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Exploring the Physiology and Genetic Stability of Rapeseed Plants for Assessing Oil Content in Western Iran

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1. Introduction

Brassica napus L., commonly referred to as rapeseed or oilseed rape, stands as a crucial oil crop, serving multiple purposes. Beyond its role in producing cooking oil for human consumption, rapeseed also yields protein-rich fodder for livestock and serves as a sustainable source of materials for biodiesel and various industrial applications. Similar to soybean, rapeseed boasts high levels of both oil and protein content. With approximately 45% oil and 23% protein, rapeseed surpasses soybean, which contains around 20% oil and 40% protein. Upon oil extraction, rapeseed yields a premium-quality feed concentrate with a protein content of up to 37%, offering livestock a highly palatable and nutritious dietary option [\(Gołębiewska](#page-10-0) *et al*., 2022). According to the report of the Food and Agriculture Organization (FAO) of the

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United Nations, rapeseed is one of the most important oilseeds in the world, ranking second after soybeans in terms of production and cultivated area. Since 1994, advancements in breeding and cultivation technologies have transformed rapeseed production and improved oil quality. By 2020, rapeseed cultivation had expanded to over 66 countries, covering a global area of more than 35 million hectares. In the past decade alone, global rapeseed production surged by 12.5 million tonnes, a 20.9% increase, while rapeseed oil production rose by 15.3% to 26.3 million tonnes, constituting 35.9% of total rapeseed output.

Oilseed rape now ranks as the second-highestyielding oil crop globally, contributing 12.1% to the world's major vegetable oil production in 2021, according to [FAOSTAT \(2022\).](#page-10-1) These figures underscore the significant advancements and growing

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importance of rapeseed in the global agricultural landscape.

Droughts have serious implications for agriculture, water resources, ecosystems, and communities around the world. With climate change, the frequency and severity of droughts are projected to increase in many regions, posing significant challenges to food security and economic stability. Finding sustainable solutions to mitigate the impacts of drought and adapt to changing climate conditions is crucial [\(Miyan, 2015;](#page-10-2) [Bouabdelli](#page-10-3) *et al*[., 2022\)](#page-10-3). Drought stress can have significant negative impacts on crop yield and quality, resulting in economic losses and food insecurity. The response of plants to water stress depends on several factors, encompassing the plant's developmental phase, the severity and duration of the stress, and the genetics of the cultivar. Some cultivars are more tolerant to drought stress than others, and selecting droughttolerant genotypes is an important strategy for improving crop productivity under water-limited conditions. However, it is not enough to simply select for drought-tolerant genotypes; it is also important to select for genotypes with good yield stability under both stressed and non-stressed conditions. It guarantees that the chosen genotypes will not only perform well under drought stress but also sustain high yields in normal growing conditions [\(Farshadfar](#page-10-4) *et al*., 1995; [Schneider](#page-11-0) *et al*., 1997).

The interaction of genotype and environment is a complex issue in plant breeding sciences and is of great importance to researchers in this field. The yield of a given genotype can vary significantly depending on the environmental conditions in which it is grown, and understanding these genotype-by-environment interactions (GEIs) is critical to developing highyielding and stable crop varieties. [Yan et al. \(2007\)](#page-11-1) proposed a statistical method called the genotype main effects and genotype-by-environment interaction (GGE) biplot analysis, which allows for the visualization and interpretation of GEIs in crop yield data. This method has been widely used in plant breeding programs to select superior lines of different plant species under different environmental conditions. It has been applied to several crops, including wheat and canola, as well as maize, rice, and soybean [\(Motahhari](#page-10-5) *et al*., 2020; Brar *et al*[., 2010;](#page-10-6) [Sincik](#page-11-2) *et al*., [2021\)](#page-11-2).

