Study of genetic stability for genotypes promising of maize (*Zea mays* L.)

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Abstract

The study included 10 genotypes of maize (*Zea mays* L.) (1- AGN 720, 2- Jameson, 3- Reserave, 4- Konsens, 5- 215479, 6- 215475, 7- 215480, 8- 215481, 9 -215482, 10- 215472), which were sourced from Debbane for Modern Agriculture Ltd, which was planted during the fall agricultural season of the year (2023-2024), in two sites, the first in Nineveh Governorate (Talkef), and the second in Erbil Governorate (Shaqlawa) according to Randomized Complete Block Design (RCBD) with three replications and three dates, to determine the best date and genotype suitable for growth and environmental stability within the conditions of the Nineveh and Erbil sites. The results of the variance table showed that the mean of genetic compositions, environments, and the linear component of environments were significant for the trait of the the number of ears per plant, while the genetic composition (215472) excelled in the linear component of the interaction of environments at the 1% level for most genetic traits. The results of stability exceeded that the genotypes (Reserave, 215482, 215472) were highly stable for all traits.

Keywords: maize, genotypes, genetic stability

Introduction

The maize (*Zea mays* L.) is one of the important grain crops that belongs to the Poaceae family and ranks third after wheat and rice in terms of area and production **[12]**. It is one of the important crops and has multiple uses for all its vegetative and fruitful parts, as its vegetative parts are used as fodder for animals, while the seeds are used for food and are used as concentrated feed for animals, because they contain (81%) carbohydrates, (10.6%) protein, (4.6%) oil, and (2%) ash, in addition to containing other minerals such as sodium, potassium, and phosphorus. Its seeds also contain vitamins B1, B2, and E, its stems are used in making paper, and oils and starch are extracted from its seeds **[4]**. Selecting crops with high yields requires knowledge of the nature and variation in genetic origins **[2]**

To ensure the development of highly productive genotypes, the introduction method is one of the official sources for the continued renewal of the breeding material, this method has been adopted in all countries of the world to create new genotypes containing genes for high yield and important qualitative traits. In order to develop an integrated program for breeding and developing new genotypes, it is necessary to estimate some genetic indicators, including the stability of genotypes within several environments, as these parameters are evidence for plant breeders in developing the new variety. There are many studies that have achieved results in the genetic stability of maize crops, including: **[13]** indicated when they studied 13 genotypes of maize plants that they were significant for the traits of the number of days to 50% tasseling the number of seeds per row, the weight of

300 seeds, and individual plant yield. **[11]** found, in their study of maize, to evaluate 108 genotypes that were significant within all environments in the grain yield trait of the individual plant. **[6]** when studying maize obtained two genotypes (SH × ZP105) and (IK58 × ZP105), which were distinguished by their stability in the traits of the number of days to 50% tasseling, the number of days to 50% silking, ear length, number of ear rows, and number of ear seeds and the weight of 300 seeds, which resulted in significant regression coefficients for the individual plant yield on the above traits. **[14]** found, during their study of maize genotypes, that the KSC705 genotype had the highest stability for the individual plant yield trait. **[7]** indicated when they studied several genotypes of maize plants that they were significant for the traits of the number of days to 50% tasseling the number of days to 50% silking, ear length, number of ear rows, number of ear seeds, the weight of 300 seeds and individual plant yield **[1]** showed, when he studied several genotypes for the maize crop, that they were significant for the yield trait of the individual plant. **[3]** found that genotype (215479) was highly stable for the ear length trait, followed by genotypes AGN720, Jameson, and 215480 for the traits of individual plant yield and ear length, respectively. The current study aims to evaluate the performance of 10 new genotypes of maize under three planting dates to test the stability of the genotypes, under varying environmental conditions.

