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Original Article

Selection of maize hybrids based on genotype × yield × trait (GYT) in different environments

Seleção de híbridos de milho com base no genótipo × rendimento × característica (GYT) em diferentes ambientes

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Abstract

This study aimed to identify the best genotypes using the genotype × yield × trait (GYT) method. To investigate the relationships was performed between yield × traits in four regions of Karaj, Birjand, Shiraz and Arak in two cropping years in a randomized complete block design (RCBD) with three replications. The average grain yield in four regions and two years of the experiment was calculated as 5966 kg/ha, and GYT was obtained based on the multiplication of grain yield with different traits. Comparing the average effect of genotype × year in different environments showed that KSC703 and KSC707 hybrids are among the most productive hybrids among the studied genotypes in grain yield. By examining the correlation coefficients between yield × traits in the tested areas, Y × TWG with Y × GW, Y × NRE, Y × NGR and Y × EL, Y × ED with Y × NGR, Y × NRE with Y × GW and the combination of Y × GW with Y × GL had a positive and significant correlation in all regions. The correlation diagrams were drawn on the evaluated areas' data and showed the correlation of most compounds except Y × GT with each other. Based on the analysis of the main components, the first three components explained the greatest diversity in the population. They were named the component ear grain profile, grain thickness component and plant height profile component.

Keywords: maize, combined analysis, GYT, correlation, cluster analysis.

Resumo

Este estudo teve como objetivo identificar os melhores genótipos usando o método "genótipo × produção × característica (GYT)". Uma análise foi realizada para investigar as relações entre "rendimento × características", em quatro regiões de Karaj, Birjand, Shiraz e Arak durante dois anos de cultivo, em um delineamento de blocos completos ao acaso (RCBD) com três repetições. O rendimento médio de grãos em quatro regiões e dois anos de experimento foi calculado em 5966 kg/ha, e o GYT foi obtido a partir da multiplicação do rendimento de grãos com diferentes caracteres. A comparação do efeito médio de "genótipo × ano" em diferentes ambientes mostrou que os híbridos KSC703 e KSC707 estão entre os híbridos mais produtivos entre os genótipos estudados na produtividade de grãos. Examinando os coeficientes de correlação entre rendimento × características nas áreas testadas, *Y × TWG com Y × GW, Y × NRE, Y × NGR e Y × EL, Y × ED com Y × NGR, Y × NRE com Y × GW e a combinação de Y × GW com Y × GL* apresentaram correlação positiva e significativa em todas as regiões. Os diagramas de correlação foram desenhados nos dados das áreas avaliadas e mostraram a correlação da maioria dos compostos exceto Y × GT entre si. Com base na análise dos componentes principais, os três primeiros componentes explicaram a maior diversidade da população. Eles foram denominados de "componente perfil de grão da espiga", "componente de espessura de grão" e "componente de perfil de altura da planta".

Palavras-chave: milho, análise combinada, GYT, correlação, análise de cluster.

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1. Introduction

Maize is one of the most important sources of human calories and has been largely independently selected for traits such as grain yield (Nagy, 2006; Bodnár et al., 2018; Mousavi et al., 2021a). It is also a staple food for humans cultivated worldwide and plays an important role in supporting the world's growing population (Prasad et al., 2017). The biplot method is a method for graphically representing multivariate data that can be a powerful tool for graphically displaying data in a scatter plot (Shojaei et al., 2022a; Mousavi et al., 2020, 2021b). Selection based on multiple traits is a useful breeding strategy for selecting optimal genotypes (Burdon and Klápště, 2019; Bojtor et al., 2021). Yan et al. (2019) developed the effect of genotype × yield × trait (GYT) to identify and select superior genotypes based on Multi-traits. The GYT biplot combines grain yield with other evaluated crop traits, ranks genotypes in trait distribution, and shows their strengths and weaknesses (Yue et al., 2022) It is also important in identifying the best genotypes in the correlation between yield and other traits (Purwati et al., 2022). Correlation between grain yield and other traits is a very important factor for the early selection of high-yield genotypes because grain yield is influenced by genetic effects and the interaction of genotype and environment (Djaman et al., 2020). Genotype evaluation based on GYT analysis consists of several steps: converting the two-way genotype × trait (GT) to the genotype × yield × trait (GYT), standardizing the GYT data, displaying the GYT as a GYT biplot, Calculation of GYT from the mean's performance × traits (Yan and Frégeau-Reid, 2018). One of the most important benefits of GYT biplot is the selection of additional compounds to reduce the measurement costs in the experiment (Mohammadi, 2019). Researchers have used the GYT method to study various plants, including the use of this method in durum wheat (Kendal et al., 2019), bread wheat (Hamid et al., 2019), sesame (Boureima and Yaou, 2019).

The objectives of this research include the following:

1) Evaluation of the effect of genotype × yield × trait (GYT)
2) Identification of superior genotypes based on GYT method
3) Relationships between yield × trait combinations in different areas studied in different years of experimentation
4) Investigating the correlation of yield × traits
5) Grouping of genotypes based on GYT.

2. Materials and Methods

2.1. Farm evaluation and data collection

This study was conducted to investigate the effect of genotype × yield × trait (GYT), evaluate the relationships between GYT compounds, and identify and select the desired genotypes using the GYT method on 12 commercial maize hybrids (Zea mays L.) in four regions. Karaj, Birjand, Shiraz and Arak and in two cropping years in a randomized complete block design (RCBD) were cultivated and evaluated in three replications. Experimental plots were designed in four rows with a distance of 75 cm and a length of 2 meters. All planting, holding, and harvesting operations were performed accurately. In order to measure grain yield, after removing the margin, effects in terms of kg/ha and ton/ha were recorded and performed. Other evaluated traits were used based on measurements of 5 random plants in each plot for statistical analysis. The code and name of genotypes, environments, traits and compounds obtained from yield × traits are presented in Table 1. Table 2 also shows the soil characteristics of the cultivated and evaluated field. Figure 1 shows the geographical and climatic characteristics of the cultivated areas.

2.2. Statistical analyzes

To perform the required analyzes and statistical analysis, was used the mean of the studied traits in the cultivated

Table 1. Code and name of hybrids, environments, traits and compounds obtained from yield × trait in experiment.

Genotypes No.	Genotypes	Traits Code	Traits	Regions code	Regions
G1	KSC 703	Y×PH	Yield × Plant height	K	KARAJ
G2	KSC 260	Y×EL	Yield × Ear length	B	BIRJAN
G3	KSC 705	Y×ED	Yield × Ear diameter	S	SHIRAZ
G4	KSC 400	Y×NGR	Yield × Number of grains in row	A	ARAK
G5	KSC 706	Y×NRE	Yield × Number of rows in ear		
G6	KSC 704	Y×GW	Yield × Grain weight		
G7	KSC 707	Y×GL	Yield × Grain Length		
G8	DC 370	Y×GT	Yield × Grain Thickness		
G9	SC 647	Y×TWG	Yield × Thousand grain weight		
G10	SC 302				
G11	SC 604				
G12	SC 301				

Table 2. Soil characteristics of cultivated fields in the experiment.

