

SABRAO Journal of Breeding and Genetics
 58 (5) 2135-2146, 2026
<http://doi.org/10.54910/sabrao2026.58.5.14>
<http://sabraojournal.org/>
 pISSN 1029-7073; eISSN 2224-8978



GENOTYPE-BY-ENVIRONMENT INTERACTIONS AND YIELD STABILITY OF SOYBEANS (*GLYCINE MAX* L.) UNDER DIVERSE AGROECOSYSTEMS

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SUMMARY

Genotype-by-environment interaction (GEI) is a critical factor influencing soybean (*Glycine max* L.) performance and stability across diverse growing conditions. For developing high-yielding and stable cultivars, it is essential to understand how soybean genotypes respond differently to environmental variations. This study aimed to assess the GEI for agro-morphological traits and evaluate the soybean advanced lines and check genotypes for grain yield under two contrasting environmental conditions using parametric and non-parametric stability measurements. This study comprehensively compared multiple parametric and non-parametric stability statistics to identify soybean genotypes with both high productivity and broad adaptability under contrasting agroecosystems. The field experiment conducted had two diverse environmental conditions: the paddy field (soil texture clay) and the dry land (soil texture dusty clay) agroecosystems using a randomized complete block design (RCBD) with three replications at the Majalengka, West Java, Indonesia. The results showed significant genotype-by-environment interaction effects for grain yield. The soybean advanced lines UM12, UM20, and UM05 emerged with the highest grain yield and adaptability to environmental variations and have the potential to be developed as new superior cultivars. The results will contribute and provide information on soybean breeding activities in the future.

Keywords: Soybean (*G. max* L.), genotype-by-environment interactions, nonparametric, parametric, stability

Communicating Editor: Dr. Tabyimbaeva Laila

Manuscript received: April 07, 2026; Accepted: June 13, 2026.

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Citation: Wijaya AA, Sukmasari MD, Karmila M, Mohammad RAP, Gaffar AA, Maulana H (2026). Genotype-by-environment interaction and yield stability of soybeans (*Glycine max* L.) under diverse agroecosystems. *SABRAO J. Breed. Genet.* 58 (5) 2135-2146. <http://doi.org/10.54910/sabrao2026.58.5.14>.

Key findings: Significant genotype-by-environment interaction effects were evident among the soybean (*G. max* L.) advanced lines for pod width, 100-grain weight, and grain yield. Genotypes UM12, UM20, and UM5 showed the highest grain yield and environmental adaptability, revealing their potential to be superior cultivars in the future.

INTRODUCTION

Soybean (*Glycine max* L.) is recognizably the legume with the highest vegetable protein content among the major legumes, ranging from 40% to 50%, depending on genotypes and environmental conditions (Kholmurodova *et al.*, 2023), which can reach 46%–55% under dry growing conditions (Kakati *et al.*, 2024). Moreover, soybean is a widely used crop in various food industries, recognized as a functional food due to its rich nutritional composition, including anthocyanins and phenolic compounds (Choi *et al.*, 2020), isoflavones (Lee *et al.*, 2021), saponins (Tamangwa *et al.*, 2023), and linoleic acid (Agyenim-Boateng *et al.*, 2023). The accumulation of these nutritional and bioactive compounds comes from strong influences of genotype-by-environment interactions (GEI), as different genotypes may respond differently to environmental conditions, resulting in variations in seed quality and nutritional composition.

Currently, soybean breeding programs mainly concentrate on the development of stable and high-yielding genotypes. However, environmental conditions on their own significantly influence soybean performance, and cultivation in different agroecosystems often results in genotypes with varied responses. Previous studies have also reported the soybean grain yield receiving significant genotype-by-environment interaction effects (Susanto *et al.*, 2023; Njoroge *et al.*, 2026). Unlike previous studies looking into general traits, this study comprehensively compared multiple parametric and non-parametric stability statistics to identify soybean genotypes with both high productivity and broad adaptability under contrasting agroecosystems. Other studies have also shown a significant impact of environmental factors on the grain yield in various crops,

including maize (Ruswandi *et al.*, 2023), potatoes (Maulana *et al.*, 2024), and rice (Nasution *et al.*, 2025). The genotype-by-environment interaction effects cause inconsistent performance of soybean genotypes across the locations and seasons, necessitating stability analysis to identify and select the stable and high-yielding genotypes (Wijaya *et al.*, 2022).