Material and methods

The factorial field experiment was carried out in fall season (2023-2024) in two environmentally distinct sites, the first in Nineveh Governorate (Talkef), in the fields of a farmer and the second in Erbil Governorate (Shaqlawa). The first factor included the cultivation of 10 genotypes of maize (*Zea mays* L.) as shown in Table (1) and the second factor is three planting dates (1/7, 5/7, and 10/7/2023) using Randomized Complete Block Design (RCBD) for three replications, where planting was done by placing (2-3) seeds in each hole and the distance between one hole and another was (25 cm). The planted plants were thinned, leaving one plant in each hole. The planted plants were irrigated during the season on a regular basis for both sites. We added the DAP fertilizer, DAP, which is an abbreviation for (Diammonium Phosphate), which is a source of concentrated phosphorous. Urea fertilizer was used, which contains (46%) nitrogen, at an average of 100 g for each cultivar (50 g for each row) for both locations for two types of fertilizer

The necessary processes for plant germination and growth were carried out under different environmental conditions. Harvesting took place at Erbil and Mosul sites on 5/11/2023 and 10/11/2023, respectively. The studied traits were: the number of days to 50% tasseling, the number of days to 50% silking, the number of ears per plant,the ear length (cm), the number of rows per ear, the number of seeds per row, the number of seeds per ear, the weight of 300 seeds (g), individual plant yield (g/plant). The data obtained from the studied traits were analyzed according to Randomized Complete Block Design (RCBD) with three replications, and the ready-to-use statistical software SAS, SPSS, and Microsoft Excel 2010 were used to conduct statistical operations. The stability of the genotypes was tested in the different environments adopted in the study using:

Eberhart and Russel method

The above method was based on the linear regression model proposed by **[10]** according to the following equation.

$$y_{ij} = \mu + b_i\ I_j + \sigma_{ij} + e_{ij} \begin{cases} i=1,2\ldots\ldots\ \ldots t \\ j=1,2\ldots\ldots\ \ldots\ldots s \end{cases}$$

Since:

Yij = mean genotype i in environment j

μ = mean of all genotypes in all environments

b_i = The regression coefficient of the genotype i on the environmental index that measures the response of the genotype to environmental changes.

I_j= environmental index, which is defined as the deviation of the mean of all genotypes in a particular environment from the general mean.

σ_{ij}= deviation from regression for genotype i at environment j

e_{ij} = mean experimental error

Two stability parameters were estimated according to what was stated in **[15]**, which are:

1- Regression coefficient: It is the regression behavior of each genotype in different environments, according to the following equation:

$$bi = \sum y_{ij}\ I_j / \sum I_j^2$$

Note that:

$\sum y_{ij}\ I_j$ = sum of the products.

$\sum I_j^2$= sum of squares.

2- The mean deviation from the linear regression (S^2 di), which is:

$$\left\{\frac{\sum \delta ij^2}{S-2}\right\} - Se^2/r$$

whereas:

(S^2) = Estimate of the clustered error.

The significance of regression coefficients below zero for each trait was tested by calculating the value of the standard error of the regression coefficient, as the linear regression coefficient between each trait of the genotype in each environment and the quotient and behavior of each trait to the environment mean is expressed as a measure of the linear response to environmental changes, and the mean variance of the regression (S^2 di) represents a measure of heterogeneity, and the stability can be judged from the parameters as follows:

1- If the regression coefficient = 1 and the deviation from the regression = zero, the sample is highly stable.
2- If the regression coefficient is > 1 and the deviation from the regression = zero, the variety thrives in good environments.
3- If the regression coefficient is < 1 and the deviation from the regression = zero, then the varieties grow in unsuitable environments as well
4- If the deviation from the regression is > zero, then the prediction of the variety is weak due to its stability.