Region	Soil electrical conductivity ds/m)	Acidity	Lime (%)	Organic carbon (%)	Organic materials (%)	Clay (%)	Silt (%)	Sand (%)
Karaj	0.20	8.2	7	32	45	32	25	22
Birjand	0.46	7.08	15	17	29	10	42	42
Shiraz	0.75	7.8	4	21	25	41	31	46.1
Arak	2.9	8	9	23	12	23	21	38

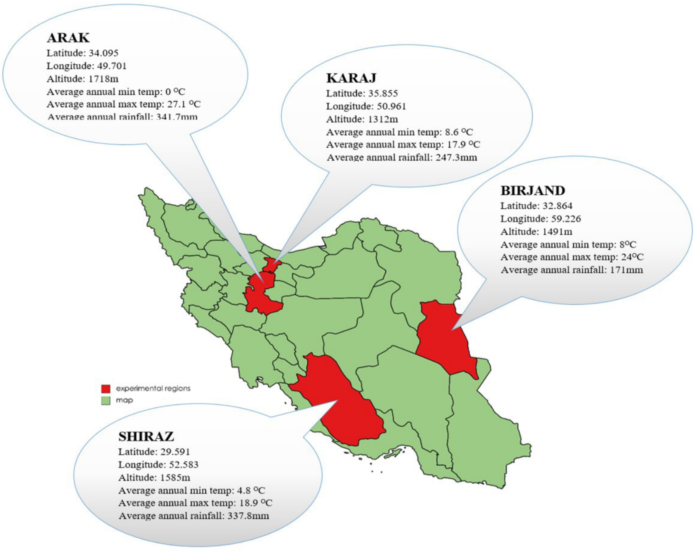

Figure 1. Geographical and climatic characteristics of the cultivated and studied environments in the experiment.

areas. GYT (genotype × yield × trait) was obtained using the product of yield × trait (Yan and Frégeau-Reid, 2018). In this method, was obtained plant height, ear length, ear width, number of grains per row, number of rows per ear, grain width, grain length, grain thickness and 1000-grain weight were multiplied separately by grain yield and GYT. Due to the existence of different units of traits, standardization of traits was used to eliminate units.

$$Z = \frac{X - \mu}{\sigma} \tag{1}$$

In this Equation 1, Z: standard score, X: initial trait data, μ: mean of the trait, σ: standard deviation of the trait.

In this study of combined analysis, comparison of the average effect of genotype × years in different experiment fields, correlation coefficient analysis, principal component analysis (PCA) and also graphical analysis method which includes correlation diagrams, polygon, ranking of genotypes based on GYT and genotype ranking based on ideal genotype was used. Cluster analysis was used to group the studied hybrids based on yield × trait combinations. Excel and SAS.v9.2 software were used for statistical analysis, Genstat.v12 and XlStat.2015 software were used for graphical analysis.

3. Result and Discussion

3.1. Variance analysis and mean comparison

The study of the average data obtained from two years in the four regions evaluated showed that the grain yield in the studied genotypes ranged from 4200 kg/ha for the KSC704 hybrid in the Birjand region to 8080 kg/ha for the KSC706 genotype in the Karaj region. The average grain yield in the Karaj region was 6399 kg/ha, in the Birjand region 5085 kg/ha, in the Shiraz region 5800 kg/ha, and in the Arak region, 6580 kg/ha. The average grain yield in the four field areas was 5966 kg/ha. Table 3 shows the average data of the studied traits in the two years under evaluation. The GYT was obtained based on the combination of each trait with grain yield according to Yan et al. (2019) method (Table 4). For this purpose, plant height, ear length, ear width, the number of grains per row, rows per ear, grain width, grain length, grain thickness, and 1000-grain weight were multiplied separately by grain yield and yield × trait combination obtained. Standardization was used on the obtained GYT data, and finally, the GYT index was calculated (Table 5). The combined analysis of variance (Table 6) showed significant differences among genotypes for all understudied traits by the F test. The effects of Environment × Genotype, Year × Genotype and Genotype × Year × Environment were significant

Table 3. Average of traits in 12 maize hybrids over two years in four evaluated areas.

	Genotype	PH	EL	ED	NGR	NRE	GW	GL	GT	TWG	Y
KARAJ	G1	179.1	18.23	40	15.37	39.55	6.6	9.01	2.59	284.67	8.06
	G2	165.38	17.22	42.49	21.51	34.83	5.69	7.29	3.56	309.83	5.57
	G3	197.87	21.77	42.41	15	51.05	6.08	10.73	2.48	299.68	6.51
	G4	192.05	15.6	38.68	14	41.08	6.11	10.82	2.66	288.12	6.17
	G5	201.12	17.77	32.19	14.33	40.85	5.6	9.86	2.9	242.67	8.08
	G6	173.63	18.22	51.87	17.5	39.18	5.97	11.86	5.49	321.32	6.86
	G7	169.08	17.73	43.47	17.24	38.9	7.26	10.68	2.69	344.9	7.53
	G8	190.77	13.78	39.16	15.26	26.62	5.71	10.03	5.43	318.38	5.59
	G9	176.65	15.43	45.97	19.22	42.35	6.91	10.67	2.42	225.5	5.92
	G10	174.4	15.58	47.95	17.06	34.58	5.69	9.82	2.89	263.15	5.52
	G11	202.12	15.75	42.22	17.2	30.35	3.22	8.6	6.26	245.63	5.78
	G12	195.88	18.2	40.84	17.48	38.07	5.04	11.97	3.17	253.53	5.2
BIRJAND	G1	163.95	14.7	37.23	12.29	31.38	6.14	10.56	2.64	271.15	5.03
	G2	151.84	13.88	39.38	17.21	27.16	5.29	8.57	3.64	297.15	5.23
	G3	181.24	17.55	39.31	12	40.08	5.66	12.71	2.44	286.45	4.26
	G4	176.63	12.58	35.85	11.65	32.02	5.69	12.41	2.63	276.28	4.64
	G5	185.08	14.33	29.84	11.7	32.39	5.21	11.43	2.86	233.06	5.07
	G6	155.54	14.69	48.07	14.67	31.08	5.56	13.96	5.43	309.45	4.12
	G7	151.22	14.3	40.32	14.18	29.14	6.98	12.54	2.65	326.4	6.24
	G8	156.37	11.12	36.29	12.26	20.07	5.5	11.65	5.35	316.4	5.73
	G9	145.07	12.44	42.61	15.63	34.84	6.64	12.44	2.39	227.44	5.12
	G10	144.09	12.57	44.44	13.87	29.36	5.46	11.33	2.89	265.67	5.24
	G11	166.6	12.7	39.13	13.76	24.81	3.08	9.91	6.19	247.5	5.79
	G12	164.43	14.68	37.85	13.98	28.75	4.86	13.34	3.14	256.26	4.55
SHIRAZ	G1	190.02	14.38	31.49	12.95	32.81	5.91	10.06	2.76	293.08	6.82
	G2	176.17	13.52	36.45	17.95	28.02	5.05	8.2	3.85	321.18	5.49
	G3	210.14	17.11	36.28	12.53	41.29	5.47	12.13	2.59	309.82	5.81
	G4	204.56	12.3	33.09	12.11	33.06	5.47	11.94	2.79	298.75	6.87
	G5	214.24	13.96	27.41	12.22	33.27	5.04	10.98	3.04	252.11	5.79
	G6	183.3	14.31	44.27	15.28	31.39	5.41	13.64	5.78	334.24	5.54
	G7	178	13.91	37.38	14.6	29.67	6.77	12.25	2.81	343.2	6.73
	G8	181.49	10.86	34.1	12.32	20.37	5.17	11.45	5.7	330.09	7.1
	G9	168.28	12.51	40.03	15.76	36.11	5.99	12.25	2.47	235.99	5.59
	G10	166.88	12.65	41.93	13.99	30.48	4.88	11.1	3	279.42	4.49
	G11	193.08	12.75	36.54	13.84	25.52	2.77	10.12	6.4	256.86	4.77
	G12	190.48	13.94	35.15	14.12	29.59	4.32	13.55	3.25	266.04	4.61
ARAK	G1	189.31	14.15	30.12	13.23	31.87	4.69	10.6	2.55	270.57	7.24
	G2	174.88	13.31	35.19	18.3	27.34	3.98	8.57	3.55	297.94	7.35
	G3	209.3	16.93	34.97	12.78	41.26	4.31	12.66	2.38	289.32	7.83
	G4	203.72	12.17	31.93	12.31	33.04	4.35	12.48	2.6	279.05	5.85
	G5	215.38	13.81	27.18	12.44	33.31	3.99	11.47	2.84	235.42	5.68
	G6	186.82	14.14	43.94	15.58	31.21	4.3	13.13	5.54	318.2	5.23
	G7	181.2	13.75	37.15	14.87	29.35	5.34	11.77	2.69	324.87	6.93
	G8	184.84	10.73	33.83	12.53	20.16	4.09	11.05	5.49	313.87	6.58
	G9	171.02	12.38	40.08	15.89	35.59	4.81	11.68	2.38	224.57	6.22
	G10	168.99	12.51	42.03	14.06	30.21	3.94	10.64	2.87	265.6	6.56
	G11	195.94	12.61	36.66	13.9	25.13	2.26	9.56	6.14	244.01	7.01
	G12	193.47	13.54	34.96	14.1	29.14	3.55	13.1	3.1	252.91	6.48

