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Research Paper

Yield response of Kabuli-type chickpea genotypes to different environmental conditions using AMMI and GGE biplot methods

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Abstract

To evaluate the genotype × environment (G × E) interaction and stability of grain yield in the Kabuli type chickpea (*Cicer arietinum* L.), 15 white chickpea genotypes were evaluated in a randomized complete block design with four replications in Kurdistan, Maragheh, and Zandjan stations during three successive years under spring dryland conditions. Combined analysis of variance showed significant variation ($p < 0.05$) among the genotypes for grain yield. The results of AMMI (additive main effects and multiplicative interaction) analysis showed that the two first components (PC_1 and PC_2) of interaction were highly significant ($p < 0.01$) and accounted for 52% and 34% of the G × E interaction, respectively. The AMMI model determined the best combinations of genotypes and environments for grain yield. FLIP 09-369C had the highest level of stability under the present test conditions, which can be considered as a new cultivar. Also, the interaction effect of GE was studied by the GGE biplot method. According to the singular value decomposition, the first two principal components explained 52% and 34% of the total variation. Based on the GGE biplot method, the genotypes FLIP 09-369c, FLIP 09-365c, and FLIP 09-247c had higher grain yield and stability than other genotypes. The GGE biplot analysis divided the environments into two mega-environments including KURDISTAN-MARAGHEH and ZANDJAN, and for each mega-environment, FLIP 09-369C and FLIP 09-251C lines were recommended, respectively. The study also indicated that FLIP 09-364C, Samin, and FLIP 09-212C were identified as lines with general adaptability.

Keywords: AMMI analysis, chickpea (*Cicer arietinum* L.), dryland agriculture, GGE biplot, stability

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Introduction

The growing population, especially in developing countries, is making the supply of food, especially protein, more and more challenging. Pulses, as a source of plant protein, are of particular importance in the human diet. Chickpea (*Cicer arietinum* L.) is the third most important pulse crop in the world and the first most important in the WANA[1] region (Maya and Maphosa 2020). This plant is cultivated as a low-input and low-cost crop in semi-arid to temperate tropical

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West Asia and North Africa

agricultural systems and is important because of its ability to adapt to a wide range of environmental and soil conditions.

Chickpeas account for 15% of the global area under pulses and 13% of world production of these crops (FAOSTAT 2022). Asia, with 17 chickpea-producing countries, accounts for 80 percent of the global area under cultivation and about 72 percent of the production. Globally, the annual yield losses of chickpeas due to biotic and abiotic stresses are estimated at 4.8 million tons and 6.4 million tons, respectively (Bhat *et al.* 2022). The most common abiotic stresses affecting chickpea yield are drought, heat, and cold (Muehlbauer and Sarker 2017).

The western provinces of Iran are among the main chickpea-producing regions in the country. Farmers in these provinces cultivate chickpeas in rotation with rain-fed wheat (*Triticum aestivum* L.), often in the spring. In these areas, chickpea cultivation is done after the spring rains and the plants complete their growth cycle by using the moisture stored in the soil profile.

Cultivars evaluated in different locations and years have different reactions to environmental changes and this differential response of cultivars from one environment to another is called the genotype × environment (GE) interaction (Crossa *et al*. 1990). Depending on the size of the interaction or the distinct response of the experimental genotypes, the ranking of the varieties can be different in different environments (Agahi *et al*. 2020). Combined analysis of variance identifies and describes the values of the main effects, however, this analysis does not provide information about the genotype × environment interaction (Kaya *et al*. 2002). Therefore, it is necessary to use stability analysis methods. In general, the genotype × environment interaction complicates the selection of superior genotypes following their evaluation in multi-environment trials.

