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The names and affiliations of all authors are provided below, following the references.

Genotype $\times$ environment interaction and stability analysis for seed yield and yield-attributing traits in soybean [*Glycine max* (L.) Merrill]

Ajit Vishnu Hiwarkar¹, SS Nichal², PV Patil³, SK Burghate⁴, PV Jadhav⁵, SP Pradhan⁶, MD Chavan⁷

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ABSTRACT

G $\times$ E interaction limits realization of genetic yield potential in soybean. Thirty genotypes (23 test entries, 7 checks) were evaluated in RBD with three replications across three Maharashtra locations (Akola, Amravati, Washim) during Kharif 2025, using the Eberhart-Russell (1966) model for stability across ten traits. Pooled ANOVA showed highly significant genotypic differences for plant height, branches/plant, pod insertion height, pods/plant, seeds/pod, 100-seed weight, and seed yield. G $\times$ E (linear) was highly significant for plant height, seeds/pod, and seed yield, indicating predictable genotypic responses. Amravati was most favorable ($I_j = +47.689$), Washim most stress-prone ($I_j = -55.144$), and Akola intermediate ($I_j = +7.456$). Grand mean yield was 1,963.41 kg/ha (921.67–2,743.33 kg/ha). AMS 26-1, AMS 25-6, and AMS 2022-1 ($b_i > 1$) showed specific adaptability to favorable environments; AMS 26-2, AMS 25-1, and AMS-MB 5-18 ($b_i < 1$) suited resource-limited conditions, while AMS 100-39 and RVSM 2011-35 were broadly stable. Results support targeted genotype selection for Maharashtra.

Keywords: *Glycine max*, Genotype $\times$ environment interaction, Stability analysis, Eberhart-Russell model, Seed yield

Introduction

Soybean [*Glycine max* (L.) Merrill, $2n = 40$], the "miracle bean" (Kumar *et al.*, 2005) [1], is a key Indian oilseed crop valued for its high protein (38–42%) and oil (18–22%) content (Basavaraja *et al.*, 2005; Dukariya *et al.*, 2020) [2, 3]. Global production reached an estimated 428.2 million metric tons in 2024–25, led by Brazil, the USA, and Argentina, with India among the top five producers (USDA, 2025) [4]. Maharashtra, particularly Vidarbha, is a major domestic contributor, though productivity varies across seasons and locations.

A key challenge in soybean improvement is genotype $\times$ environment (G $\times$ E) interaction, which shifts genotype rankings across environments and complicates cultivar selection (Comstock *et al.*, 1963) [5]. Eberhart *et al.* (1966) [6] addressed this by defining a stable genotype as one with high mean performance, a regression coefficient (b_i) near unity, and a deviation from regression (S^2d_i) near zero — partitioning G $\times$ E interaction into predictable and unpredictable components. This model, along with related approaches (AMMI, GGE biplot), has been widely applied in soybean, consistently revealing significant G $\times$ E interaction for yield and component traits (Deka and Talukdar, 1997 [7]; Hossain *et al.*, 2003 [8]; Katna *et al.*, 2017 [9]; Pallavi *et al.*, 2019 [10]; Habtegebriel and Abebe, 2023 [11]; Abebe *et al.*, 2024) [12], highlighting the need for multi-location testing.

This study evaluated 30 soybean genotypes across three Maharashtra locations (Akola, Amravati, Washim) during Kharif 2025 to (i) assess seed yield potential across environments and (ii) characterize G $\times$ E interaction for yield and component traits using the Eberhart–Russell (1966) [6] model, identifying genotypes suited to broad or specific adaptation for future breeding.

