Plant Archives Vol. 19 No. 1, 2019 pp. 1797-1803 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

USE OF GGE-BIPLOT TECHNOLOGY TO STUDY THE GENETIC-ENVIRONMENTAL INTERACTION OF THE MAIZE

Riyadh Jabbar Al-Maliki[1]* and Nadhum Yonis Abed[2]

[1]College of Agriculture, Wasit University, Wasit, Iraq.
[2]College of Agriculture, Baghdad University, Baghdad, Iraq.

Abstract

The data analyses the grain yield of eight inbreed line genetic of maize tested within nine Environments in Iraq ofseason 2017 Using the GGE-Biplot Technology. The objectives of the experiments were to study the of GGE. To determine the optimal genotype and the ideal environment as well as to determine the pattern of interference using technology as a new method to employ biostatistics in the field of plant breeding through the selection of varieties in different environments in other areas as an important tool for plant breeders.

The results showed that the genetic variability and the genetic-environmental interaction was significant. The first two components (PC1 & PC2) were sufficient to explain the genetic-environmental interference, with a ratio of 63.5%, heterogeneity GGE. Genotypes are classified as high when they have PC1 values greater than zero and low combinations when PC1 values are less than zero. Similarly, PC2 values near zero are constant, while high PC2 values (regardless of signal) indicate instability. Thus, the inbreed line (Ast-B strain) was ideal on the basis of high yield and stability, while the inbreed line(Zm-17) was characterized by high stability but low, and all studied environments had PC1 values greater than zero, so the environments represented a non-crossover type. The highest average plant yield was 276.17 g / plant in Al-Kut location. The Australian (inbreed line Ast-B) recorded the highest cross environment - rate of 331.36 g / plant while the combination inbreed line Ast-B in Al-Kut location recorded the highest rate of 416.05 g / plant. Compatible and an effective tool in the selection and identification of the inbreed line within the preferred environment which means Bur new and important technology.

Key words : GGE biplot, *Zea mays*, multi-environment, yield trial.

Introduction

This is the third largest crop in the world after wheat and rice in terms of cultivated area and production. The most important maize producing areas in the world are: North and South America, Eastern Europe and Russia, China, India, South Africa.

The effect is quantitative and usually shows great genetic-environmental interaction. Therefore, the difference in the composition of the tested genotype is significant among the studied environments (Delacy and Cooper, 1990; Kaya *et al.*, 2006). The main environmental factors specific to the production are the duration of the lighting and the temperature and their relation to the change in the lines. Therefore, multi-environment experiments (MEYT) are applied to assess genotypes during a number of sites and years, and are usually applied in areas with geographic variation. This process is not easy because phenotypic heterogeneity is a mixture of G, environmental, E and environmental genetics.

The latter reduces the association between phenotypic and genotypic and thus complicates the selection process for distinct genotypes and contributes to the process of instability (Delacy *et al.*, 1996; Hammer and Cooper, 1996; Kaya *et al*., 2002). G and GE do the task of evaluating genetics, especially when GE is constant and repetitive (Hariprasanna *et al*., 2008). Department of Evans (Evan, 1993) concept of stability to the first: stability during the seasons or years (Temporal Stability) and stability during sites or environments (Spatial Stability or Adaptability).