Studying the GE interaction can help us understand the concept of stability. One of the main goals of plant breeding is to develop cultivars that can adapt to a wide range of environments. However, a farmer won't care how the variety performs at other locations; he would care how it performs at his location year after year. Therefore, farmers need temporal stability (across years) rather than spatial stability (across locations). Many methods have been proposed for stability analysis, including parametric methods (univariate and multivariate) and nonparametric methods (Kang 1993). The AMMI analysis has been used to evaluate the stability of grain yield and grain chemical composition in regional experiments in many crops (Farshadfar *et al.* 2012; Mohammadi *et al.* 2013; Abebe *et al.* 2015; Nowosad *et al.* 2016; Tadesse *et al.* 2017). Another biplot model that has been extensively used for this purpose, is the GGE (G+GE) biplot analysis (Yan and Kang 2003; Yan and Tinker 2006). Plant breeders and agronomists have found GGE biplot analysis to be useful for genotype evaluation (Kang *et al*. 2006). This analysis helps to determine whether the target cropping region is homogeneous or should be divided into different mega-environments (Yan and Rajcan 2002; Tadesse *et al*. 2017).

Since the Kabuli-type chickpea variety

with high plant height (suitable for mechanized harvesting) and adapted to terminal drought stress, is not available in Iran, it is necessary to research to introduce a cultivar with these characteristics. This study aimed to investigate the GE interaction about the promising white chickpea genotypes in spring cultivation and to identify a superior genotype for all target environments or a cultivar for a specific environment.

Material and Methods

In this study, 14 selected Kabuli- type chickpea genotypes as well as a check variety (Samin), were evaluated in a randomized complete block design with four replications in Kurdistan, Maragheh, and Zandjan stations during the 2016 to 2019 cropping seasons. The list of experimental genotypes is presented in Table 1. The geographical and climatic characteristics of the research stations are presented in Table 2. The data in Table 2 show that the highest amount of rainfall was 495 mm at the Maragheh station in the third year of the study and the lowest amount of rainfall was 289 mm at the Kurdistan station in the first year. Seeds were planted in late March every year under dryland conditions. Before planting, 25 kg of net nitrogen per hectare was spread evenly on the surface of the experimental plots and then, mixed with the soil. Before planting, the seeds were inoculated with Vitavax fungicide (75% WP) at a concentration of 0.2 percent and during the vegetative growth period, the necessary field operations were carried out.

Table 1. List of chickpea varieties evaluated in the experiment.

No.	Entry name	Code	No.	Entry name	Code
1	FLIP 09-369C	369C	9	FLIP 09-214C	214C
2	FLIP 09-365C	365C	10	FLIP 09-292C	292C
3	FLIP 09-300C	300C	11	FLIP 09-345C	345C
4	FLIP 09-434C	434C	12	FLIP 09-251C	251C
5	FLIP 09-385C	385C	13	FLIP 09-364C	364C
6	FLIP 09-212C	212C	14	FLIP 09-247C	247C
7	FLIP 09-400C	400C	15	Samin (ILC 1799)	Samin
8	FLIP 09- 73C	73C			

In all of the experiments, the plants were monitored weekly to record traits, including plant stand, days to flowering, days to maturity, pods per plant, seeds per pod, plant height, 100-seed weight, and grain yield. Data collected from each station were analyzed separately, and after testing for uniformity of variance, combined analysis was conducted to determine the effects of years, genotypes, and their interactions.

To evaluate the GE interaction for the yield data, the AMMI model was used (Vargas

Table 2. Climatic and geographical information of the experimental stations during 2016-19.

Station	Longitude and Latitude	Altitude (m)	Year	Code	Temperature (^{O}C)		Precipitation (mm)
					Min.	Max.	
Kurdistan	35° 42' N 48° 08' E	2120	2016-17	KURDISTAN_17	-18.8	32.8	289.4
			2017-18	KURDISTAN_18	-15.6	33.8	333.9
			2018-19	KURDISTAN_19	-18.5	31.6	444.5
Maragheh	37° 12' N 46° 05' E	1720	2016-17	MARAGHEH_17	-17.7	33.3	299.7
			2017-18	MARAGHEH_18	-19.2	35.3	312.4
			2018-19	MARAGHEH_19	-14.4	37.2	494.6
Zandjan	36° 09' N 48° 49' E	1875	2016-17	ZANDJAN_17	-15.8	35.4	309.3
			2017-18	ZANDJAN_18	-14.6	37.2	390.0
			2018-19	ZANDJAN_19	-10.2	32.8	430.1

and Crossa 2000). The mathematical model of the AMMI biplot is as below (Gauch 2006):

