Iran Agricultural Research (2026) 45(1) 90-98

Shiraz University

Iran Agricultural Research

Journal homepage: https://iar.shirazu.ac.ir/?lang=en

Research Article

Assessment of grain yield stability in soybean (*Glycine max* (L.) merril) genotypes with various parameters

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ARTICLE INFO

Keywords:
Genotype × environment interaction
Grain yield
Stability analysis

Received: 14 September 2025
Revised: 21 November 2025
Accepted: 25 November 2025

ABSTRACT- Knowledge of genotype × environment interactions (GEI) and yield stability is essential for developing new cultivars with improved adaptation to diverse environmental constraints. Soybean (*Glycine max* (L.) Merrill) is a major source of food, protein, and oil; therefore, enhancing its yield under varying conditions remains an important research priority. In this study, the stability of soybean genotypes for grain yield was evaluated across four regions of Iran in 2019. The effects of environment, genotype, and their interaction on grain yield were all significant. The environment and GEI components contributed the largest proportions to the total sum of squares, highlighting their strong influence on soybean performance and the importance of stability assessment. Consequently, several stability analyses were conducted to identify stable genotypes. A comprehensive set of stability parameters was employed, including environmental variance, coefficient of variability (CVi), Wricke's ecovalence (Wi), Shukla's stability variance (σ^2i), coefficient of determination (Ri^2), Eberhart and Russell's joint linear regression, Tai's regression analysis, deviation from regression (S^{2}di), and the α and λ stability parameters in Tai's model. Based on environmental variance and the methods of Roemer and Francis and Kannenberg, genotypes 16, 19, and 13 were identified as the most stable. According to Shukla's stability variance (σ^2i) and Wi, genotypes 19 and 16 were classified as both high-yielding and stable. Tai's regression analysis placed genotypes 1, 16, and 19 within the stability zone. Among them, genotypes 16 and 19 were preferred due to their superior yields and were therefore considered stable genotypes. Overall, integrating the results of all stability parameters indicated that genotype 19 was the most stable and is recommended for cultivation across all regions. This study demonstrates the accuracy and effectiveness of multiple stability assessment methods in identifying stable soybean genotypes.

INTRODUCTION

Soybean is one of the most important grain legumes due to its economic significance (Dugje et al., 2009) and high protein content (Agwu et al., 2008). It is a diploid species (Chen et al., 2015) rich in protein and oil, particularly essential fatty acids (Sritongtae et al., 2022). Owing to its economic value, soybean is a suitable and strategically important crop for developing countries (Yirga et al., 2022; Chen et al., 2015). In crop breeding programs, genotypes are evaluated in multi-environment trials to assess their yield performance under different conditions and to identify superior genotypes for specific environments. Genotype × environment interaction (GEI) is a major challenge in such programs. For quantitative traits like grain yield, significant GEI can markedly reduce selection progress, as GEI constitutes a substantial proportion of the phenotypic variance (Hallauer and Miranda, 1983). When genotypes are tested across environments, their yields often vary due to differential responses to environmental factors. These are variations commonly referred to as GEI (Kang et al., 2006).

GEI arises either from changes in the relative ranking of genotype yields or from differences in the magnitude of yield variation across environments. GEI affects breeding progress by complicating the identification of genuinely superior genotypes (Magari and Kang, 1993; Ebdon and Gauch, 2002). Another consequence is a reduced correlation between phenotypic and genotypic values, which diminishes selection efficiency and introduces bias into heritability estimates and predictions of genetic gain (Comstock and Moll, 1963). Therefore, understanding the extent and nature of GEI is crucial for designing effective breeding strategies. The widespread occurrence of GEI for many quantitative traits has led to the development of numerous statistical techniques for assessing genotype stability across environments.

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DOI: 10.22099/iar.2026.51160.1633

Francis and Kannenberg (1978) categorized maize genotypes into four groups using mean yield and the coefficient of variability: (i) high yield–low variability, (ii) high yield–high variability, (iii) low yield–low variability, and (iv) low yield–high variability. Another widely used method is the regression approach of Eberhart and Russell (1966), which evaluates stability using regression coefficients (b) and deviations from regression. A significant linear component indicates a strong relationship between genotype yield and the environmental index, whereas non-significant GEI suggests similar genotype responses across environments. The regression coefficient reflects sensitivity: values greater than 1 indicate high responsiveness (better in favorable but poorer in unfavorable environments); values less than 1 imply stability in unfavorable conditions but lower performance in good environments; values near 1 denote average responsiveness. Deviations from regression capture unpredictable fluctuations, with significant deviations indicating instability. In this study, most genotypes exhibited significant deviations, indicating variable performance across environments, although none differed significantly from the expected regression coefficient of b = 1, suggesting average responsiveness.