Material and methods

The experimental material comprised 30 soybean genotypes (23 advanced test lines and 7 commercial checks: AMS 100-39, AMS-MB 5-18, JS 335, JS 93-05, JS 20-34, RVSM 2011-35, and MAUS 158) obtained from the All India Coordinated Research Project (AICRP) on Soybean, Regional Research Centre, Dr. Panjabrao Deshmukh Krishi Vidyapeeth (PDKV), Akola, Amravati, and evaluated during Kharif 2025 at three locations in Maharashtra treated as distinct environments E_1 : Oilseeds Research Unit, Dr. PDKV, Akola (sown 04 July 2025); E_2 : AICRP on Soybean (Dr. PDKV, Akola), Amravati (sown 25 June 2025); and E_3 : Agriculture Research Station, Washim (sown 03 July 2025) using a Randomized Block Design (RBD) with three replications per location, each plot comprising five rows of 4 m length sown at 45 $\times$ 5 cm spacing

Corresponding Author:
 Ajit Vishnu Hiwarkar
 PG Scholar, Department of
 Agricultural Botany,
 Genetics and Plant
 Breeding, Post Graduate
 Institute, Dr. Panjabrao
 Deshmukh Krishi
 Vidyapeeth (Dr. PDKV),
 Akola, Maharashtra, India

with a basal fertilizer dose of 30:60:30 kg N:P₂O₅:K₂O per hectare, and standard agronomic and plant-protection practices followed uniformly across locations. Observations were recorded on five randomly selected competitive plants per genotype per replication (and on a whole-plot basis for yield) for ten quantitative traits days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, height of first pod insertion (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), seed yield per plot (kg), and seed yield per hectare (kg) with genotypic differences at each location tested following Panse *et al.* (1967) [13] and stability analysis performed using the joint linear regression model of Eberhart *et al.* (1966) [6].

3. Result and discussion

3.1 Mean performance

Highly significant genotypic variation was observed for most traits at the individual-location level. Grand mean values across the three environments were: days to 50% flowering, 42.23 days; days to maturity, 99.71 days; plant height, 52.47 cm; branches per plant, 3.40; height of first pod insertion, 14.14 cm; pods per plant, 45.57; seeds per pod, 2.48; 100-seed weight, 11.89 g; seed yield per plot, 1.77 kg; and seed yield per hectare, 1,963.41 kg/ha.

Table 1. Mean seed yield (kg/ha) of 30 soybean genotypes across three environments (Kharif 2025)

Sr. No.	Genotype	Akola E 1	Amravati E2	Washim E3	Mean
1	AMS 2022-1	2,554	2,944	2,407	2,635.00
2	AMS 22-14	2,336	1,889	1,907	2,044.00
3	AMS 2021-3	1,505	593	2,244	1,447.33
4	AMS 23-8	1,533	1,796	1,163	1,497.33
5	AMS 24-7	1,470	648	1,660	1,259.33
6	AMS 25-3	2,381	2,833	2,026	2,413.33
7	AMS 25-21	1,168	1,630	1,686	1,494.67
8	AMS 22-2	1,549	870	1,444	1,287.67
9	AMS 26-1	2,765	2,981	2,484	2,743.33
10	AMS 26-2	2,093	2,019	1,960	2,024.00
11	AMS 24-3	926	1,000	839	921.67
12	AMS 24-12	1,904	1,852	1,744	1,833.33
13	AMS 25-1	2,006	2,148	2,381	2,178.33
14	AMS 25-2	2,454	2,778	2,204	2,478.67
15	AMS 25-5	2,363	2,981	2,278	2,540.67
16	AMS 25-6	2,582	3,037	2,481	2,700.00
17	AMS 25-7	2,167	2,815	2,265	2,415.67
18	AMS 25-9	2,424	1,019	2,123	1,855.33
19	AMS 25-17	1,406	852	1,651	1,303.00
20	AMS 25-19	2,426	2,926	2,467	2,606.33
21	AMS 25-20	1,445	1,426	1,054	1,308.33
22	AMS 25-22	2,486	2,870	2,196	2,517.33
23	AMS 25-23	2,026	2,500	2,037	2,187.67
24	AMS 100-39 (C)	2,204	2,463	2,019	2,228.67
25	AMS-MB 5-18 (C)	1,926	2,074	1,963	1,987.67
26	JS 335 (C)	1,611	1,815	1,704	1,710.00
27	JS 93-05 (C)	1,796	1,833	1,611	1,746.67
28	JS 20-34 (C)	1,548	1,741	1,574	1,621.00
29	RVSM 2011-35 (C)	2,091	1,981	1,819	1,963.67
30	MAUS 158 (C)	1,981	2,019	1,857	1,952.33
	Mean	1,970.00	2,011.00	1,908.27	1,963.41
	SE(m)	108.84	126.86	107.43	—
	CD at 5%	308.11	359.12	304.12	—
	CV (%)	9.61	10.93	9.75	—