$$Y_{ij} = \mu + \alpha i + \beta_j + \Sigma\ \lambda_n \rho_{in}\delta_{jn} + \theta_{ij} + e_{ij}$$

where Y_{ij} is yield of the ith genotype in the jth environment, μ is the grand mean, α_i (i = 1,…, s) is the mean deviation of the genotype (mean of the genotype minus the grand mean), β_j (j = 1,…, t) is the mean deviation of an environment from the grand mean, λ_n singular values for n-principal component decomposition axis, ρ_{in} and δ_{jn} principal component analysis (PC) scores or singular vectors for the genotype and environment, respectively in the nth axis of PC, N number of PC axes in the model, θ_{ij} matrix of residuals, and e_{ijk} residual error related to the kth replication (k = 1,…, r). In the AMMI1 model, the response of genotypes consists of linear functions of environmental first principal component (PC_1) scores that are very similar to the Finlay-Wilkinson regression (Finlay and Wilkinson 1963), where the response of genotypes is represented as a linear function of environmental means. The PC_1 usually has a clear agroecological interpretation for both genotypes and environments, while, higher degree PCs are less interpretable.

The GGE biplot was built according to the formula given by Yan *et al.* (2000):

$$Y_{ij} - \mu - \beta_j = \lambda_1\xi_{i1}\eta_{j1} + \lambda_2\xi_{i2}\eta_{j2} + \epsilon ij$$

where Y_{ij} is the mean for the i^{th} genotype in the j^{th} environment, μ is the grand mean, β_j is the main effect of the environment j, λ_1, and λ_2 are the singular values of the 1st and 2nd principal components, ξ_{i1} and ξ_{i2} are the PC_1 and PC_2 scores, respectively, for the genotype i^{th}, η_{j1}, and η_{j2} are the eigenvectors for the j^{th} environment for PC_1 and PC_2, and ϵij is the residual error term. To perform the combined analysis of variance, the assumption of uniformity of experimental errors must be confirmed. Therefore, to check the homogeneity of the error variances, Bartlett’s test (Bartlett 1999) was conducted. Combined analysis of variance and comparison of means was performed via SAS software version 9.1 (SAS Institute 2008). The AMMI analysis was performed with AMMISOFT version 1.0 (available at https://css.cornell.edu/ammisoft/AMMISOFT 10.pdf). The GGE Biplot methodology was applied for visual examination of the GE interaction pattern of multi-environmental trial data by using the GGE biplot software.

Results and Discussion

Analysis of variance

Bartlett’s test (χ^2= 10.91, df = 8) showed that the experimental errors were homogeneous. Then, assuming the effects of years and stations as random and the effect of varieties as fixed, the combined analysis of variance was performed (Table 3).

Table 3. Combined analysis of variance for various traits of chickpea genotypes in three experimental stations during three cropping seasons (2016-19).

SOV	Degrees of freedom	Mean Squares					
		STD	DF	DM	PHT	SW	YLD
Station (S)	2	17.87^{ns}	37080*	17145^{ns}	2150.42^{ns}	0.27^{ns}	18.61^{ns}
Y (Year)	2	11.94^{ns}	5286^{ns}	7297^{ns}	1369.69^{ns}	79.63^{ns}	14.89^{ns}
Y × S	4	6.28**	5450**	5047**	1959.56**	16.79*	12.09**
Rep/Y × S	27	0.77	56.0	5.0	17.37	5.49	0.23
Genotype (G)	14	0.34^{ns}	32.5**	20.6**	38.91**	238.69**	0.11*
G × S	28	0.32^{ns}	9.8*	6.6**	7.01^{ns}	34.91**	0.06^{ns}
G × Y	28	0.48^{ns}	8.1^{ns}	4.5^{ns}	14.31*	19.42^{ns}	0.03^{ns}
G × Y × S	56	0.41*	5.5**	2.7^{ns}	7.82**	14.36**	0.05*
Error	378	0.27	2.5	2.2	3.31	4.47	0.03
Coefficient of variation (CV)%		38.92	2.32	1.44	6.72	6.17	20.54

ns, * and ** non-significant and significant at 5% and 1% probability levels, respectively.