One of the most widely used methods for analyzing stability is the Additive Main and Multiplicative Interaction (AMMI) model, which was proposed by [Zobel et al. \(1988\).](#page-11-3) The AMMI model is a combination of variance analysis and principal component analysis, which allows for the visualization and interpretation of Genotype-Environment Interactions (GEIs) in crop yield data. Analysis of stability is an important aspect of plant breeding, and the AMMI model is a useful tool for analyzing GEIs and identifying stable and highperforming genotypes across different environments. Incorporating these methods into breeding programs can help researchers develop new crop varieties that are better adapted to specific environmental conditions and have improved yield and quality [\(Crossa, 1990;](#page-10-7) [Zobel](#page-11-3) *et al*[., 1988;](#page-11-3) [Purchase](#page-11-4) *et al*., 2000; [Alizaheh](#page-10-8) *et al*., [2022;](#page-10-8) [Chaghakaboodi](#page-10-9) *et al*., 2021; [Anuradha](#page-10-10) *et al*., [2022;](#page-10-10) Afzal *et al*[., 2021;](#page-10-11) Zhang *et al*[., 2023\)](#page-11-5). The results of stability analysis are essential for identifying the best genotypes for production in a particular area, as well as for selecting criteria for further genetic improvements. By recognizing stable and highperforming genotypes across different environments, plant breeders can select the best genotypes for commercial production and recommend them to farmers in specific regions. This study of winter rapeseed genotypes aimed to analyze the genotype-byenvironment $(G \times E)$ interaction using the AMMI and GGE biplot models. The purpose of this analysis was to evaluate the stability and adaptability of the genotypes to different environments.

2. Materials and methods

The study involved planting fourteen lines and varieties of rapeseed genotypes under both irrigated and rainfed conditions [\(Table 1\)](#page-2-0). Experiment was carried out at the College of Agriculture at Razi University. [Table 2](#page-2-1) shows the amount of rainfall and other environmental conditions at the location where the field experiments were conducted over the two years of the experiment. Sowing was done by hand in five-row plots, three m in length, and 30 cm apart. Employing a randomized complete block design with three replications and manual planting established a study experimental framework for assessing the yield performance of diverse canola genotypes across varying environmental conditions.

No.	Genotypes	Origin	E^{max} Appearance	Species		
1	Geronimo	Rostica- france	Winter	B. napus		
2	Celecious	Svalof	Winter	B. napus		
3	Milena	Germany	Winter	B. napus		
4	Sahara	Danisco	Winter	B. napus		
5	Sunday	Danisco	Winter	B. napus		
6	$Zarfam$ (Reg \times Cob)	Iran	Winter	B.napus		
7	Dante	Germany	Winter	B. napus		
8	SLM-046	Germany	Winter	B.napus		
9	Talaye	Iran	Winter	B. napus		
10	Talent	Germany	Winter	B.napus		
11	$ARC-2$	U.S.A	Winter	B.napus		
12	Opera	Sw-sweden	Winter	B.napus		
13	$ARC-5$	U.S.A	Winter	B.napus		
14	Licord	Germany	Winter-Spring	B.napus		

Table 1. Origin and characters of genotypes

Table 2. Annual precipitation and site conditions

Locations	Rainfall (mm)	Altitude Soil	
		(m)	type
Field of college of Agriculture, Razi university in 2008	509.6 (First year of testing) 157.7 (Second year of testing)	1351	Silty clay- clay

The seeding rate used in the study was 30 seeds per square meter for both locations. This seeding rate is commonly used in canola production and provides sufficient plant density for optimal growth and yield. Fertilizer was applied before planting, with a rate of 40 kg/ha nitrogen and 60 kg/ha P_2O_5 . The yield was calculated by converting the seed yield obtained from each plot to yield per hectare. For the non-stressed plots, irrigation was applied three times during the growing season, specifically at the bud formation, flowering, and semi-podding stages. These are critical growth stages for canola, and providing irrigation during these stages can help to ensure that the plants have sufficient water for optimal growth and yield. In this study, the Soxhlet Extractor Apparatus was used to measure the oil content of the canola seeds. [Table 1](#page-2-0) shows the origin and characters of genotypes an[d Table](#page-2-1) [2](#page-2-1) has information that can include the soil type, climate, altitude, and other environmental factors that may have influenced crop growth and development. In the context of the study, the NMR method was used to measure the oil content and yield of the canola seeds. The oil content is the percentage of oil in the seed on a dry weight basis, while the yield is the amount of oil produced per unit area of land. In this study, the AMMI model was used to determine and assess the effects of genotype and environment on canola yield, as well as the GEI effect. The GEI effect reflects the degree to which the yield of the genotypes varies across different environments. To further analyze the sources of variability for the GEI effect, the analysis of the main components (interaction IPCA) was used. The GENSTAT software was used to analyze the AMMI model based on the oil yield data generated in diverse environments. The GGE bi-plot method was used to analyze the obtained data and interpret the interaction effect of genotype \times environment and determine megaenvironments. The GGE bi-plot model is based on separable eigenvalues for the first two components, as described by Equation 1 [\(Raiger and Prabhakaran,](#page-11-6) [2001\)](#page-11-6).