Plant height (PH), Ear length (EL), Ear diameter (ED), Number of grains in row (NGR), Number of rows in ear (NRE), Grain weight (GW), Grain length (GL), Grain thickness (GT), Thousand grain weight (TWG), Yield (Y).

for all traits. Suppose there is no significant difference between the genotypes in the evaluated agronomic traits in terms of G × E and the genetic relationship between the experimental genotypes. In that case, it indicates the similar behaviour of the genotypes in the experimental environments. The significance of genotype-environment interaction indicates different reactions of genotypes in different environments. The significance of genotype-year interaction is a sign of different reactions of genotypes in different years. The highest percentage of coefficient of variation was related to grain yield (21.33), and the lowest was related to cob length (6.23). Due to the widespread use

Table 4. Genotype × yield × trait (GYT) data obtained from traits for 12 maize hybrids in four experiment areas.

	Genotype	Y*PH	Y*EL	Y*ED	Y*NGR	Y*NRE	Y*GW	Y*GL	Y*GT	Y*TWG
KARAJ	G1	1444.1	147.02	322.53	123.90	318.90	53.223	72.62	20.86	2295.38
	G2	921	95.87	236.61	119.79	193.98	31.66	40.62	19.83	1725.42
	G3	1288.11	141.70	276.07	97.65	332.33	39.58	69.85	16.11	1950.93
	G4	1185.80	96.32	238.81	86.44	253.66	37.73	66.79	16.42	1778.96
	G5	1624.57	143.51	260.05	115.78	329.97	45.2	79.66	23.44	1960.20
	G6	1191.70	125.02	355.99	120.10	268.92	40.96	81.38	37.69	2205.30
	G7	1273.01	133.51	327.25	129.83	292.87	54.65	80.40	20.27	2596.71
	G8	1066.1	77.03	218.83	85.26	148.75	31.91	56.03	30.32	1779.40
	G9	1046.5	91.39	272.35	113.88	250.90	40.95	63.23	14.33	1335.96
	G10	962.10	85.96	264.51	94.08	190.78	31.37	54.19	15.93	1451.71
	G11	1168.2	91.03	244.04	99.41	175.42	18.58	49.71	36.20	1419.76
	G12	1018.5	94.64	212.3	90.88	197.94	26.19	62.25	16.47	1318.37
BIRJAND	G1	824.13	73.91	187.16	61.79	157.75	30.84	53.06	13.26	1362.96
	G2	794.81	72.67	206.12	90.07	142.15	27.66	44.86	19.04	1555.41
	G3	772.10	74.77	167.44	51.12	170.72	24.11	54.15	10.40	1220.29
	G4	818.75	58.31	166.17	53.99	148.45	26.38	57.53	12.17	1280.70
	G5	938.75	72.67	151.34	59.35	164.28	26.41	57.97	14.52	1182.13
	G6	640.48	60.49	197.95	60.42	127.98	22.89	57.47	22.36	1274.22
	G7	943.42	89.22	251.54	88.46	181.78	43.53	78.26	16.55	2036.36
	G8	896.35	63.71	208.02	70.26	115.02	31.51	66.80	30.67	1813.69
	G9	742.76	63.69	218.14	80.05	178.39	34.02	63.67	12.24	1164.51
	G10	754.40	65.79	232.66	72.63	153.73	28.60	59.30	15.13	1390.93
	G11	965.16	73.58	226.71	79.716	143.70	17.85	57.42	35.85	1433.83
	G12	748.13	66.78	172.23	63.61	130.79	22.09	60.68	14.30	1165.99
SHIRAZ	G1	1296.14	98.06	214.79	88.32	223.76	40.32	68.62	18.81	1999.13
	G2	967.17	74.20	200.12	98.53	153.8	27.75	45	21.14	1763.25
	G3	1221.82	99.51	210.92	72.85	240.09	31.81	70.50	15.04	1801.41
	G4	1405.54	84.48	227.38	83.22	227.15	37.61	82.02	19.17	2052.73
	G5	1240.22	80.80	158.68	70.75	192.62	29.20	63.54	17.62	1459.42
	G6	1016.11	79.30	245.42	84.70	173.99	29.98	75.60	32.05	1852.78
	G7	1198.11	93.66	251.62	98.27	199.70	45.59	82.47	18.91	2310.09
	G8	1288.75	77.14	242.11	87.48	144.66	36.68	81.33	40.49	2344.02
	G9	941.41	70.01	223.94	88.17	202.02	33.48	68.50	13.84	1320.22
	G10	749.47	56.82	188.28	62.82	136.89	21.89	49.85	13.49	1254.92
	G11	921.61	60.87	174.44	66.07	121.79	13.22	48.31	30.56	1226.09
	G12	877.27	64.18	161.89	65.02	136.23	19.88	62.39	14.95	1225.27
ARAK	G1	1371.21	102.49	218.18	95.85	230.87	33.942	76.74	18.44	1959.86
	G2	1285.15	97.83	258.6	134.46	200.93	29.25	62.94	26.08	2189.55
	G3	1637.85	132.51	273.64	100.02	322.85	33.72	99.10	18.63	2264.11
	G4	1191.32	71.18	186.71	71.99	193.20	25.45	72.95	15.19	1631.79
	G5	1222.86	78.43	154.33	70.64	189.13	22.634	65.14	16.10	1336.65
	G6	977.90	74.03	230	81.54	163.34	22.52	68.72	28.98	1665.58
	G7	1256.33	95.33	257.60	103.11	203.47	37.05	81.57	18.62	2252.45
	G8	1217.05	70.65	222.74	82.51	132.77	26.91	72.73	36.16	2066.64
	G9	1064.14	77.02	249.38	98.84	221.43	29.93	72.68	14.81	1397.30
	G10	1108.75	82.05	275.76	92.26	198.21	25.82	69.80	18.85	1742.62
	G11	1373.35	88.41	256.94	97.40	176.16	15.82	66.98	43.06	1710.23
	G12	1253.28	87.73	226.48	91.35	188.74	22.99	84.85	20.083	1638.27

Plant height (PH), Ear length (EL), Ear diameter (ED), Number of grains in row (NGR), Number of rows in ear (NRE), Grain weight (GW), Grain length (GL), Grain thickness (GT), Thousand grain weight (TWG), Yield (Y).

of grain yield trait in the experiments and the significant effect of genotype × year in terms of grain yield trait, the average in terms of this trait in different regions was made in two years of experiment (Figure 2).