STD= Stand score, DF= Days to flowering, DM= Days to maturity, PHT= Plant height, SW= 100-seed weight, YLD= Grain yield

Based on the results, the difference between grain yield of experimental genotypes was significant at the 5% probability level and for the number of days from planting to flowering, number of days to maturity, plant height, and 100 seed weight at the 1% probability level. The difference between the lines was not significant concerning the plant establishment score. The stand score of all genotypes was favorable and less than 2. Line 369C gave the highest mean yield (919 kg ha^{-1}) and 385C had the lowest mean yield (722 kg ha^{-1}) across environments. The maximum and minimum plant height belonged to 214C (38.51 cm) and Samin (25.82 cm), respectively. The highest and lowest weight of 100 seeds was observed in 400C (37.85 g) and 364C (30.39 g) genotypes, respectively. (Table 4).

Stability analysis

Based on the AMMI analysis of variance, the first interaction principal component (PC_1), with 21 degrees of freedom, accounted for about 52% of the total variability in the GE interaction sum of squares (Table 5). The second and third principal components accounted for 34% and 4% of the total GE sum of squares, respectively. In the AMMI1 graph, the horizontal axis represents the additive main effects or the mean yield of genotypes and environments, and the vertical axis represents the multiplicative interaction or values of the principal components for genotypes and environments.

Table 6 contains the mean grain yield of each genotype for each of the experimental environments. In this table, the winner genotype in each environment was marked in bold. These results revealed that some genotypes showed stable performance across all environments. The genotypes selected by the AMMI model across the experimental environments are presented in Table 7. None of the lines under study had a clear advantage concerning stability over other lines. The 369C

Table 4. Mean of characteristics of 15 chickpea genotypes in three experimental stations during three cropping seasons (2016-19).

Genotypes	STD	DF	DM	PHT (cm)	SW (g)	YLD (kg ha^{-1})
FLIP 09-369C	1.306	66.69	103.2	35.77	32.44	919.0
FLIP 09-365C	1.389	67.89	104.2	28.84	36.55	893.9
FLIP 09-300C	1.306	67.36	104.0	37.63	32.19	836.7
FLIP 09-434C	1.333	68.83	104.9	38.01	36.61	813.2
FLIP 09-385C	1.333	67.89	105.0	37.41	37.61	722.4
FLIP 09-212C	1.361	68.69	104.4	37.49	36.05	789.7
FLIP 09-400C	1.306	68.50	104.4	37.39	37.85	762.4
FLIP 09- 73C	1.528	67.58	103.9	37.24	35.93	815.7
FLIP 09-214C	1.222	67.89	105.1	38.51	37.42	792.8
FLIP 09-292C	1.139	68.08	104.6	35.20	35.19	832.4
FLIP 09-345C	1.167	67.75	104.5	37.47	34.47	755.3
FLIP 09-251C	1.389	67.67	103.6	35.92	32.96	850.0
FLIP 09-364C	1.361	67.25	103.4	36.76	30.39	826.2
FLIP 09-247C	1.361	66.25	104.3	37.05	32.43	914.6
Samin (ILC 1799)	1.417	65.19	102.3	25.82	33.56	845.4
$LSD_{5\%}$	0.239	0.726	0.694	0.844	0.980	78.51

STD= Stand score, DF= Days to flowering, DM= Days to maturity, PHT= Plant height, SW= 100-seed weight, YLD= Grain yield line ranked at the top in environments E2, E8, and E9, and the 247C line in environments E1, E5, and E6. However, the fluctuation of the performance of these genotypes in other environments was so great that the selection of these genotypes was questioned.

Table 5. Analysis of variance for additive main effects and multiplicative interactions (AMMI) for 15 chickpea genotypes.

SOV	df	MS	Explained SS (%)
Treatments	134	912787**	-
Environments (Env.)	8	14423530**	82.75
Block/Env.	27	232736**	4.51
Genotypes (Gen.)	14	114790*	1.15
Gen.× Env.	112	47483**	3.81
IPCA1	21	109419**	52.1
IPCA2	19	62526**	34.1
IPCA3	17	45665ns	4.25
Residual	55	19201	9.56
Error	378	28698	-
Total	539	-	-

ns, * and ** non-significant and significant at 5% and 1% probability levels, respectively

The mean squares attributable to PC_1 and PC_2 were significant at the 1% level of probability and cumulatively about 86% of the variation associated with GE interaction was explained by these two components. In addition, the best model resulted from two components plus the genotypic main effect, and the use of other PCs did not help to improve the model. Although the residual value was not significant, it accounted for about 20% of the total GE sum of squares.