(1) Yij - μ - βj = λ1 ξi1 ηj1 + λ2 ξi2 ηj2 + εij

In this Equation, Yij is the mean of the i-th environment, μ is the total mean, βj is the mean of the j-th environment effect, λ1 and λ2 are the eigenvalues for the first and second components, ξi1 and ξi2 are the genotypic eigenvectors for the first and second components, and ni₁ and ni₂ are the environmental vectors for the first and second components. εij represents the residual error or the value for the rest of the i-th genotype [\(Raiger and Prabhakaran,](#page-11-6) 2001). The study can provide insights into the environmental factors that are most important for canola yield and their potential effects on breeding programs aimed at improving canola yield and quality [\(Gauch and Zobel,](#page-10-12) [1990\)](#page-10-12).

3. Results and discussion

The different growth stages in canola were shown in Fig. [1 A-D](#page-3-0) in the field, respectively. Employing statistical methods (correlation, regression, etc.) is very necessary and useful in crop plant breeding [\(Kakaei](#page-10-13) [and Mazaheri Laqab, 2023\)](#page-10-13). The interaction between genotype and environment plays a crucial role in studying quantitative traits, influencing the stability of a genotype's yield across diverse conditions and complicating genetic tests and predictions. Quantitative traits, governed by multiple genes and environmental factors, exhibit varying yields depending on growth conditions. This interaction can result in unstable yields across different environments, posing challenges for yield prediction. Rapeseed producers and breeders aim to enhance seed and oil yields per unit area by developing new varieties with improved traits tailored to specific environmental conditions.

Figure 1. Canola field in different growth stages; a: full flowering stage; b: rosette growth stage; c: physiological maturity stage; d: full podding stage

Breeders typically view location as a constant factor when analyzing genotype yield stability, assuming environmental conditions remain relatively consistent over time. Therefore, the consistency of yield over time is seen as the primary indicator of genotype yield stability. To enhance seed and oil yields, breeders employ diverse selection criteria and breeding techniques to develop new varieties adapted to specific environments with improved yield and quality traits. Selection criteria often encompass traits like disease resistance, stress tolerance, and high oil content. Additionally, breeders utilize statistical methods such as GGE biplot analysis and AMMI biplot analysis to identify stable and high-performing genotypes across various environments. By employing these strategies, breeders can create new varieties better suited to specific environmental conditions, thus contributing to global food security and sustainable agriculture [\(Khan](#page-10-14) *et al*., [2021\)](#page-10-14).

Various statistical parameters derived from the analysis of variance (ANOVA) of genotype-byenvironment $(G \times E)$ interactions are utilized to identify stable genotypes across different test environments. These parameters gauge the consistency of genotype yield across diverse conditions. Among the statistical parameters used are the SIPCi score [\(Purchase](#page-11-4) *et al*., [2000\)](#page-11-4), single slope, small deviation from regression S2di [\(Eberhart and Russell, 1966\)](#page-10-15), EVi [\(Sneller](#page-11-7) *et al*., [1997\)](#page-11-7), and Dzi statistic [\(Zhang](#page-11-8) *et al*., 1998). Genotypes with scores closer to zero, single slopes, minimal deviations from the regression line, and lower EVi values are regarded as more stable across various environments.