Table (1) Names and sources of maize genotypes and their numbers used in the study

No.	Name	Source
1	AGN 720	American Genetics
2	Jameson	American Genetics
3	Reserave	American Genetics
4	Konsens	Syngenta
5	215479	KWS
6	215475	American Genetics
7	215480	American Genetics
8	215481	American Genetics
9	215482	American Genetics
10	215472	American Genetics

Results and Discussion

Table (2) shows the results of the analysis of variance for stability according to the method (Eberhert and Russel Model, 1966) for the studied traits. It is noted that the mean squares of the genotypes were significant at 1% for the traits: number of days to 50% tasseling the number of ears per plant, ear length, and number of seeds per row. While the mean squares for the environments were significant at 5% for the two traits: the number of days to 50% silking, and the number of ears per plant,. It is clear that the mean squares of the environments (linear) were significant at 1% for the three traits: the number of days to 50% silking, and the number of ears per plant, and the number of rows per ear, while they were significant at 5% for the trait number of days to 50% tasseling This indicates that the response to different environments is under genetic control (**[5]**; **[8]**), and the mean square of the linear component of the interaction of environments x genotypes was significant at 1% when tested against the clustering deviation for the trait: number of days to 50% tasseling was significant at 1% for most of the genotypes, except for genotypes (AGN 720 and 215479), and for the trait for the number of days to 50% silking, it was significant at 1% for most of the traits except for the two genotypes Konsens and 215472, it was significant at 5%. While the trait for the number of ears per plant, was significant for the genotypes (Jameson, Reserave, 215480, 215472) were significant at 1% and at 5% for the two genotypes (AGN 720) and (215482). It was noted that the rest of the yield traits were significant at 1% for most of the genotypes, with the exception of the number of seeds per row, which was significant at 5% for the genotype (Jameson). We conclude from the above that the genotype (215472) was significant at the 1% level for most genetic traits, and the significance of the means of squares for the genotypes and the aforementioned traits indicates the significance of the deviation on the regression from zero for these genotypes and traits .

Table (2) Analysis of variance for stability according to (Eberhert and Russel Model) method

Differences	df	Mean squares number of days to 50% tasseling	the number of days to 50% silking	the number of ears per plant	Length of the ear
Genotypes	9	4.175**	8.408 N. S	0.078**	12.240**
Environments	5	1.123 N. S	2.338 *	0.064*	0.518 N. S
Genotypes x environments	45	1.109 N. S	0.995 N. S	0.028 N. S	1.149 N. S
Environments + genotypes + environments	50	1.110 N. S	1.130 N. S	0.031 N. S	1.086 N. S
Environments (Linear)	1	5.617*	11.689**	0.320**	2.591 N. S
Environments x Genotypes (Linear)	9	1.957*	1.527 N. S	0.021 N. S	0.931 N. S
Aggregate deviation	40	0.807 N. S	0.776 N. S	0.026 N. S	1.083 N. S
AGN 720	4	2.833 N. S	1.111 N. S	0.139*	3.026*
Jameson	4	4.759**	2.000 N. S	0.202**	5.882**
Reserave	4	4.611**	6.148**	0.264 **	6.128**
Konsens	4	3.926**	3.481*	0.093 N. S	3.053**
215479	4	2.444 N. S	1.111 N. S	0.095 N. S	8.750**
215475	4	5.648**	16.815**	0.059 N. S	5.428**
215480	4	10.222**	1.259 N. S	0.299**	6.413**
215481	4	4.593**	10.981**	0.093 N. S	6.750**
215482	4	11.259**	10.315**	0.142*	3.881**
215472	4	5.204**	3.259*	0.175**	4.983**
Experimental error	108	2.396	2.548	0.117	2.107**

*Significant at the probability level (5%).

** Significant at the probability level (1%).

Appendix to Table (2)