Based on the graph obtained in the Karaj region (Figure 2A), KSC703 and KSC706 genotypes in the second crop year were identified as hybrids with high average yield and good rank and SC301 SC302 genotypes in the second year of the experiment as low-grade hybrids. In the first year of the experiment, the SC302 genotype had a better rank than other genotypes. Based on the graph obtained in the Birjand region, SC604 and KSC703 hybrids in the

Table 5. The standardized genotype by yield × trait.

	Genotype	Y*PH	Y*EL	Y*ED	Y*NGR	Y*NRE	Y*GW	Y*GL	Y*GT	Y*TWG	GYT index
KARAJ	G1	1.28	1.43	1.19	1.11	1.14	1.48	0.61	-0.18	1.18	1.03
	G2	-1.28	-0.56	-0.72	0.85	-0.82	-0.57	-1.86	-0.31	-0.23	-0.61
	G3	0.52	1.22	0.15	-0.56	1.34	0.18	0.40	-0.77	0.33	0.31
	G4	0.02	-0.54	-0.67	-1.27	0.12	0.01	0.16	-0.73	-0.10	-0.33
	G5	2.16	1.29	-0.20	0.59	1.31	0.72	1.15	0.14	0.35	0.84
	G6	0.05	0.57	1.93	0.87	0.35	0.31	1.29	1.90	0.95	0.91
	G7	0.44	0.90	1.29	1.49	0.73	1.61	1.21	-0.25	1.92	1.04
	G8	-0.57	-1.29	-1.12	-1.34	-1.52	-0.55	-0.67	0.99	-0.10	-0.69
	G9	-0.67	-0.73	0.07	0.47	0.07	0.31	-0.12	-0.99	-1.19	-0.31
	G10	-1.08	-0.94	-0.10	-0.78	-0.87	-0.60	-0.81	-0.79	-0.90	-0.76
	G11	-0.07	-0.75	-0.56	-0.44	-1.11	-1.81	-1.16	1.72	-0.98	-0.57
	G12	-0.80	-0.61	-1.26	-0.99	-0.75	-1.09	-0.19	-0.72	-1.23	-0.85
BIRJAND	G1	0.04	0.51	-0.38	-0.58	0.32	0.43	-0.77	-0.61	-0.16	-0.13
	G2	-0.25	0.36	0.24	1.60	-0.44	-0.05	-1.78	0.13	0.54	0.04
	G3	-0.49	0.62	-1.02	-1.40	0.94	-0.59	-0.63	-0.97	-0.68	-0.47
	G4	-0.01	-1.36	-1.06	-1.17	-0.13	-0.24	-0.21	-0.75	-0.46	-0.60
	G5	1.21	0.36	-1.55	-0.76	0.63	-0.24	-0.16	-0.45	-0.82	-0.20
	G6	-1.82	-1.09	-0.03	-0.68	-1.13	-0.77	-0.22	0.55	-0.48	-0.63
	G7	1.25	2.34	1.72	1.47	1.48	2.35	2.34	-0.19	2.30	1.67
	G8	0.78	-0.71	0.30	0.07	-1.75	0.53	0.93	1.60	1.49	0.36
	G9	-0.78	-0.71	0.63	0.83	1.32	0.91	0.54	-0.74	-0.89	0.12
	G10	-0.66	-0.46	1.10	0.26	0.12	0.09	0.00	-0.37	-0.06	0.00
	G11	1.47	0.47	0.91	0.80	-0.36	-1.53	-0.23	2.26	0.10	0.43
	G12	-0.73	-0.34	-0.87	-0.44	-0.99	-0.89	0.17	-0.47	-0.88	-0.60
SHIRAZ	G1	0.98	1.41	0.20	0.62	1.10	1.06	0.16	-0.30	0.68	0.66
	G2	-0.61	-0.29	-0.26	1.43	-0.63	-0.31	-1.63	-0.02	0.11	-0.25
	G3	0.62	1.51	0.08	-0.61	1.50	0.13	0.30	-0.74	0.20	0.33
	G4	1.52	0.44	0.60	0.21	1.18	0.76	1.17	-0.25	0.81	0.72
	G5	0.71	0.18	-1.55	-0.77	0.33	-0.16	-0.22	-0.44	-0.62	-0.28
	G6	-0.38	0.07	1.16	0.33	-0.13	-0.07	0.69	1.26	0.33	0.36
	G7	0.51	1.10	1.35	1.41	0.50	1.64	1.21	-0.29	1.43	0.98
	G8	0.95	-0.08	1.06	0.55	-0.86	0.66	1.12	2.25	1.51	0.80
	G9	-0.74	-0.59	0.49	0.61	0.56	0.31	0.15	-0.88	-0.96	-0.12
	G10	-1.67	-1.52	-0.62	-1.40	-1.05	-0.95	-1.26	-0.92	-1.12	-1.17
	G11	-0.84	-1.24	-1.06	-1.15	-1.43	-1.90	-1.38	1.08	-1.19	-1.01
	G12	-1.05	-1.00	-1.45	-1.23	-1.07	-1.18	-0.31	-0.75	-1.19	-1.03
ARAK	G1	0.74	0.82	-0.44	0.15	0.63	1.13	0.22	-0.50	0.43	0.35
	G2	0.23	0.55	0.68	2.44	-0.02	0.35	-1.15	0.35	1.15	0.51
	G3	2.31	2.54	1.09	0.40	2.64	1.10	2.45	-0.48	1.39	1.49
	G4	-0.33	-0.97	-1.32	-1.27	-0.19	-0.29	-0.16	-0.86	-0.59	-0.66
	G5	-0.14	-0.56	-2.22	-1.35	-0.27	-0.76	-0.93	-0.76	-1.52	-0.95
	G6	-1.59	-0.81	-0.12	-0.70	-0.84	-0.78	-0.58	0.68	-0.49	-0.58
	G7	0.06	0.41	0.65	0.58	0.04	1.66	0.70	-0.48	1.35	0.55
	G8	-0.17	-1.00	-0.32	-0.64	-1.50	-0.04	-0.18	1.48	0.77	-0.18
	G9	-1.08	-0.64	0.42	0.33	0.43	0.46	-0.18	-0.91	-1.33	-0.28
	G10	-0.81	-0.35	1.15	-0.06	-0.08	-0.23	-0.47	-0.45	-0.25	-0.17
	G11	0.75	0.02	0.63	0.24	-0.56	-1.90	-0.75	2.25	-0.35	0.04
	G12	0.04	-0.02	-0.21	-0.12	-0.28	-0.70	1.03	-0.32	-0.57	-0.13

Plant height (PH), Ear length (EL), Ear diameter (ED), Number of grains in row (NGR), Number of rows in ear (NRE), Grain weight (GW), Grain length (GL), Grain thickness (GT), Thousand grain weight (TWG), Yield (Y).

first year of the experiment, KSC707 hybrid in both years of the experiment and SC307 genotype in the second year of the experiment were identified as desirable genotypes. KSC704, KSC705 and SC301 hybrids were selected as low-ranking genotypes (Figure 2B). Based on the mean effect of genotype × year in the Shiraz region, the KSC707 genotype in the first year of the experiment was identified as a favorable hybrid compared to other hybrids and the SC302 in the first year and SC604 in the second year of the experiment as undesirable hybrids. In the second year of the experiment, the KSC703 genotype can also be considered a hybrid with the desired rank (Figure 2C). According to the

Table 6. Composition analysis of variance in the evaluated traits in 12 maize hybrids in two years of experiment.