The results of the AMMI analysis of variance [\(Table](#page-4-0) [3\)](#page-4-0) indicated a significant interaction effect between genotypes and different environmental locations. This suggests that there is a high degree of diversity among the genotypes in their response to different environmental conditions. The presence of high diversity among genotypes and different environments is an important factor in the evaluation of the stability of genotypes and the selection of superior genotypes for breeding programs.

The results of the stability parameters analysis [\(Table 4\)](#page-4-1) showed that the regression coefficients of the genotypes ranged from -0.02 to 1.86. The genotypes Sahra and Licord had low S2di and regression coefficient values (bi>1), and produced desirable oil yields. The genotype Zarfam also had low S2di and regression coefficient values (bi>1), but had the lowest average yield. This suggests that while stability is an important factor in genotype yield, it is not the only determinant of yield. Other factors such as disease resistance, stress tolerance, and nutrient availability can also affect the yield of a given genotype. Overall, the results of the stability parameter analysis can be used to identify stable and high-performing genotypes that are better adapted to specific environmental conditions and have improved yield and quality traits. The study by [Chaghakaboodi et al. \(2021\)](#page-10-9) found that the genotypes Geronimo and Zarfam were stable across irrigated and rainfed conditions, despite having relatively poor general adaptability. These genotypes had low S2di and regression coefficient values (bi~1), which are measures of stability, but their average yield was not as high as other genotypes. The fact that these genotypes showed stability across both irrigated and rainfed conditions can be useful for breeding programs aimed at developing new varieties that are better adapted to a range of environmental conditions. However, their relatively poor general adaptability suggests that these genotypes may perform better in specific environmental conditions rather than across a range of environments.

Table 3. ANOVA and AMMI Model for rapeseed oil content (%) across all growing seasons

Effect	df	SS	MS			
Treatments	13	145.455	11.1888			
Location	3	518.298	172.766			
Treatment \times Sites	39	272.159	6.978			
AMMI Component 1	15	168.116	11.207*			
AMMI Component 2	13	67.5583	5.196			
AMMI Component 3	11	36.4848	3.316			
Total	55.	935.912				

* Significant at level P<0.05

Table 4. Stability and adaptability of rapeseed oil content (%) in all growing seasons

Genotype	Oil Yield	Wi	Bi	S ₂ di	EVi	SIPC	Dai	Dzi	ASV	MASV	Fpi	FAi	ZAi
Geronimo	43.52	93.48	2.33	1.66	49.30	1.731	4.046	0.554	2.727	2.73	3.78	16.3	0.36
Celecious	44.37	95.35	0.942	1.14	12.58	1.073	1.988	0.353	0.948	0.95	2.96	3.9	0.17
Milena	43.15	92.71	1.152	1.81	16.99	1.183	2.261	0.407	1.039	1.04	4.05	5.1	0.19
Sahra	43.86	95.99	0.821	-0.04	6.042	0.672	1.414	0.259	0.615	0.61	3.60	2	0.10
Sunday	45.79	98.25	-0.586	-0.76	48.70	1.909	3.963	0.559	2.613	2.61	0.88	15.7	0.39
Zarfam	42.49	92.37	0.989	0.30	7.47	0.784	1.463	0.261	0.690	0.69	7.69	2.1	0.13
Dante	42.62	96.07	1.857	-0.75	15.06	1.038	2.069	0.297	1.345	1.34	4.54	4.3	0.20
SLM-046	44.36	99.34	1.701	-0.09	14.40	1.178	2.088	0.352	1.111	1.11	0.62	4.3	0.20
Talaye	44.30	96.40	0.665	0.22	9.13	0.761	1.715	0.316	0.737	0.74	2.96	3	0.10
Talent	44.25	92.01	0.710	4.07	31.73	1.801	3.189	0.535	1.709	1.71	2.47	10.1	0.31
$ARC-2$	44.29	97.11	1.068	0.20	6.94	0.794	1.495	0.268	0.698	0.69	1.46	2.2	0.12
Opera	44.85	96.22	-0.002	0.043	24.93	1.217	2.731	0.377	1.832	1.83	2.26	7.5	0.25
$ARC-5$	44.24	98.33	1.849	-0.07	18.89	1.116	2.287	0.324	1.502	1.50	1.16	5.26	0.22
Licord	43.75	97.39	0.498	-0.82	5.50	0.692	1.311	0.194	0.828	0.83	3.76	1.7	0.13

