Heliyon 10 (2024) e39105

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon

Research article

GGE biplot analysis for genotype × environment interactions affecting the seed shattering of *Psathyrostachys juncea*

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A R T I C L E I N F O

Keywords:
GGE biplot
Genotype-environment interaction
Psathyrostachys juncea (fisch.) nevski
Seed shattering

A B S T R A C T

The *Psathyrostachys juncea* (Fisch.) Nevski. Is an important forage grass in cold and arid regions. However, its high seed shattering (SS) traits affects seed yield. The SS phenomenon arises from the intricate interplay between its genotype and environment (GE). To gain a comprehensive understanding of SS variations in different *Psathyrostachys juncea* (Fisch.) Nevski materials under the influence of GE interactions, a two-year experiment was conducted on 300 individual plants at two locations. Utilizing the GGE biplot method, the current research aimed to assess the adaptability and stability of *Psathyrostachys juncea* (Fisch.) Nevski *on SS trait*, with a focus on identifying genotype materials conducive to breeding. The analysis of variance indicated that genotype, environment, year, and their interactions exhibited extremely significant effects on SS. Among these factors, the GE interaction showed as the primary contributor to variability in the SS trait of *Psathyrostachys juncea* (Fisch.) Nevski. The GGE biplot illustrated that Hohhot and Baotou emerged as representative locations with strong discriminative power for the materials. Genotypes 18 and 120 exhibited high SS rates in Hohhot, while 118 and 111 showed high SS rates in Baotou. Genotypes 132 and 177 were identified as ideal genotypes with both high and stable SS rates. These findings serve as valuable references for applications in grazing pastures and provide genotype materials for the genetic improvement and mechanistic analysis of SS traits in *Psathyrostachys juncea* (Fisch.) Nevski.

1. Introduction

Psathyrostachys juncea (Fisch.) Nevski., a diploid chromosome plant (2n = 2x = 14) in the Triticeae Dumort of the Gramineae family, is a cross-pollinated perennial grass native to Central and Northern Asia [1]. Their distribution has spread to East Asia, Europe, and North America due to introduction and domestication [2]. Its primary distribution includes Inner Mongolia, Tibet, and Xinjiang in China [2]. It is accustomed to grow in arid and cold environments and is frequently utilized in natural grasslands and cultivated pastures within cold and arid regions [3]. *Psathyrostachys juncea* (Fisch.) Nevski has clustered leaves, multiple tillers, and a strong root system [4]. Thriving during summer and autumn when the soil retains some moisture, it offers high nutritional value as forage [4,5]. Consequently, *Psathyrostachys juncea* (Fisch.) Nevski stands out as an exceptional forage grass with economic and breeding significance for livestock [6]. However, the challenge lies in its high seed shattering (SS), a self-regulating mechanism for wild grass to adapt to the

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https://doi.org/10.1016/j.heliyon.2024.e39105
Received 20 June 2024; Received in revised form 2 October 2024; Accepted 7 October 2024
Available online 13 October 2024

environment, ensuring life continuity through seed dispersal and pasture regeneration [7]. Despite these advantages, the high SS of forage grass reduces seed yield, limiting its application in agricultural production. Notably, research on the SS traits of *Psathyrostachys juncea* (Fisch.) Nevski is yet to be conducted. This study measured the SS rate of 300 individual plants to evaluate the degree of SS for each material.

In agricultural ecosystems, SS traits in plants are intricately determined by the interplay of genetic regulation, environmental influences, and management practices [8]. The dynamic interaction between genetics and the environment (GE) across diverse environmental conditions leads to variations in plant phenotypic traits. Because of this complexity, breeders routinely conduct multi-year, multi-site regional trials on plant materials. While traditional statistical analysis methods such as joint variance analysis and linear regression exist, they prove cumbersome in practical application and may lack systematic and comprehensive results [9,10].

The GGE model (genotype main effect plus genotype × environment interaction model) is an effective analytical method for environmental discrimination and comprehensive evaluation of various varieties in regional trials [11]. Functioning as a valuable tool, the GGE model facilitates efficient statistical analysis and visually intuitive representation of the stability and multifactor interactions of plant traits in different environments [12]. It provides an objective assessment of GE interactions [13], effectively mitigating the association between phenotypic and genotypic values and influencing the progress of selection [14]. Knowledge of GE interaction can help plant breeders to reduce the cost of genotype evaluation by eliminating unnecessary testing locations [15].

The GGE model proves invaluable in discerning the optimal performance of different materials across diverse environments. It evaluates the discriminative power and representativeness of the environment, aiding in the selection of ideal varieties characterized by high yield, stability, quality, and broad adaptability [16–18]. This methodology has been successfully applied in various contexts, such as barley germplasm resource screening [19] and the evaluation of experimental environments for maize [20]. The growth of edible peanuts, influenced by the interaction of GE, has been effectively assessed using the GGE biplot to identify stable and high-yielding peanut genotypes [21]. Similarly, sorghum, a crucial source of human nutrition, underwent a two-year experiment involving 13 newly developed varieties at seven trial locations. The GGE biplot analysis shed light on the GE interaction's impact on sorghum yield, pinpointing the optimal trial locations for each variety [22]. The research group led by Wang Tian investigated the tillering-related traits of 21 *Psathyrostachys juncea* (Fisch.) Nevski materials, identifying materials suitable for cultivation in different environments [23]. In contrast, the current research on *Psathyrostachys juncea* (Fisch.) Nevski underscores a significant gap in the utilization of the GGE biplot for analyzing SS traits. This study actively bridges this gap by identifying optimal planting environments for diverse *Psathyrostachys juncea* (Fisch.) Nevski materials and precisely delineating superior genotypes exhibiting stable SS performance. The outcomes not only provide valuable insights for deploying high-performing genotypes in grassland settings but also furnish alternative materials for refining SS genotypes through strategic breeding efforts. The findings from this study stand as a pivotal reference for subsequent transcriptome sequencing technology focused on mechanistically unraveling the intricacies of SS traits in *Psathyrostachys juncea* (Fisch.) Nevski.

2. Materials and methods

2.1. Plant materials and experimental site

The 21 accessions of *Psathyrostachys juncea* (Fisch.) Nevski selected for this study were procured from eight countries, encompassing China, the United States, Mongolia, and Russia. One accession (CF005043) originated from the China National Medium-term

Table 1
Sources, geographic coordinates, and cultivation methods of *Psathyrostachys juncea* (Fisch.) Nevski accessions.