Several stability analyses have gained wide usage in selecting stable genotypes, such as additive main effects and multiplicative interaction, or AMMI (Gauch, 2013; Amien *et al.*, 2022); parametric and non-parametric measurements analysis (Aulia *et al.*, 2022); and GGE biplot analysis (Maulana *et al.*, 2023). The use of combined stability analysis tended to have better accuracy in selecting stable and high-yielding genotypes (Maulana *et al.*, 2024). Numerous researchers have successfully identified and selected the stable and high-yielding genotypes by using combined stability analysis in various crops, including soybeans (Susanto *et al.*, 2023), turmeric (Aulia *et al.*, 2022), and peas (Filio *et al.*, 2023).

In Indonesia, soybean cultivation occurs in both paddy fields and dryland agroecosystems, which differ in soil properties, water availability, and management practices. These contrasting environments contribute to GEI, highlighting the importance of multi-environment testing to identify high-yielding and stable genotypes across diverse production systems. Comprehensive information on GEI is crucial for refining selection strategies and developing soybean cultivars with the highest grain yield and stability across the diverse agroecosystems. Therefore, this study aimed to identify the genotype-by-environment interaction effects for agromorphological traits and evaluate the soybean genotypes for yield performance under diverse environmental conditions using parametric and non-parametric stability analysis.

MATERIALS AND METHODS

Plant materials

In this study, the genetic material comprised 25 soybean (*G. max* L.) advanced lines derived from crossbreeding in the F₅ generation. Crossbreeding proceeded to obtain genetic recombination of large-seeded and high-yielding soybean genotypes with tolerance to rainy-season conditions. The soybean standard cultivars Deja 2 and Detam 4 served as check genotypes. Information about the 25 studied soybean advanced lines and the two check cultivars appears in Table 1.

Experimental design and procedure

The conducted experiment continued under two agroecosystems, viz., the paddy field agroecosystem (PS) and the dryland agroecosystem (FL), carried out in 2025. Information on soil fertility, soil texture, and

the agroclimatological conditions at the experimental location is available in Table 2. The type of soil at the research site is latosol (USDA, 1999). Despite having similar agroclimatic conditions, the paddy field and dryland sites differed in several edaphic characteristics, including soil texture, organic carbon content, and nutrient availability. The dryland site had higher organic carbon (3.73%), available K₂O (45.03), and slightly greater rainfall, whereas the paddy field showed characteristics of clay soil with lower fertility status. Differences in soil texture (clay vs. dusty clay) may also influence water-holding capacity, aeration, and nutrient uptake by plants. Such environmental heterogeneity is an important source of genotype × environment interaction (GEI), as soybean genotypes could respond differently to variations in soil fertility and physical conditions, thereby affecting yield performance and stability across environments.

Table 1. Soybean genetic materials used in the study.

No.	Genotypes	Pedigree
1	UM01	GK x Mut 3 (2)
2	UM02	GK x Det 4 (1)
3	UM03	GK x Det 4 (2)
4	UM04	GK x Det 4 (3)
5	UM05	Deja 2 x Mut 3 (1)
6	UM06	Deja 2 x Mut 3 (2)
7	UM07	Deja 2 x Mut 3 (3)
8	UM08	Deja 2 x Det 5 (1)
9	UM09	Deja 2 x Det 5 (2)
10	UM10	Deja 2 x Det 5 (3)
11	UM11	Deja 2 x Det 1 (1)
12	UM12	Deja 2 x Det 1 (2)
13	UM13	Mut 3 x Det 4 (1)
14	UM14	Mut 3 x Det 5 (1)
15	UM15	Mut 3 x Det 5 (2)
16	UM16	Mut 3 x Bio (1)
17	UM17	Mut 3 x Bio (2)
18	UM18	Mut 3 x Bio (3)
19	UM19	Det 4 x Deja 2 (1)
20	UM20	Det 4 x Deja 2 (2)
21	UM21	Det 4 x Det 5 (1)
22	UM22	Det 4 x Det 5 (2)
23	UM23	Det 4 x Det 5 (3)
24	UM24	Det 4 x Bio (1)
25	UM25	Det 4 x Bio (2)
26	Deja 2	Commercial variety
27	Detam 4	Commercial variety

Table 2. Environmental conditions of the sites used in the soybean study.