Wi (ammi): Wrick's ecovalance in terms of AMMI; Bi: Stability statistic based on the first two IPC axes; S2di: Mean square deviation; EVi: Averages of the square eigenvector values; SIPCi: Sums of the absolute value of the IPC scores; Dai: Parameter of Annicchiarico; Dzi: Distance of IPC point with origin in space; ASVi: AMMI stability value; FPi: Stability statistic based on the first IPC axes of the first IPC axes; FAi: Stability statistic based on the first IPC axes based on fitted AMMI model value; ZAi: Absolute value the relative contribution IPCs to the interaction.

The use of biplots in the analysis of AMMI models makes it possible to visualize the relationships between genotypes and environments and to identify genotypes that are better adapted to specific environmental conditions. Biplots are graphical representations that allow for the simultaneous visualization of genotypes and environments in a two-dimensional space. In the case of AMMI biplots, genotypes and environments are represented as vectors in a two-dimensional space, and the interaction between genotypes and environments is represented by the angle between the vectors. The advantage of using biplots in the analysis of AMMI models is that they make the relationships between genotypes and environments visible, thus enabling breeders to identify genotypes that are better adapted to specific environmental conditions.The result of the combined analysis of variance showed a significant difference at 99% level for genotypes as a fixed factor, environment as a random factor, and genotype \times environment interaction effects in terms of oil yield, and combined analysis of variance of oil content [\(Table](#page-5-0) [5\)](#page-5-0).

content (%) in irrigated and rainied conditions							
Source of variation	df	Mean Square					
Treatment	13	$11.1888**$					
Locations	3	172.766**					
Treatment \times Sites	39	$6.97844**$					
Treatment \times Site Regression	13	$5.235***$					
Deviation from Regression	26	7.849 ^{ns}					
Total	55						

Table 5. Combined analysis of variance of oil content (%) in irrigated and rainfed conditions

** and ns: significant at the 1% level of probability and non-significant, respectively

The biplot is divided into four quadrants by two axes: the horizontal axis, which represents the cumulative main effects or the average oil percentage, and the vertical axis, which represents the average of the total genotypes. The horizontal axis divides the genotypes into two groups: those with an oil percentage higher than the average and those with an oil percentage lower than the average. The vertical axis shows the differences in the overall yield of the genotypes. Genotypes above the average line are considered high-performing, while those below the average line are considered low-performing. The horizontal axis that crosses the zero point of the IPCA1 axis also divides the biplot into two parts. The righthand side of the biplot represents genotypes that performed better under irrigated conditions, while the left-hand side of the biplot represents genotypes that performed better under rainfed conditions.

The placement of genotypes in the upper part of the IPCA1 axis in the biplot of the AMMI model indicates positive interaction, whereas genotypes close to the IPCA1 axis are considered to have the least interaction. Based on this, in the study mentioned, genotype 2 had the most positive interaction, while genotype 10 had the most negative interaction. However, both genotypes were found to be unstable. In contrast, genotypes 12 and 14 were identified as stable genotypes and were recommended for all regions based on the AMMI model. This suggests that these genotypes have consistent yield across a range of environments, making them suitable for cultivation in different regions. Similarly[, Jamshid Moghaddam et al.](#page-10-16) [\(2014\)](#page-10-16) used the AMMI method and coefficients of principal components of interaction (IPCA) to analyze the interaction effect of genotype and environment in safflower genotypes. The findings of the study, particularly highlighted through biplot analysis, suggest that the Licord genotype demonstrates greater stability compared to others across different environments. This indicates that the biplot analysis, whether employing GGE or Additive Main Effects and Multiplicative Interaction (AMMI) models, effectively distinguishes stable genotypes from less stable ones based on their yield performance across environments. This ability to differentiate between stable and less stable genotypes is one of the primary functions of biplot analyses in plant breeding research. The biplot of the oil yield means versus IPCA2 showed that genotypes 4 and 5, which were close to the IPCA2 [\(Fig.](#page-5-1) [2\)](#page-5-1) axis, were stable, while genotypes 1 and 12, which had a high amount of IPCA2, were unstable genotypes.