Accession	Individual plant number	Sample size	Longitude	Latitude	Origin	Cultivation
PI 531828	1–14	14	113°51′45″W	45°26′0″N	Idaho, U.S.	Wild
PI 595135	15–28	14	86°31′6″E	43°36′43″N	Xin jiang, China	Wild
PI 619487	29–42	14	92°4′35″E	49°51′50″N	Mongolia	Wild
CF 005043	43–56	14	110°46‴E	40°51′0″N	China	Cultivate
PI 502577	57–70	14	113°51′0″E	62°31′0″N	Russian Federation	Cultivate
PI 549118	71–84	14	111°46′0″E	40°51′0″N	Utah, U.S.	Cultivate
PI 502576	85–98	14	113°51′0″E	62°31′0″N	Russian Federation	Cultivate
PI 565060	99–112	14	112°48′30"E	63°21′2"N	Russian Federation	Wild
PI 565051	113–123	11	112°48′30"E	63°21′2"N	Russian Federation	Wild
PI 578854	124–138	15	106°7′0″W	52°2′0"N	Canada	Cultivate
PI 619483	139–153	15	90°7′58″E	49°29′13″N	Mongolia	Wild
PI 565052	154–167	14	112°50′28"E	63°50′2"N	Russian Federation	Wild
PI 531827	168–182	15	24°28′0″E	59°22′0″N	Estonia	Wild
PI 272136	183–195	13	76°55′0″E	43°19′0″N	Alma-Asa, Kazakhstan	Cultivate
PI 502573	196–210	15	164°9′5″E	65°17′0″N	Former Soviet Union	Cultivate
PI 598614	211–224	14	50°30′0″E	50°25′0″N	Kazakhstan	Wild
PI 476299	225–237	13	99°59′55″W	46°1′42″N	U.S.	Cultivate
PI 619565	238–251	14	94°55′45″E	49°22′50″N	Mongolia	Wild
PI 531826	252–268	17	93°51′45″E	42°22′6″N	China	Wild
PI 502572	269–284	16	164°9′5″E	65°17′0″N	Former Soviet Union	Cultivate
PI 598610	285–300	16	58°45′0″E	46°45′0″N	Kazakhstan	Wild

Gene Bank for Forage Germplasm, while the remaining 20 were supplied by the U.S. National Plant Germplasm Resources Conservation System (NPGS). Table 1 outlines individual plant numbers, source countries, and cultivation methods. The geographical location, soil conditions, and climatic details of Hohhot and Baotou are comprehensively presented in Tables 2 and 3.

2.1.1. *Field experimental design*

The accessions of *Psathyrostachys juncea* (Fisch.) Nevski were individually cultivated in the greenhouse at Inner Mongolia Agricultural University in October 2018. Upon seedling formation, they were divided into two clone populations at the tillering node position and subsequently transplanted into cultivation bowls. In June 2019, the two clone populations were separately transplanted to Hohhot and the Vocational Technology College of Inner Mongolia Agricultural University in Baotou. Using a randomized complete block experimental design, each accession was planted with 30 individual plants at spacings of 50 cm. Conventional field management practices were diligently applied, and after heading, artificial watering was judiciously regulated. (Although the study was initiated in 2018, the primary data collection and major experimental work were conducted from 2022 to 2023. The early years were focused on initial plant cultivation and experimental setup. The comprehensive analysis and final data collection were carried out during the years 2022–2023.)

The method for determining SS in Gramineae forage grass, as outlined by Steven [24], served as the reference for SS assessment. We selected 300 individual plants that survived in both locations (Table 1) and chose three inflorescences from each plant that exhibited similar shapes and consistent maturity (The materials we introduced have a relatively short cultivation time, and their domestication level is low. The materials come from natural populations, and there are differences between different individuals of the same material. Therefore, it is necessary to analyze individual plants). Each inflorescence underwent ten shakes with equal force on the edge of a bucket, causing the seeds to detach and fall into the container. The number of shed seeds was meticulously recorded. The sum of the shed seeds and the remaining seeds on the inflorescence yielded the total seed count. The SS rate was calculated using the formula: Seed Shattering Rate (%) = (Number of shed seeds per inflorescence/Total number of seeds per inflorescence) × 100 % [24]. Measurements were conducted 30 days after the peak flowering of *Psathyrostachys juncea* (Fisch.) Nevski in the years 2022–2023 (July, when seeds were fully matured). Since 2020, we have been exploring methods suitable for measuring the seed shattering rate of *Psathyrostachys juncea* (Fisch.) Nevski. We have ultimately settled on this method, which, despite being laborious and time-consuming, offers high accuracy.

2.2. *Statistical analysis*

Data plotting and statistical analyses were conducted using GraphPad Prism 8.0 software (https://www.graphpad.com/). Detailed statistical parameters, including means ± SDs (standard deviations), skewness, and kurtosis, are presented in the table. Joint variance analysis utilized SAS 9.4, while GE interaction effects analysis was carried out using the R language GGEBiplot-GUI package [25]. Each individual plant was assigned a numerical identifier (Table 1). The left figures (a, c, e, g) correspond to the year 2022, while the right figures (b, d, f, h) depict the year 2023. A and B represent Hohhot and Baotou, respectively. Statistical significance is denoted by asterisks: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$.

3. Results

3.1. *Genetic variation and analysis of variance*

In the years 2022–2023, seed shattering (SS) rates were assessed for 300 individual plants of *Psathyrostachys juncea* (Fisch.) Nevski in Hohhot and Baotou. The analysis revealed notable disparities in SS rates between the two locations within the same year, as depicted in Fig. 1 (where red and blue colors represent Hohhot and Baotou, respectively) and detailed in Table 4. Specifically, in 2023, the SS rates in the two locations exhibited significant differences at the 0.001 significance level. In 2022, the disparity in SS rates between the two locations was minimal. However, in 2023, the SS rates ranged from 0 percent to 64.35 percent in Hohhot and from 0 percent to 40.98 percent in Baotou, demonstrating a marked distinction between the two locations. The high variability rate of SS (55.51 %–73 %) indicates that the 300 individual plants of *Psathyrostachys juncea* (Fisch.) Nevski exhibit rich variability. The skewness and kurtosis values presented in Table 4, when combined with the data distribution illustrated in Fig. 1 (where red and blue colors represent Hohhot and Baotou, respectively), suggest that the SS rates were relatively concentrated under different environmental conditions and across various years, conforming to a normal distribution. These findings indicate strong environmental influences on SS rates, particularly in

Table 2
Environmental parameters of Hohhot and Baotou, including soil type, temperature, precipitation, and humidity.

Climate index	Hohhot						Baotou					
	2022			2023			2022			2023		
	May	Jun.	Jul.	May	Jun.	Jul.	May	Jun.	Jul.	May	Jun.	Jul.
Average temperature/°C	16.1	22.4	23.3	16.2	22.2	23.4	17.4	23.3	23.5	17.3	23.1	23.3
Average relative humidity/%	30.8	41.4	52.1	38.5	33.0	52.0	35.4	45.8	60.4	44.7	41.0	62.8
Average precipitation/mm	4.7	31.3	37.2	29.7	27.3	58.5	11.0	36.7	50.0	23.9	16.3	97.4
Average effective sunshine hours/h	289.5	246.8	263.1	226.1	321.7	241.6	302.5	281.0	273.8	253.1	343.6	269.3

Table 3
Climate indices of Hohhot and Baotou, including temperature, precipitation, humidity, and sunshine hours.