Differences	df	Mean squares				
		the number of rows per ear	Number of seeds in the row	Number of seeds per ear	Weight of 300 seeds	Individual plant yield
Genotypes	9	0.126 N. S	8.599**	1,096.197 N. S	72.596 N. S	210.320 N. S
Environments	5	0.714 N. S	4.175 N. S	1,474.464 N. S	55.742 N. S	629.894 N. S
Genotypes x environments	45	0.528 N. S	4.122 N. S	1,865.195 N. S	47.249 N. S	448.071 N. S
Environments + genotypes + environments	50	0.546 N. S	4.128 N. S	1,826.122 N. S	48.099 N. S	466.254 N. S
Environments (Linear)	1	3.572**	20.874*	7,372.322*	278.711*	3,149.468*
Environments x Genotypes (Linear)	9	0.470 N. S	6.424 N. S	1,954.728 N. S	36.166 N. S	177.561 N. S
Aggregate deviation	40	0.488 N. S	3.192 N. S	1,658.530 N. S	45.018 N. S	464.129 N. S
AGN 720	4	2.734**	23.251**	11,247.047**	239.704**	1,977.719**
Jameson	4	1.286 **	14.187*	5,180.366**	568.759**	1,354.806**
Reserave	4	2.208 **	23.571**	9,819.387**	150.167**	2,719.639**
Konsens	4	2.860**	18.196**	8,288.832**	484.370**	1,708.859**
215479	4	4.651**	26.526**	14,908.353**	167.111**	4,771.013**
215475	4	3.442**	19.477**	8,760.820**	40.093 N. S	1,500.187**
215480	4	4.145**	17.410**	7,736.885**	359.500**	3,455.517**
215481	4	1.465**	19.539**	7,158.150**	132.611**	2,046.246**
215482	4	2.836 **	23.691**	8,577.001**	106.222**	2,794.673**
215472	4	1.688**	20.533**	9,629.249**	156.389**	984.024**
Experimental error	108	0.820	10.478	2,708.209	56.825	276.575

*Significant at the probability level (5%).

** Significant at the probability level (1%).

[10] pointed out that the values of the regression coefficient (Bi), the deviation from the regression, and the means of the genotypes and the traits under study are all important in judging the stability of the genotypes. When the regression coefficient is close to one (not significant) and is associated with a deviation from the regression equal to zero (not significant), this indicates that the genotypes are highly responsive to environmental changes and highly stable. If the regression coefficient

