proximity to the ideotype and, therefore, superior multi-trait performance. Among the evaluated genotypes, ASb-101 exhibited the lowest MGIDI value and was identified as the most desirable genotype, followed by MAUS-816 which also showed relatively small distances from the ideotype. These genotypes were selected as they combined favorable performance across multiple agronomic traits. In contrast, genotypes such as, THPS-06, JS335, AMS-22-16, and DS-1589 displayed higher MGIDI values, indicating greater deviation from the ideotype and comparatively inferior multi-trait performance. These genotypes were therefore not selected.

It is noteworthy that the genotypes, ASb-101, RSC -11-95, KSS-225 and MAUS 816 were identified as superior to the best check variety in grain yield over locations and will be evaluated in multi-location trial followed by adoptive trials for possible release as varieties across soybean-growing regions of Telangana state.

In cluster analysis, genotypes in the Group 3 are genetically more diverse and may carry unique traits crosses between genotypes belonging to different clusters—especially between Cluster III and Clusters I or II—are expected to produce greater heterosis and wider variability compared to crosses within the same cluster.

In the present investigation, grain yield showed a significant positive correlation with 100-seed weight, corroborating earlier reports (Shivakumar *et al*., 2011; Maranna *et al*., 2021) [12, 6]. These associations suggest that direct positive selection for this trait would be effective in improving grain yield in soybean. Grain yield exhibited weak or non-significant correlations with most phonological traits, except for its positive association with HSW, suggesting that yield improvement in this population may be more strongly influenced by seed weight than by flowering or maturity duration

Table 1: Pooled Analysis of Variation (ANOVA) for quantitative traits over two seasons (2023 & 2024)

Source of variation	df	MSS									
		PHT	DTF	DTM	HSW	CLS	POD	BRC	SPP	GY	FPH
Environment	1	315.60	29.53	92.62	13.88	0.33	21.24	9.48	3.77	148673	2.47
Genotypes	12	1781.32*	27.43*	117.348*	9.29*	8.90*	289.26*	0.93*	3.80	422656*	17.75*
Genotypes x Environment	12	102.84	3.17	29.82	1.57	4.90	170.55	0.63	7.11	476842	0.31
Residuals	48	9.22	0.20	0. 0. 49	0.07	2.15	13.28	0.12	2.49	34192	0.45
CV (% at 5%)		4.67	1.14	0 0.65	1.92	12.13	6.96	13.98	6.07	5.64	9.66

Where, PHT = Plant height (cm); DTF= Days to 50% flowering; DTM= Days to maturity; HSW= 100 seed weight (g);
CLS= Number of clusters per plant; POD= Number of pods per plant, BRC= Number of branches per plant;
SPP = Seeds per pod; GY=Grain yield (kg/ha); FPH=First pod height (cm)

Table 2: Genotypic means for advanced breeding lines evaluated over two seasons (pooled 2023 & 2024)

Genotypes	PHT	DTF	DTM	HSW	CLS	POD	BRC	SPP	GY	FPH
KBLS -23-36	97.66^{a}	39.00^{cd}	105.33^{de}	13.93^{bcd}	11.03^{cd}	43.26^{e}	2.66^{abc}	2.83^{a}	3112^{def}	9.41^{ab}
DLSB 5	97.20^{a}	40.66^{b}	109.83^{bc}	14.23^{bc}	11.60^{bcd}	49.66^{cde}	2.50^{abc}	2.26^{b}	3178^{cdef}	9.96^{a}
AMS-22-16	77.73^{b}	44.66^{a}	113.33^{a}	13.15^{d}	13.26^{ab}	65.00^{a}	2.13^{bcd}	2.20^{b}	3191^{abcde}	8.76^{ab}
RSC-11-95	74.33^{b}	41.50^{b}	113.33^{a}	14.67^{b}	12.73^{bcd}	56.10^{bc}	2.50^{abc}	2.16^{b}	3606^{ab}	8.38^{cd}
MACS -1810	66.83^{c}	41.33^{b}	111.66^{ab}	15.88^{a}	12.96^{abc}	61.26^{ab}	2.90^{a}	2.86^{a}	3369^{abcd}	6.16^{f}
LOKSOYA-03	60.60^{cd}	37.00^{e}	107.50^{cde}	13.57^{cd}	11.40^{bcd}	47.90^{de}	2.56^{abc}	2.70^{a}	3210^{bcdef}	5.15^{gh}
AISb 50 (C)	59.60^{de}	40.66^{b}	108.06^{cd}	13.76^{cd}	14.98^{a}	59.86^{ab}	2.00^{cd}	2.70^{a}	3110^{def}	6.15^{f}
KSS-225	57.90^{def}	38.00^{de}	104.66^{e}	14.31^{bc}	11.23^{bcd}	49.66^{cde}	2.73^{ab}	2.76^{a}	3596^{ab}	6.16^{f}
MAUS-816	55.26^{def}	38.83^{cd}	105.50^{de}	15.74^{a}	12.06^{bcd}	50.80^{cd}	3.00^{a}	2.76^{a}	3544^{abc}	6.40^{f}
ASb-101	54.76^{def}	37.00^{e}	96.66^{f}	14.13^{bc}	12.80^{bcd}	56.76^{bc}	2.30^{abc}	2.73^{a}	3665^{a}	7.60^{de}
THPS-06	54.03^{ef}	39.33^{c}	109.16^{bc}	12.17^{e}	11.46^{bcd}	51.73^{cd}	2.70^{abc}	2.36^{b}	3155^{cdef}	5.26^{g}
JS 335 (C)	51.41^{f}	38.33^{cd}	110.50^{abc}	11.40^{e}	10.80^{d}	45.91^{de}	1.56d	2.70^{a}	2851^{f}	7.26^{e}
DS-1589	40.43^{g}	38.33^{cd}	107.50^{cde}	13.24^{d}	10.76^{d}	42.96^{e}	2.70^{abc}	2.73^{a}	2903^{ef}	4.45^{h}