Sites	Paddy field	Dryland
Agro-climate		
t _{avg} (°C)	29.68	29.68
RH (%)	84.74	84.74
Mean of rainy day (day)	25	29
Rainfall (mm/month)	547.50	600
Altitude (masl)	139	146
Soil fertility		
pH	6.50 (Neutral)	6.72 (Neutral)
C -Organic	1.47 (Poor)	3.73 (High)
N	0.22 (Medium)	0.41 (Medium)
C/N	6.73 (Poor)	9.00 (Poor)
P ₂ O ₅	4.94 (Poor)	4.29 (Poor)
K ₂ O	27.42 (Medium)	45.03 (High)
Texture	Clay	dusty clay

Agroclimatological data collected during the experiment, including daily temperature, air humidity, and rainfall, came from BMKG Kertajati, Majalengka Regency, Indonesia. The study obtained soil fertility data from the Soil Chemistry and Fertility Laboratory, Faculty of Agriculture, Padjadjaran University, Bandung, West Java, Indonesia. The experiment layout was in a randomized complete block design (RCBD) with three replications. The plot size used in the study was 3 m × 3 m, with a planting distance of 40 cm × 15 cm. The genotypes used included 25 soybean advanced lines and two check cultivars (Deja 2 and Detam 4).

Traits measurement and data collection

In all the studies of soybean genotypes, the data recorded consisted of the following traits: pod length (PL, mm); pod width (PW, mm); the number of filled pods per plant (NFP); the number of empty pods per plant (NEP); the number of seeds per plant (NSP); seed weight per plant (SW, g); 100-grain weight (S100, g); and seed weight per plot (grain yield, g). The environmental factors observed in this study were agroclimatology and soil fertility.

Each plot consisted of 140 plant populations. Ten plants became samples from each plot, with field observations conducted on the sample plants. The observed data entailed tabulation and analysis using the statistical methods. The obtained agro-climatological

conditions were from the Kertajati Meteorology, Climatology, and Geophysics Agency (BMKG), while soil fertility data for the experimental site came from soil samples analyzed at the Soil Fertility Laboratory of Padjadjaran University.

Statistical analysis

An estimation of the genotype-by-environment interactions (GEI) effects took place for all the soybean genotypes. The statistical model for combined analysis of variance (ANOVA) of the environments was as follows:

$$Y_{efgh} = \mu + G_e + E_f + GE_{ef} + R_{g(f)} + B_{h(g)} + \epsilon_{efgh}$$

Where Y_{efgh} is the value in plot h of genotype e and the value in environment f of each replication g; μ is the grand mean; G_e is the influence of genotype e; E_f is the influence of the environment; GE_{ef} is the influence of interaction between genotype e and environment f; $R_{g(f)}$ is the influence of replicate g on environment f; $B_{h(g)}$ is the influence of replicate g on plot h; and ϵ_{efgh} is the influence error of genotype e in plot h and replicate g of environment f, respectively.

Yield stability estimation engaged parametric and nonparametric measurements. Parametric measurements estimation followed the linear regression by Eberhart and Russell (1966), the mean variance component (θ_i) by Plaisted and Peterson (1959), and the GE

variance component ($\theta_{(i)}$) by Plaisted (1960). Other parametric measurements comprised the ecovalence value (Wi^2) by Wricke (1962), Shukla's stability variance (σ^2i) (Shukla 1972), and the coefficient of variance (CVi) by Francis and Kannenberg (1978). The nonparametric stability measurements were according to Nassar and Huhn (1987) and Huehn (1990) ($S^{(i)}$), Thennarasu (1995) ($NP^{(i)}$), and Kang Rank (KR) by Kang (1988). Grain yield stability analysis relied on both parametric and nonparametric measurements, as carried out by using STABILITYSOFT (online software) (Pour-aboughadareh *et al.*, 2019). The use of combined stability analysis (parametric and non-parametric) is considerably more accurate than using a single stability analysis. Additionally, this combined analysis is more suitable for use in two test environments.