3.2 Analysis of variance

Pooled analysis of variance based on the Eberhart *et al.* (1966) [6] model (Table 2) showed highly significant genotypic mean squares for plant height, branches per plant, height of first pod insertion, pods per plant, seeds per pod, 100-seed weight, seed yield per plot, and seed yield per hectare, but non-significant genotypic differences for days to 50% flowering and days to maturity when tested against the pooled G × E interaction. The Environment + (Genotype × Environment) component was highly significant for plant height,

branches per plant, pods per plant, 100-seed weight, seed yield per plot, and seed yield per hectare, confirming substantial environmental influence.

Partitioning of the environmental component revealed that Environment (linear) was highly significant for the same major traits, indicating that a large share of environmental variance followed a predictable linear trend. The G × E (linear) component was highly significant for plant height, seeds per pod, seed yield per plot, and seed yield per hectare traits for which genotypic responses to environ

mental change can therefore be reliably predicted by linear regression. Pooled deviation (the non-linear component) was also highly significant for plant height, branches per plant, pods per plant, seed yield per plot, and seed yield per hectare, indicating that unpre-

dictable, non-linear responses contributed meaningfully to $G \times E$ interaction for these traits as well consistent with reports by Katna *et al.* (2017) [9] and Pallavi *et al.* (2019) [10] in soybean.

Table 2. Pooled analysis of variance (mean sum of squares) based on the Eberhart *et al.* (1966) [6] model

Sr. No.	Character	Genotypes (df = 29)	Environment (df = 2)	$G \times E$ (df = 58)	$E + (G \times E)$ (df = 60)
1	Days to 50% flowering	56.286**	18.100	3.928	4.400
2	Days to maturity	127.637**	2.033	4.526	4.733
3	Plant height (cm)	375.600**	5,226.304**	89.441**	260.669**
4	Branches/plant	1.279**	12.516**	0.405**	0.812**
5	First pod insertion height (cm)	20.051**	6.261	0.026	0.233
6	Pods/plant	419.320**	1,274.707**	48.084**	88.972**
7	Seeds/pod	0.407**	0.086	0.007	0.009
8	100-seed weight (g)	18.856**	44.217**	0.821*	2.267**
9	Seed yield/plot (kg)	1.852**	0.196*	0.269**	0.267**
10	Seed yield/ha (kg)	2,286,817.50**	241,682.63**	332,408.67**	329,384.47**

* Significant at 5%; ** Significant at 1%

3.3 Environmental indices

The environmental index quantified the relative favorability of each test location for each trait (Table 3). **Amravati (E₂)** emerged as the most favorable environment overall, with positive indices for seed yield per hectare (+47.689), seed yield per plot (+0.043), pods per plant (+4.337), plant height (+8.000), seeds per pod (+0.034), and days to 50% flowering (+0.500). **Akola (E₁)** was moderately favor-

able, showing positive indices for seed yield per hectare (+7.456), seed yield per plot (+0.007), 100-seed weight (+0.783), and first pod insertion height (+0.285). **Washim (E₃)** was the most unfavorable environment for yield and most yield components, with negative indices for seed yield per hectare (-55.144), seed yield per plot (-0.050), pods per plant (-1.927), and plant height (-0.827), though it favored branching intensity (+0.432).