is greater than one (significantly positive) and the deviation from the regression is not significant, then the genotypes are sensitive to environmental changes and adapt in highly productive (good) environments, but when the regression coefficient is less than one (significantly negative) and the deviation from the regression is not significant, then the genotype is considered responsive to environments that are not good **[9]**. Finally, if the deviation from the regression is significant, it weakens the prediction of the stability of the genotypes. The linear regression coefficient for the rate of any of the traits under study for the genotypes on the mean of all the genotypes in each environment resulted in values of regression coefficients that ranged between (-1.968) and (3.541) for the trait: number of days to 50% tasseling, and for the trait: the number of days to 50% silking, ranged between (-0.095) and (2.956), while the values of the number of ears per plant, ranged from (-0.944) to (1.972), and the trait of the length of the ear ranged from (-1.338) to (3.744). The values of the trait of the number of rows per ear, in the ear ranged between (-0.943) and (2.641), and the trait of the number of seeds per row, ranged from (-1.469) to (3.305), while the traits of the number of seeds per ear, ranged between (-1.986) and (2.635), and for the 300-seed weight trait, it ranged between (-1.100) and (2.759), and for the individual plant yield trait, it ranged between (0.178) and (2.647). It is clear from Table (3), as it is noted that the trait of number of days to 50% tasseling is that the regression coefficient for the genotypes (AGN 720, Reserave, 215479, 215480, 215482, 215472), significantly positive (greater than one). furthermore, the deviation from the regression for it was not significant, as it is distinguished by its performance in appropriate environmental conditions, and the regression coefficient for the genotypes (Jameson, Konsens, 215475, 215481) was negative, while the deviation from its regression was not significant, as the genotype is responsive to bad environments, and for the trait of the number of days to 50% silking, the regression coefficient for the two genotypes (AGN 720, 215479) was negative, and since the deviation from its slope is not significant, they are characterized by responding to bad environments, while the regression coefficient for the genotypes (Jameson, Reserave, Konsens, 215480) was insignificant (close to one) and the deviation from its regression was not significant, thus the genotype is highly stable to environmental changes, while the genotypes (215475, 215481, 215482, 215472) had a significantly positive regression coefficient (greater than one), furthermore, the deviation from the regression was not significant, and this indicates that the genotypes adapt to good environments. It is noted from the trait of the the number of ears per plant, is that the regression coefficient for the genotypes (AGN 720, Jameson, Reserave, 215479, 215480) is significantly positive. furthermore, the deviation from its regression is not significant, and this indicates that the genotypes adapt to good environments, while the regression coefficient for the genotypes (Konsens, 215475, 215481, 215482) was not significant (close to one), and the deviation from its regression is not significant, and thus the genotype is highly stable to environmental changes, while the genotype (215472) is significantly negative and the deviation from its regression is not significant, thus the genotype is responsive to bad environments. The trait of the ear length shows that the regression coefficient for the genotypes (AGN 720, Reserave, 215475, 215472) is significantly positive, and furthermore, the deviation from its regression is not significant, and this indicates that the genotypes adapt to good environments, while the genotypes (Jameson, Konsens, 215479, 215480, 215482) were significantly negative, while the deviation from their regression was not significant, so the genotype is responsive to poor environments, while the genotype (215481) for this trait is unique in that its regression coefficient is not significant (close to one) and the deviation from its regression is not significant, thus the genotype is highly stable to environmental changes. As for the number of rows per ear, in the stem, the regression coefficient for the genotypes (Reserave, 215479, 215475, 215480, 215481, 215482, 215472) was significantly positive (greater than one). furthermore, the deviation from its regression was not significant, and this indicates that the genotypes adapt to good environments. While the two genotypes (Jameson, Konsens) were significantly negative, while the deviation from their regression was insignificant, as the genotype is responsive to bad environments. While the genotype (AGN 720) is not significant (close to one) and the deviation from its regression is not significant, thus the genotype is highly stable to environmental changes. The characteristic of the number of seeds per row, is that its regression coefficient for the genotypes (215479, 215475, 215480, 215481, 215482, 215472) is significantly positive (greater than one), furthermore, the deviation from its regression is not significant, and this indicates that the genotypes adapt to good environments. The regression coefficient of the genotypes (AGN 720, Jameson, Reserave, Konsens) is significantly negative, while the deviation from their regression is not significant, as the genotype is responsive to bad environments. It is noted that the trait of the number of seeds per ear, is that the deviation from its regression for the genotypes (AGN 720, Reserave, Konsens, 215479, 215475, 215480) is significant (greater than one), thus weakening the prediction of the stability of the genotypes, while the regression coefficient for the two genotypes (215481, 215482) was significantly positive (greater than one), and furthermore, the deviation from its regression is not significant, and this indicates that the genotypes adapt to good environments, while the genotype (Jameson) is uniquely significantly negative, and since the deviation from its regression is not significant, it is characterized by responding to not good environments, and for the trait: weight of 300 seeds, the regression coefficient for the genotypes (Jameson, Reserave, Konsens, 215481, 215472) is significantly positive (greater than one). furthermore, the deviation from its regression is not significant, and this indicates that the genotypes adapt to good environments. While the regression coefficient for the genotypes (AGN 720, 215479, 215475) is not significant (close to one), and the deviation from its regression is not significant, thus the genotype is highly stable to environmental changes, and the two genotypes (215480, 215482) had a negative significance. Since the deviation from its slope is not significant, it is characterized by the response to bad environments, and for the individual plant yield trait, the regression coefficient for the genotypes (AGN 720, Reserave, 215479, 215481, 215472) is significantly positive (greater than one). In contrast, the deviation from its regression is not significant, and this indicates that the genotypes adapt to good environments, while the regression coefficient for the genotypes (Jameson, Konsens, 215480, 215475, 215482) was not significant (close to one) and the deviation from its regression was not significant, and thus the genotype is highly stable to environmental changes. We conclude from the results of Table (3) that the genotypes (Reserave, 215482, 215472) were highly stable for all traits, followed by the two genotypes (Jameson, 215480, Konsens, 215481) which were highly stable for 8 traits except for one trait for each of the two genotypes (the number of days to 50% silking, the number of ears per plant, respectively. These results make it possible to benefit from highly stable genotypes in future hybrid breeding programs to find new genotypes that are characterized by good production and quality traits and are stable over a wide range of environmental changes. This is in line with what was mentioned by **[3]**, **[7]** and **[1]**