Basic facts	Hohhot (A)	Baotou (B)
Latitude	40°44′58.3188"	40°35′54.8124"
Longitude	111°50′46.6116"	110°34′42.7512"
Altitude/m	1048.0	1019.0
Soil pH value	8.0	7.6
Soil Organic matter/g·kg-1	20.7	26.6
Total nitrogen/g·kg-1	1.0	1.7
Rapidly available phosphorus/mg·kg-1	20.5	6.4
Rapidly available potassium/mg·kg-1	171.8	205.6

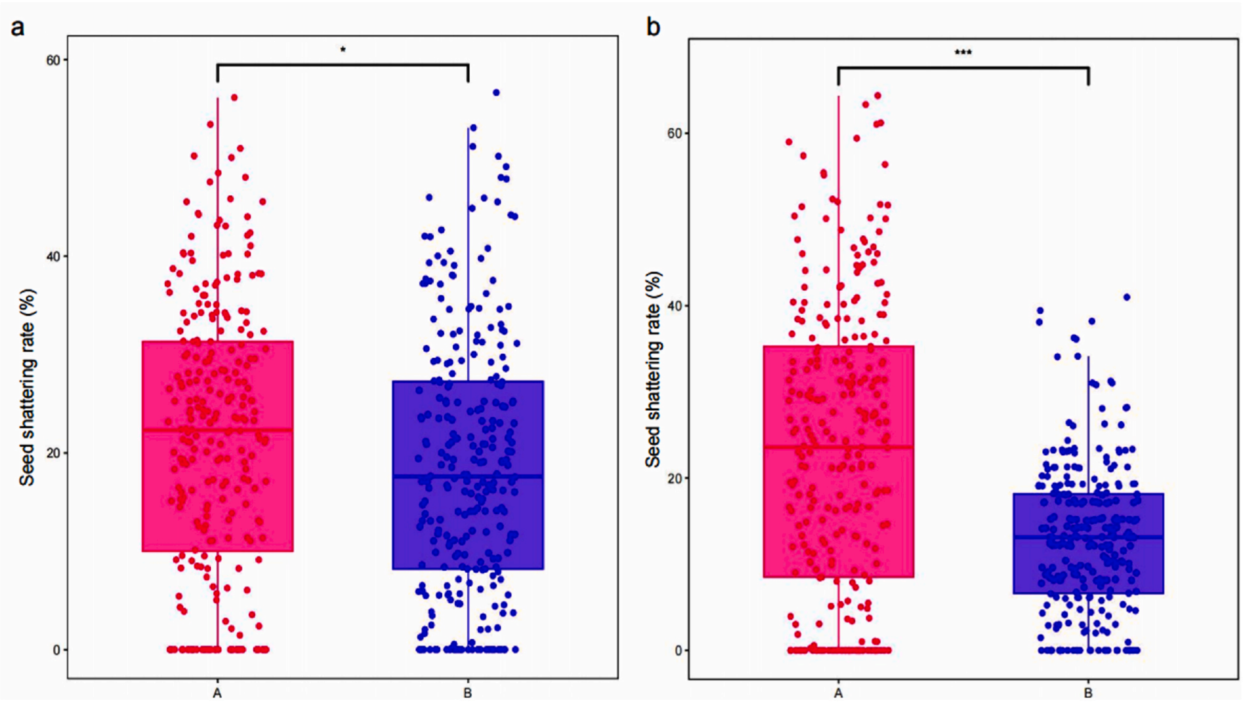

Fig. 1. Boxplots of seed shattering rate of *Psathyrostachys juncea* (Fisch.) Nevski at two locations from 2022 to 2023. "A" and "B" denote Hohhot and Baotou, respectively. The red and blue figures correspond to seed shattering rate analysis in 2022 and 2023, respectively. Statistical significance is denoted by asterisks: $^{*}P < 0.05$, $^{***}P < 0.001$. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

Table 4
Seed shattering rates of *Psathyrostachys juncea* (Fisch.) Nevski at Hohhot and Baotou over two years (2022–2023).

Environment	Year	Range of variation	Mean ± SD	CV/%	Skewness	Kurtosis
Hohhot	2022	0.00–56.15	25.22 ± 14.00	55.51	0.15	−0.45
	2023	0.00–64.35	23.15 ± 16.90	73.00	0.20	−0.56
Baotou	2022	0.00–56.66	18.72 ± 13.16	70.30	0.50	−0.31
	2023	0.00–40.98	12.86 ± 8.63	67.11	0.71	0.87

2023, where significant differences at the 0.001 level were observed between the two locations. Additionally, while the disparity in SS rates was minimal in 2022, it became more pronounced in 2023, highlighting potential year-specific environmental factors affecting SS rates. The high variability rate (55.51 %–73 %) among the 300 individual plants indicates rich genetic diversity within the studied *Psathyrostachys juncea* (Fisch.) Nevski population.

Table 5 further examined the SS rates of *Psathyrostachys juncea* (Fisch.) Nevski from diverse sources, revealing high variability rates ranging from 48.02 percent to 64.08 percent. Notably, germplasm materials from the United States exhibited the highest variability rate (64.08 %), while materials from Mongolia showed the lowest variability rate (48.02 %). Chinese and Russian materials had similar variability rates, at 59.25 percent and 59.18 percent, respectively.

To elucidate the magnitude of the impact of environment, year, genotype, and their interactions on SS traits, an analysis of variance was performed for the SS rate, as presented in Table 6. The results revealed that Location, Year, Genotype, Location × Year, Location × Genotype, Year × Genotype, and Location × Year × Genotype were all statistically significant at the 0.0001 level. Among these factors, Location, Year, Genotype, and Location × Year contributed smaller proportions to the total sum of squares. Location × Genotype, Year × Genotype, and Location × Year × Genotype accounted for 64 percent, 25.35 percent, and 10.37 percent of the total sum of squares, respectively. Remarkably, Location × Genotype exhibited the most substantial proportion in the total sum of squares, indicating that the interaction of GE was the primary driver of variations in SS traits, followed by the interaction between year and genotype.

3.2. GGE biplot analysis of G × E interaction

The "Which Won Where/What" method is employed to group experimental points based on the interaction of GE. This grouping technique highlights genotype performance in different categories and aids in the analysis of the most suitable planting zones for the tested materials. The polygon depicted in Fig. 2 is formed by connecting the "vertices," which are farthest from the origin, one by one, encompassing all genotypes. Perpendicular lines drawn from the center to each side divide the polygon into several sectors. Within each sector, the "vertex" corresponds to the genotype that performs relatively well. Genotypes situated within the polygon and close to the origin are considered less sensitive to the environment, with SS rates approaching the mean. The horizontal axis (AXIS1) represents genotype, while the vertical axis (AXIS2) represents the interaction of GE. In 2022 (Fig. 2-c), the first principal component (PC) accounted for 57.92 percent of the total variation, while the second principal component explained 42.08 percent of the variation. Genotypes 118 and 30 exhibited high SS rates in Baotou, originating from materials 565051 and 619487, respectively. Genotypes 18 and 119 showed elevated SS rates in Hohhot, sourced from 595135 to 565051, respectively. Moving to 2023 (Fig. 2-d), PC1 and PC2 accounted for 56.21 percent and 43.79 percent of the total variation, respectively. Genotype 120 displayed high SS rates in Hohhot, originating from 565051, while genotypes 111 and 47 demonstrated elevated SS rates in Baotou, sourced from 565060 to 005043, respectively. Over the two consecutive years of experiments, 565051 consistently exhibited characteristics indicative of a superior genotype at the individual plant level.