Sources of variations	Degrees of freedom	PH	EL	ED	NGR	NRE	GW	GL	GT	TWG	Y
Location	3	12122.3*	230.2^{ns}	671.4*	141.4^{ns}	1036.8^{ns}	38.6^{ns}	37.9^{ns}	0.53^{ns}	4740.4^{ns}	36.7*
Year	1	256.7^{ns}	37.7**	386.7*	0.12^{ns}	21.1^{ns}	16.33*	235.9*	3.1^{ns}	14427.4*	35.2*
Replican / LY	3	0.47^{ns}	0.12*	0.44*	1.44^{ns}	17.4^{ns}	0.88*	7.1**	0.02^{ns}	62.4^{ns}	4.33*
Error1	16	184.1	7.18	212.5	6.89	64.9	0.83	7.4	1.36	4222.4	3.28
Genotype	11	4495.1**	67.9**	527.9**	72.2**	697.8**	20.7*	49.1**	35.8**	28437.9**	4.50*
Location × Genotype	33	133.3*	0.51**	3.07*	0.54**	4.3*	0.12*	0.35*	0.01**	93.6*	2.57**
Year × Genotype	11	208.7*	5.95**	22.5**	9.2**	65.5*	3.01**	22.6**	8.31	15404.9**	2.97**
Loc×Year×Gen	33	1.33*	0.02*	0.17*	0.06**	1.18**	0.02**	0.07*	0.003*	8.18*	2.64**
Error2	176	418.3	0.8	8.8	1.65	29.5	0.39	3.22	1.01	2186.7	1.68
Coefficient of variation %	--	11.29	6.23	7.74	8.8	16.7	12.16	16.05	27.9	16.49	21.33

Plant height (PH), Ear length (EL), Ear diameter (ED), Number of grains in row (NGR), Number of rows in ear (NRE), Grain weight (GW), Grain length (GL), Grain thickness (GT), Thousand grain weight (TWG), Yield (Y). *,**, and ns Show differences in the probability level of 0.01, 0.05 and no significant, respectively.

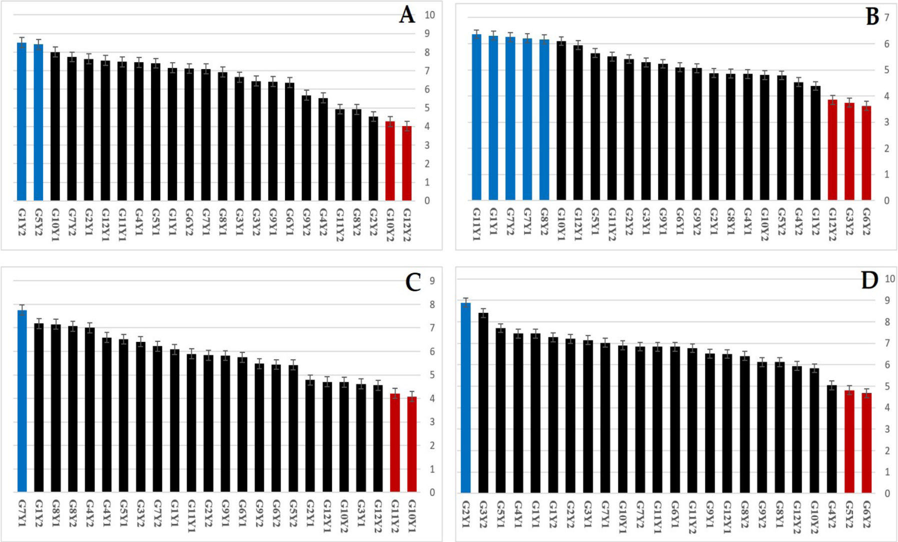

Figure 2. Comparison of mean genotype × year interaction in grain yield of 12 maize hybrids in two crop years and test areas. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

diagram obtained in the Arak region, the KSC260 hybrid in the first year of the experiment was more desirable than other genotypes. KSC706 and KSC704 genotypes were selected as low-ranking genotypes in the second year. The KSC705 genotype can be selected as a hybrid with a high average yield (Figure 2D). By reviewing the results obtained from different regions in the two years of the experiment, KSC703 and KSC707 genotypes can be selected and identified as hybrids with average yield and optimal rank.

3.2. Correlation analysis

Correlation coefficients were analyzed on compounds obtained from yield × traits in different experiment areas. Accordingly, in the Karaj region, a positive and significant correlation was identified between Y × PH combination with Y × EL, Y × NRE, Y × GW, Y × GL and Y × TWG. Also, Y × EL combination had a positive and significant correlation with all compounds except Y × GT. The combination of Y × ED with the compounds Y × NGR, Y × NRE, Y × GW, Y × GL and Y × TWG showed a positive and significant correlation. There was also a positive correlation between Y × NGR with Y × NRE, Y × GW and Y × TWG and also a positive correlation between Y × NRE with the compounds Y × GW, Y × GL and Y × TWG. A positive correlation was observed between Y × GW with Y × GL and Y × TWG and also between the combination of Y × GL and Y × TWG (Table 7-Karaj). In Birjand region, a positive and significant correlation was observed between Y × PH with Y × ED and Y × TWG. There was also a positive correlation between Y × EL and Y × TWG

Table 7. Analysis of correlation coefficients based on yield × trait combinations in four experimental regions.

Region		**Y×PH**	**Y×EL**	**Y×GD**	**Y×NGR**	**Y×NRE**	**Y×GW**	**Y×GL**	**Y×GT**	**Y×TWG**
KARAJ	Y×PH	1								
	Y×EL	0.834**	1							
	Y×GD	0.40^{ns}	0.667*	1						
	Y×NGR	0.37^{ns}	0.617*	0.732**	1					
	Y×NRE	0.799**	0.930*	0.616*	0.529*	1				
	Y×GW	0.613**	0.752**	0.710**	0.670*	0.801**	1			
	Y×GL	0.730**	0.759**	0.686**	0.406^{ns}	0.796**	0.75**	1		
	Y×GT	0.130^{ns}	-0.021^{ns}	0.232^{ns}	0.092^{ns}	-0.240^{ns}	-0.241^{ns}	0.052^{ns}	1	
	Y×TWG	0.590*	0.757**	0.740**	0.624*	0.636*	0.81**	-0.241^{ns}	0.18^{ns}	1
BIRJAND	Y×PH	1								
	Y×EL	0.570*	1							
	Y×GD	0.158^{ns}	0.341^{ns}	1						
	Y×NGR	0.287^{ns}	0.427^{ns}	0.811**	1					
	Y×NRE	0.186^{ns}	0.556*	0.137^{ns}	0.140^{ns}	1				
	Y×GW	0.218^{ns}	0.449^{ns}	0.483^{ns}	0.446^{ns}	0.503*	1			
	Y×GL	0.336^{ns}	0.302^{ns}	0.480^{ns}	0.247^{ns}	0.234^{ns}	0.642*	1		
	Y×GT	0.399^{ns}	-0.024^{ns}	0.406^{ns}	0.354^{ns}	-0.583*	-0.287^{ns}	0.091^{ns}	1	
	Y×TWG	0.512*	0.536*	0.663*	0.602*	-0.034^{ns}	0.636*	0.549*	0.41^{ns}	1
SHIRAZ	Y×PH	1								
	Y×EL	0.803**	1							
	Y×GD	0.413^{ns}	0.488^{ns}	1						
	Y×NGR	0.399^{ns}	0.495^{ns}	0.734**	1					
	Y×NRE	0.690*	0.846**	0.391^{ns}	0.374^{ns}	1				
	Y×GW	0.732**	0.785**	0.754**	0.747**	0.712**	1			
	Y×GL	0.715**	0.615*	0.718**	0.398^{ns}	0.567*	0.77**	1		
	Y×GT	0.196^{ns}	-0.07^{ns}	0.358^{ns}	0.201^{ns}	-0.399^{ns}	-0.015^{ns}	0.216^{ns}	1	
	Y×TWG	0.761**	0.716**	0.790**	0.716**	0.428^{ns}	0.83**	0.72**	0.41^{ns}	1
ARAK	Y×PH	1								
	Y×EL	0.858**	1							
	Y×GD	0.222^{ns}	0.483^{ns}	1						
	Y×NGR	0.301^{ns}	0.520*	0.690*	1					
	Y×NRE	0.674*	0.861**	0.349^{ns}	0.301^{ns}	1				
	Y×GW	0.293^{ns}	0.521*	0.278^{ns}	0.397^{ns}	0.556**	1			
	Y×GL	0.616*	0.690*	0.303^{ns}	0.021^{ns}	0.705*	0.512*	1		
	Y×GT	0.059^{ns}	-0.146^{ns}	0.226^{ns}	0.120^{ns}	-0.503*	-0.536*	-0.315^{ns}	1	
	Y×TWG	0.568*	0.639*	0.545*	0.583*	0.322^{ns}	0.620*	0.435^{ns}	0.18^{ns}	1

