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Evaluation of Some Corn Genotypes as a Second Crop by Trait (GT) Biplot Method

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IT is extremely important to grow more than one product in a production season to obtain the maximum income per unit area. Maize is one of the most suitable crops for the second product. This research was carried out in Tilkitepe village of Artuklu district of Mardin province in the 2021 growing season to determine the second crop conditions in the borders of Mardin province using hybrid cultivars with different characteristics. The study was conducted according to a randomised block design with three replications. The data obtained from the traits investigated in this study were subjected to an analysis of variance and interpreted using the GT biplot technique. Significant differences at the 1% level ($p<0.01$) were found between the genotypes in terms of the traits studied, except for the protein ratio. In the results of the study; plant height (PH) varied between 209-254 cm, height of first ear (HFC) between 59.4-87.7 cm, ear length (CL) between 17.7-21.7 cm, number of rows on ear (NRC) between 39.2-43.8 pieces, 100 grain weight (100 GW) between 30. 3-43.5 g, cob weight (CW) between 186-254 g, number of grains on the cob (NGC) between 584-696 pieces, hectolitre weight (HW) between 75.1-82.2 kg/hl, protein ratio (PR) 6.6-9.5%, grain yield (GY) between 9629-13220 kg/ha. According to the results and biplot graphs, Dekalb-6050(G39) was the most suitable genotype among the genotypes based on grain yield and traits as a second crop. As a result, this variation showed that the maize cultivar had good results as a second crop under the Mardin condition. Therefore, the Dekalb-6050(G39) genotype can be recommended for cultivation as a second crop in the following years under Mardin conditions.

Keywords: Corn, Hybrid, Trait, GT, Turkey.

Introduction

Corn (Zea mays L.) is an important plant used in human and animal nutrition and cultivated in large areas. It is an important hot climate fodder plant that produces more dry matter per unit area than other species, is easily harvested and is loved by animals. It is considered as a green and silage plant. Corn plant is grown as the main or secondary crop. In the planting, which is planned as a second crop in agricultural production, the front plant is requested to leave the field in a short time. Approximately 73% of the corn produced in the world is used for animal feeding (Öztürk and Orak, 2020).

Corn is one of the leading forage crops with high yield potential, which is considered as harvest and silage in many regions of Turkey. It is possible to say that the environmental conditions of many regions in Turkey are suitable for corn plant as a second product in terms of grain product cultivation. Corn cultivation area in Turkey has increased rapidly in recent years. In 2018, 23,412,979 tons were produced from the 472,643 ha corn silage area (Anonymous, 2018). The Southeastern Anatolia Region of Turkey is a region where second crop corn is grown in large areas, since the vegetation period is quite long, the autumn rains come late and it is a dry region, and it has extremely favorable environmental conditions for the cultivation of second crop corn for grain purposes.

Corn is the most suitable plant to increase the yield per unit area among the cereals consumed daily. Since corn is an extremely suitable plant for animal feed and human food (Abdel Settar et al., 2024, Abdelrazek et al., 2025), newly bred varieties are registered and presented to the market every year (Doğan et al., 2020). There are many factors affecting yield and quality in grain corn production.

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Geographical conditions (temperature, photoperiod and exposure time, drought), cultural processes (planting time, harvest period, plant density and irrigation conditions), genetic characteristics of the variety are the factors that determine yield and quality (Doğan et al., 2015).

In order to grow plants as a second crop, some factors such as environmental conditions, especially low rainfall during the harvest period, long vegetation period, and early corn varieties are very important. In regions that do not have these environmental conditions, corn for grain purposes cannot be grown in the second product, but it can be grown as silage.

Different statistical models are used to determine the most suitable genotypes in terms of traits studied in a region. The aim is to reveal the genotype trait relationship. GT technique is one of the analyzes that best reveals these relationships with different visuals (Kendal, 2019). The GT biplot technique has been used by many researchers to visualize the relationships between genotypes and traits in different plants. Breeding programs have made effective selections based on the interaction between genotypes and traits. Thus, it is important to identify the relationships between genotypes and trait profiles (Aktaş, 2020).

The primary objective of breeders is to define varieties that can produce favorable results under various environmental conditions. Therefore, this study aimed to use a GT biplot to identify the traits associated with grain yield in corn and to classify cultivars based on high yield, quality, and agronomic traits as a second crop.