Superscripts a,b,c,d etc. were used to denote the differences among genotypes. If difference found then, denoted with different letter and if no difference between genotypes then denoted with same letters.

Table 3: Estimates of selection differential, selection gain and heritability based on MGIDI for ten quantitative traits evaluated for 2023 and 2024 seasons

Characters	Year	Xo	Xs	SD	SD%	h^2	SG	SG%
Plant Height (cm)	2023	63.20	51.00	-12.20	-19.30	0.99	-12.1	-19.2
	2024	67.20	59.30	-7.97	-1.19	0.98	-7.86	-1.17
Days 50% flowering	2023	39.00	37.90	-1.12	-2.86	0.97	-1.09	-2.80
	2024	40.20	38.00	-2.19	-5.44	0.99	-2.17	-5.40
Days to maturity	2023	107.00	99.40	-7.49	-7.01	0.99	-7.47	-6.99
	2024	109.00	103.00	-6.10	-5.60	0.98	-6.01	-5.51
Number of branches per plant	2023	2.83	3.11	0.27	9.83	0.82	0.23	8.14
	2024	2.13	2.13	-4.44	-2.08	0.87	-3.89	-1.82
Number of clusters per plant	2023	12.00	12.30	0.25	2.13	0.36	0.09	0.76
	2024	12.20	12.10	-1.47	-1.21	0.81	-1.20	-9.88
Number of pods per plant	2023	51.90	54.00	2.13	4.11	0.96	2.05	3.96
	2024	52.90	53.5	5.57	1.05	0.92	5.16	9.76
100 seed weight (g)	2023	14.30	15.30	1.01	7.06	0.98	0.99	6.93
	2024	13.40	14.60	1.12	8.30	0.99	1.11	8.23
Grain yield (kg/ha)	2023	3320	3618	298	8.96	0.89	266	8.01
	2024	3233	3538	305	9.42	0.94	287	8.87
First pod height (cm)	2023	7.19	7.44	0.25	3.49	0.96	0.24	3.36
	2024	6.83	6.57	-2.65	-3.87	0.93	-2.4	-3.62
Seeds per pod	2023	2.60	2.85	0.24	9.44	0.92	0.22	8.70
	2024	2.60	2.63	2.65	1.02	0.79	2.10	8.08

Xo= overall mean of genotypes; Xs= mean of the selected genotypes; SD= selection differential; SG= selection gain or impact; h^2= heritability

Conclusion

The study identified superior soybean genotypes across two seasons, with lower values indicating closer proximity to the ideotype and better multi-trait performance. ASb-101 and MAUS-816 were the most desirable genotypes due to their consistently favorable agronomic traits, while genotypes with higher MGIDI values were excluded. ASb-101, RSC-11-95, KSS-225, and MAUS-816 outperformed the best check variety. Cluster analysis revealed significant genetic diversity, especially in Cluster III, offering opportunities for heterosis through crosses between genetically distant clusters. Overall, these outperformed genotypes are valuable resources for the direct release as a variety or for further testing in large-scale through adoptive trials in farmers' fields.

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Competing Interests

Authors have declared that no competing interests exist.

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