Table 3. Environmental index (I_j) for ten characters at Akola, Amravati, and Washim

Sr. No.	Character	Akola (E ₁)	Amravati (E ₂)	Washim (E ₃)
1	Days to 50% flowering	-0.367	+0.500	-0.133
2	Days to maturity	+0.156	-0.011	-0.144
3	Plant height (cm)	-7.173	+8.000	-0.827
4	Branches/plant	-0.208	-0.224	+0.432
5	First pod insertion height (cm)	+0.285	-0.236	-0.049
6	Pods/plant	-2.410	+4.337	-1.927
7	Seeds/pod	-0.008	+0.034	-0.026
8	100-seed weight (g)	+0.783	-0.568	-0.215
9	Seed yield/plot (kg)	+0.007	+0.043	-0.050
10	Seed yield/ha (kg)	+7.456	+47.689	-55.144

3.4 Stability analysis

Because significant $G \times E$ interaction was detected for most traits, stability parameters (mean, b_i , S^2d_i) were estimated for all ten characters following Eberhart *et al.* (1966) [6]. Full genotype-wise results for

the primary economic trait, seed yield per hectare, are given in Table 4; a synthesis of stability classification across all ten traits is given in Table 5.

Table 4. Stability parameters (mean, b_i , S^2d_i) for seed yield per hectare (kg/ha) of 30 soybean genotypes

Sr. No.	Genotype	Mean	b_i	S^2d_i
1	AMS 2022-1	2,635.00	1.66	8,080.813
2	AMS 22-14	2,044.00	0.14	113,878.246**
3	AMS 2021-3	1,447.33	-5.23	33,295.485
4	AMS 23-8	1,497.33	2.04	-13,005.755
5	AMS 24-7	1,259.33	-3.08	105,977.487**
6	AMS 25-3	2,413.33	2.55	-973.984

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Sr. No.	Genotype	Mean	b_i	S^2d_i
7	AMS 25-21	1,494.67	-0.40	140,528.748**
8	AMS 22-2	1,287.67	-1.65	122,369.827**
9	AMS 26-1	2,743.33	1.60	-12,855.409
10	AMS 26-2	2,024.00	0.23	-6,974.258
11	AMS 24-3	921.67	0.51	-13,080.652
12	AMS 24-12	1,833.33	0.39	-7,329.501
13	AMS 25-1	2,178.33	-0.86	22,519.785
14	AMS 25-2	2,478.67	1.81	-6,672.462
15	AMS 25-5	2,540.67	2.12	64,033.533*
16	AMS 25-6	2,700.00	1.69	23,849.623
17	AMS 25-7	2,415.67	1.58	109,786.104**
18	AMS 25-9	1,855.33	-3.13	608,273.614**
19	AMS 25-17	1,303.00	-2.48	25,083.732
20	AMS 25-19	2,606.33	1.34	54,222.009*
21	AMS 25-20	1,308.33	1.28	4,609.459
22	AMS 25-22	2,517.33	2.13	-3,662.098
23	AMS 25-23	2,187.67	1.36	43,127.125*
24	AMS 100-39 (C)	2,228.67	1.40	-8,386.355
25	AMS-MB 5-18 (C)	1,987.67	0.31	-5,983.245
26	JS 335 (C)	1,710.00	0.28	3,761.753
27	JS 93-05 (C)	1,746.67	0.74	-11,528.774
28	JS 20-34 (C)	1,621.00	0.48	-2,463.884
29	RVSM 2011-35 (C)	1,963.67	0.60	6,569.595
30	MAUS 158 (C)	1,952.33	0.53	-12,737.362
	Grand mean	1,963.41	1.00	—

* Significant at 5%; ** Significant at 1%

For seed yield per hectare, checks **AMS 100-39** ($b_i = 1.40$, $S^2d_i = -8,386.355$, non-significant) and **RVSM 2011-35** ($b_i = 0.60$, $S^2d_i = +6,569.595$, non-significant), which yielded above and near the grand mean respectively, showed the closest approach to the ideal stability combination among genotypes with non-significant S^2d_i . High-yielding genotypes **AMS 2022-1**, **AMS 25-3**, **AMS 26-1**, **AMS 25-6**, **AMS 25-2**, and **AMS 25-22** combined mean yields well above the grand mean with regression coefficients above unity ($b_i > 1$) and non-significant S^2d_i , marking them as below-average in stability but specifically

and strongly responsive to favorable, high-input environments such as Amravati. Conversely, **AMS 26-2**, **AMS 25-1**, and **AMS-MB 5-18** showed $b_i < 1$ with non-significant S^2d_i , denoting above-average stability and buffering capacity suited to resource-limited or stress-prone environments such as Washim. Genotypes with significant S^2d_i (e.g., AMS 22-14, AMS 24-7, AMS 25-21, AMS 22-2, AMS 25-9, AMS 25-7) showed unpredictable, non-linear responses across environments and are not recommended for either broad or targeted release without further evaluation.