RESULTS AND DISCUSSION

Genotype-by-environment interaction effects

The studies on soybean (*G. max* L.) advanced lines and check cultivars grown under different environments showed inconsistent performance for various morpho-yield traits, which can be due to genotype-by-environment interaction effects. The combined analysis of variance (ANOVA) on soybean genotypes grown in two different environments is available in Table 3. Genotypes and the environments significantly affect the traits, such as pod length, the number of filled and empty pods, and the number of seeds per plant (Table 3), revealing a robust contribution of the phenotypic variance. Genotype-by-environment interactions (GEI) significantly

Table 3. Genotype-by-environment Interaction effects for agro-morphological traits in soybeans.

Source	S.O.V.	Genotypes	Environments	GEI	Residual	Total	CV
PL	SS	1523.3	110.45	128.31	265.25	2039.50	
	F pr.	11.49**	110.45	0.97			6.27
	%SS	86.45	6.27	7.28			
PW	SS	49.78	32.54	20.98	16.29	121.38	
	F pr.	6.11**	36.23*	2.58**			6.60
	%SS	48.19	31.50	20.31			
NFP	SS	2.23	1.07	1.96	2.63	7.93	
	F pr.	1.70	61.28*	1.49			11.19
	%SS	42.40	20.34	37.26			
NEP	SS	29.73	83.98	17.38	84.87	244.32	
	F pr.	0.70	5.93	0.41			47.37
	%SS	22.68	64.06	13.26			
NSP	SS	2.68	0.82	2.09	3.03	8.70	
	F pr.	1.77*	21.97*	1.38			10.43
	%SS	47.94	14.67	37.39			
SW	SS	1.36	3.02	1.34	2.14	7.89	
	F pr.	1.27	196.67**	1.25			14.12
	%SS	23.78	52.80	23.43			
S100	SS	51.48	686.7	170.32	140.55	1516.76	
	F pr.	7.38**	1921.73**	2.42**			11.75
	%SS	5.67	75.59	18.75			
Yield	SS	1.38	0.18	1.27	1.39	4.22	
	F pr.	1.98*	43.45*	1.83*			10.78
	%SS	48.76	6.36	44.88			

Note: S.O.V. = Source of variation; SS = Sum of square; F pr. = F Probability; GEI = genotype-by-environment interactions; CV = Coefficient of variations; * = significant at the 95% level; ** = significant at the 99% level.

influenced the pod width, 100-seed weight, and plot yield. These results were greatly analogous to the findings by Abebe *et al.* (2024). The GEI is crucial in determining genotypes' performance across the environments and enables the identification of stable genotypes with optimal environments (Valencia-Ramírez and Tibocho-Ardila, 2023).

Biologically, the emergence of GEI indicates the performance of a genotype is not always consistent across various environmental conditions, so that a genotype producing high yields in one location may not necessarily produce the same results in another location (Amien *et al.*, 2022). This interaction occurs because environmental factors, such as rainfall, temperature, soil fertility, water availability, and cultivation practices, influence the expression of genes controlling plant growth and yield (Adediran *et al.*, 2023). Consequently, each genotype has a different level of adaptation to certain environmental conditions, which is a reflection of differences in productivity, yield stability, and adaptability (Waly *et al.*, 2026).

Environmental conditions between the two agroecosystems showed notable differences (Table 2), with an average temperature of 29.68 °C, relative humidity of 84.74%, 25–29 rainy days per month, and rainfall ranging from 547.50 to 600 mm, while altitude slightly varied between 139 and 146 masl. High rainfall combined with clay-based soils could induce poor drainage and waterlogging, which can negatively affect soybean root development; rainfall and water availability have had reports to strongly influence soybean growth and yield (Chauhan *et al.*, 2023), and environmental conditions are critical determinants of plant growth and yield, emphasizing the importance of appropriate cultivar selection (Sobari *et al.*, 2026). Soil fertility was generally comparable between sites, characterized by neutral pH, moderate nitrogen, low C/N ratio and P₂O₅, and clay texture. Although differences were prominent in organic carbon and K₂O content, with lower C-organic and medium K₂O in the paddy field and higher levels in the dryland. The interaction between high rainfall and clay soil may reduce infiltration and increase runoff,

leading to nutrient losses, particularly nitrogen (Yao *et al.*, 2021); therefore, proper drainage management is essential to maintain soil structure and fertility.