Karimizadeh et al. (2012) evaluated lentil yield stability using several criteria, including environmental variance, coefficient of variation (CV), ecovalence, stability variance, regression slope, deviation from regression, coefficient of determination, and genotypic stability. These were categorized into variance-based (Type I), regression-based (Type II), adaptation-specific (Type III), and residual-based (Type IV) methods. Joint regression and deviation-from-linearity analyses showed that the best rice cultivars had linear responses and non-significant deviations, indicating good adaptability, highlighting the value of using multiple stability criteria for release decisions and targeting mega-environments (El-Aty et al., 2024). Similarly, the application of stability variance, coefficient of determination, CV, regression slope, and deviation from regression helped identify favorable oat genotypes, although different indices emphasized various aspects of stability, i.e., variance, responsiveness, or predictability, suggesting that breeders should triangulate across methods (Safavi et al., 2024). In quinoa, the use of environmental variance, CV, stability variance, ecovalence, regression coefficient, and deviations from linearity produced inconsistent genotype rankings; some genotypes appeared stable according to variance-based methods but not according to the regression-based approaches (Souri Laki et al., 2025).

The aim of this study was to evaluate and compare statistical methods for assessing the stability of grain yield in soybean genotypes across four locations during the 2019 growing season and to identify stable genotypes based on these stability parameters.

MATERIALS AND METHODS

Plant materials

Twenty soybean genotypes (Table 1) were evaluated at four locations in Iran, i.e., Gorgan, Moghan, Karaj, and Shahrekord, during the 2019 growing season (Table 2). These locations represent the major soybean-producing regions of the country. The experiment was conducted using a randomized complete block design (RCBD) with four replications. Each block contained 20 plots, and each plot consisted of four rows, 4 meters in length, with 60 cm row spacing and 5–8 cm plant spacing. Planting was carried out in May at a target density of 350,000 plants per hectare. Grain yield was recorded as kilograms per plot and then converted to tons per hectare at 12% seed moisture.

Data analysis

ANOVA was first performed separately for each experiment. Prior to the combined ANOVA, data normality and homogeneity of variances were assessed using the Kolmogorov–Smirnov and Levene tests, respectively. A combined analysis of variance was then conducted to estimate the main effects of the four locations (L), twenty genotypes (G), and their interaction (GEI) on total soybean grain yield. In this model, genotype was treated as a fixed effect, while replication and location were considered random effects. F-tests were performed according to the expected mean square values, E(MS), and comparisons of mean grain yield were carried out using Duncan's multiple range test. Following the detection of significant GEI, grain-yield stability analysis for the genotypes was performed separately for each environment using SAS (2014). To assess grain yield stability of the soybean genotypes, eight of the most widely used stability parameters were applied as follows: environmental variance (Roemer, 1917), coefficient of variability (CV_i) (Francis and Kannenberg, 1978), Wricke's (1962) ecovalence (Wi), Shukla's (1972) stability variance (σ^2_i), coefficient of determination (R_i^2) (Pinthus, 1973), Eberhart and Russell's (Eberhart and Russell, 1966) joint linear regression analysis, Tai's (1971) regression analysis, deviation from regression (S^2_{di}) (Eberhart and Russell, 1966; Perkins and Jinks, 1968), α and λ stability parameters in Tai's (1971) regression, genotypic variances across environments (Si2) (Roemer, 1917), and non-parametric methods for genotype ranking. The analysis was performed with SAS 9.4 M3 software.