***Author for correspondence :** E-mail: ralmaliki@uowasit.edu.iq

Several methods of studying G.E. In MEYT experiments including joint regression (Eberhart and Russel, 1966; Gabriel, 1971; Phakamas *et al*., 2008), AMMIA (Additive Main Multiplicative Interaction Analysis) by Gauche (Hamdalla *et al*., 2011) and genetic correlation type B (Yan and Tinker, 2005). Biplot technology was proposed by Gabriel (Gauch, 1992) and developed by Yan and Hunt (2001). This technology identifies the genotype-environmental interference pattern through the interference pattern diagram in MEYT experiments. The GGE-Biplot analysis consists of two main phases. The first is based on the aggregate analysis of the separation of the aggregate effect from the interference and the second stage is based on the analysis of the components (PCA). The main objectives of this technology are to analyze the mega-environment and to evaluate the genetic composition in terms of its performance and stability and assessment of the environment in terms of its ability to classify genotypes. GGE-Biplot is based on two concepts: the first is the graphical representation (Gauch, 1992; Mekontchou1 *et al*., 2006) and the second is the estimation of G and G.E (Yan and Hunt, 2001). GGE-Biplot analysis was used by a number of researchers in field pistachio kernel experiments (Banterng *et al*., 2006; Finlay and Wilkinson, 1963; Kang, 1990; Mothilal *et al*., 2010; Phakamas *et al*., 2010; Putto *et al*., 2009; Roozeboom *et al*., 2008). This study was conducted to study the pattern of interference. For the grain of eight inbreed line Different genetically modified maize in nine environments using GGE-Biplot technology, identification of the ideal inbreed line and the ideal environment, as well as determining the appropriate lineage for each environment.

Materials and Methods

Field experiment

Field trials were carried out in nine environments in Wasit province during the 2017 season to study the effect of genetic-environmental interference on eight inbreed line of maize (table 1). The seeds were planted on a 75 cm cedar and 25 cm in diameter with two seeds. Superphosphate fertilizer was added at a rate of 200 kg / ha at tillage and urea fertilizer was added at an average of 200 kg / ha after germination. Incineration and weeding operations were carried out as needed. Ten random plants were selected and harvested at maturity.

Statistical analysis

GGE-Biplot is based on two concepts: the first is G and G.E. (GGE). The second concept is that Biplot technology is used to display GGE in MEYT experiments.

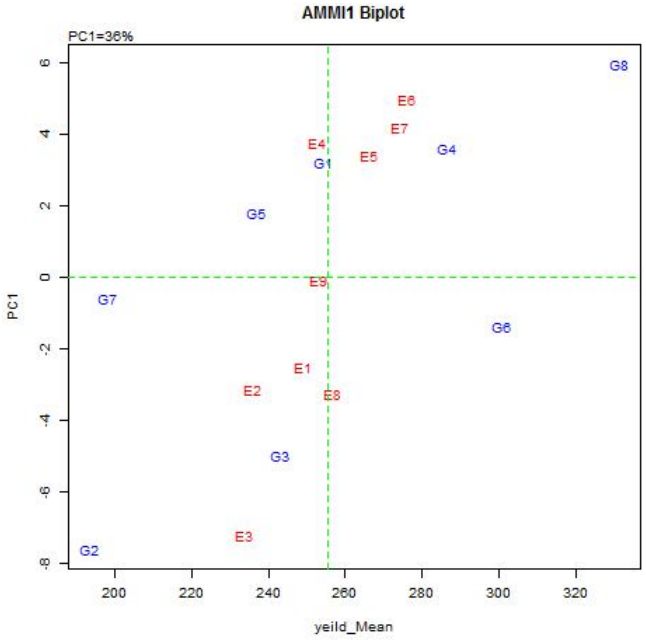

Fig. 1 : Distribution of breeds to studied environments.