The presence of GEI necessitates stability analysis to identify genotypes that combine high-yield potential with consistent performance across contrasting environments. Grain yield appeared as the primary selection criterion in soybean breeding programs due to its direct reflection of genotypic productivity and agronomic adaptation under field conditions. Consequently, stability analysis in this study had restrictions on grain yield, as it represents the most economically important trait and serves as a key determinant for cultivar recommendation and adoption by farmers.

Yield-stability analysis of soybean genotypes

Soybean genotypes' evaluation across the diverse environments is essential to identify the stable and high-yielding genotypes. Grain yield stability reflects the genotype's potential to maintain its performance under varying environmental conditions; thus, stability analysis sought to assess the genotype-by-environment interaction effects and determine whether the genotypes were specifically or broadly adapting to the existing environments (Aulia *et al.*, 2022; Njoroge *et al.*, 2026). Therefore, the single stability method may not be sufficient, and multiple parametric and nonparametric approaches were crucial for a more precise evaluation (Ruswandi *et al.*, 2023).

Stability analysis results showed considerable variations among the different methods (Tables 4 and 5). By integrating multiple parameters, it was therefore recommendable to select the soybean genotypes with both stability and high-yield potential (Susanto *et al.*, 2023). Combined stability indices (SR, AR, and SD) further supported the soybean genotypes' selection. The most stable genotypes were those with the lowest average ranking (AR), enunciating consistent performance across diverse environments. Based on AR values, the

Table 4. Soybean advanced lines with yield stability based on parametric and non-parametric measurements.

Genotypes	Y	S ⁽¹⁾	S ⁽²⁾	S ⁽³⁾	S ⁽⁶⁾	NP ⁽¹⁾	NP ⁽²⁾	NP ⁽³⁾	NP ⁽⁴⁾	KR	W _i ²	σ^2_i	s ² d _i	b _i	CV _i	$\theta_{(i)}$	θ_i
UM01	3.78	8	32.00	2.00	0.50	8.00	0.25	0.50	0.50	28	0.28	0.24	1.59E-17	2.64	22.45	1.49	0.90
UM02	4.44	7	24.50	1.09	0.31	10.00	0.38	0.44	0.31	25	0.69	0.69	7.93E-18	-1.59	11.47	1.48	1.11