RESULTS AND DISCUSSION

Simple and combined ANOVA

Simple analyses of variance showed significant differences among genotypes at all locations ($P < 0.01$). The Levene homogeneity test confirmed uniform variances, allowing the use of a combined ANOVA. In the combined analysis (Table 3), the location effect was significant, indicating that grain yield varied markedly from one location to another. These differences can be attributed to the factors such as soil chemical and physical properties, as well as geographical characteristics such as latitude and longitude. The genotype effect was also significant ($P < 0.01$), demonstrating the presence of substantial variation among the evaluated genotypes. In addition, the genotype × environment interaction was significant ($P < 0.01$), revealing that genotypes responded differently across locations. Consequently, stability analysis was conducted to further examine the GEI and identify stable genotypes. The significance of GEI observed in this study aligns with the findings of Rao et al. (2002), who reported significant location × year and genotype × environment interactions in soybean. The present results are also consistent with those reported by Aslam et al. (2002) and Kobraee et al. (2011). Rao et al. (2002) further noted significant differences in grain yield among soybean genotypes, supporting the outcomes obtained in this study.

Stability parameters

Environmental variance and the coefficient of variation (Type I parameters)

Based on environmental variance, genotypes 16, 19, 13, and 1 exhibited the lowest variance and were therefore identified as the most stable genotypes, respectively (Table 4). Among these, genotypes 16, 19, and 13 had mean yields higher than the grand mean, indicating that they were not only stable but also high-performing and thus suitable candidates for selection. In contrast, genotypes 7, 8, 18, and 12 displayed the highest environmental variances, reflecting pronounced yield fluctuations and low stability across environments. Similar findings were reported by Shahriari et al. (2018) in Plantago species, where no single genotype showed high stability for multiple traits, although certain species contained more than one genotype with stable trait performance. The most desirable genotypes are those positioned in the first stability group. Accordingly, genotypes assigned to this group were considered the best performers. In addition to genotypes 16, 19, 13, 4, and 15, which were categorized as the most favorable, genotypes 2 and 20 were also selected because they were located within a representative environment (Fig. 1). Conversely, genotypes 7, 8, 6, and 9 showed the highest coefficients of variability, indicating the lowest stability (Table 5).

Table 1. Pedigree of soybean genotypes used in the experiment

Genotype	Pedigree
1	Liana (8) × Telar
2	Liana (14) × Telar
3	Liana (16) × Telar
4	L6 (6) × Hacheston
5	Williams × G.non-Photo (1)
6	Williams × G.non-Photo (2)
7	Williams × G.non-Photo (5)
8	Williams × G.non-Photo (7)
9	Williams × G.non-Photo (9)
10	Williams × G.non-Photo (10)
11	Williams × G.non-Photo (11)
12	Will.82 × L87- 0174 (1)
13	Will.82 × L87- 0174 (2)
14	Will.82 × L87- 0174 (3)
15	L17 × Lavina (3)
16	Williams × Steele (2)
17	Williams × Steele (3)
18	Williams × Steele (4)
19	L8.P79
20	Williams (Check)

Table 2. The geographical and climatic features of the locations

Location	Longitude	Latitude	Average rainfall (mm)	Elevation AMSL (m)
Karaj	51°0´E	35°48´N	251	1297
Gorgan	54°25´E	36°50´N	584	155
Moghan	39°30´E	47°48´N	360	40
Shahrekord	50°86´N	32°32´E	275	2070

Table 3. Combined analysis of variance for grain yield in twenty soybean genotypes

Source of variation	df	Mean of Squares
Location (L)	3	6477679.4**
Replication/Location	8	106995.0
Genotype (G)	19	1005920.8**
G × L	57	1230734.8**
Error	152	65256.2
Coefficient of variability (%)		9.59

** significant at $P < 0.01$

Table 4. Stability methods based on analysis of variance for the 20 genotypes studied

Genotype	Yield mean	Environmental variance	Coefficient of variability	Shukla's stability variance	Wricke's ecovalence
1	2098.51	231304.9	22.91	52835.3	155417.0
2	2763.48	443047.7	24.08	468234.2	1276993.8
3	2553.15	345608.4	23.02	122214.1	342739.6
4	2859.17	286088.7	18.7	500281.1	1363520.5
5	2147.37	257554.3	23.33	137698	384546.1
6	2227.73	607325.3	34.98	319185.6	874562.6
7	2817.57	1293047.3	40.35	1008868.2	2736705.8
8	2702.84	1105108.5	38.89	911348.9	2473403.4
9	2418.56	630194.8	32.82	492632.7	1342869.7
10	2357.19	424576.5	27.64	572253.1	1557844.7
11	2541.27	523558.7	28.47	232245.1	639823.3
12	2887.93	665316.7	28.24	630919.4	1716243.8
13	2789.21	228141.8	17.12	182537.4	505612.5
14	2573.30	538085.8	28.5	419210.4	1144629.5
15	2784.24	373018.9	21.93	557975.9	1519296.5
16	2761.53	32930.3	6.57	57343.8	167589.8
17	2920.11	647816.0	27.56	332610.5	910809.7
18	3141.16	745399.9	27.48	881323.6	2392335.3
19	2772.66	47653.7	7.87	120613.5	338417.9
20	3094.29	528398.2	23.49	565766.2	1540330.1