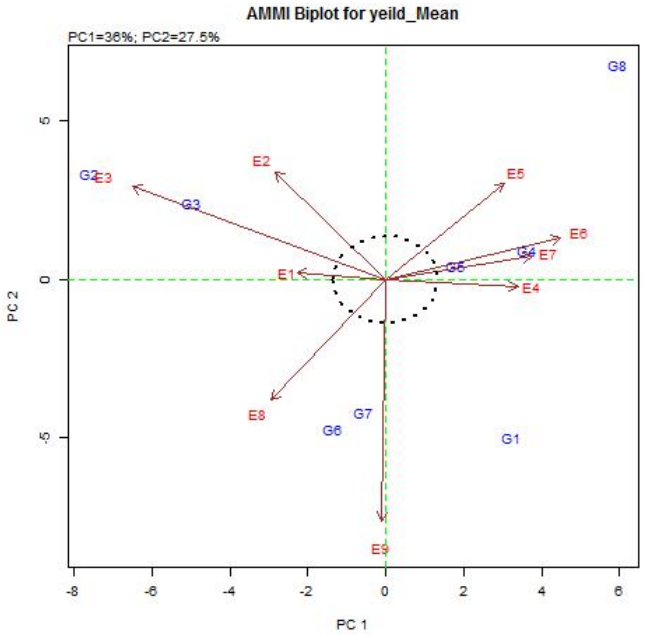

Fig. 2 : Link between environments and breeds.

GGE-Biplot based on the initial and secondary effects of the basic components PC1 and PC2 (Principle Components Analysis) resulting from exposing the environment centered data to a single primary analysis (Yan *et al*., 2000; Yan and Hunt, 2001), which are used to analyze the interference effect of Synthesis model and thus aggregation of aggregates based on similarity of performance in contrasting environments. The GGE-Biplot analysis model, based on (Yan *et al*., 2001) is based on single value analysis (SVD) for the first components two:

Table 1 : Inbreed line and environments.

Inbreed line	Sours	Icon	Environments	Icon
Inp-6	Locale	G1	sowure	E1
Pio-17	Yugoslavia	G2	Sheksaad	E2
Syn-9	French	G3	Al hiy	E3
Zm-17	Yugoslavia	G4	shehmeae	E4
Pio-3	Yugoslavia	G5	degely	E5
S-10	Australian	G6	ahrar	E6
MGW-1	Yugoslavia	G7	kut	E7
Ast-B	Australian	G8	azezeae	E8
			nomaneae	E9

ij-μ- β_j = λ_ (1) __i1 K_j1 + λ_ (2) __i2 K_ (j2) + £ _ij (1y)

Where, _ij is a measurement of the performance of the composition i in the environment j, μ: the general rate, β_j: the main effect of the environment j, μ + β_j: the sum of all compositions in environment j, λ_ (1) and λ_ (2). For the primary components I and II (PC1 and PC2) sequentially, __i1 and __i2 are the eigenvectors for installation i of the first two components, K_j1 and K_j2: are the eigenvectors of environment j of the first two components, _ij.

The individual value is fragmented by:

g_i1 =[(λ)_ (1)] ^ (s_i) _i1 and e_1j = [(λ)_ (1)] ^ [(01-s)] _i) K_1j (2 y)

Where, s_1 is the retail factor for PC1 values whose values are between 1 and 0

For GGE-Biplot generation, Equation (1) will be written as follows:

ij-μ- β_j = g_i1 e_1j + g_i2 e_2j + £ _ij (3y)

When adjusting data, the last equation becomes:

yIj-μ-β_j) s_j = Σ_(i = 1) ^ k g_i1 e_1j+£_ij (4 y).

Where, s_j: the standard deviation in environment j, i = 1,2, ..., k, g_i1 and e_1j are PC1 values for installation i and environment j sequentially.

Equation (4) was used to form Fig. 2 and Equation (3) to evaluate the relationship between structure and environment. The analysis and graph were performed using GGE biplot (26).

Results and Discussion

The aggregate analysis table showed a significant effect on the environment and genetic structure and their interaction in the grain yield of maize (table 2). The environment, genotypes and their interactions contributed 35.8%, 30.8% and 23.3%, respectively. The biplot analysis also shows that the main components PC1 and PC2 were significant and explained 63.5%. % of total GGE variance.