Plant height (PH), Ear length (EL), Number of grains in row (NGR), Number of rows in ear (NRE), Grain weight (GW), Grain length (GL), Grain thickness (GT), Thousand grain weight (TWG), Yield (Y). *, **, and ns Show differences in the probability level of 0.01, 0.05 and no significant, respectively

and also Y × NGR with Y × TWG. Y × NRE had a positive correlation with Y × GW and a negative correlation with Y × GT. Y × GW had a positive and significant correlation with Y × GL and Y × TWG and Y × GL with Y × TWG (Table 7-Birjand). In the study of correlation coefficients between compounds in the Shiraz region, a positive and significant correlation was observed between Y × PH combination with all compounds except Y × ED, Y × NGR and Y × GT. A positive correlation was observed between Y × EL combination with Y × NRE, Y × GW, Y × GL and Y × TWG and between Y × ED combination with Y × NGR, Y × GW, Y × GL and Y × TWG. Y × NGR also had a positive correlation with Y × GW and Y × TWG compounds and also Y × NRE with Y × GW and Y × GL compounds. A positive and significant correlation was observed between Y × GW with Y × GL and Y × TWG as well as the combination of Y × GL with Y × TWG (Table 7-Shiraz). In the study of correlation coefficients between compounds in Arak region between Y × PH with compounds Y × EL, Y × NRE, Y × GL and Y × TWG and between Y × EL with all compounds except Y × ED and Y × GT Positive and significant were observed. A positive correlation was observed between Y × ED with Y × NGR and Y × TWG and also Y × NGR with Y × TWG. There was a significant positive correlation between Y × NRE with Y × GW and Y × GL and a negative correlation with Y × GT combination. Y × GW was positively correlated with Y × GL and Y × TWG and negatively correlated with Y × GT (Table 7-Arak).

By examining the correlation coefficients between yield × traits in the experiment areas, Y × TWG with Y × GW, Y × NRE, Y × NGR and Y × EL, Y × ED with Y × NGR, Y × NRE with Y × GW and the combination of Y × GW with Y × GL had a positive and significant correlation in all regions.

According to the correlation diagram between the compounds in the Karaj region, all compounds except Y × GT had a positive correlation. Also, the correlation between Y × GT and Y × GL to the 90 ° angle between the vectors of these two compounds was estimated to be zero (Figure 3A). In the Birjand region, a positive correlation was observed between Y × GW, Y × EL, Y × GL, Y × PH, Y × NGR and Y × TWG. Also, Y × GT had a positive correlation with Y × TWG, Y × NGR and Y × PH. Y × NRE also showed a positive correlation with Y × GW, Y × EL and Y × GL. Considering the 90-degree angle between the vectors of Y × GT with Y × GL and also Y × NRE with Y × TWG and Y × NGR, the correlation in these compounds was estimated to be zero (Figure 3B). In the study of the correlation between yield × traits in the Shiraz region, all compounds except Y × GT had a positive correlation.

On the other hand, Y × GT also showed a positive correlation with Y × ED, Y × TWG and Y × NGR. The correlation between Y × GT and Y × PH was estimated to be zero (Figure 3C). The correlation diagram between the compounds obtained in the Arak region also showed a positive correlation between the compounds Y × ED, Y × NGR, Y × TWG, Y × PH and Y × EL in one group and in the other group a positive correlation between the compounds Y × GW, Y × GL, Y × NGR, Y × PH and Y × EL It was observed that Y × PH and Y × EL can be identified as compounds that have a positive correlation with all compounds except Y × GT (Figure 3D).

3.3. Principal Component Analysis (PCA)

The principal component analysis (PCA) results are presented in Table 8. The first three components explained more than 88% of the total diversity of compounds in the study population in the Karaj region. The first component had positive coefficients for all compounds evaluated and among these compounds, Y × EL and Y × NRE had the most impact on the first component. The second component had the highest positive coefficient for the combination Y × GT and the compounds Y × GD, Y × NRE and Y × TWG also had a positive effect on this component. This component also had negative coefficients for Y × PH, Y × EL, Y × NRE, Y × GW and Y × GL. The third component also had positive coefficients in the compounds Y × PH, Y × EL, Y × NRE, Y × GL and Y × GT, and among these the combination Y × PH had the greatest effect on this component. The rest of the compounds had a negative effect on this component (Table 8-Arak). In Birjand region, based on the results obtained from the special value diagram (Figure 4B), the first three components explained more than 79% of the total variance of the data.

The first component covered more than 44% of the total diversity of compounds in the study population and had positive coefficients in all compounds of yield × traits studied. The most positive effect on this component was related to the combination of Y × GW. The second component also had positive coefficients for the compounds Y × GD, Y × NGR, Y × GL, Y × GT and Y × TWG, which had the most positive effect on this component related to the combination Y × GT. The rest of the compounds had a negative effect on this component. In the third component, Y × PH, Y × EL, Y × NRE, Y × GL, Y × GT and Y × TWG had positive effects and the highest positive effect was estimated for Y × PH combination (Table 8-Brijand).

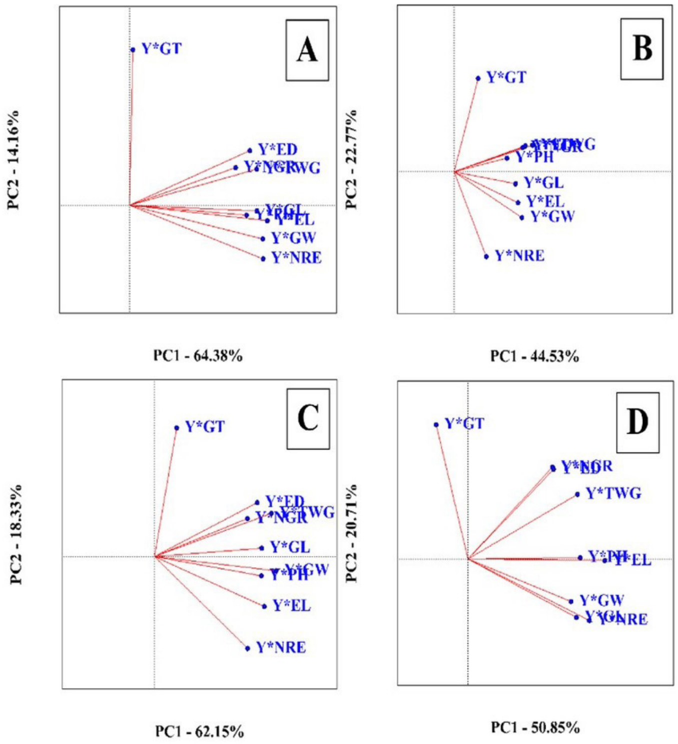

Figure 3. Correlation diagram between yield × trait combinations in the four regions. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

Table 8. Principal component analysis (PCA) based on yield × trait combinations in the four regions.