Table 5. Rank of yield mean and stability parameters for soybean genotypes

Genotype	Yield mean	Environmental variance	Coefficient of variability	Shukla's stability variance	Wricke's ecovalence
1	20	4	6	1	1
2	10	10	10	11	11
3	14	7	7	4	4
4	5	6	4	13	13
5	19	5	8	5	5
6	18	14	18	8	8
7	6	20	20	20	20
8	12	19	19	19	19
9	16	15	17	12	12
10	17	9	13	16	16
11	15	11	15	7	7
12	4	17	14	17	17
13	7	3	3	6	6
14	13	13	16	10	10
15	8	8	5	14	14
16	11	1	1	2	2
17	3	16	12	9	9
18	1	18	11	18	18
19	9	2	2	3	3
20	2	12	9	15	15

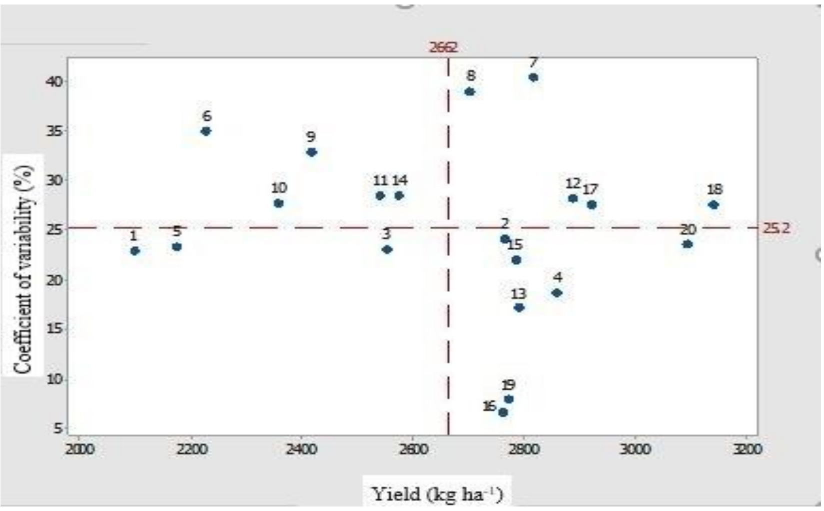

Fig. 1. Distribution of soybean genotypes according to grain yield (kg ha^{-1}) and coefficient of variability (%).

Fig. 2 presents the three-dimensional plot of genotype performance in relation to the coefficient of variability and environmental variance based on Roemer's (1917) stability parameter. According to this graph, genotypes positioned in the region characterized by low variance and a low coefficient of variability are considered highly stable. Genotypes 19, 16, 13, 4, 1, 5, 3, and 15 were identified as stable according to both Roemer (1917) and Francis and Kannenberg (1978). In contrast, genotypes 7, 8, 18, 6, 9, and 12 exhibited high variance and high coefficients of variability, indicating low stability. Among the stable group, genotypes 16, 19, and 13 showed mean yields exceeding the grand mean and were therefore recognized as the most stable and consistent genotypes. These genotypes are recommended for planting across all regions. Such findings also help breeders reduce time and costs by facilitating the identification of representative environments and high-performing, stable genotypes for grain yield trials (Hassani et al., 2018).

Shukla's stability variance and Wricke's ecovalence (Type II parameters)

Based on stability variance (σ^2_i), genotypes 1, 16, 19, 3, and 5 exhibited the lowest variances and were therefore identified as the most stable genotypes (Table 4 and Table 5). Among these, genotypes 16 and 19 also produced grain yields higher than the grand mean, indicating that they combine both stability and superior performance, making them the most favorable genotypes for selection. Wricke's (1962) ecovalence (Wi) was used to determine the contribution of each genotype to the GEI sum of squares and its magnitude as a stability measure. The results of Shukla's (1972) stability variance (σ^2_i) and Wricke's ecovalence (Wi) were consistent. Since Shukla's stability variance is a linear combination of Wricke's ecovalence, and both parameters yielded identical genotype rankings, the use of either parameter is sufficient. Based on both criteria, genotypes 19 and 16 were classified as stable, high-yielding genotypes and are therefore recommended for cultivation across all studied environments. Conversely, genotypes 7, 8, 18, and 12 were identified as the most unstable genotypes (Table 4 and Table 5). It should be noted that Wricke's ecovalence represents the proportion of each genotype's contribution to the overall GEI sum of squares; thus, stable genotypes are characterized by lower Wi values.