The ideal genotype demonstrates both high and stable yields in specific environments. The "Mean vs. Stability" method is employed to concurrently identify the high-yielding and stable characteristics of materials. In Fig. 3, the direction along the arrow indicates higher yields. Genotypes on the left side of the vertical axis, perpendicular to the horizontal axis, have yields below the average, while those on the right side have yields above the average. The length of the perpendicular line from a genotype to the average environment axis reflects the genotype's stability, with longer lines indicating less stability and vice versa. The first two principal components in Fig. 3-e and Fig. 3-f collectively incorporated 100 percent of the variation information. In Fig. 3-e, genotypes 61, 132, and 177 exhibited high and stable SS rates, originating from materials 502577, 578854, and 531827, respectively. In Fig. 3-f, 171 exhibited the highest SS rate, sourced from 531827 but with instability. Genotype 131, originating from 578854, showed a high and stable SS rate. In summary, there are genotypes with consistently high and stable SS rates from the same materials in both years. Therefore, 132 and 177 were selected as ideal genotypes.

The "Discriminativeness vs. Representativeness" analysis method is employed to illustrate the correlation of different locations in the assessment of material adaptability. In Fig. 4, the lines originating from the origin represent vectors, with the length of the vector indicating discriminative power. Longer vectors suggest a stronger discriminative ability of the location for the materials. The lines with arrows passing through the circles represent the "average environment axis." The angle between the vector and the average environment axis reflects the representativeness of the environment, with a smaller angle indicating stronger representativeness. Furthermore, the angle between testing points can unveil the correlation between environments. An angle less than 90° indicates a positive correlation, suggesting similar effects of environments on materials. Conversely, an angle greater than 90° signifies a negative correlation, indicating opposing effects of environments on materials. An angle equal to 90° represents no correlation between environments. In this investigation, the elongated vectors observed in both Hohhot and Baotou indicated a robust discriminative power. The angles between the vectors and the average environment axis were less than 90° in both locations, highlighting the strong representativeness of Hohhot and Baotou. Nevertheless, the angle between the two locations was close to 90°, indicating that the impacts of the two test points on the materials were independent of each other.

Table 5
Seed shattering rates of *Psathyrostachys juncea* (Fisch.) Nevski from different geographic sources.

Source	Max	Min	Mean ± SD	CV/%
China	64.35	0.00	21.45 ± 12.71	59.25
Mongoliae	61.04	0.00	25.49 ± 12.24	48.02
Russia Federation	63.32	0.00	22.81 ± 13.50	59.18
Kazakhstan	51.46	0.00	20.39 ± 11.99	58.80
Estonia	41.29	0.00	18.70 ± 11.56	61.82
America	48.77	0.00	17.26 ± 11.06	64.08
Former Soviet Union	51.72	0.00	21.84 ± 13.16	60.26
Canada	61.21	0.00	27.47 ± 13.89	50.56

Table 6
Combined analysis of variance for seed shattering rates of *Psathyrostachys juncea* (Fisch.) Nevski genotypes in two locations and two years (2022–2023).

Sources of variation	df	Sum of square	*P* ****	% of total sums of squares
Location	1	416,278.3	<0.0001	0.18
Year	1	119,049.7	<0.0001	0.05
Genotype	20	1641.1	<0.0001	0.00
Location × Year	1	103,964.5	<0.0001	0.04
Location × Genotype	20	144,232,482.4	<0.0001	64.00
Year × Genotype	20	57,139,597.8	<0.0001	25.35
Location × Year × Genotype	20	23,363,789.4	<0.0001	10.37
Error	189	3253.9		0.00
Total	272	225,380,057.2		

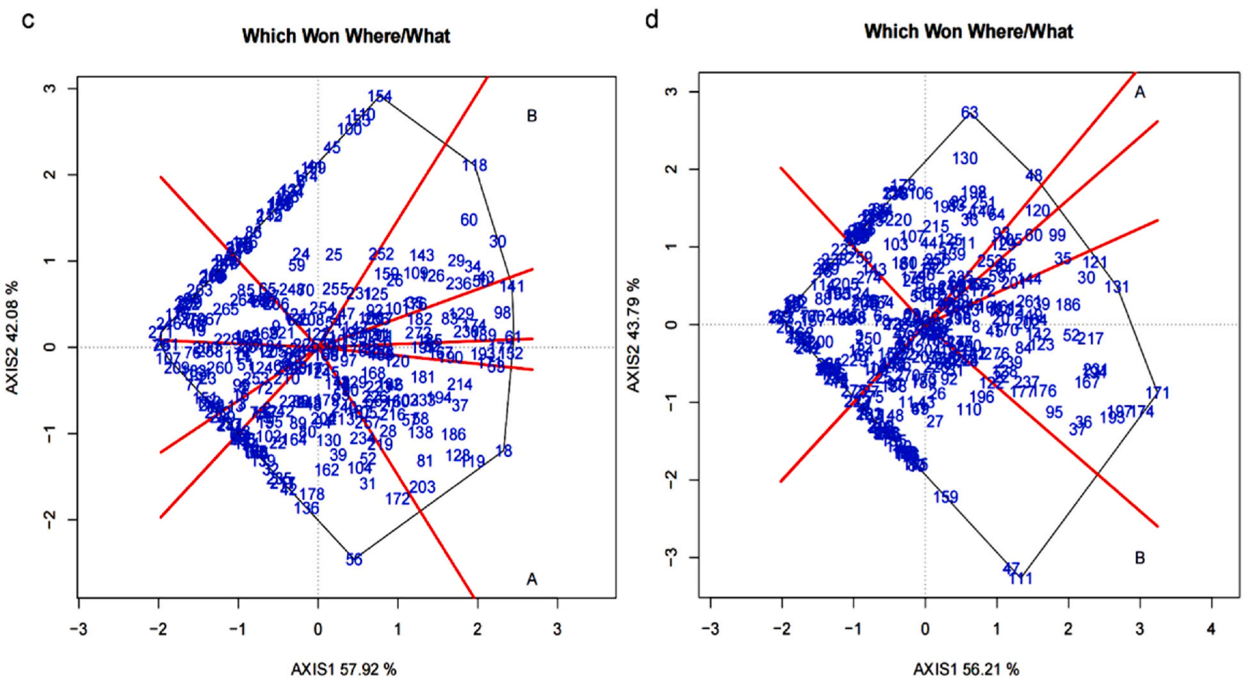

Fig. 2. "Polygon" view of the GGE biplot showing the performance of *Psathyrostachys juncea* (Fisch.) Nevski Genotypes in seed shattering across different locations. "A" and "B" denote Hohhot and Baotou, respectively. c) Which won where polygon view for the year 2022. d) Which won where polygon view for the year 2023.