Materials and Methods

Materials

Ten corn genotypes (cultivars and hybrids) were evaluated in Tilkitepe village of Artuklu district of Mardin province in the 2021 growing season. The information on the genotypes is given in Table 1, the climatic data are given in Table 2 and the physical and chemical characteristics of the soil in the trial area are given in Table 3. The trials were established in Tilkitepe village of Mardin province, during the second crop corn growing season in 2021.

Methods

The studies were set up as three replications according to the Random Blocks Experimental Design. It consisted of 30 plots in total, with 10 plots in each block of the experiment. The seedbed was sown by hand at a depth of 4-5 cm in the seed bed, which was prepared with 6 rows in each plot, 70 cm between rows, 5 m row length and 20 cm row spacing. The plot area is planned as 5 m x 3.5 m = 17.5 m2.

After the wheat, which is the pre-plant for trial planting, was harvested (June), the trial area was irrigated and the pan was brought, and then deep plowing was made. Then, the soil preparation was made by drawing a disc harrow and a milling cutter. Sowing, after the soil was ready, 150 kg/ha P2O5 (42% TSP) was mixed with the soil before planting. Nitrogen fertilizer was applied at 200 kg/ha (33% AN), half of which was applied at planting time, and the remaining part was applied during the stemming period (40 cm).

After the rows were opened with a tractor, hand sowing was done on 17 June 2021. Plant maintenance procedures; considering the development status of the plant, irrigation was done 6 times with the drip irrigation system. Weed treatment was done by hoeing method and no chemical control was applied. The harvest date was done in 22-30 November 2021. In order to make sampling in the parcels with a moisture content of 20% in the cobs of the plants that have reached the harvest maturity, 10 plants representing the parcels were taken from each parcel and the plant characteristics were examined by sampling.

Data analysis

Variance analysis of the data obtained from the study was performed (ANOVAs) by using JMP5, Significance ($p < 0.05$, $p < 0.01$) levels were determined by ANOVA and differences between means were determined by LSD testing. On the other hand, the data of ten corn genotypes in trial analyzed by GT biplot method, as recommended by Yan and Thinker (2005). The biplot method was implemented to examine all scored traits of the genotypes with the aid of Genstat 14 launch software program. The information have been interpreted the use of GGE biplot software program. Figure 1 depicts the performance of every genotype for each trait, Figure 2 indicates the sector and group of each genotype and trait, Figure 3 illustrates the stability of genotypes based on traits, and Figure 4 distinguishes the best genotypes based on ideal center and traits.

TABLE 1. The code, name, origin, of corn genotypes

Code	Name of cultivar and pedigree of hybrids	Company
G1	P0900	Pioner
G2	May	Capuzi
G3	DKC6050	Dekalb
G4	SY Prosperic	Sygenta sy prosperic
G5	LG 30.500	Helen
G6	DKC6664	Dekalb
G7	P0937	Pioner
G8	KWS	Kefrancos
G9	Mumtez	Rayal-Mumtez
G10	DS2024	Hektas

TABLE 2. Long-term temperature, precipitation and humidity values of Mardin province (1960-2021) and growing season(2021)

	Temperatures (°C)		Precipitation (mm)		Humidity (%)	
Montly	2021	Long Term	2021	Long Term	2021	Long T.
June	28.3	228.3	0.0	2.7	20.7	223.9
July	33.3	332.5	0.5	0.9	19.5	220.0
August	31.8	330.9	0.0	00.2	25.3	227.4
Seotember	25.2	426.6	0.0	1.3	33.0	228.5
October	20.8	821.0	2.4	21.5	31.2	334.2
Novomber	15.2	113.6	4.1	28.5	42.6	447.0
December	8.5	88.7	25.7	333.0	49.7	661.2
Total			32.7	559.6		
Average	23.3	23.1			31.7	334.6

TABLE 3. Some physical and chemical properties of trial area soils

Depth (cm)	Clay (%)	Plate (%)	Hair (%)	Texture Sınıfı	pH (1:2.5 su)	Loam (%)	Phosphorus (ppm)	Potassium (me/100g)	Organic matter (%)	Salt (%)
0-20	25.5	3.3	36.8	clay-loamy	7.85	15.9	6.53	2.54	1.67	0.018
0-40	28.7	3.1	38.9	clay-loamy	8.37	13.8	4.35	1.25	1.52	0.020

Results and Discussion:

Plant height (PH cm)