Eberhart and Russell method

According to Eberhart and Russell's (1966) joint linear regression analysis (Fig. 3), the most stable genotype with high grain yield is one that has a regression coefficient equal to unity (b = 1) and a non-significant deviation from regression ($S^2di = 0$). Genotypes with b > 1 are better adapted to favorable environments, whereas those with b < 1 are more adapted to unfavorable environments. In the present study, the regression coefficients were not significant for any genotype; therefore, stability assessment relied mainly on the deviation from regression and mean yield. The deviation from regression (S^2di) was significant for most genotypes, indicating variable responses across environments and considerable yield dispersion around the regression line. Similar findings were reported by Ghaed-Rahimi et al. (2015), who showed that regression models, GEI variances, and yield performance could effectively identify stable wheat genotypes for breeding purposes. Because not all genotypes clustered around b = 1, the influence of unpredictable environmental factors on stability was evident. A t-test was used to evaluate whether regression coefficients differed significantly from unity, and results confirmed that none of the genotypes showed a significant deviation from b = 1. According to Eberhart and Russell (1966), stable genotype selection should consider three components simultaneously: the regression coefficient (bi), the deviation from regression (S^2di), and mean yield. Ideally, a stable genotype exhibits b = 1, minimal deviation from regression, and high grain yield. Given that the regression coefficients were not significant, this criterion alone was insufficient for identifying stable genotypes; however, regression coefficients together with grain yield provided useful information on general adaptability. Fig. 3 illustrates the distribution of genotypes based on mean yield and regression coefficients. It is evident that genotypes 12, 4, 7, 19, 2, and 8 produced mean yields higher than the grand mean, and all had non-significant regression coefficients.

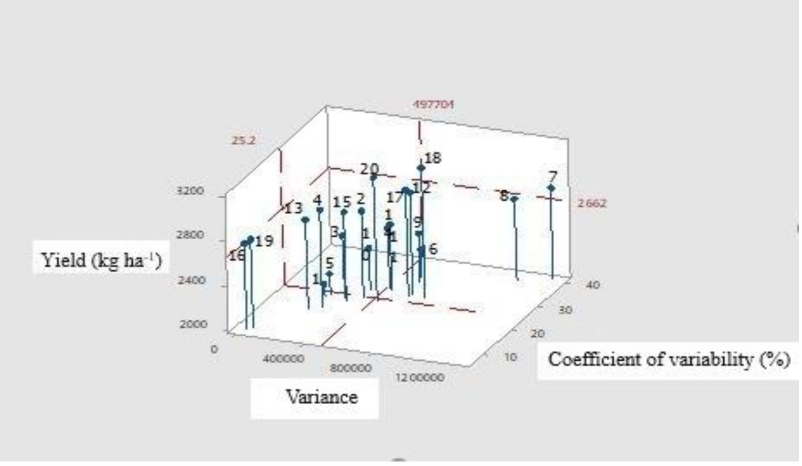

Fig. 2. Three-dimensional plot of stability parameters of environmental variance and coefficient of variability of grain yield (kg ha^{-1}) in studied soybean genotypes.

Therefore, these genotypes exhibited favorable general adaptability. Among them, genotypes 19 and 4 showed the lowest deviation from regression, indicating higher stability compared to the others. Genotypes with low mean yield but non-significant regression coefficients, i.e., genotypes 1, 5, and 6, were classified as moderately stable but possessing poor general adaptability. Genotypes 9, 11, and 14 were identified as stable genotypes with moderate general adaptability, as their mean yields were close to the grand mean and their regression coefficients were non-significant (Fig. 3). The identification of stable genotypes and representative environments provides valuable support for breeding programs aimed at developing improved *Glycine max* cultivars (Shahriari et al., 2018).