4. Discussion

4.1. Combined analysis of variance for seed shattering trait

Seed shattering is more prevalent in wild forage grass varieties [26]. In agricultural production, SS can result in a reduction in seed yield [27]. This trait is influenced by environmental factors such as moisture, temperature, and humidity [28,29]. We assessed the SS rate of *Psathyrostachys juncea* (Fisch.) Nevski in Hohhot and Baotou and identified significant differences in the SS rate between the two locations in 2022 and extremely significant differences in 2023. Analyzed of meteorological data reveals that in 2023, Baotou experienced the highest average precipitation and relative humidity in July. Given that the maturity period of *Psathyrostachys juncea* (Fisch.) Nevski also coincides with July, the overall measured SS rate was lower. The study concludes that harvesting *Psathyrostachys juncea* (Fisch.) Nevski seeds in a relatively humid environment can mitigate the loss of seed yield.

The examination of distribution using skewness and kurtosis provides insights into the nature of gene action and the number of genes governing traits [30]. Positive skewness is linked to complementary gene action, while negative skewness is associated with duplicate (additive × additive) gene interactions [31]. Positive kurtosis (leptokurtosis) suggests a limited number of genes regulating the trait (single gene or oligogenic inheritance, i.e., minimal environmental impact), whereas normal distribution at zero (mesokurtosis) and negative kurtosis (platykurtosis) are indicative of numerous genes influencing the trait (polygenic inheritance, i.e., substantial environmental impact) [32]. This study revealed positive skewness in all four replications of the SS rate, indicating

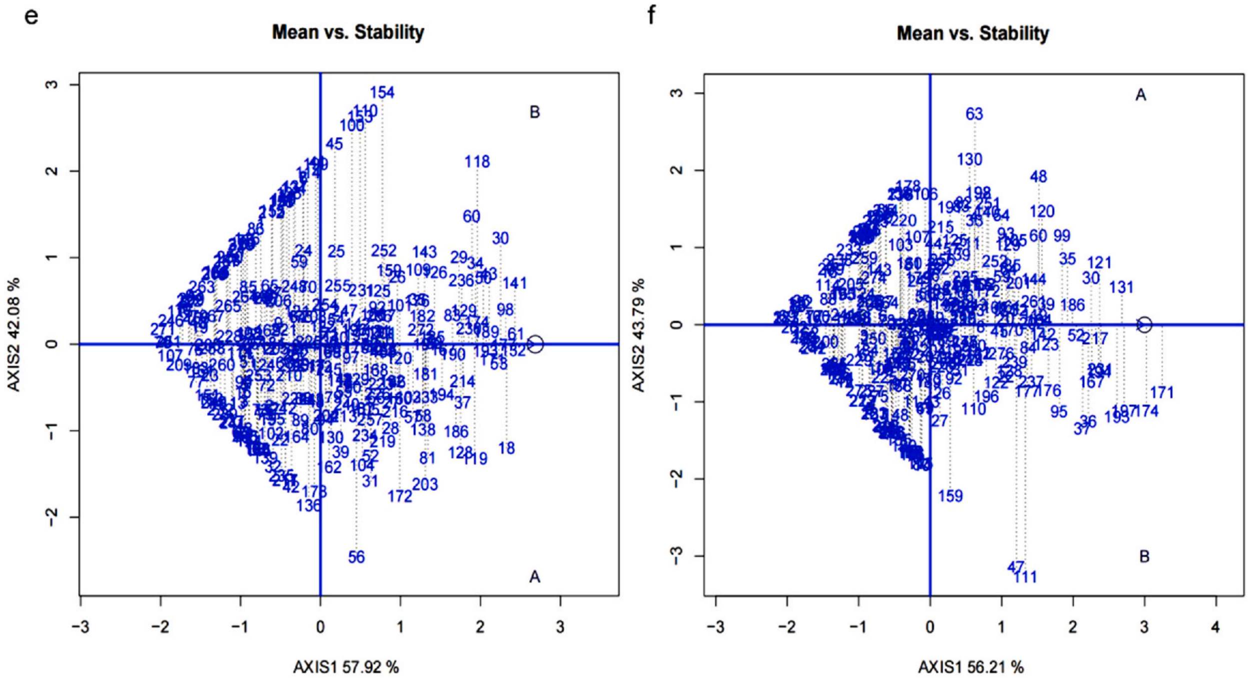

Fig. 3. GGE biplot showing the ranking of *Psathyrostachys juncea* (Fisch.) Nevski genotype based on seed shattering performance and stability. "A" and "B" denote Hohhot and Baotou, respectively. e) Means performance and stability view of genotypes for the year 2022. f) Means performance and stability view of genotypes for the year 2023.

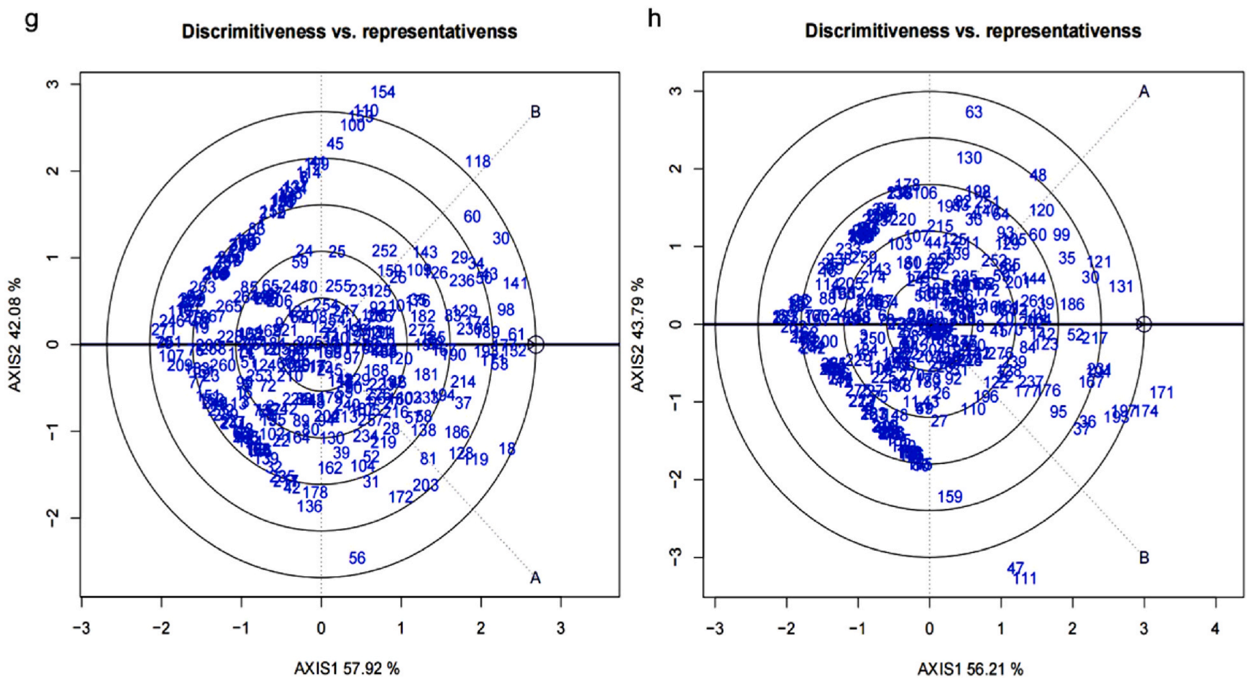

Fig. 4. GGE biplot showing the discrimitiveness and representativeness of location. "A" and "B" denote Hohhot and Baotou, respectively. g) Environment view for correlation among environments for the year 2022. h) Environment view for correlation among environments for the year 2023.

complementary gene interactions. The kurtosis of the Baotou SS rate in 2023 was 0.87, reinforcing the notion that the influence of a humid environment on SS in *Psathyrostachys juncea* (Fisch.) Nevski was relatively small. In the other three replications, negative kurtosis was observed, suggesting a significant impact of dry conditions on SS, likely regulated by interactions among multiple genes. Overall, the genetic complexity of SS appears to be higher in arid environments, presenting challenges in terms of selection intensity and the improvement of varieties under complementary gene interaction [33]. The study proposes exploring genes related to SS and improving high SS varieties through gene editing. This approach could expedite the breeding process of superior varieties. In the context of natural grassland applications, the inclination for seeds to shed more easily facilitates propagation. The experiment's results demonstrated abundant variability in SS traits among the 300 individual plants of *Psathyrostachys juncea* (Fisch.) Nevski, with the highest variability observed in the materials from the United States. Further utilization of these materials can be pursued based on specific needs.