Figure 1 shows the polygon view for the present experiment including 15 chickpea genotypes in 9 environments. In this figure, the genotypes 369C, 365C, 247C, 345C, 385C, 212C, and 251C, which formed the vertex of the polygon, had the greatest distance from the center of the biplot and were the best or poorest lines in their respective environments (Yan and Kang 2003). The rest of the genotypes were located within the polygon. The lines drawn from the origin of the coordinate perpendicular to the sides of the polygon define environmental groups or mega environments (Yan and Kang 2003). In this study, the environments were divided into two mega-environmental groups. The first mega-environment included the environments of Kurdistan in all three years and Maragheh in the second and third years. The most superior and stable genotypes in this mega-environment were 369C, 365C, and 247C, respectively. The second mega-environment included Zandjan in all three years, and superior and stable

Table 6. Winner genotypes by environment for 15 chickpea genotypes at nine environments.

No.	Genotype	Kurdistan			Maragheh			Zandjan		
		2017 (E1)	2018 (E2)	2019 (E3)	2017 (E4)	2018 (E5)	2019 (E6)	2017 (E7)	2018 (E8)	2019 (E9)
G1	FLIP 09-369C	1024.6	**1028.4**†	884.3	1030	2077	562.0	852.1	**364.5**	**447.8**
G2	FLIP 09-365C	1014.2	1011.7	**899.8**	981	2044	584.3	812.7	332.0	415.1
G3	FLIP 09-300C	847.8	899.7	569.0	1100	2000	490.4	**862.4**	337.5	424.1
G4	FLIP 09-434C	847.5	878.5	569.1	1035	2035	471.8	815.7	291.5	374.6
G5	FLIP 09-385C	658.3	815.2	517.2	1134	1448	328.4	825.1	332.8	442.3
G6	FLIP 09-212C	741.1	828.9	395.8	**1151**	1919	445.3	874.0	330.8	421.3
G7	FLIP 09-400C	726.6	824.5	461.5	1110	1781	402.6	835.1	312.5	407.4
G8	FLIP 09- 73C	811.9	852.4	441.0	1095	2105	486.9	855.0	306.6	388.0
G9	FLIP 09-214C	820.0	851.6	520.2	1025	2034	454.7	802.0	272.3	354.7
G10	FLIP 09-292C	862.8	914.5	648.2	1068	1931	475.7	839.6	331.3	420.2
G11	FLIP 09-345C	795.7	852.6	633.8	979	1785	389.0	753.4	258.7	350.3
G12	FLIP 09-251C	879.5	936.4	681.0	1089	1917	429.5	858.4	354.1	444.5
G13	FLIP 09-364C	879.4	933.9	751.8	1031	1828	454.8	811.8	326.0	418.4
G14	FLIP 09-247C	**1038.3**	991.9	772.5	979	**2342**	**589.9**	828.0	309.3	379.6
G15	Samin (ILC 1799)	930.0	943.0	753.2	989	2015	492.1	799.1	301.8	385.4

†Bold figures are mean yield of genotypes (G1-G15) in different environments (E1-E9), that indicate which genotype wins where.

Table 7. First four AMMI selections per environment for 15 chickpea genotypes.