Table 3 shows the superiority of the inbreed line (G9) on all the studied structures on the basis of the rate obtained through environments and reached the highest rate of 331.36 g/plant and the lowest rate of (2) was 175.43 g/plant across the environment. (1) and the genetic characteristics of each breeder to demonstrate maximum genetic capacity under environmental conditions. The eighth inbreed line was superior in all environments and gave it the highest rate compared to other inbreeds except the sixth inbreed line which surpassed the number in the eighth and ninth environment. The table indicates that

Table 2 : Aggregate analysis of the grain yield of eight inbreed line of maize in nine environments.

s.o.v.	d.f.	s.s.	m.s.	f-cal.	Sig	% s.s.	% of Eigen values cumulative
Env.	8.00	43187.60	5398.40	46.28	**		
Reps./env.	16.00	1634.10	102.10	0.88	Ns		
Gen.	7.00	441866.50	63123.80	541.17	**		
Gen.×Env.	56.00	180856.00	3229.60	27.69	**		
IPCA1	14.00	65026.84	4644.77	40.63	**	36.00	36.00
IPCA2	12.00	49745.66	4145.47	36.26	**	27.50	63.50
IPCA3	10.00	31227.40	3122.74	27.32	**	17.30	80.80
IPCA4	8.00	18084.60	2260.57	19.77	**	10.00	90.80
IPCA5	6.00	10034.14	1672.36	14.63	**	5.50	96.30
IPCA6	4.00	4462.36	1115.59	9.76	**	2.50	98.80
IPCA7	2.00	2275.05	1137.53	9.95	**	1.20	100.00
Residual	142.00	16563.50	116.60				

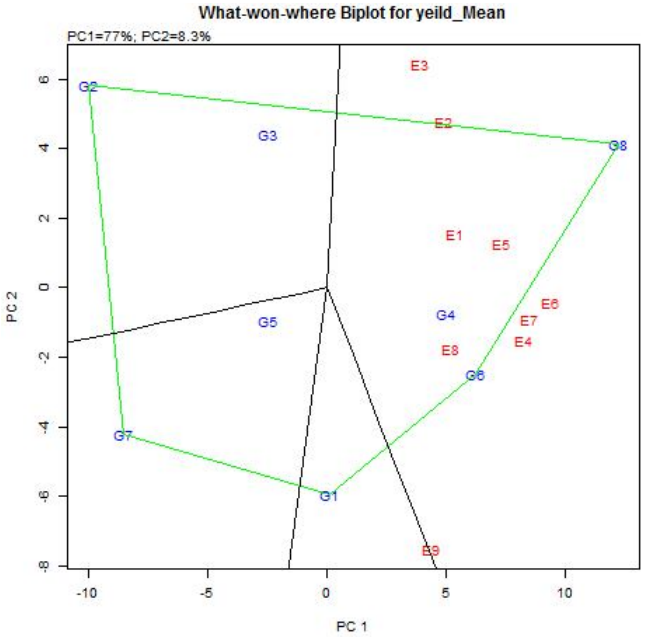

Fig. 3 : Preferred breeds within environments.

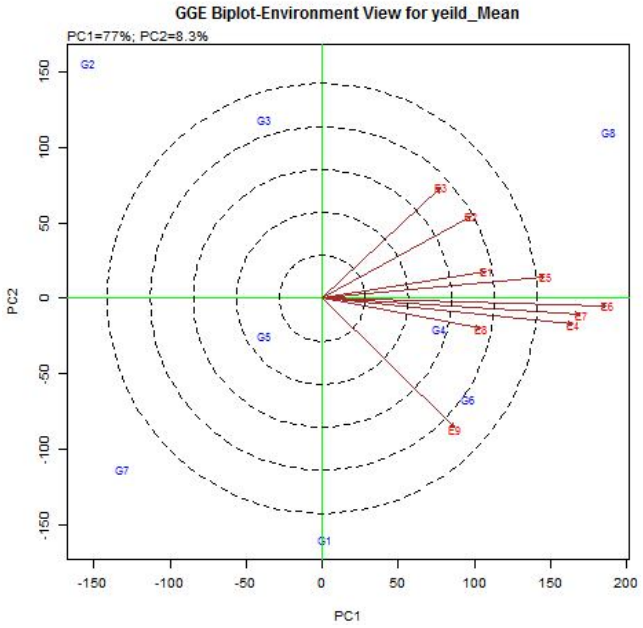

Fig. 4 : Stability of genotypes in environments.