The evident interaction of GE highlights the variation in the growth status of plants across different environments. Consequently, cross-regional experiments become an indispensable prerequisite for the selection of optimal planting materials [34,35]. In multi-year, multi-location experiments, the manifestation of plants in phenotypic traits is governed by the interplay of genotype, environment, and their interactive effects [36]. The analysis of variance in this study underscored that the primary factor influencing SS in *Psathyrostachys juncea* (Fisch.) Nevski was the interaction of GE. This observation emphazised the importance, in regional trials, of prioritizing both the selection of materials and the representativeness of the trial environment. The interaction of GE should not be overlooked. It is crucial to tailor the selection of *Psathyrostachys juncea* (Fisch.) Nevski materials for cultivation based on local conditions. Consequently, we employed the GGE biplot to further refine the selection of genotypic materials that exhibit high adaptability and stability.

4.1.1. GGE biplot

The GGE biplot emerges as a valuable tool for comprehending the growth patterns of genotypes in intricate environments [37]. Recognized for its efficacy in detecting stable and high-yielding genotypes, this method elucidates the performance of each genotype at every trial site and has found validation across numerous plant studies [36,38–41]. The "which-won-where" biplot uncovered mega-environment disparities, revealing environments conducive to genotypic adaptability, the best-performing genotypes in each mega-environment, and the ideal genotype exemplifying high agronomic performance and stability [42]. Our research findings exhibited diverse excellent genotypes across different years and environments. In 2022, materials displaying high SS rates in Baotou were 565051 and 619487, while in Hohhot, they were 565051 and 595135. In 2023, materials with elevated SS rates in Hohhot were 565051, and in Baotou, they were 565060 and 005043. In regional trials, evaluating the adaptability of plant agronomic traits necessitates a thorough analysis of both the high yield and stability of each material in multi-location trials [43,44]. Zhang emphasized that varieties with high and stable yields are suitable for extensive cultivation, whereas low-yielding varieties, even with stable yields, are not recommended for widespread planting [45]. Noteworthy for their high and stable SS rates, 61, 132, and 177 prove suitable for cultivation in both cultivated pastures and natural grasslands in both Hohhot and Baotou. Some varieties, while lacking stability, exhibit high yields and exceptional performance in specific environments, demonstrating adaptability and potential for local cultivation [46]. Although 171 displayed the highest SS rate, its instability maked it suitable for forage use in Baotou. The discriminative ability and representativeness of the GGE biplot serve as vital metrics for test environments, offering unbiased insights into the tested genotypes [47]. In multi-year studies, environments with longer vectors were observed to possess greater discriminative abilities between genotypes, while those with shorter vectors provided limited or no information on genotype differences [48]. Both Hohhot and Baotou exhibited representation and robust discriminative power for materials, unveiling significant differences in the SS performance of each genotype.

Our analyzed results corresponded closely with the actual climatic conditions, affirming the reliability of the GGE biplot analysis outcomes. Divergent soil conditions across distinct experimental sites can give rise to intricate and diverse mechanisms governing the interaction between plants and the environment, thereby yielding inconsistent performance across various environments. While the concept of an "ideal" genotype may not necessarily reflect a tangible reality, it functions as a benchmark for evaluating the relative desirability of the tested materials.

5. Conclusions

The study evaluated the SS traits of 300 individual plants of *Psathyrostachys juncea* (Fisch.) Nevski over two years at two locations, revealing significant genetic variability in SS. This information holds value for subsequent hybrid breeding efforts. The analysis of variance indicated that genotype, environment, year, and their interactions exhibited extremely significant effects on SS. Notably, the interaction effect between genotype and environment emerged as the primary factor contributing to variation in SS traits. The GGE biplot illustrated that Hohhot and Baotou emerged as representative locations with strong discriminative power for the materials. Genotypes 18 and 120 exhibited high SS rates in Hohhot, while 118 and 111 showed high SS rates in Baotou. Genotypes 132 and 177 were identified as ideal genotypes with both high and stable SS rates. Through GGE biplot analysis, we have deepened our understanding of the SS traits in *Psathyrostachys juncea* (Fisch.) Nevski and provided a reference tool for data analysis of SS traits. The genotypes with high SS obtained from these research results can serve as reference materials for subsequent transcriptome sequencing technology and the establishment of natural grasslands.

CRediT authorship contribution statement

Yuru Lv: Writing – review & editing, Writing – original draft, Investigation, Formal analysis, Data curation. **Lan Yun:** Writing – review & editing, Project administration, Methodology, Data curation. **Miaomiao Jia:** Writing – review & editing, Visualization, Formal analysis. **Xiaodi Jia:** Writing – review & editing, Resources, Project administration, Conceptualization.

Data availability

All data from this study is included in this published article. Requests for the data should be directed to the corresponding author.

Ethical approval

This is not applicable since the work does not use either humans or animals by any of the listed authors.

Funding

This work was supported by the National Natural Science Foundation of China Grant No.32371762 and the Key Project of Natural Science Foundation Inner Mongolia of China Grant No. 2023ZD07.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Yuru Lv reports administrative support and equipment, drugs, or supplies were provided by the Ministry of Education Key Laboratory of Grassland Resources and Processing and High Efcient Utilization of the Ministry of Agriculture, Grassland Resource and Environment College, Inner Mongolia Agricultural University. Lan Yun reports a relationship with the National Natural Science Foundation of China Grant No.32371762 and the Key Project of Natural Science Foundation Inner Mongolia of China Grant No. 2023ZD07 that includes: funding grants. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

We thank the test support laboratory staff in the Ministry of Education Key Laboratory of Grassland Resources and Processing and High Efcient Utilization of the Ministry of Agriculture, College of Grassland Science, Inner Mongolia Agricultural University. Special thanks for the valuable comments and suggestions from the anonymous reviewers.

References

[1] Editorial board of flora of China, Flora Reipublicae Popularis Sinicae, Science Press, Beijing, 1987.

[2] J.F. Yun, Y. Wang, C.B. Xu, L. Yun, Biological characteristics and production performance of Psathyrostachys juncea, Chinese J. Grassland. 5 (2006) 1–7.