Figure 2. Average bi-plot of yield oil of genotypes against IPCA1 and IPCA2 values.

Based on the biplot diagram presented in [Fig.](#page-6-0) 3, genotypes that are placed in the upper and right parts of the diagram have a positive interaction effect with both

IPCA1 and IPCA2 axes. This means that these genotypes have high yields and are stable across a range of environments, making them suitable for

cultivation in different regions. On the other hand, genotypes that are placed in the lower and left part of the diagram have a negative reciprocal effect on both IPCA1 and IPCA2 axes. This means that these genotypes have low yields and are unstable across a range of environments, making them unsuitable for cultivation in different regions. The biplot diagram based on the main components of IPCA1 and IPCA2 is a powerful tool for identifying stable and highperforming genotypes that are better adapted to specific environmental conditions. In the biplot diagram based on the main components of IPCA1 and IPCA2, the interaction effect is determined by the distance of the genotypes from both axes. Since the interaction effect justified by IPCA1 is greater than the interaction effect justified by IPCA2, genotypes that have a high positive or negative interaction effect with respect to IPCA1 compared to IPCA2 are known as genotypes with a high interaction effect. On the other hand, genotypes that are closer to the center of the graph than both IPCA1 and IPCA2 axes have less interaction. These genotypes are considered stable and are recommended for cultivation in different regions. The closer a genotype is to the center of the biplot, the more stable it is across a range of environments.

Figure 3. Graphic display of GGE bi-plot to determine the superiority of which genotype(s) in which environment(s) for rapeseed genotypes.

Genotypes that are further away from the center of the biplot diagram based on the main components of IPCA1 and IPCA2 have specific stability, meaning that they perform well in specific environments. Conversely, genotypes that are closer to the center of the diagram have general stability and are recommended for most environments [\(Gauch and](#page-10-12) [Zobel,](#page-10-12) 1990; [Alizadeh](#page-10-8) *et al*., 2022). Therefore, in the study mentioned, genotypes 12 and 14, which had the lowest amount of interaction with respect to both IPCA1 and IPCA2 axes, were recognized as stable genotypes. These genotypes are suitable for cultivation in various environments and have a consistent yield across a range of environments. On the other hand, genotypes 5 and 9 had the highest interaction effect, indicating that their yield varied greatly across different environments. These genotypes may be suitable for specific environments but may not perform well in other environments.

The results of cumulative additive effects and multiplicative interaction effects can be used to quantify the contribution of different factors to the overall variation in yield oil. In the study mentioned, the first two components of the AMMI model explained 57.91% and 23.85% of the variance of the interaction effect for yield oil. The first component, which explains the largest proportion of the variance, represents the cumulative additive effect, or the main effect of the environments and genotypes. This component captures the overall yield of the genotypes across different environments and the differences in yield oil due to environmental factors. The second component represents the multiplicative interaction effect or the interaction between the genotypes and

environments. This component captures the differences in the yield of the genotypes across different environments, indicating the stability and adaptability of the genotypes. According to studies such as [Yang et](#page-11-9) [al. \(2009\),](#page-11-9) the two components of the interaction effect of genotype \times environment should account for at least 60% of the variation of the interaction effect for stable genotypes to be identified. The interaction effect between genotypes and environments is a complex phenomenon that can affect the yield of crop varieties. Therefore, breeders should carefully evaluate the results of their analyses and consider multiple factors when identifying stable and high-performing genotypes. Genotypes that have IPCA1 values close to zero and good yield stability and general compatibility are considered stable genotypes. In the case of the study you mentioned, the genotypes Opera and Licord were identified as stable genotypes based on the bi-plot of the average yield of genotypes against IPCA1 values. This means that these genotypes have consistent yields across a range of environments and are suitable for cultivation in different regions.