Table 5. Summary of stability classification of soybean genotypes across ten traits (Eberhart *et al.*, 1966) [6]

Character	Average stability ($b_i \approx 1$; broadly adaptable)	Below-average stability ($b_i > 1$; favorable environments)	Above-average stability ($b_i < 1$; unfavorable environments)
Days to 50% flowering	AMS 2022-1, AMS 25-3, AMS 24-3	AMS 25-21, AMS 26-2, AMS 26-1, AMS 25-20, AMS 25-23	AMS 24-12, AMS 25-5, AMS 25-22, JS 20-34
Days to maturity	AMS 25-21, AMS 25-5, AMS 25-22, MAUS 158	AMS 100-39, JS 20-34, AMS 25-3, AMS 26-1, AMS 24-12, AMS 25-6	AMS 2022-1, AMS 25-23, JS 93-05
Plant height (cm)	MAUS 158, AMS 24-7, AMS 25-17, AMS 25-19	AMS 2021-3, AMS 23-8, AMS 22-2, AMS 25-2, AMS 25-9	—
Branches/plant	AMS 2022-1, AMS 25-6, AMS 25-7, AMS-MB 5-18, MAUS 158	AMS 25-1, AMS 25-9, AMS 25-5	AMS 25-3, AMS 25-22, RVSM 2011-35

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Character	Average stability ($b_i \approx 1$; broadly adaptable)	Below-average stability ($b_i > 1$; favorable environments)	Above-average stability ($b_i < 1$; unfavorable environments)
First pod insertion height (cm)	AMS 2021-3, AMS 24-3, AMS 24-12, AMS 25-5, AMS 25-1, JS 20-34	—	AMS 2022-1, AMS 26-2
Pods/plant	AMS 26-2, AMS 25-20, AMS 25-22, AMS 100-39	AMS 2022-1, AMS 22-14, AMS 25-5, AMS 25-6, AMS 25-7, AMS 25-19	—
Seeds/pod	AMS 25-6, AMS 25-7, AMS 25-19, AMS 25-23, JS 93-05, RVSM 2011-35	AMS 2022-1, AMS 25-3, AMS 25-2, AMS 25-5, AMS 100-39	AMS 26-1, AMS 26-2
100-seed weight (g)	AMS 25-5, AMS 25-6, AMS 25-22, AMS 25-23, AMS 100-39, JS 20-34, MAUS 158	AMS 26-1, AMS 26-2, AMS 24-12, AMS 25-1, AMS 25-2, RVSM 2011-35	AMS 2022-1, AMS 25-3, AMS 25-19, JS 93-05
Seed yield/plot (kg)	AMS 100-39, RVSM 2011-35	AMS 2022-1, AMS 25-3, AMS 26-1, AMS 25-2, AMS 25-6, AMS 25-22	AMS-MB 5-18, AMS 26-2, AMS 25-1
Seed yield/ha (kg)	AMS 100-39, RVSM 2011-35	AMS 2022-1, AMS 25-3, AMS 26-1, AMS	AMS-MB 5-18, AMS 26-2, AMS 25-1

Overall, genotype **AMS 26-1** distinguished itself through the combination of the highest mean seed yield (2,743.33 kg/ha), the highest 100-seed weight (15.94 g), the highest branching intensity (4.03 branches/plant), and a strong pod count (56.47 pods/plant), consistently outperforming all seven commercial checks across locations. **AMS 25-6** and **AMS 2022-1** followed closely, both combining high yield with strong responsiveness to favorable conditions ($b_i > 1$). These results parallel earlier findings by Tyagi *et al.* (2013) [14] and Ramteke *et al.* (2012), who similarly reported that high-yielding soybean genotypes with regression coefficients above unity performed best under favorable, high-input management, while genotypes with b_i near or below unity were more dependable under variable or resource-limited conditions.