[3] P.G. Jefferson, R. Muri, Competition, light quality and seedling growth of Russian Wildrye Grass (Psathyrostachys juncea), Acta Agron. Hung. 55 (2007) 49–60, https://doi.org/10.1556/AAgr.55.2007.1.6.

[4] G.M. Sbatella, R.G. Wilson, S.F. Enloe, C. Hicks, Propoxycarbazone- sodium and imazapic effects on downy brome (Bromus tectorum) and newly seeded perennial grasses, Invasive Plant Sci. Manage. 4 (2011) 78–86, https://doi.org/10.1614/IPSM-D-10-00010.1.

[5] T. Lawrence, C.D. Ratzlaff, Performance of some native and introduced grasses in a semiarid region of Western Canada, Can. J. Plant Sci. 69 (1989) 251–254, https://doi.org/10.4141/cjps89-033.

[6] W.X. Liu, L.H. Li, W.H. Liu, Z.M. Zhang, Z.H. Wu, C.S. Wang, SSR analysis on the sampling strategy of Psathyrostachys Huashanic keng population, Acta Tritici Sinica 26 (2006) 16–20.

[7] Y. Dong, Y.Z. Wang, Seed shattering: from models to crops, Front. Plant Sci. 6 (2015) 476, https://doi.org/10.3389/fpls.2015.00476.

[8] A. Maity, A. Lamichaney, D.C. Joshi, A. Bajwa, N. Subramanian, M. Walsh, M. Bagavathiannan, Seed Shattering: a Trait of evolutionary importance in plants, Front. Plant Sci. 12 (2021) 657773, https://doi.org/10.3389/fpls.2021.657773.

[9] Y. Shahriari, B. Heidari, A. Dadkhodaie, Dissection of genotype×environment interactions for mucilage and seed yield in Plantago species: application of AMMI and GGE biplot analyses, PLoS One 13 (2018) e0196095, https://doi.org/10.1371/journal.pone.0196095.

[10] S. Sood, V. Bhardwaj, V. Kumar, V.K. Gupta, BLUP and stability analysis of multi-environment trials of potato varieties in sub-tropical Indian conditions, Heliyon 6 (2020) e05525, https://doi.org/10.1016/j.heliyon.2020.e05525.

[11] W. Yan, L.A. Hunt, Q. Sheng, Z. Szlavnics, Cultivar evaluation and mega-environment investigation based on the GGE biplot, Crop Sci. 40 (2000) 597–605, https://doi.org/10.2135/cropsci2000.403597x.

[12] H. Dehghani, A. Ebadi, A. Yousefi, Biplot analysis of genotype by environment interaction for barley yield in Iran, Agron. J. 98 (2006) 388–393, https://doi.org/10.2134/agronj2004.0310.

[13] W. Yan, J.B. Holland, A heritability-adjusted GGE biplot for test environment evaluation, Euphytica 171 (2010) 355–369, https://doi.org/10.1007/s10681-009-0030-5.

[14] E. Saeidnia, M.M. Majidi, A. Mirlohi, M.R. Dehghani, B. Hosseini, Yield stability of contrasting orchardgrass (Dactylis glomerata L.) genotypes over the years and water regimes, Euphytica 217 (2021) 1–23, https://doi.org/10.1007/s10681-021-02871-3.

[15] H.G. Gauch, H.P. Piepho, P. Annicchiarico, Statistical analysis of yield trials by AMMI and GGE: further considerations, Crop Sci. 48 (2008) 866–889, https://doi.org/10.2135/cropsci2007.09.0513.

[16] F. Flores, M. Hybl, J.C. Knudsen, P. Marget, F. Muel, S. Nadal, L. Narits, B. Raffiot, O. Sass, I. Solis, J. Winkler, F.L. Stoddard, D. Rubiales, Adaptation of spring faba bean types across European climates, Field Crops Res. 145 (2013) 1–9, https://doi.org/10.1016/j.fcr.2013.01.022.

[17] W.K. Yan, D. Pageau, Fré, J. Geaureid, J. Lajeunesse, J. Goulet, J. Durand, D. Marois, Oat mega-environments and test-locations in Quebec, Can. J. Plant Sci. 91 (2011) 643–649, https://doi.org/10.4141/cjps10139.

[18] Z. Yu, L. Luo, F. Zhang, M. Hong, X. Zhang, R. Guo, Evaluation of yield, stability and adaptability of national winter rapeseed regional trials in the upper Yangtze River region in 2017-2018, Oil Crop Sci 5 (2020) 121–128, https://doi.org/10.1016/j.ocsci.2020.07.001.

[19] J. Xi, T.K. Turkington, P. Juskiw, J. Nyachiro, F. Capettini, Field screening is effective for identifying genetic resistance to scald of barley, Crop Sci. 59 (2019) 1479–1493, https://doi.org/10.1002/csc2.20057.

[20] B. Badu-apraku, R.O. Akinwale, Biplot analysis of line× tester data of maize (Zea mays L.) inbred lines under stress and nonstress environments, Cereal Res. Commun. 47 (2019) 518–530, https://doi.org/10.1556/0806.47.2019.25.

[21] P. Kona, B.C. Ajay, K. Gangadhara, N. Kumar, R.R. Choudhary, M.K. Mahatma, S. Singh, K.K. Reddy, S.K. Bera, C. Sangh, K. Rani, Z. Chavada, K.D. Solanki, AMMI and GGE biplot analysis of genotype by environment interaction for yield and yield contributing traits in confectionery groundnut, Sci. Rep. 14 (2024) 2943, https://doi.org/10.1038/s41598-024-52938-z.

[22] Q. Wang, H. Wang, S. Huang, Y. Zhao, E. Chen, F. Li, L. Qin, Y. Yang, Y. Guan, B. Liu, H. Zhang, Assessment of yield performances for grain sorghum varieties by AMMI and GGE biplot analyses, Front. Plant Sci. 14 (2023) 1261323, https://doi.org/10.3389/fpls.2023.1261323.

[23] T. Wang, L. Yun, Z. Li, Y.R. Lv, Genotype × Environment interactions for some traits of Psathyrostachys juncea based on GGE bipot, Acta Agrestia Sinica 31 (2023) 489–497. https://link.cnki.net/urlid/11.3362.S.20221229.0937.001.

[24] R.L. Steven, A.K. Elizabeth, Genetic dissection of seed production traits and identification of a major-effect seed retention QTL in hybrid Leymus (Triticeae) Wildryes, Crop Sci. 49 (2009) 29–40, https://doi.org/10.2135/cropsci2008.05.0277.

[25] E. Frutos, M.P. Galindo, V. Leiva, An interactive biplot implementation in R for modeling genotype-by-environment interaction, Stoch Env Res Risk A. 28 (2014) 1629–1641, https://doi.org/10.1007/s00477-013-0821-z.

[26] X.H. Zhao, J. Xu, K. Zhao, X.H. Zhao, Y. Jin, W.G. Xie, Screening of germplasm with low seed shattering rate and evaluation on agronomic traits in Elymus sibiricus L, J. Plant Genet. Resour. 16 (2015) 691–699. https://link.cnki.net/doi/10.13430/j.cnki.jpgr.2015.04.003.