	Yield×Traits	**Principal Component**								
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
KARAJ	Y×PH	0.329	-0.053	0.563	0.334	-0.129	0.306	0.392	-0.339	-0.283
	Y×EL	0.387	-0.083	0.164	0.301	0.037	-0.493	-0.267	-0.287	0.57
	Y×GD	0.338	0.295	-0.322	-0.275	0.464	-0.279	0.469	-0.288	-0.145
	Y×NGR	0.298	0.23	-0.538	0.565	0.092	0.368	-0.303	-0.007	-0.15
	Y×NRE	0.375	-0.289	0.142	0.139	0.262	-0.247	0.061	0.735	-0.243
	Y×GW	0.374	-0.182	-0.243	-0.22	-0.3	0.387	0.373	0.212	0.542
	Y×GL	0.358	-0.031	0.256	-0.525	0.31	0.371	-0.531	-0.101	-0.435
	Y×GT	0.009	0.84	0.325	0.046	0.011	0.063	0.032	0.349	0.243
	Y×TWG	0.357	0.195	-0.101	-0.236	0.12	-0.308	-0.185	0.0005	-0.368
	Relative	0.643	0.141	0.098	0.048	0.032	0.02	0.008	0.003	0.002
	Cumulative	0.643	0.785	0.884	0.932	0.966	0.986	0.995	0.998	1
BIRJAND	Y×PH	0.291	0.093	0.692	-0.139	0.116	0.494	0.056	-0.315	-0.213
	Y×EL	0.352	-0.212	0.426	0.267	-0.185	-0.633	-0.25	0.138	-0.244
	Y×GD	0.393	0.177	-0.392	0.248	0.307	-0.184	0.401	-0.394	-0.389
	Y×NGR	0.378	0.165	-0.219	0.511	0.009	0.371	-0.576	0.025	0.217
	Y×NRE	0.177	-0.582	0.116	0.258	0.42	0.085	0.369	0.193	0.437
	Y×GW	0.374	-0.314	-0.272	-0.235	-0.345	0.338	0.13	0.462	-0.407
	Y×GL	0.339	-0.082	-0.148	-0.654	0.462	-0.195	-0.397	-0.039	0.126
	Y×GT	0.133	0.64	0.161	-0.004	0.257	-0.072	0.213	0.652	0.055
	Y×TWG	0.432	0.181	-0.1	-0.185	-0.53	-0.127	0.287	-0.212	0.564
	Relative	0.445	0.227	0.125	0.096	0.049	0.031	0.015	0.006	0.002
	Cumulative	0.445	0.673	0.798	0.894	0.943	0.975	0.991	0.997	1
SHIRAZ	Y×PH	0.352	-0.104	0.5	0.281	-0.296	0.322	-0.347	-0.121	-0.455
	Y×EL	0.362	-0.269	0.138	0.316	0.429	-0.406	0.499	0.06	-0.273
	Y×GD	0.339	0.29	-0.319	-0.41	0.441	-0.049	-0.389	-0.031	-0.424
	Y×NGR	0.306	0.205	-0.6	0.389	-0.152	0.406	0.301	-0.267	-0.0007
	Y×NRE	0.307	-0.495	0.018	-0.044	0.419	0.404	-0.214	-0.002	0.52
	Y×GW	0.401	-0.076	-0.2	-0.069	-0.388	-0.095	-0.035	0.788	0.067
	Y×GL	0.353	0.044	0.257	-0.659	-0.24	0.107	0.479	-0.258	0.073
	Y×GT	0.073	0.694	0.396	0.164	0.311	0.251	0.13	0.316	0.226
	Y×TWG	0.385	0.232	0.054	0.177	-0.167	-0.562	-0.35	-0.347	0.451
	Relative	0.621	0.183	0.09	0.053	0.023	0.015	0.008	0.003	0.0003
	Cumulative	0.621	0.804	0.895	0.948	0.972	0.988	0.996	0.997	1
ARAK	Y×PH	0.362	0.005	0.528	0.055	-0.35	-0.517	0.072	-0.667	-0.101
	Y×EL	0.441	-0.007	0.201	-0.16	-0.18	0.095	-0.131	0.552	-0.611
	Y×GD	0.276	0.41	-0.225	-0.369	0.575	0.233	-0.108	-0.354	-0.213
	Y×NGR	0.273	0.42	-0.377	-0.276	-0.388	-0.558	0.158	0.065	0.193
	Y×NRE	0.392	-0.281	0.068	-0.405	-0.062	0.432	0.087	0.145	0.614
	Y×GW	0.332	-0.194	-0.487	0.445	-0.033	0.235	0.564	-0.082	-0.183
	Y×GL	0.35	-0.267	0.247	0.13	0.588	-0.573	0.146	0.127	0.124
	Y×GT	-0.102	0.614	0.422	0.159	0.107	0.2	0.518	0.26	0.139
	Y×TWG	0.353	0.296	-0.066	0.594	-0.014	0.106	-0.569	0.084	0.294
	Relative	0.508	0.207	0.122	0.073	0.059	0.013	0.007	0.005	0.003
	Cumulative	0.508	0.715	0.837	0.911	0.97	0.983	0.991	0.997	1

Plant height (PH), Ear length (EL), Number of grains in row (NGR), Number of rows in ear (NRE), Grain weight (GW), Grain length (GL), Grain thickness (GT), Thousand grain weight (TWG), Yield (Y).

In the study of principal components analysis in the Shiraz region according to the special value diagram (Figure 4C), the first two components covered more than 80% of the data variance. The first component had positive coefficients for all studied compounds, of which Y × GW had the most positive effect on this component. The compounds Y × GD, Y × NGR, Y × GL, Y × GT and Y × TWG had a positive effect on the second component and among these compounds, Y × GT had the most positive effect on this component (Table 8-Shiraz). Based on the eigenvalue diagram obtained in Arak region, the first three components explained more than 80% of the variance of the data (Figure 4D), which in the first component had positive coefficients for all compounds except Y × GT, which from Among these compounds, Y × EL had the greatest effect. The compounds Y × PH, Y × GD, Y × NGR, Y × GT and Y × TWG also had a positive effect on the second component and the combination Y × GT had a more positive effect on this