UM03	3.305	5	12.50	1.19	0.48	4.00	0.33	0.38	0.48	23	0.03	-0.03	-9.9E-19	0.46	4.49	1.50	0.77
UM04	3.215	6	18.00	1.50	0.50	5.00	0.25	0.42	0.50	30	0.23	0.19	1.59E-17	2.49	24.85	1.50	0.87
UM05	4.775	0	0.00	0.00	0.00	2.00	0.42	0.08	0.00	11	0.04	-0.01	0	1.65	11.11	1.50	0.78
UM06	5.445	22	242.00	15.13	1.38	13.00	0.69	0.81	1.38	28	18.02	19.41	-2.5E-16	-12.22	72.07	0.76	10.11
UM07	2.265	8	32.00	6.40	1.60	11.00	1.80	2.20	1.60	51	1.95	2.05	6.34E-17	5.35	75.86	1.42	1.77
UM08	2.285	4	8.00	2.00	1.00	7.00	2.50	1.75	1.00	40	0.26	0.22	-3.2E-17	2.58	36.21	1.49	0.89
UM09	2.465	3	4.50	1.00	0.67	3.00	2.11	0.67	0.67	29	0.02	-0.04	9.91E-19	0.59	7.75	1.50	0.76
UM10	3.005	14	98.00	8.91	1.27	10.00	0.64	0.91	1.27	41	0.95	0.96	3.17E-17	4.03	43.06	1.47	1.24
UM11	3.885	18	162.00	10.13	1.13	12.00	0.56	0.75	1.13	34	3.27	3.47	-1.3E-16	6.63	54.78	1.37	2.45
UM12	4.61	1	0.50	0.02	0.04	1.00	0.38	0.04	0.04	8	0.01	-0.04	-4E-18	1.37	9.51	1.50	0.76
UM13	3.535	1	0.50	0.03	0.06	1.00	0.10	0.06	0.06	17	0.00	-0.06	0	1.12	10.20	1.50	0.75
UM14	3.865	11	60.50	3.90	0.71	9.00	0.35	0.58	0.71	29	0.65	0.65	0	-1.52	12.62	1.48	1.09
UM15	3.845	5	12.50	0.68	0.27	4.00	0.24	0.22	0.27	22	0.22	0.17	-3.2E-17	2.44	20.41	1.50	0.86
UM16	2.41	1	0.50	0.11	0.22	2.00	2.11	0.44	0.22	26	0.00	-0.06	0	0.97	12.91	1.50	0.75
UM17	2.985	3	4.50	0.53	0.35	6.00	0.65	0.71	0.35	31	0.08	0.03	-3.1E-20	0.11	1.18	1.50	0.79
UM18	3.195	6	18.00	1.64	0.55	6.00	0.27	0.55	0.55	32	0.24	0.20	1.59E-17	2.53	25.45	1.49	0.88
UM19	4.005	24	288.00	19.20	1.60	13.00	0.80	0.87	1.60	33	5.97	6.39	-1.3E-16	8.61	69.03	1.26	3.85
UM20	5.005	1	0.50	0.02	0.04	3.00	0.45	0.12	0.04	11	0.07	0.02	-1.6E-17	1.83	11.73	1.50	0.79
UM21	3.525	2	2.00	0.13	0.13	0.00	0.07	0.00	0.13	19	0.00	-0.05	0	1.17	10.63	1.50	0.75
UM22	2.95	17	144.50	13.76	1.62	12.00	0.81	1.14	1.62	45	1.72	1.80	-3.2E-17	-3.08	33.56	1.43	1.64
UM23	4.365	5	12.50	0.61	0.24	9.00	0.32	0.44	0.24	24	0.58	0.57	-3.2E-17	3.37	24.79	1.48	1.05
UM24	3.63	4	8.00	0.53	0.27	5.00	0.13	0.33	0.27	21	0.04	-0.01	0	0.35	3.12	1.50	0.77
UM25	2.515	10	50.00	8.33	1.67	11.00	1.33	1.83	1.67	45	1.35	1.40	1.59E-17	-2.62	33.46	1.45	1.45
Deja 2	3.825	9	40.50	2.61	0.58	7.00	0.29	0.45	0.58	28	0.39	0.36	-4E-18	-0.95	7.95	1.49	0.96
Detam 4	3.98	10	50.00	2.94	0.59	8.00	0.29	0.47	0.59	25	0.56	0.54	-7.9E-18	-1.32	10.66	1.48	1.04