Table 3 : Average grain yield (g / plant) of eight inbred lines of maize in nine environments.

	Genotybe1	Genotybe2	Genotybe3	Genotybe4	Genotybe5	Genotybe6	Genotybe7	Genotybe8	Mean
env1	230.00	205.00	250.00	284.00	231.00	300.00	190.00	305.00	249.38
env2	240.32	212.33	260.89	230.00	220.66	244.74	157.82	322.00	236.10
env3	171.03	247.86	240.19	250.67	205.19	291.23	173.56	291.42	233.89
env4	242.66	170.67	188.33	262.89	291.33	328.86	181.67	358.31	253.09
env5	250.19	180.83	258.80	345.16	258.66	262.20	210.00	364.55	266.30
env6	292.35	181.14	244.81	305.70	231.23	319.05	219.00	416.05	276.17
env7	290.06	183.47	251.41	349.21	249.72	305.59	197.89	368.97	274.54
env8	276.82	184.59	285.52	269.14	204.81	330.08	213.60	291.29	256.98
env9	294.51	175.02	207.17	281.76	240.33	322.82	241.17	264.63	253.43
lsd 5%				**17.432**			**6.163**		
mean	254.22	193.43	243.01	286.50	236.99	300.51	198.30	331.36	**255.54**
lsd 5%				**5.811**					

the number of inbreed line (Baker, 1988 and Evan, 1993) in the environment decreased, which negatively affected the general average. Which exceeded the other environments at a rate of 276.17 g/plant, which did not differ significantly from the seventh environment.

Table 4 indicates the difference in rank of most breeds in most environments. This indicates that these inbreed lines may be crossover except the (G8 and G6) genotype, which have been stable throughout most environments. The crossover overlap is usually accompanied by a genotypic rank and therefore this type of interference is important in evaluating the compositions in MET (Baker, 1988).

GGE biplot data were graphically presented to study the relationship between genotypes and environments. The inbreedlines that owned PC1 values were higher than zero as high and the structures that had PC1 values were less than zero as low (fig. 1). Also, the structures that had PC2 values (close to zero) were adaptive and had high PC2 values are not adaptive. On the basis of this, the structures were divided into three groups in terms of the following: the first is higher than the general average and the G8 and G4 inbreed lines are the lowest and the lowest is the G5 and the third group (G7).

The lines connecting the origin point and the environment locations are called the environment vectors and the full-angle between any vectors of any two environments corresponds to the correlation between them. Also, the length of the environment vectors represents the standard deviation and reflects the susceptibility of the environment to the classification of