Env.	Name	Yield (kg ha^{-1})	IPCA score	Genotype Rank			
				1st	2nd	3rd	4th
E4	MARAGHEH_17	1053	23	G6	G5	G7	G3
E9	ZANDJAN_19	405	8	G1	G12	G5	G3
E7	ZANDJAN_17	828	7	G6	G3	G12	G8
E8	ZANDJAN_18	317	7	G1	G12	G3	G5
E2	KURDISTAN_18	904	-1	G1	G2	G14	G15
E6	MARAGHEH_19	471	-2	G14	G1	G2	G15
E1	KURDISTAN_17	859	-7	G14	G1	G2	G15
E3	KURDISTAN_19	633	-7	G2	G1	G14	G15
E5	MARAGHEH_18	1951	-18	G14	G8	G1	G2

genotypes in this mega-environment were 369C and 251C. The superior genotypes of the left-alone environment, MARAGHEH_17 were 212C and 385C. The genotype 345C was not superior in any of the environments. Some genotypes such as 364C, Samin, and 212C, which were located near the center of the biplot, had average performance and general adaptability in the experiments. Based on Figure 1, two mega-environments including KURDISTAN_17, _18, and _19 plus MARAGHEH_18 and _19 as well as ZANDJAN_17, _18 and _19, were identified in the western and northwestern regions of the country, and these two environments corresponded well with the geographical distribution of the locations. These results are consistent with the results of previous research (Guru *et al*. 2020; Kanouni *et al*. 2021).

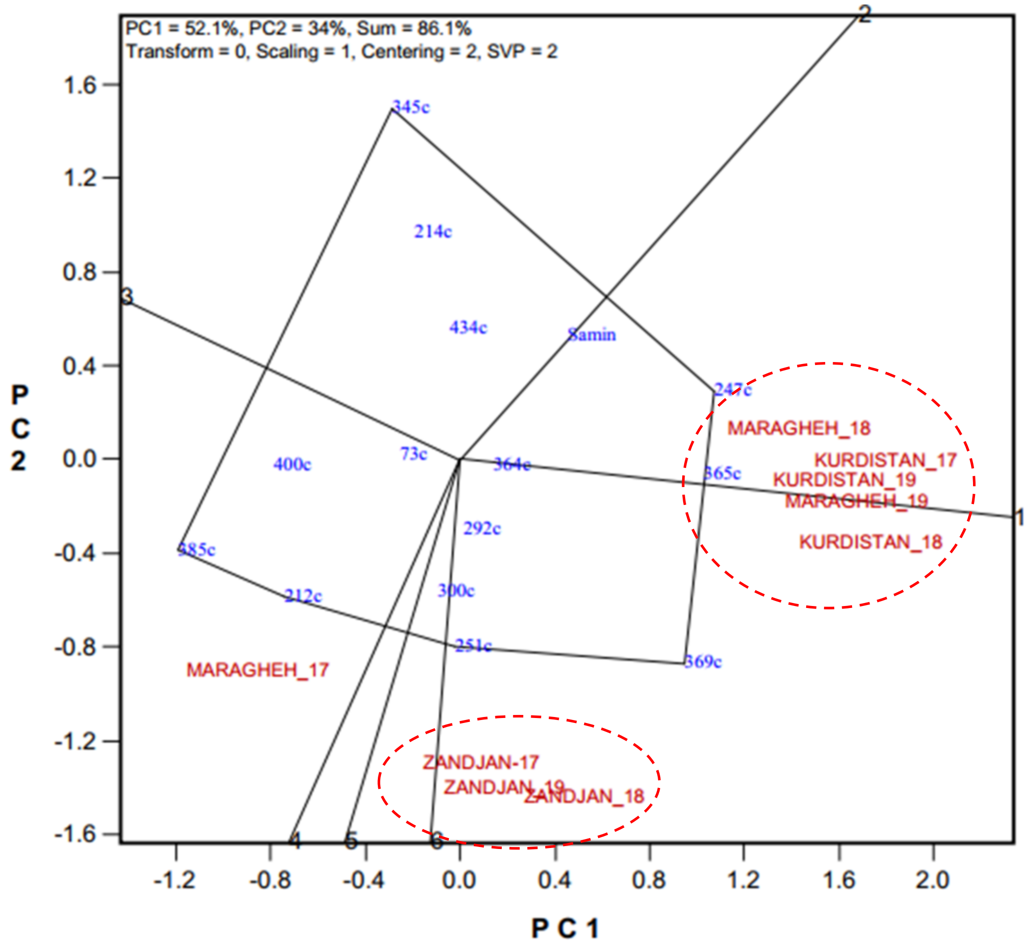

Figure 1. Which won where polygon pattern for 15 chickpea genotypes grown in nine environments of Iran.