4. Conclusions and recommendations

This multi-location evaluation of 30 soybean genotypes under the Eberhart *et al.* (1966) [6] stability model confirmed significant genotype $\times$ environment interaction for seed yield and its major component traits, with the linear component predominating for plant height, seeds per pod, seed yield per plot, and seed yield per hectare. Amravati was identified as the most environmentally favorable test site, Washim as the most stress-prone, and Akola as intermediate. Based on combined mean performance and stability parameters: **AMS 26-1**, **AMS 25-6**, and **AMS 2022-1** are recommended for cultivation in favorable, high-input environments (e.g., Amravati), owing to their high mean seed yields (2,743.33, 2,700.00, and 2,635.00 kg/ha, respectively) and above-unity regression coefficients ($b_i > 1$), and are recommended as prime candidates for multi-location release trials and as donor parents for high-yield breeding.

1. **AMS 100-39 (C) and RVSM 2011-35 (C)** displayed the closest approach to general (average) stability for seed yield per hectare among genotypes with non-significant S^2d_i , supporting their continued use as broadly dependable check cultivars.
2. **AMS 26-2, AMS 25-1, and AMS-MB 5-18**, with regression coefficients below unity, are better suited to low-input or stress-prone environments such as Washim and merit inclusion in breeding programs targeting drought- or stress-resilient soybean cultivars.

3. Genotypes with significant deviation from regression ($S^2d_i > 0$), such as AMS 22-14, AMS 24-7, AMS 25-21, AMS 22-2, and AMS 25-9, exhibited unpredictable performance and require further multi-season testing before recommendation.
4. Given its superior seed mass (15.94 g/100 seeds) and pod load, AMS 26-1 is additionally recommended as a valuable donor parent for improving seed size and sink capacity in future hybridization programs, while genotypes AMS 25-2, AMS 2022-1, and AMS 2021-3, with first pod insertion heights of 17.47, 16.13, and 15.78 cm respectively (compared with 8.84 cm in JS 20-34), are recommended for breeding mechanical-harvest-compatible cultivars.
5. Genotypes with significant deviation from regression ($S^2d_i > 0$), such as AMS 22-14, AMS 24-7, AMS 25-21, AMS 22-2, and AMS 25-9, exhibited unpredictable performance and require further multi-season testing before recommendation.
6. Given its superior seed mass (15.94 g/100 seeds) and pod load, AMS 26-1 is additionally recommended as a valuable donor parent for improving seed size and sink capacity in future hybridization programs, while genotypes AMS 25-2, AMS 2022-1, and AMS 2021-3, with first pod insertion heights of 17.47, 16.13, and 15.78 cm respectively (compared with 8.84 cm in JS 20-34), are recommended for breeding mechanical-harvest-compatible cultivars.

Continued multi-environment and multi-season testing of these genotypes is recommended to validate stability estimates before formal release for cultivation in Vidarbha and comparable agro-climatic zones of Maharashtra.

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Authors

Ajit Vishnu Hiwarkar

PG Scholar, Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. Panjabrao Deshmukh Krishi Vidyapeeth (Dr. PDKV), Akola, Maharashtra, India

SS Nichal

Professor [CAS], Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. PDKV, Akola, Maharashtra, India

PV Patil

Assistant Professor, Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. PDKV, Akola, Maharashtra, India

SK Burghate

Assistant Professor, Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. PDKV, Akola, Maharashtra, India

PV Jadhav

Professor [CAS], Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. PDKV, Akola, Maharashtra, India

SP Pradhan

PG Scholar, Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. Panjabrao Deshmukh Krishi Vidyapeeth (Dr. PDKV), Akola, Maharashtra, India

MD Chavan

PG Scholar, Department of Agricultural Botany, Genetics and Plant Breeding, Post Graduate Institute, Dr. Panjabrao Deshmukh Krishi Vidyapeeth (Dr. PDKV), Akola, Maharashtra, India