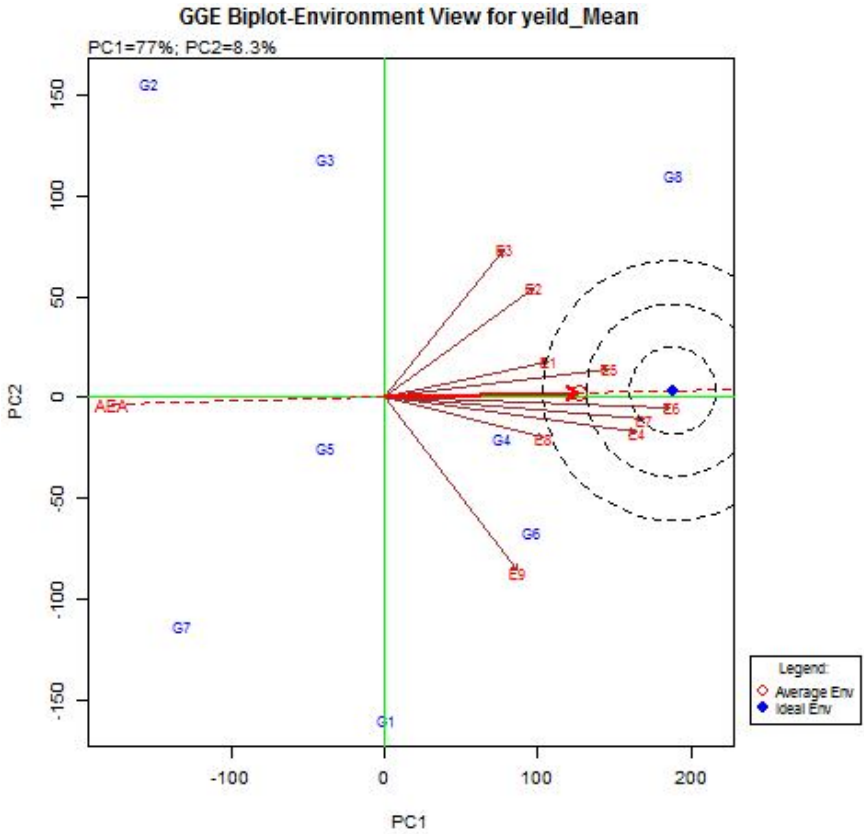

Fig. 5 : The relationship between genetic strains.

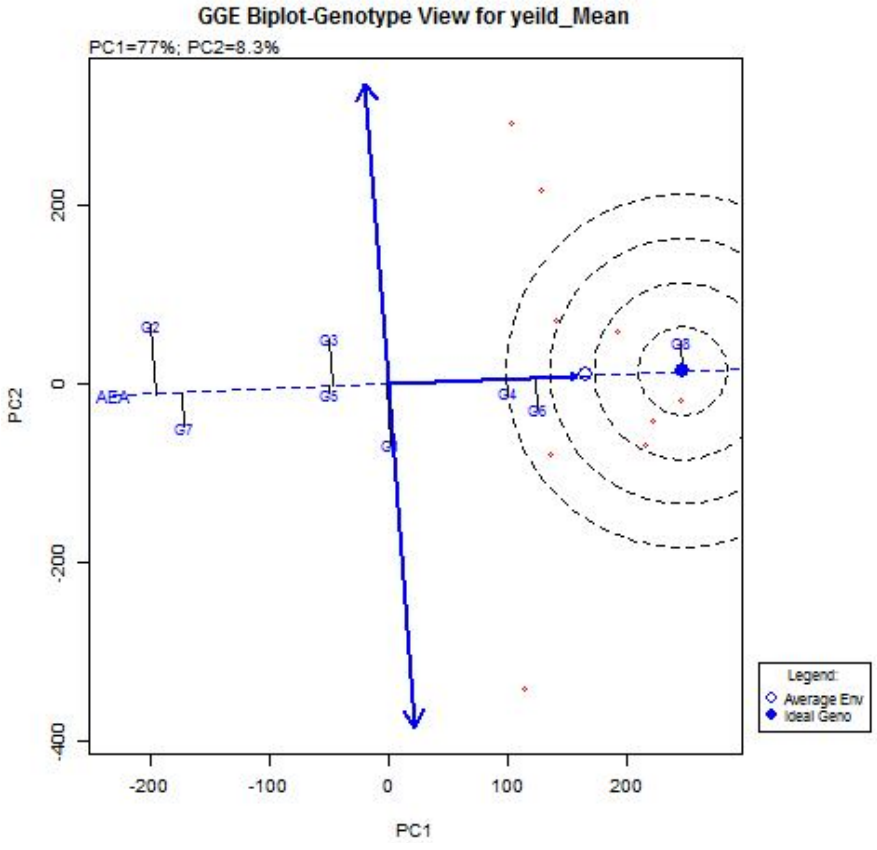

Fig. 6 : Types of environmental genetic interference.