Simultaneous selection for yield and stability performance is shown in Figure 2. In this figure, 15 chickpea genotypes were ranked based on their mean yield and stability. The axis marked with an arrow determines stability, and any line that is closer to this axis is more stable. The average tester coordinate, which is called ATC, is an index that compares the average performance of experimental genotypes with the overall average (Erdemci 2018, Karimizadeh *et al*. 2022). The genotypes on the right side of the ATC have an average higher than the mean yield and the genotypes on the left side of this axis have an average yield below the mean, so genotypes such as 369C, 365C, and 247C, which are connected to the stability axis with a shorter line, have higher stability than other genotypes. Lines 212C, 434C, and 345C had an above- average performance, and lines 251C, 300C, and 292C had a below-average performance. Among these genotypes, 369C was recognized as the most productive and stable genotype. On the other hand, 345C was recognized as the least productive genotype with poor stability. Through this biplot, genotypes with a high yield but with moderate or poor stability (such as 251C line) can be selected for particular environments. This genotype showed a very good adaptation to the environment of Zandjan.

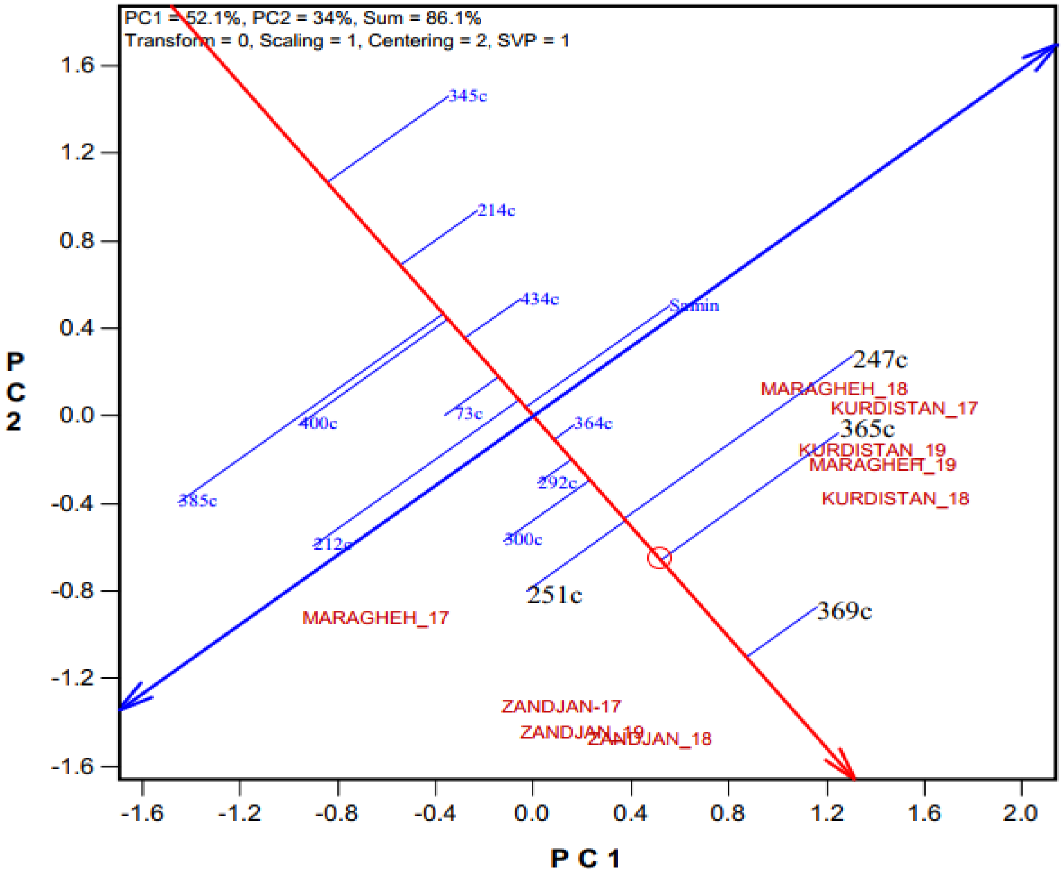

Figure 2. Simultaneous selection for grain yield and stability of 15 chickpea genotypes grown in nine environments based on the average tester coordinate (ATC).