Table (3) The parameters and mean for nine traits of the maize

No.	Genotypes	number of days to 50% tasseling			the number of days to 50% silking			the number of ears per plant		
		Mean	Bi	S^2di	Mean	Bi	S^2di	Mean	Bi	S^2di
1	AGN 720	54.500	1.949	-0.623	57.667	-0.095	-0.574	1.756	1.333	-0.018
2	Jameson	53.389	-0.564	0.347	55.667	0.970	-0.624	1.633	1.667	-0.011
3	Reserave	54.833	1.869	-0.137	57.889	0.105	0.684	1.767	1.972	-0.004
4	Konsens	53.111	-0.257	0.174	55.222	0.086	0.019	1.656	0.944	-0.023
5	215479	54.667	1.424	-0.472	58.333	-0.067	-0.573	1.911	1.528	-0.034
6	215475	52.722	-1.968	0.069	56.111	2.956	0.800	1.711	0.611	-0.027
7	215480	54.333	3.541	-0.004	58.444	0.143	-0.541	1.978	1.361	0.021
8	215481	53.222	-1.108	0.177	56.722	2.338	0.298	1.678	0.778	-0.021
9	215482	55.111	3.244	0.538	58.056	2.101	0.440	1.867	0.750	-0.008
10	215472	53.611	1.869	0.012	56.222	1.464	-0.661	1.778	-0.944	-0.002
	SE(b)		1.198			0.815			0.906	

Appendix to Table (3)

No.	Genotypes	Length of the ear			the number of rows per ear			the number of seeds per row		
		Mean	Bi	S^2di	Mean	Bi	S^2di	Mean	Bi	S^2di
1	AGN 720	25.856	2.064	-0.222	14.039	0.029	0.410	37.484	-0.070	2.317
2	Jameson	22.967	-0.308	0.762	13.918	-0.545	0.022	34.524	-1.469	-1.071
3	Reserave	25.611	2.987	0.252	13.866	1.396	0.105	36.747	-0.599	2.213
4	Konsens	23.656	-0.632	0.035	13.921	-0.943	0.362	35.321	-1.427	-0.006
5	215479	25.878	-0.420	1.474	14.201	2.641	0.266	37.343	2.872	-1.165
6	215475	22.956	3.744	-0.253	13.928	1.626	0.351	34.658	1.718	-0.164
7	215480	25.478	-0.316	0.894	13.880	1.301	0.612	37.234	2.288	-1.873
8	215481	22.522	0.753	0.949	14.308	1.076	-0.011	35.010	1.503	0.214
9	215482	25.444	-1.338	0.152	14.040	2.150	0.023	36.942	3.305	-3.268
10	215472	22.928	3.468	-0.235	14.043	1.269	0.005	35.272	1.879	-0.202
	SE(b)		2.045			1.169			1.237	

Appendix to Table (3)

No.	Genotypes	Number of seeds per ear			Weight of 300 seeds			Individual plant yield		
		Mean	Bi	S^2di	Mean	Bi	S^2di	Mean	Bi	S^2di
1	AGN 720	513.367	-0.709	1,816.417	113.111	0.715	37.420	185.456	1.329	263.070
2	Jameson	487.546	-1.986	-334.384	119.389	1.741	102.130	192.311	0.585	219.564
3	Reserave	511.000	-0.467	1,511.870	112.500	1.908	-6.776	186.944	1.473	416.827
4	Konsens	493.534	0.137	1,166.000	117.444	2.759	49.122	196.689	0.178	332.529
5	215479	525.844	2.420	1,745.149	109.333	0.470	21.297	187.600	2.647	548.948
6	215475	487.047	2.409	217.631	115.722	0.727	-12.599	197.667	0.261	277.502
7	215480	509.894	1.870	386.889	112.167	-0.312	70.255	187.356	0.655	737.888
8	215481	503.178	2.213	-15.584	116.833	1.699	-5.914	196.844	1.264	293.611
9	215482	512.489	2.635	-38.208	110.000	-1.100	-0.816	184.367	0.374	595.464
10	215472	487.811	1.478	1,102.161	117.833	1.393	6.644	200.489	1.234	33.974
	SE(b)		1.500			1.271			1.214	