Tai's regression

In Tai's (1971) regression model, all genotypes exhibited non-significant α values, indicating moderate stability. However, based on the λ parameter, genotypes 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, and 20 showed significant deviations from linear response and were therefore not positioned within the representative stability region. According to this method, genotypes located within the hyperbolic curves and between the vertical boundaries of the α–λ plot are considered stable (Fig. 4). Theoretically, $\alpha = -1$ reflects complete stability, whereas $\alpha = 0$ indicates moderate stability. In the present study, genotypes 1, 16, and 19 were positioned within the designated stability region, with genotypes 16 and 19 selected as the most desirable due to their superior grain yield. These findings align with previous reports that regression-based stability models can effectively identify varieties with high adaptability and stability suitable for breeding programs (Ghaed-Rahimi et al., 2014). The continued success of plant breeding initiatives ultimately depends on providing farmers with genotypes that consistently deliver high yield across diverse and unpredictable environmental conditions (Hassani et al., 2018).

Comparison of various methods

This study highlights the pervasive influence of GEI on soybean grain yield, consistent with previous findings showing that GEI accounts for a substantial proportion of total variation, often exceeding the main effects of genotype and environment, and plays a decisive role in determining yield performance (Habtegebriel, 2022). Similar results from recent soybean trials also confirmed significant GEI effects, reinforcing its importance in cultivar evaluation and selection (Abebe et al., 2024). The use of univariate stability parameters provided a comprehensive assessment of genotype behavior across environments. The consistent identification of genotypes 16 and 19 as both stable and high-yielding across multiple indices aligns with reports from other crops, where different stability metrics converged on the same superior genotypes (Abdelghany et al., 2021; Vymyslický et al., 2025). The convergence observed in the present study, particularly the repeated identification of genotype 19 as the most stable, demonstrates the value of integrating multiple statistical approaches for robust genotype selection. This is in agreement with current recommendations from multi-environment trials advocating for combined evaluation of mean performance and stability to guide cultivar release decisions (Matei et al., 2017; Rani et al., 2023). The findings of this study hold important implications for soybean breeding. Genotype 19, with its consistent performance and low sensitivity to environmental variation, emerges as a strong candidate for widespread cultivation. The results reaffirm the central role of GEI in shaping soybean yield and highlight the importance of combining several stability parameters to ensure accurate and reliable genotype selection. Identifying genotypes that exhibit both high yield and stability benefits both breeders and farmers. For breeders, incorporating stable genotypes such as 16 and 19 into crossing programs can accelerate the development of cultivars with reliable performance across diverse conditions, reducing the time and cost associated with multi-environment testing. For farmers, the adoption of stable and high-yielding genotypes reduces production risk and enhances productivity under fluctuating environmental conditions. As climate variability intensifies, the development and deployment of broadly adapted genotypes become increasingly crucial. Stable genotypes form a strong foundation for breeding cultivars that are resilient to unpredictable climatic and environmental changes. The present study highlights the essential role of stability analysis in soybean improvement and provides valuable insights for enhancing the resilience and productivity of soybean cultivation. Genotype 19 stands out as a highly promising cultivar for broad adaptation in Iran, demonstrating how the integration of statistical rigor with practical breeding objectives can accelerate the development of robust and productive soybean genotypes.

CONCLUSION

The various stability parameters largely identified similar genotypes as stable across environments. Based on environmental variance, genotypes 16, 19, 13, and 1 were recognized as the most stable. The coefficient of variation indicated genotypes 16, 19, 13, 4, and 5 as stable. Shukla's stability variance and Wricke's ecovalence both identified genotypes 19 and 16 as the most stable. According to the Eberhart and Russell regression method, genotypes 19 and 4 were considered stable, while Tai's regression analysis indicated genotypes 16 and 19 as stable. Overall, genotype 19 consistently demonstrated high stability across all four environments based on multiple stability parameters and also exhibited superior grain yield. The identification of stable genotypes can support soybean breeding programs by facilitating the development of improved *Glycine max* cultivars with reliable performance across diverse environments. Furthermore, the results of this study can assist breeders in identifying representative testing locations for grain yield trials, thereby reducing both the time and cost required for multi-environment evaluation.