Based on the results of the GGE biplot and AMMI, it was possible to select advanced chickpea genotypes with high stability and performance compared to the control variety, Samin. The GGE biplot in examining the compatibility and stability performance of the genotypes in different environments was effective and may be used in the investigation of genotypes in different locations and years in the chickpea breeding programs (Karimizadeh *et al*. 2022). In the GGE biplot, the main effect of genotype and genotype × environment interaction cannot be separated, therefore Gauch (2006) believes that the AMMI However, other investigators (Yan *et al*. 2007) believe that the GGE biplot method is more successful than the AMMI method in terms of analysis of GE data because from the point of view of the breeders, selecting genotypes only based on the main effect of genotype, or only considering the GE interaction will not be effective.

Conclusion

Based on the results, genotypes with high yield but with different sensitivity to environmental conditions were identified as compared with the check cultivars of chickpea. Therefore, the adaptable and high-yielding genotypes identified in this study can be used to increase the yield of white chickpeas in the region. Genotypes FLIP 09-369C followed by FLIP 09-365C and FLIP 247C showed the highest stability across different environments. These lines can be introduced as spring cultivars to chickpea farmers in northwest Iran after additional studies.

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Conflict of interest

The authors declare that they have no conflict of interest with any organization concerning the subject of the manuscript.

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بررسی پاسخ عملکرد ژنوتیپ‌های نخود تیپ کابلی به شرایط محیطی متفاوت با استفاده از روش‌های AMMI و بای‌پلات GGE

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چکیده

برای بررسی اثر متقابل ژنوتیپ × محیط و پایداری عملکرد دانه در نخود تیپ کابلی، ۱۵ ژنوتیپ نخود سفید در قالب طرح بلوک‌های کامل تصادفی با چهار تکرار در ایستگاه‌های کردستان، مراغه و زنجان طی سه سال متوالی در شرایط دیم بهاره مورد ارزیابی قرار گرفتند. تجزیه واریانس مرکب نشان داد که تغییرات بین ژنوتیپ‌ها از لحاظ عملکرد دانه معنی دار است ($p \leq 0.05$). نتایج تجزیه اثرات اصلی افزایشی و اثرات متقابل ضربی (AMMI) نشان داد که دو مؤلفه اصلی اول (PC1) و دوم (PC2) بسیار معنی‌دار هستند ($p \leq 0.01$) که به ترتیب ۵۲٪ و ۳۴٪ از اثرمتقابل ژنوتیپ × محیط را به خود اختصاص دادند. مدل AMMI بهترین ترکیب ژنوتیپ‌ها و محیط‌ها را برای عملکرد دانه تعیین کرد. بر اساس نتایج حاصل، FLIP 09-369C بالاترین سطح پایداری را در شرایط آزمایش حاضر داشت که می‌تواند به عنوان رقم جدید در نظر گرفته شود. همچنین، اثرمتقابل GE توسط روش بای پلات بررسی شد. با توجه به تجزیه مقادیر منفرد، دو مؤلفه اصلی اول (PC1 و PC2) به ترتیب ۵۲٪ و ۳۴٪ تغییرات در کل داده ها را توجیه کردند. بر اساس نمودارهای بای پلاتGGE ، ژنوتیپ های ۳۹۶C، ۳۶۵C و ۲۴۷C نسبت به سایر ژنوتیپ‌ها عملکرد و پایداری بیشتری داشتند. تجزیه و تحلیل بای پلات GGE محیط‌ها را به دو محیط کلان شامل کردستان+ مراغه و زنجان تقسیم کرد و برای هر محیط کلان به ترتیب ژنوتیپ‌های FLIP 09-369C و FLIP 09-251C توصیه شدند. همچنین در این مطالعه FLIP 09-364C، Samin و FLIP212C به عنوان ژنوتیپ‌های با سازگاری عمومی شناسایی شدند.

واژه‌های کلیدی: بای‌پلات GGE، پایداری، تجزیه AMMI، کشاورزی دیم، نخود (*Cicer arietinum* L.)