Analysis of variance revealed that PH was significantly influenced by genotype (P<0.01). The plant height of the genotypes varied between 209-254 cm and the highest plant height was obtained from Mumtez (G10) variety with 254 cm, and the lowest plant height was obtained from LG 30.500 (G5) variety with 209 cm (Table 5). Zaim, (2020) reported that while the highest plant height value was reported as 205.7 cm in Pioneer P2088 variety, the lowest plant height was determined as 186.3 cm in May Capuzi variety. The data we obtained from this study are similar to the results of the previous study. Kebede and Gebissa, (2020), reported that the plant 117-170 cm was changed. Hassan et al., (2018) reported that PH values varied between 158.9 and 203.8 cm in maize cultivars, which is a genetically inherited trait.On the other hand, the results of this study are consistent with the findings of Umakanth et al., (2000), who reported similar results regarding genetic differences in plant height in maize genotypes. The varyans analysis data of 10 corn genotypes are showing in Table 4, the mean data of tarits of 10 corn genotypes are showing in Table 5.

In the study, significant differences at the level of 1% (p<0.01) were found between the genotypes in terms of the examined traits, except for the protein ratio (Table 4).

TABLE 4. The results of varyans analysis (mean of squares)

Source	DF	PH	HFC	CL	NRC	100 GW	CW	NGC	HW	PR	GY
Genotype	9	706.2**	278.0**	4.4**	8.2**	48.9**	1596.4**	7640.5**	16.1**	1.9ns	4854333**
Rep.	2	211.40	91.53	1.06	1.55	12.65	12.46	3237.10	1.36	0.43	356833
Error	18	73.64	19.56	0.65	0.91	2.80	306.50	935.21	1.16	0.84	404256
CV(%)		3.71	6.06	4.06	2.28	4.44	8.28	4.44	1.36	11.77	5.86

**: P< 0.01 probability level, *:P< 0.05 probability level. ns: not significant, PH: plant height, HFC: height of first cob, CL: cob length, NRC: number of rows on the cob, 100GW: 100 grain weight, CW: cob weight, NGC: number of grains on the cob, HW: hectoliter weight, PR: protein ratio, GY: grain yield

Height of first cob (HFC cm)

The analysis of variance revealed that the high-frequency component (HFC) was significantly influenced by the genotypes (P<0.01). The height of first cob genotypes varied between 59.4-87.7 cm and the highest height of firs cob was obtained from Mumtez (G10) variety with 87.7 cm, and the lowest height of firs cob was obtained from Dekalb 6554 (G6) variety with 59.4 cm(Table 5). Zaim (2020), reported that while the highest height of firs cob value was recorded as 76.9 cm in Dekalp DK6664 variety, the lowest height of first cob was determined as 63.1 cm in May Capuzi variety. It is estimated that the differences in the results of the research are due to the locations where the research was conducted.

Cob length (CL cm)

Analysis of variance revealed that CL was significantly influenced by the main effect of genotype (P<0.01). The cob length of genotypes varied between 17.7-21.7 cm and the highest cob length was obtained from Dekalb 6554 (G6) variety with 21.7 cm, and the lowest height cob length was obtained from SY Prosperic (G4) variety with 17.7 cm (Table 5). Zaim (2020), reported that while the highest cob length value was recorded as 18.1 cm in P2088 ve SY Zoan variety, the lowest cob length was determined as 16.5 cm in May Capuzi variety. It is estimated that the differences in the results of the research are due to the locations where the research was conducted. On the other hand, Uddin et al., (2020), reported that the cob length ranged from 16.12 – 23.90 cm in the study. Number of rows on the cob (NRC cm)

Analysis of variance showed that NRC was significantly influenced by the main effect of genotype (P<0.01). The number of rows on the cob varied between 39.2-43.8 cm and the highest number of rows on the cob was obtained from May Capuzi (G3) variety with 43.8 cm with Mumtez (G10), and the lowest number of rows on the cob was obtained from P0937 (G7) variety with 39.2 cm (Table 5). Bhargavi et al., (2016) reported that the number of rows on the cob ranged from 20.7 to 32.3 in the study.