[27] A. Elgersma, J.E. Leeuwangh, H.J. Wilms, Abscission and seed shattering in perennial ryegrass (Lolium perenne L.), Euphytica 39 (1988) 51–57, https://doi.org/10.1007/BF00043367.

[28] M.S. Taghizadeh, S. Crawford, M.E. Nicolas, R.D. Cousens, Water deficit changes the anatomy of the fruit abscission zone in Raphanus raphanistrum (Brassicaceae), Aust. J. Bot. 57 (2009) 708–714, https://doi.org/10.1071/BT09165.

[29] J.E. Taylor, C.A. Whitelaw, Signal in abscission, New Phytol. 151 (2001) 323–340, https://doi.org/10.1046/j.0028-646x.2001.00194.x.

[30] P. Govintharaj, S. Manonmani, S. Robin, Variability and genetic diversity study in an advanced segregating population of rice with bacterial blight resistance genes introgressed, Cienc. Agrotec. 42 (2018) 291–296, https://doi.org/10.1590/1413-70542018423022317.

[31] J.H. Kamdar, M.D. Jasani, B.C. Ajay, S.K. Bera, J.J. Georrge, Effect of selection response for yield related traits in early and later generations of groundnut (Arachis hypogaea L.), Crop Breed, Appl. Biotechnol. 20 (2020) 1–7, https://doi.org/10.1590/1984-70332020v20n2a31.

[32] A. Neelima, C. Sarankumar, M. Sudha, K.N. Ganesan, R. Ravikesavan, N. Senthil, Estimation of variability, heritability, genetic advance and assessment of frequency distribution for morphological traits in intercross population of Maize, Electron. J. Plant Breed. 12 (2020) 574–580, https://doi.org/10.37992/2020.1102.095.

[33] H.B. Dinesh, K.P. Viswanatha, H.C. Lohithaswa, R. Pavan, S. Poonam, Genetic association estimates using third and fourth degree statistics in early segregating generations of cowpea, Int. J. Curr. Microbiol. 7 (2018) 867–873, https://doi.org/10.20546/ijcmas.2018.701.105.

[34] M. Dia, T.C. Wehner, R. Hassell, D.S. Price, G.E. Boyhan, S. Olson, S. King, A.R. Davis, G.E. Tolla, Genotype×environment interaction and stability analysis for watermelon fruit yield in the United States, Crop Sci. 56 (2016) 1645–1661, https://doi.org/10.2135/cropsci2015.10.0625.

[35] P. Senguttuvel, N. Sravanraju, V. Jaldhani, B. Divya, P. Beulah, P. Nagaraju, Y. Manasa, A.S.H. Prasad, P. Brajendra, C. Gireesh, M.S. Anantha, K. Suneetha, R. M. Sundaram, M.S. Madhav, M.D. Tuti, L.V. Subbarao, C.N. Neeraja, V.P. Bhadana, P.R. Rao, S.R. Voleti, D. Subrahmanyam, Evaluation of genotype by environment interaction and adaptability in lowland irrigated rice hybrids for grain yield under high temperature, Sci. Rep. 11 (2021) 15825, https://doi.org/10.1038/s41598-021-95264-4.

[36] I. Ansarifard, K. Mostafavi, M. Khosroshahli, M. Reza Bihamta, H. Ramshini, A study on genotype-environment interaction based on GGE biplot graphical method in sunflower genotypes (Helianthus annuus L.), Food Sci. Nutr. 8 (2020) 3327–3334, https://doi.org/10.1002/fsn3.1610.

[37] J. Luo, Y.B. Pan, Y. Que, H. Zhang, M.P. Grisham, L. Xu, Biplot evaluation of test environments and identification of mega-environment for sugarcane cultivars in China, Sci. Rep. 5 (2015) 15505, https://doi.org/10.1038/srep15505.

[38] J. Angelini, G.S. Faviere, E.B. Bortolotto, L. Arroyo, G.H. Valentini, L.C. Domingo, Gerardo, Biplot pattern interaction analysis and statistical test for crossover and non-crossover genotype-by-environment interaction in peach, Sci. Hortic. 252 (2019) 298–309, https://doi.org/10.1016/j.scienta.2019.03.024.

[39] V.I. Esan, G.O. Oke, T.O. Ogunbode, I.A. Obisesan, AMMI and GGE biplot analyses of Bambara groundnut [Vigna subterranea (L.) Verdc.] for agronomic performances under three environmental conditions, Front. Plant Sci. 13 (2023) 997429, https://doi.org/10.3389/fpls.2022.997429.

[40] F. Saeidnia, M. Taherian, S.M. Nazeri, Graphical analysis of multi-environmental trials for wheat grain yield based on GGE-biplot analysis under diverse sowing dates, BMC Plant Biol. 23 (2023) 198, https://doi.org/10.1186/s12870-023-04197-9.

[41] E. Tian, H. Liu, D. Zhang, M. Hu, F. Zhang, S. Ding, K. Yang, Screening of salt tolerance of maize (Zea mays L.) lines using membership function value and GGE biplot analysis, PeerJ 12 (2024) e16838, https://doi.org/10.7717/peerj.16838.

[42] W. Yan, L.A. Hunt, Interpretation of genotype environment interaction for winter wheat yield in Ontario, Crop Sci. 41 (2001) 19–25, https://doi.org/10.2135/cropsci2001.41119x.

[43] M. Enyew, T. Feyissa, M. Geleta, K. Tesfaye, C. Hammenhag, A.S. Carlsson, Genotype by environment interaction, correlation, AMMI, GGEbiplot and cluster analysis for grain yield and other agronomic traits in Sorghum (Sorghum bicolor L. Moench), PLoS One 16 (2021) e0258211, https://doi.org/10.1371/journal.pone.0258211.

[44] R.H. Wang, D.H. Hu, H.Q. Zheng, S. Yan, R.P. Wei, Genotype×environmental interaction by AMMI and GGE biplot analysis for the provenances of Michelia chapensis in South China, J. For. Res. 27 (2016) 659–664, https://doi.org/10.1007/s11676-015-0181-2.

[45] H.J. Zhang, H.J. Wang, X.L. Ma, B.C. Li, Y.X. Meng, Yield stability of cultivars and representativeness of test sites in barley regional rest of northen China barley cultivars based on GGE-biplot analysis, J. Triticeae Crop. 35 (2015) 1250–1256. https://link.cnki.net/urlid/61.1359.s.20150906.0946.022.

[46] Q. Liu, L. Huang, C. Fu, T. Zhang, W. Ding, C. Yang, Genotype-environment interaction of crocin in Gardenia jasminoides by AMMI and GGE biplot analysis, Food Sci. Nutr. 10 (2022) 4080–4087, https://doi.org/10.1002/fsn3.3003.

[47] W. Yan, I. Rajcan, Biplot analysis of test sites and trait relations of soybean in Ontario, Crop Sci. 42 (2002) 11–20, https://doi.org/10.2135/cropsci2002.1100.

[48] W. Yan, N.A. Tinke, Biplot analysis of multi-environment trial data: principles and applications, Can. J. Plant Sci. 86 (2006) 623–645, https://doi.org/10.4141/P05-169.