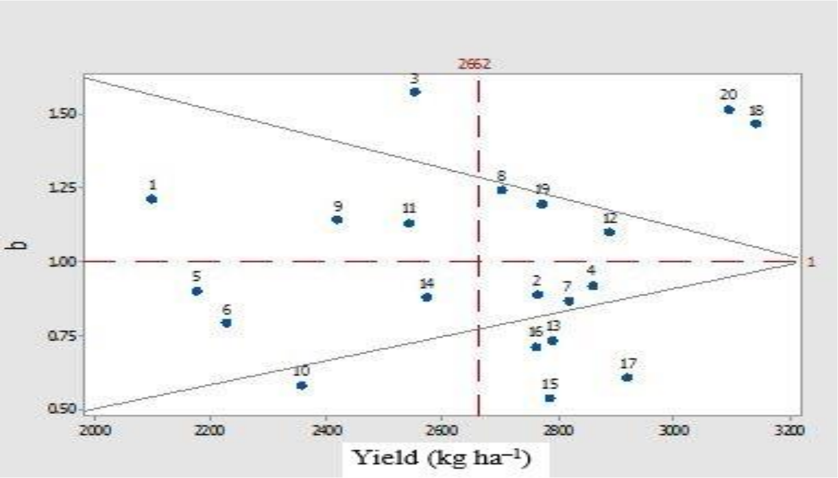

Fig. 3. Eberhart and Russell scatterplot of genotypes according to grain yield (kg ha^{-1}) and regression coefficient (b).

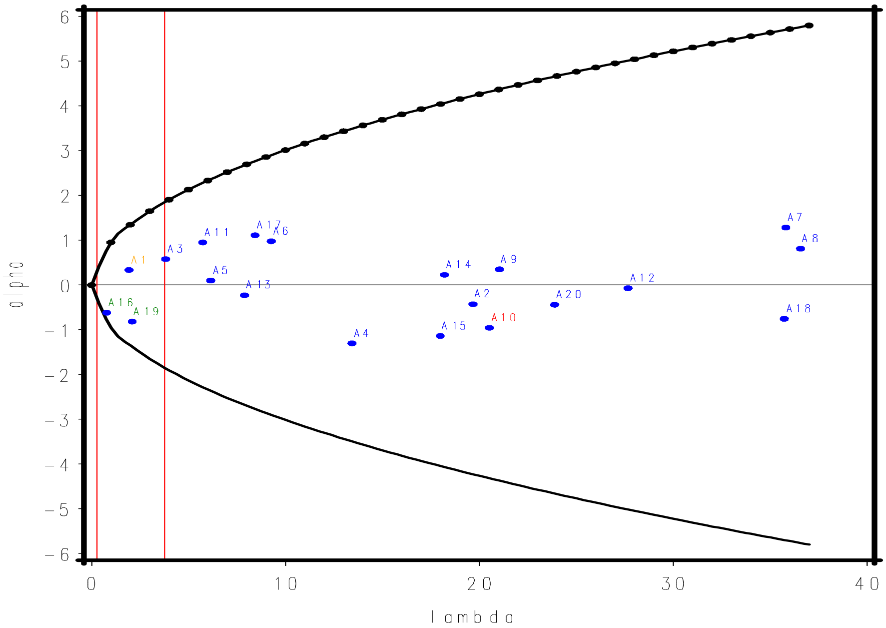

Fig. 4. The scatterplot of soybeans genotypes in Tai regression for determining stability.

FUNDING

The authors declare that no funds were received during the preparation of this manuscript.

Credit AUTHORSHIP CONTRIBUTION STATEMENT

Conceptualization: Alireza Pourmohammad and Mahdieh Roshandel; Methodology: Hamidreza Babaei; Software: Hamidreza Babaei; Validation: Mahdieh Roshandel, Alireza Pourmohammad, and Hamidreza Babaei; Formal analysis: Mahdieh Roshandel; Investigation: Mahdieh Roshandel; Resources: Alireza Pourmohammad; Data curation: Mahdieh Roshandel; Writing—original draft preparation: Alireza Pourmohammad; Writing—review and editing: Alireza Pourmohammad; Visualization: Mahdieh Roshandel; Supervision: Alireza Pourmohammad; Project administration: Hamidreza Babaei.

DECLARATION OF COMPETING INTEREST

The authors declare no conflicts of interest.

ETHICAL STATEMENT

Not applicable.

DATA AVAILABILITY

The data presented in this study are uploaded during submission as a supplementary file and are openly available for readers upon request.

ACKNOWLEDGMENTS

The authors are thankful to Seed and Plant Improvement Institute (SPII), Karaj, Iran for receiving necessary help for this project work**.**

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