100 Grain yield (100GW g)

Analysis of variance revealed that 100 GW was significantly influenced by the main effect of genotype (P<0.01).The 100 grain yield of the maize cultivars ranged from 30.3 g from (G10) to 43.5 g (G6) (Table 5). Mut et al., (2022) reported that the 100 grain yield of mays cultivars ranged from 20.0 - to 38.0 g with a mean value of 31.8 g, they reported that the difference between cultivars in terms of thousand grain yield may be due to the difference in the FAO group, genetic structure. On the other hand, Sahin and Kara (2021) reported that cultivars with a high thousand grain yield had high grain yield and test weight, while cultivars with low thousand grain yield had the lowest values of test weight and grain yield due to having a higher number of grains per ear.

Cob weight (CW cm)

The analysis of variance showed that the CW was significantly influenced by the main effect of genotypes (P<0.01). The cob weight of the maize cultivars ranged from 186-254 g and the highest number of cob weight was obtained from G6 with 254 g, and the lowest cob weight was obtained from with Mumtez (G10) variety with 39.2 cm (Table 5). Bhargavi et al., (2016) reported that the cob length ranged from 159 to 205 g, Uddin et al., (2020), reported that the cob weight ranged from 233.12 - 289.48 g in the study.

Number of grains on the cob (NGC piece)

The analysis of variance showed that the HW was significantly influenced by the main effect of genotypes (P<0.01). The number of grains on the cob of the maize cultivars ranged from 548-696 piece and the highest number of grains on the cob was obtained from G6 with 696 p, and the lowest cob weight was obtained from with G7 and G8 with 548-584 piece (Table 6). Bhargavi et al., (2016), reported that the number of grains on the cob of mays cultivars ranged from 333.1 - to 499.3 with a mean value of 491.4.

Hectoliter weight (HW kg/hl)

Analysis of variance showed that HW was significantly influenced by the main effect of genotype (P<0.01). The test weight of the maize cultivars ranged from 75.1 kg/hl from (G10) to 82.2 kg/hl (G6).The cultivars G2 (80.1 kg/hl) and G3 (80.9 kg/hl) were placed in same statistical group (Table 5). Mut et al., (2022), reported that the 100 grain yield of mays cultivars ranged from 70.0 - to 76.9 kg/hl with a mean value of 373.9 kg/hl and they reported that the difference between cultivars in terms of test weight may be due to the difference in the FAO group, genetic structure. On the other hand, Sahin and Kara (2021) reported that cultivars with a high test weight had high grain yield and thousand grain yield, while cultivars with low test weight had the lowest values of thousand grain and grain yield due to having a higher number of grains per ear.

Protein ratio (%)

Analysis of variance indicated that the PR was not significantly. The protein ratio of the maize cultivars ranged from 6.6% from (G10) to 8.6 % (G1) (Table , Table 6). According to Doğan et al., (2019), the protein ratio is affected by various factors such as the genetic characteristics of the varieties and planting time (I. crop and II crops), climate, and characteristics of the research location, cultivation techniques, fertilizer doses and sources, cultivation purpose, and harvest period. The results showed that the protein contents were ranged from 10.82 to 13.59 % (Ilyas et al., 2014).

Grain yield (GY t ha^{-1})

The analysis of variance revealed that the grain yield (GY) was significantly influenced by the genotypes (P<0.01). The grain yield of the maize cultivars ranged from 9.6 from (G10) to 13.8 t ha-1 (G6) (Table 5). The cultivars G3 (13.2 t ha-1) were placed in same statistical group with (G6),and the cultivars G8(19.7 t ha-1) and G7(9.8 t ha-1) were placed in same statistical group with(G10). Mut et al. (2022), reported that the grain yield of mays cultivars ranged from 9.6 - to 16.4 t ha-1 they reported that the difference between cultivars in terms of grain yield may be due to the difference in the FAO group, genetic structure. Zhou et al., (2016) reported that maize growth and yield are primarily affected by climatic factors such as temperature, sunshine hours, and precipitation, in addition to genetic factors. Conversely, According to Şahin and Kara (2021) reported that varieties with high grain yield have high thousand grain weight, while varieties with low grain yield have lower grain yield due to the higher number of grains per spike. Kalkan and Sade (2009) reported in their study that grain yield in hybrid maize varieties may vary depending on and according to maturity groups. Varieties in FAO 400, 250 and 200 groups exhibited lower yields compared to other varieties.

TABLE 5. The mean data of 10 corn genotypes.