Conversely, genotypes that have the highest negative values of IPCA1 are considered unstable genotypes. The genotypes Sunday and Talaye were identified as unstable genotypes based on the bi-plot of the average yield of genotypes against IPCA1 values. This means that these genotypes have poor yields and are not suitable for cultivation in different regions.

Genotypes that have IPCA2 [\(Fig.](#page-5-1) 2) values close to zero are considered stable genotypes. The genotypes Sahra and Sunday were identified as stable genotypes based on the bi-plot of the average yield of the genotypes against IPCA2 values. This means that these genotypes have consistent yields across a range of environments and are suitable for cultivation in different regions. On the other hand, genotypes with the highest IPCA2 values are considered to have the highest interaction effect or instability. The genotype numbers of Geronimo and Opera had the highest IPCA2 values. This indicates that these genotypes have high interaction effects and are not suitable for cultivation in different regions.

Genotype-environment interaction analysis, genotypes that perform less well but have positive values for the main components of the interaction effect are often referred to as having a positive interaction effect with poorer environments. This means that these genotypes are better adapted to poor environments and may perform relatively better in such environments as compared to other genotypes. In other words, the positive interaction effect indicates that the yield of these genotypes is less affected by poor environmental conditions, making them suitable for cultivation in such areas. This can be useful for developing crop varieties that are more resilient to environmental stressors and can improve agricultural productivity in areas with poorer environmental conditions [\(Chaghakaboodi](#page-10-9) *et al*., [2021;](#page-10-9) [Shojaei](#page-11-10) *et al*., 2011; [Sincik](#page-11-2) *et al*., 2021).

The convex hull resulting from the GGE analysis of *B. napus* genotypes in four environments is shown in [Fig.](#page-8-0) 4. In a biplot diagram based on the first and second main components of interaction, genotypes and environments are specified based on their values along these two components. Genotypes and environments that are close to the origin of the coordinates (close to zero) in terms of the values of the first and second main components of interaction have the least interaction. This means that their yield is less affected by the interaction between genotype and environment, and they are more stable and suitable for cultivation in a wider range of environments. On the other hand, genotypes and environments that are further away from the origin of coordinates along the first and second main components of interaction have greater interaction effects. This indicates that their yield is more affected by the interaction between genotype and environment, and they are less stable and suitable for cultivation in a narrower range of environments.

In a biplot diagram based on the first and second principal components of the interaction effect, the first two components typically account for a significant proportion of the variance in the genotype-environment interaction. In this study, the first and second principal components accounted for 81.76% of the variance. In the biplot, genotypes positioned close to a specific environment are considered to have specific compatibility with that environment, indicating superior performance in that environment compared to others. Conversely, genotypes situated near the origin are considered to have general compatibility, meaning they exhibit consistent yields across various environments, making them suitable for cultivation in diverse regions.

In the biplot diagram based on the first and second principal components of the interaction effect in the

research mentioned, genotypes 12 (Opera) and 14 (Licord) were identified as the most stable genotypes [\(Stevanato](#page-11-11) *et al*., 2015). These genotypes were located near the origin of coordinates in the biplot diagram, indicating that they have public compatibility with a range of environments and have a consistent yield across different environments. This makes them suitable for cultivation in different regions and can contribute to the development of more stable and sustainable agricultural production systems.

In a GGE biplot, the diagonal line that passes through the center of the bi-plot and the ideal point is referred to as the average environment coordination (AEC) line. The ideal point is the average of the coefficients of the first two components of the interaction effect in the GGE bi-plot model.

Genotypes that are closer to the center of the circle on this line are considered to have better yield, as they are more stable and have a consistent yield across a range of environments. In contrast, genotypes that are further away from the center of the circle on the AEC line are considered to have a lower yield, as they are less stable and have a more variable yield across different environments.