Note: Y = Grain yield; S⁽¹⁾, S⁽²⁾, S⁽³⁾, S⁽⁶⁾ = Nassar and Huhn; NP⁽¹⁾, NP⁽²⁾, NP⁽³⁾, NP⁽⁴⁾ = Thennarasu; KR = Kang rank; W_i² = Wricke's ecovalence; σ^2_i = Shukla's stability variance; s²d_i, b_i = linear regression; CV_i = coefficient of variance; $\theta_{(i)}$ = GE variance component; and θ_i = mean variance component.

Table 5. Soybean advanced lines with yield-stability ranking based on parametric and non-parametric measurements.

Genotypes	Y	S ⁽¹⁾	S ⁽²⁾	S ⁽³⁾	S ⁽⁶⁾	NP ⁽¹⁾	NP ⁽²⁾	NP ⁽³⁾	NP ⁽⁴⁾	KR	W _i ²	σ^2_i	s ² d _i	b _i	CV _i	$\theta_{(i)}$	θ_i	SR	AR	SD
UM01	13	17	17	16	13	16	5	15	13	13	15	15	22	15	16	15	13	249	14.65	3.23
UM02	5	16	16	12	10	20	13	11	10	10	20	20	21	20	11	20	8	243	14.29	4.99
UM03	17	11	11	13	12	8	11	8	12	8	6	6	12	6	3	6	22	172	10.12	4.48
UM04	18	14	14	14	13	10	5	9	13	18	12	12	22	12	18	12	16	232	13.65	3.86
UM05	3	1	1	1	1	4	15	4	1	2	8	8	14	8	10	8	20	109	6.41	5.57
UM06	1	26	26	26	23	26	20	21	23	13	27	27	1	27	26	27	1	341	20.06	9.48
UM07	27	17	17	21	24	22	24	27	24	27	24	24	27	24	27	24	4	384	22.59	5.54
UM08	26	9	9	16	20	14	27	25	20	23	14	14	4	14	22	14	14	285	16.76	6.30
UM09	24	7	7	11	18	6	25	18	18	16	5	5	20	5	4	5	23	217	12.76	7.51
UM10	20	23	23	23	22	20	18	23	22	24	21	21	26	21	23	21	7	358	21.06	3.93
UM11	9	25	25	24	21	24	17	20	21	22	25	25	2	25	24	25	3	337	19.82	7.46
UM12	4	2	2	3	3	2	13	2	3	1	4	4	10	4	6	4	24	91	5.35	5.52
UM13	15	2	2	4	4	2	2	3	4	4	2	2	14	2	7	2	26	97	5.71	6.41
UM14	10	22	22	20	19	18	12	17	19	16	19	19	14	19	13	19	9	287	16.88	3.82
UM15	11	11	11	10	9	8	4	6	9	7	11	11	4	11	15	11	17	166	9.76	3.28
UM16	25	2	2	5	6	4	25	11	6	12	1	1	14	1	14	1	27	157	9.24	8.78
UM17	21	7	7	7	11	12	19	19	11	19	10	10	13	10	1	10	18	205	12.06	5.31
UM18	19	14	14	15	15	12	7	16	15	20	13	13	22	13	19	13	15	255	15.00	3.41
UM19	7	27	27	27	24	26	21	22	24	21	26	26	2	26	25	26	2	359	21.12	8.35
UM20	2	2	2	2	2	6	16	5	2	2	9	9	8	9	12	9	19	116	6.82	5.12
UM21	16	6	6	6	5	1	1	1	5	5	3	3	14	3	8	3	25	111	6.53	6.13
UM22	22	24	24	25	26	24	22	24	26	25	23	23	4	23	21	23	5	364	21.41	6.32
UM23	6	11	11	9	7	18	10	10	7	9	18	18	4	18	17	18	10	201	11.82	4.77
UM24	14	9	9	8	8	10	3	7	8	6	7	7	14	7	2	7	21	147	8.65	4.27
UM25	23	20	20	22	27	22	23	26	27	25	22	22	22	22	20	22	6	371	21.82	4.50
Deja 2	12	19	19	18	16	14	8	13	16	13	16	16	10	16	5	16	12	239	14.06	3.70
Detam 4	8	20	20	19	17	16	9	14	17	10	17	17	9	17	9	17	11	247	14.53	4.10

Note: Y = Grain yield; S⁽¹⁾, S⁽²⁾, S⁽³⁾, S⁽⁶⁾ = Nassar and Huhn; NP⁽¹⁾, NP⁽²⁾, NP⁽³⁾, NP⁽⁴⁾ = Thennarasu; KR = Kang rank; W_i² = Wricke's ecovalence; σ^2_i = Shukla's stability variance; s²d_i, b_i = linear regression; CV_i = coefficient of variance; $\theta_{(i)}$ = GE variance component; and θ_i = mean variance component.

soybean advanced lines UM12, UM13, UM05, UM21, and UM20 were identifiably the most stable genotypes, consistent with previous findings that low AR corresponds to high stability and yield potential (Aulia *et al.*, 2022).

Furthermore, confirmation of the genotypes' grouping based on stability and yield potential ensued using cluster analysis visualized in the form of a dendrogram. The said analysis used the ranking value of each stability parameter as a basis for grouping; thus, genotypes with similar stability patterns reached grouping in the same cluster. Genotype grouping based on the stability ranking of all measurements appears in Figure 1. Through this approach, close relationships among the genotypes can be more obviously evident, which facilitates the identification of groups of genotypes with on-par stability characteristics. The cluster analysis approach to grouping genotypes based on their response to the environment has also been a widely used method in various studies involving multi-

location and multi-season testing of various crops (Vaezi *et al.*, 2019).