Genotype	PH (cm)		HFC (cm)		CL (cm)		NRC		100GW (g)		CW		NGC		HW (kg hl)		PR (%)	GY (t ha^{-1})	
G1	211	ef	64.7	ce	19.1	de	39.4	ef	34.0	e	193	ce	673	ab	82.2	a	8.6	10.6	bc
G2	225	ce	62.0	de	19.4	ce	41.6	cd	36.4	de	216	bd	668	ab	82.1	a	8.3	11.4	bc
G3	231	cd	75.8	b	21.4	ab	43.8	a	41.7	ab	241	ab	696	a	80.9	a	7.5	13.2	a
G4	247	ab	76.2	b	17.7	f	41.7	bd	39.9	bc	193	ce	637	bc	78.6	b	9.5	10.3	c
G5	209	f	59.4	e	19.7	ce	41.1	de	39.6	bc	221	bc	588	cd	78.2	b	7.5	10.4	bc
G6	246	ab	86.7	a	21.7	a	43.0	ac	43.5	a	254	a	676	ab	78.0	b	7.9	13.8	a
G7	236	bc	71.8	bc	18.7	ef	39.2	f	39.8	bc	206	ce	548	d	77.9	b	7.9	9.9	c
G8	219	df	68.1	cd	20.1	bd	41.0	de	33.9	e	187	de	584	d	77.3	b	7.4	9.8	c
G9	234	bc	76.5	b	20.5	ac	43.3	ab	37.4	cd	217	bc	589	cd	76.8	bc	7.4	10.34	bc
G10	254	a	87.7	a	20.1	be	43.6	a	30.3	f	186	e	660	ab	75.1	c	6.6	9.6	c
LSD (0.05)	14.70		7.50		1.30		1.63		2.87		30.02		52.45		1.84		1.56	1090.70	

PH: plant height, HFC: height of first cob, CL: cob length, NRC: number of rows on the cob, 100GW: 100 grain weight, CW: cob weight, NGC: number of grains on the cob, HW: hectoliter weight, PR: protein ratio, GY: grain yield.

TABLE 6. Pairwise corelations among traits of 10 corn genotypes.

	PH	HFC	CL	NRC	100GW	CW	NGC	HW	PR
HFC	0.755**								
CL	-0.030ns	0.296							
NRC	0.366*	0.532*	0.462*						
100GW	0.033ns	0.0423ns	0.263ns	0.012ns					
PCW	0.027ns	0.056ns	0.566*	0.240ns	0.666**				
NGC	0.166ns	0.181ns	0.2656ns	0.404*	0.051ns	0.272ns			
HW	-0.188ns	-0.249ns	0.019ns	-0.100ns	0.155ns	0.294ns	0.493*		
PR	-0.167ns	-0.207ns	-0.284ns	-0.186ns	0.289ns	0.070ns	0.180ns	0.255ns	
GY	0.083ns	0.212ns	0.586**	0.307ns	0.621*	0.749**	0.597**	0.423*	0.0890ns

*Value significant for 0.05 probability level. ns: not significant, PH: plant height, HFC: height of first cob, CL: cob length, NRC: number of rows on the cob, 100GW: 100 grain weight, CW: cob weight, NGC: number of grains on the cob, HW: hectoliter weight, PR: protein ratio, GY: grain yield

The Biplot of genotype by trait (GT)

With the biplot technique, in the analysis, the two-dimensional PCA score constituted 66.01% of the total variation, while PC2 covered 40.04% and PCI 25.97% respectivelly. The relationship between GT (genotype x trait) can be examined visually from different angles. GT technique shows the relationship between genotypes and traits and each other by the scatter plot (Figure 1), the grouping of genotypes and traits with sector analysis, by the sector analysis (Figure 2), the stability of genotypes in terms of the average of the traits by the ranking biplot plot (Figure 3), the situation of the genotypes according to the ideal center created in terms of the average of the traits by the comparison biplot plot (Figure 4). The genotypes used in the study were examined in terms of the examined traits by these Figure.