References

[1]Abd El-Latif, M. S Y. A. Galal, M. S. Kotp, W. M. El Sayed, H. A., Aboyousef & M. M. B. Darwich (2023). Yield stability and relationships among parameters in maize. *African Crop Science Journal*, *31*(1), 75-84

[2]Al-Badrani, Qusay Amer Youssef (2020). Study of union ability, genetic action, and hybrid vigor in individual crosses of maize (*Zea mays* L.), Master's thesis, College of Agriculture and Forestry, University of Mosul.

[3]Al-Najmawi, D. A. R. F., M. S. Al-Taweel, Z. Alhabbar, K. M. D., Al-Zubaidy & H. A. M. Issa . (2023). Genetic Stability for New Genotypes of Maize (*Zea mays* L.) under Different Fertilizer Combinations. In *IOP Conference Series: Earth and Environmental Science* (Vol. 1213, No. 1, p. 012021). IOP Publishing

[4]Al-Nasrawi, Abdul Karim Hussein Rumi (2015). Response Evaluation of The Genotypes of Maize (*Zea mays* L.), PhD thesis, College of Education for Pure Sciences, University of Karbala.

[5]Al-Rawi, K.M.,Z. Abdulyas and J.Poles (1983). Regression analysis of genotype- environment interaction in cotton (*Gossypium hirsutum* L.).J.Agric. and Water Resource Res.. 2: 85-93.

[6]Al-saddi, K. A. A., & W. M. H, Al-Rawi (2021). Phenotypic and phylogenetic behavior of some strains of maize (Zea mays L.) using partial diallel cross. *Journal of Education and Scientific Studies*, *3*(17). 43-62

[7]Chaurasia, N. K., R. B. P. Nirala, B. Singh, J. P., Prasad, R. K. Roy, &, D. Thakur (2023). Assessment of stability parameters for multiple traits in newly developed single cross hybrids of maize (*Zea mays* l.). *JAPS: Journal of Animal & Plant Sciences*, *33*(4). 936-948

[8]Dawod, Khalid Mohammed (2008). Genetic stability in some cotton cultivars (*Gossypium hirsutum* L.). Fourth Agricultural Scientific Conference, Tikrit University April 29-30.

[9]Dawod, Khalid Mohammed and Abdel Sattar Ahmed Mohamed (2000). Combining ability analysis for some quantitative traits in maize. Mesopotamia Journal of Agriculture, 32(1): 107-113.

[10]Eberhart, S. A. and W. A. Russell. (1966). Stability parameters for comparing varieties. crop sci 6: 36-40.

[11]Eze, C. E., R. O. Akinwale, S. Michel, & H. Bürstmayr (2020). Grain yield and stability of tropical maize hybrids developed from elite cultivars in contrasting environments under a rainforest agro-ecology. *Euphytica*, *216*(6), 1-13.

[12]Kazar, Walaa Abdul Amir Ibrahim (2022). Responses of maize to combinations of organic fertilizer and Nano potassium spray, Master's thesis, College of Agriculture, University of Karbala.

[13]Patil, S. N., Duppe, M. V., & R. M. Bachkar (2020). Stability analysis in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, *11*(02), 382-385.

[14]Seyed Habib Shojaei, Khodadad Mostafavi, Ali Omrani, Saeed Omrani, Seyed Mohammad Nasir Mousavi, ´Arpad Illes, Csaba Bojtor, And Janos Nagy,(2021). yield stability analysis of maize (*Zea mays* l.) hybrids using parametric and ammi methods, hindawi scientifica volume, article id 5576691, 9 pages.

[15]Singh, R. k. And B. D. Chaudhary (2007). Biometrical methods in quantitative genetic analysis Kalyani pubishers, new delhi. Ludhiana. pp: 102 – 127.