The dendrogram divided the soybean genotypes into five groups based on the combination of their stability and grain yield, viz., stable high yield, stable medium yield, stable low yield, unstable high yield, and unstable low yield (Figure 1). The stable high-grain-yield group consisted of three soybean genotypes (UM12, UM20, and UM05), which demonstrated the highest adaptability to environmental variations and had the potential to be developed as new superior cultivars. A stable line will exhibit consistent grain yields across varied agroecosystem conditions. This is due to the line's ability to optimize existing resources to produce consistent grain (Wijaya *et al.*, 2022). The unstable high-yield group included the genotypes UM11, UM19, UM6, DETAM4, DEJA2, UM14, UM23, and UM02, which, despite their high yields, were less stable and therefore more suitable for development under specific environments.

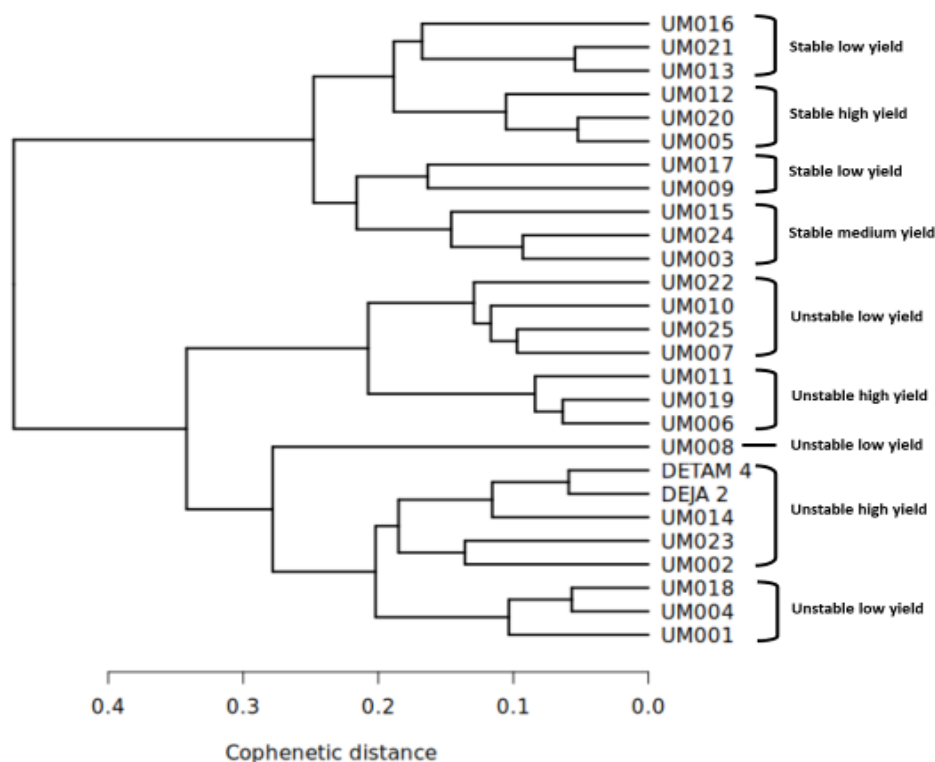


Figure 1. Dendrogram for grain yield stability in soybean advanced lines based on parametric and non-parametric measurements.

Meanwhile, the unstable low-yield group showed genotypes with low grain yield and low stability, making them less desirable for further development. Overall, the analysis revealed the combination of various stability methods and cluster analysis can provide a comprehensive picture of soybean genotype performance. This approach not only allows the identification of stable and high-yielding genotypes but also helps identify the potential genotypes for development under specific environments and as candidates for new superior cultivars in the future. Past studies also recommended to selecting the soybean genotypes with both stability and high-yield potential (Susanto *et al.*, 2023).

CONCLUSIONS

The results showed significant genotype-by-environment interaction effects for pod width, 100-grain weight, and grain yield in soybean genotypes. The genotypes UM12, UM20, and UM5 achieved inclusion in the stable high-yield group by showing the highest adaptability to environmental variations and potential to be developed as new superior cultivars in the future. These results will contribute to and provide information on soybean breeding activities in the future.

ACKNOWLEDGMENTS

The authors would like to express their deepest gratitude and appreciation to the Ministry of Higher Education, Science, and Technology for funding this research under the Regular Fundamental Research Scheme in 2025, under Contract No. 121/C3/DT.05.00/PL/2025, PT. Dwipapuri Abadi and the Rector of Majalengka University.

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