Figure 1 illustrates the relationships between properties and traits based on genotype profiles. A biplot, which is a graph that can be interpreted in two directions, is used to explain this concept (Yan et al., 2000; Yan and Tinker, 2006; Aktaş, 2020). The cosine of the angle between the vectors of the two properties approximates their Pearson correlation. Therefore, an angle of less than 90° indicates a positive correlation, an angle greater than 90° indicates a negative correlation, and an angle of 90° indicates zero correlation. If the vector of a trait is longer than that of the other vectors, the variation of this trait in genotypes is higher than that of the other traits. If the vector length of any trait is much shorter than that of the other traits, the variation in this trait is very low. The angle between the genotype vector and trait provides information regarding the state of the genotype. A sharp and narrow angle indicates that the genotype is below average for that trait, whereas a large angle indicates that the genotype is below the mean data for traits. The length of the genotype vector indicated the strength or weakness of the genotype for all trait profiles. Based on the principles of the GT biplot technique, the observations made are presented in Figure 1.

Considering the observations on this figure indicated that grain yield was significant and positively correlated with NGC, CW, 100 GW, CL and HW. In the study, G3 and G6 had good results based on traits because they located the center of traits, and G4,G7,G8 and G10 was not correlated with any traits because they located backwards of traits in Figure 1.

Figure 2 shows the polygon of which-won-where/what of the GT biplot based on the across-season data. The figure is divided by a thick axis from the center, and each zone separated by two thick lines is referred to as a "sector" and is indicated by numbers 1, 2, 3, etc. Genotypes and traits that are located in the same sector are very similar (Yan and Tinker, 2006; Shrestha et al., 2021). When considering Fig. 2 and its associated prediction, it is important to note that the figure is divided into six sectors, separated by a tik line. Different traits were associated with different genotypes for each sector. Genotype G6 is the winner of sector 1, which is located in the same sector as G3 and is correlated with NGC, CW, 100 GW, CL, and HW. Similarly, G1 is the winner of sector 3 and is located in the same sector as G2 and G5, with PR. In sector 5, genotype G10 was the most successful and was correlated with PH and HWC. Genotypes G8 and G9 were also located in sector 5. In sector 4, genotypes G7 and G4 were present, but were not correlated with any trait

Figure 3 illustrates the stability of the genotypes based on their traits. The vertical axis represents the mean values, whereas the horizontal axis represents stability. The genotypes were evaluated based on their positions on these axes. Those located below the vertical axis were considered unfavorable, whereas those located above were preferable. If the genotypes were located near or at the center of the horizontal line, they were considered stable. Conversely, if they are located away from the horizontal line, they are considered unstable (Yan and Rajcan, 2002; Kendal, 2019; Ahmed et al., 2020). Based on this prediction, G3 and G6 were stable because they were located at the center of the horizontal axis. In contrast, G2, G6, and G9 are unstable because they are located far from the center of the horizontal axis. The remaining six genotypes were considered unpredictable because they were located below the vertical axis. Of the eight genotypes, only G2 and G9 were located above the vertical axis, making them the preferred genotypes based on the trait profiles.

Figure 4 illustrates the discriminative and representative nature of the genotypes based on traits. It presents an 'ideal center, ' which represents the mean values of the properties and allows for the evaluation of genotypes based on their proximity to or distance from the center (Yan and Tinker, 2005; Özata, 2020If the genotypes were located in the center, they were considered ideal. If they are located on the average perpendicular axis, but far from the center, they are still considered ideal. However, if they were located below the perpendicular axis (red line), they were considered undesirable. Based on the prediction in Fig. 4, G6 is more ideal than G3, G2, or G9 because it is located at the 'ideal center.' The other six genotypes were located under the perpendicular axis and far from the 'ideal center,' making them undesirable.

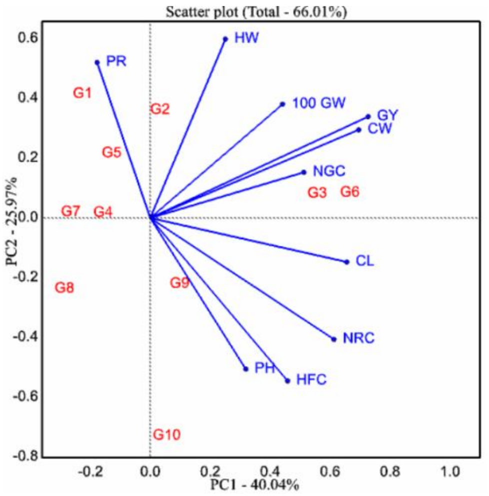

Fig. 1. The relationship of Genotype by trait.