genotypes, the longer the length of the vectors expressed the greater ability of the environment to classify the structures (discriminative). Fig. 2 showed that all angles between vectors for all environments were less than 90 degrees. This indicates that all correlation coefficients were positive and that the lack of negative correlation between environments is a sign that there has been no significant change in the structure of structures during environments. Note that the lowest angle occurred between the sixth and eighth environments, which indicates the high correlation between these two environments. Meaning the possibility of election on the basis of the appearance of a particular installation in one environment and the dissemination of results to the other environment. In any case, fig. 3 shows the preferred inbreeds of each environment and depends on polygon formation by passing points of genotype far from the origin of the biplot to include all other genotype inside. G4, G6, and G8 have a high yield in the seventh environment, while G3 and G2 are suitable for environments 1, 2 and 3. Fig. 3 shows that there are two mega-environments, the first included the sixth and the second included the fifth and eighth environments.

The stability of genotypes was studied in the studied environments using the AEC (Average Environment Coordination) method by Yan and Hunt (2001) and Yan (2002). Based on this method, the environment rate is determined by the PC1 and PC2 values for all environments and represents a small circle (fig. 4) and then draws a line passing through the environment and the point of origin. This line is called the AEC. It is based on the AEC and represents the Y-coordinate and contains two arrows that indicate the greatest effect of interference (GE) and the low stability by moving away from the point of origin. On this basis, the

Table 4 : The behavior of inbreed lines in different environments according to the individual plant yield of the grains.

9	8	7	6	5	4	3	2	1	Environments
6G	6G	8G	8G	8G	8G	8G	8G	8G	Inbreed lines
4G	8G	4G	6G	4G	6G	6G	3G	6G	
1G	3G	6G	4G	6G	5G	4G	6G	G4	
8G	1G	1G	1G	3G	4G	2G	1G	3G	
7G	4G	3G	3G	5G	1G	3G	4G	5G	
5G	7G	5G	5G	1G	3G	5G	5G	1G	
3G	5G	2G	7G	7G	7G	7G	2G	2G	
2G	2G	7G	2G	2G	2G	1G	7G	7G	

structures that have the shortest vector (PC2 lowest values) are the most stable and include G4 and G5 The most heterogeneous structures are G7 and G1 (fig. 3). The composition G4 cannot be adopted for election despite its high stability due to the decrease occurring.

The results in fig. 5 showed the nature of the relationship between the studied structures. The length of the vector between the site of the genotype and the origin point shows how the specific genotype differs from the general average, so the composition with the longest vector is either better or worse in one or more environments and table 3. Either structures near the origin point are close to the general average. Consequently, the G5 and G7 are the top two, while the lowest G4 is obtained. That's the corner of the corner.

A vector of any two genotypes measures the degree of similarity to the interference response. Therefore, the performance of the G1 and G2 inbreed line are similar, while the G4 and G5 compositions are very different. The ideal structure should be characterized by high reliability and good stability in all studied environments with a value of G.E. (fig. 5), so the G5 is an ideal combination, either the G4 is the farthest from the ideal. Getting the ideal structure is very difficult because of the complexity of the work of the genes and the difficulty of collecting and interacting with the environment, so it may not exist in fact, it can be used as a test to evaluate the rest of the structures, so researchers seek to find the desirable structure, to the ideal structure (near the center of the circle). Fig. 5 shows that G3 and G7 are desirable structures. Based on the above, the ideal structure can be defined as the structure that has the least deviation from its average during the studied environments and the largest deviation from the general average.

The analysis of genetic-environmental interference can determine the patterns and causes of the interference and this leads to the characterization of the characteristic composition and environmental factors that can help in the effective evaluation of the studied structures. An efficient assessment of adaptive genotypes for local conditions and analysis of their interactions with the environment is necessary to cope with climate change on our planet (fig. 6).

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