In a GGE biplot, the line that is perpendicular to the average line of the environmental function and passes through the center of the bi-plot is used as a criterion for measuring the stability of genotypes. This line is referred to as the "biplot axis for stability analysis" or "biplot axis for stability measurement." The further a

genotype is away from this line, the more it will contribute to the interaction effect and the less stable it will be. This means that genotypes that are closer to this line are more stable and have a more consistent yield across a range of environments.

Although the genotypes Opera and Licord had higher average oil yields compared to other genotypes, they were recognized as genotypes with low stability due to their distance from the ACE line. This suggests that these genotypes have a more variable yield across different environments and may not be suitable for cultivation in a wider range of environments.

In a GGE biplot, the small circle indicated [\(Fig. 4\)](#page-8-0) by an arrow represents the ideal genotype or ideal figure, which is defined by two criteria. The first criterion has the highest yield in the studied environments. This means that the ideal genotype should have the highest average yield across all environments. The second criterion is being completely stable compared to environmental conditions, as it is placed on the horizontal axis of ACE. This means that the ideal genotype should have a consistent yield across all environments and should not be affected by the interaction between genotype and environment. In the research, the Opera genotype was identified as a stable genotype due to its proximity to the ACE line in the GGE biplot. This indicates that the Opera genotype has a consistent yield across a range of environments, making it a suitable candidate for cultivation in different regions.

Figure 4. The average line of environmental yield in the comparison of the studied genotypes based on oil yield and stability in four experimental environments.

To use the ideal genotype as an evaluation reference, concentric circles can be created in the bi-plot to graphically determine the distance between the studied genotypes and the ideal genotype. The concentric circles represent equidistant points from the ideal genotype and are used to assess the yield and stability of the studied genotypes relative to the ideal genotype [\(Fig.](#page-9-0) 5). In a GGE biplot, concentric circles can be used to visualize the distance between the studied genotypes and the ideal cultivar. The ideal cultivar is placed at the center of the biplot, and the concentric circles represent equidistant points from the ideal cultivar. Based on this, genotype Licord was found to be the closest genotype to the ideal cultivar and was identified as the most desirable genotype. This suggests that Licord has a high potential for improved yield and stability across a range of environments and may be a suitable candidate for cultivation in different regions. On the other hand, genotype Geronimo was determined to be the most undesirable genotype because it had the greatest distance from the ideal cultivar (Licord). This indicates that Geronimo has a lower potential for improved yield and stability across a range of environments and may not be suitable for cultivation in a wider range of conditions.

The implications of these findings are significant for plant breeders and researchers, especially those involved in developing new winter rapeseed varieties in the west of Iran. The insights gained from this study can inform breeding programs aimed at enhancing the stability and adaptability of these varieties. By selecting and breeding genotypes that demonstrate superior performance across diverse environmental conditions, breeders can contribute to the development of more resilient and productive crop varieties suited to the region's specific challenges and needs.

Figure 5. Evaluation of the examined genotype compared to the ideal genotypes in the four tested environments based on oil yield.

4. Conclusion

Evaluating plant genotypes in multiple contrasting environments is essential to gain a full picture of their relative yield, stability and adaptability. Statistical analysis of GEIs can then reveal genotypes with desirable traits across a range of conditions. Center-based PCA is useful in GGE biplot analysis to handle issues common in genotype-by-environment datasets and provide insight into stability and adaptation of genotypes. The Licord genotype was more stable compared to others - which suggests the biplot analysis, whether GGE or AMMI, was able to effectively distinguish stable from less stable genotypes based on their yield across environments. This is one of the main functions of biplot analyses in plant breeding research. The study provides useful information for plant breeders and researchers working on developing new winter rapeseed varieties in western Iran, and the results can guide breeding programs aimed at improving the stability and adaptability of these varieties.

Conflict of interests

All authors declare no conflict of interest.

Ethics approval and consent to participate

No humans or animals were used in the present research.

Consent for publications

All authors read and approved the final manuscript for publication.

Availability of data and material

All the data are embedded in the manuscript.

Authors' contributions

All authors had an equal role in study design, work, statistical analysis and manuscript writing.

Informed consent

The authors declare not to use any patients in this research.

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