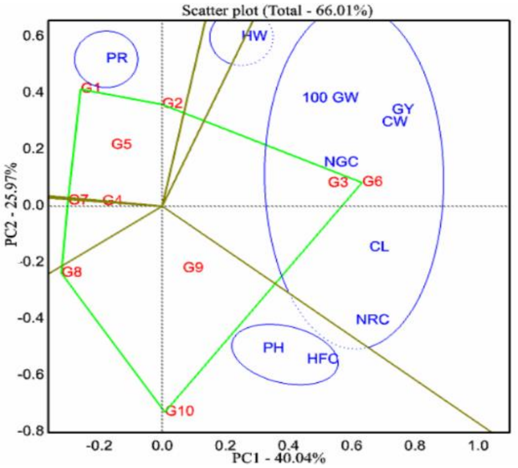

Fig. 2. The sector analysis of genotype and traits.

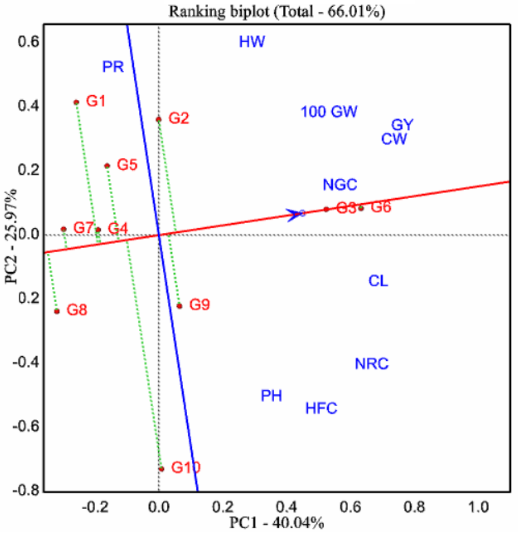

Fig. 3. The stability of genotypes based on traits.

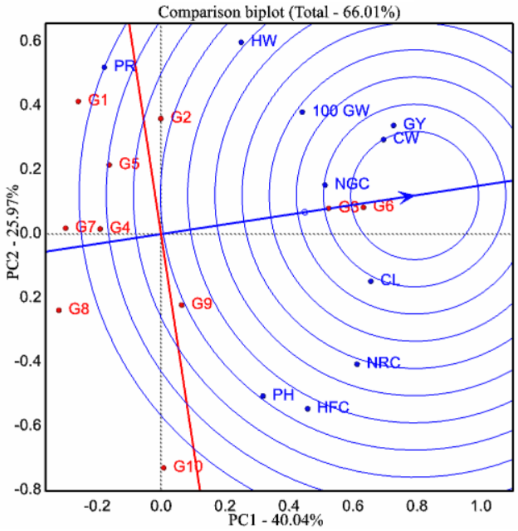

Fig.4.Definite of ideal genotype based on traits

Conclusion

In conclusion, the moisture content of the grain is crucial for harvesting, particularly in years with varying climatic conditions during second crop grain maize cultivation in Mardin Province. Following the maize harvest, it is essential to promptly sow the main wheat crop with sufficient time for sowing. Our study found no issues related to the timing of wheat sowing. It was concluded that there is sufficient time for planting second-crop maize after wheat harvest in the region. In years when the air temperature and climate are suitable, it is appropriate to harvest until the end of November or the beginning of December. Therefore, the selection of high-yielding and early harvesting varieties is crucial. The objectives of genotypes x traits suggest that this method is useful in various plant studies. The GT biplot technique reveals a special relationship between all traits and yield. It provides information on the general and specific adaptability capabilities of genotypes. G3 and G6 were found to be the most stable and best genotypes among all. The stability of the G3 and G6 genotypes make them suitable for maize cultivation as a second crop in the Kızıltepe district of Mardin province. The GT biplot technique is a valuable tool for visually evaluating genotypes based on all traits.

The objectives of genotypes x trait suggested that there are more reason to use this method in different plant and studies, it is seen that there is a special variation relationship between all traits and yield in GT biplot technique. In terms of all traits, the GT biplot technique provides information on the general adaptability and specific adaptability capabilities of genotypes. In terms of all traits, G3 and G6 were stable and the best genotypes among all genotypes. It has been concluded that the G3 and G6 genotypes are quite stable and can be recommended in the research and cultivation of maize as a second crop in the Kızıltepe district of Mardin province. In addition, it has been determined that the GT biplot technique provides extremely useful results for visually evaluating genotypes in terms of all traits.

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All authors declare their consent for publication.

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The author declares no conflict of interest.

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