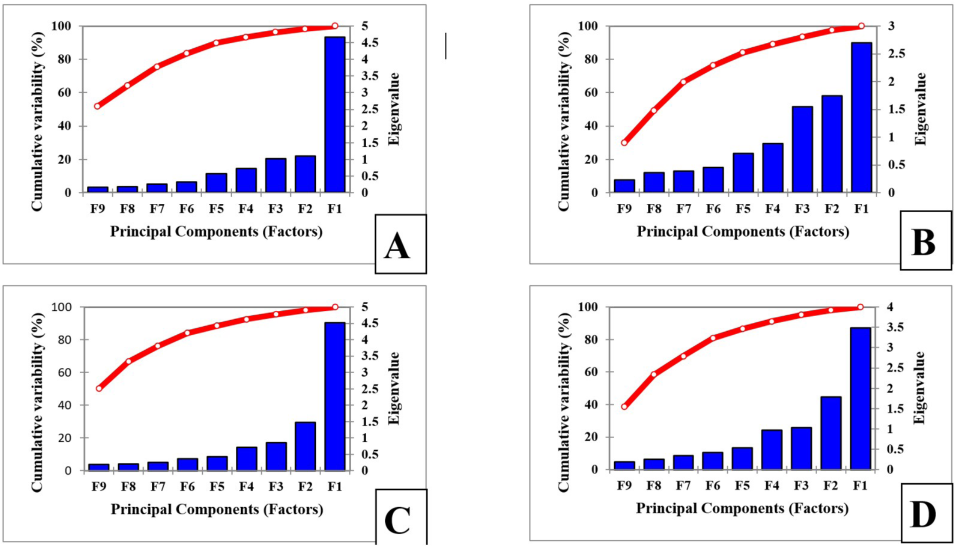

Figure 4. Eigenvalue diagram in different experimental regions. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

component than other compounds. The third component also had positive coefficients in the compounds Y × PH, Y × EL, Y × NRE, Y × GL and Y × GT, which the most positive effect on this component was estimated to be related to the composition Y × PH (Table 8-Arak).

The principal components examined in different regions of the experiment concluded that the first three components explain the greatest diversity in the population. The most positive coefficients in the first component were related to the compounds Y × GT, Y × GW and Y × EL, which can be named as the component of cob seed characteristics. In the second component, the compound Y × GT had the most positive effect, based on which this component was named as the seed thickness component. In the third component, the most positive effect is related to the composition of Y × PH, which can be named as the component of plant height characteristics, so the selection of genotypes with this component can distinguish tall hybrids.

To investigate the distribution of genotypes and identify superior hybrids were used principal component diagrams based on yield × trait combinations. The horizontal and vertical axes represent the two main components separating genotypes (Figure 5). Accordingly, in Karaj region, SC604, SC307 and KSC260 genotypes were placed in one group, SC301, SC302, KSC400 and SC647 genotypes in the second group and KSC705, KSC706, KSC703 and KSC707 hybrids in the third group. The KSC704 hybrid was placed in the fourth group alone and this hybrid was selected as the preferred genotype according to this diagram (Figure 5A). According to the diagram obtained in Birjand region, KSC705, KSC706, KSC703, SC302 and SC647 genotypes in the first group, KSC400, SC301 and KSC704 hybrids in the second group, KSC260, SC604 and SC307 hybrids in the third group and the KSC707 genotype placed in the fourth group. The two genotypes SC647 and KSC707 can be identified as desirable genotypes (Figure 5B). According to the diagram obtained from Shiraz region, SC604 and KSC260 hybrids were in the first group, SC301, KSC706 and SC647 hybrids in the second group, KSC400, KSC703 and KSC705 genotypes in the third group and KSC707, KSC704 and SC307 genotypes in the fourth group. The genotypes in the fourth group were selected as the preferred hybrids (Figure 5C). In Arak region, SC302, SC601, SC307 and KSC704 genotypes were in the first group, SC301, SC647, KSC400 and KSC706 hybrids in the second group, KSC703, KSC707 and KSC705 hybrids in the third group and KSC260 genotype in the fourth group. The two hybrids SC302 and KSC260 were identified as desirable hybrids based on this diagram (Figure 5D). Various researchers have used principal component analysis diagrams in which the axes of the diagram represent the first and main components in their research (Khatibi et al., 2022; Shojaei et al., 2022b; Emami et al., 2020; Shojaei et al., 2021).

3.4. Polygon diagram

A polygon diagram was used to identify the preferred genotypes regarding yield × trait compositions (Figure 6). This diagram is obtained by connecting the desired genotypes that are farthest from the origin of the diagram. In each section, any hybrid that is close to the evaluated compounds is selected as the desired genotype in terms of that combination. The Which-Won- Where polygon diagram allows researchers to identify genotypes that combine well with different traits (Yan and Hunt, 2002). Paramesh et al. (2016) believed that in this type of diagram, the best genotype for the evaluated traits is displayed at the vertex of the polygon. Based on the polygon diagram obtained on the data of Karaj region, the first and second components explained 64.38 and 14.16%, respectively, and in total more than 78% of the variance of the data. KSC704, KSC707, KSC703, KSC706, KSC705, KSC400, SC301, SC307 and SC604 hybrids had the longest distance from the origin of the graph and were identified as desirable hybrids.

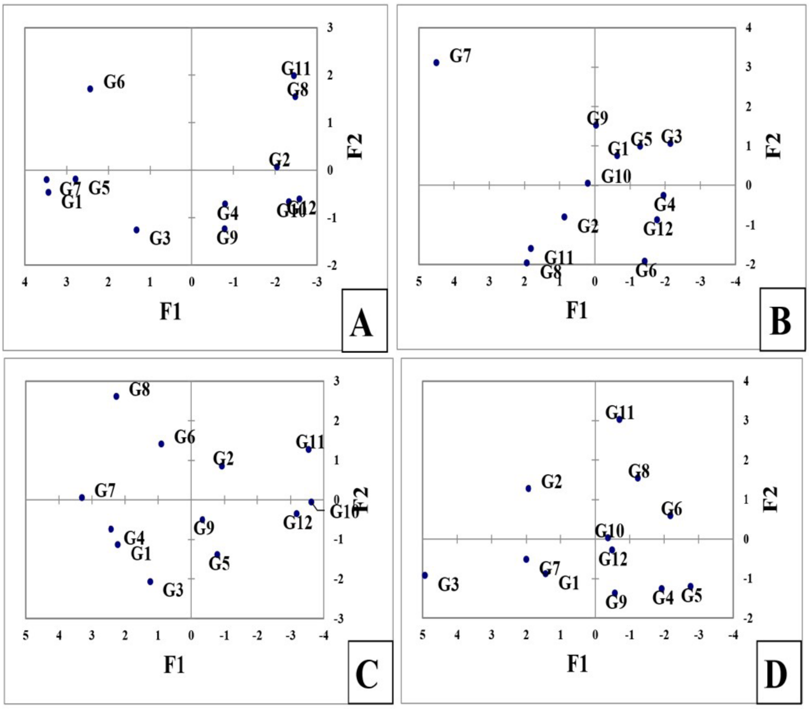

Figure 5. Distribution of genotypes based on the first and second main components in terms of yield × trait in four experimental regions. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

Also, KSC704 genotype in terms of Y × GT combination and KSC707, KSC703 and KSC706 genotypes in terms of Y × GL, Y × PH, Y × EL, Y × GW and Y × NRE combinations were more desirable than other hybrids (Figure 6A). In the diagram obtained from Birjand region, the first component explained 44.53% and the second component 22.77% and a total of 67.3% of the total variance of the data. The genotypes SC604, SC307, KSC707, KSC705, KSC400 and KSC704 had the longest distance from the chart's origin and were identified as superior hybrids. The SC604 and SC307 genotypes performed better in terms of Y × GT composition and the SC647 hybrid in terms of Y × NRE composition and the KSC707 hybrid in terms of Y × GW combination than other hybrids (Figure 6B). Based on the polygon diagram drawn on genotype × yield × trait data in the Shiraz region, the first component explained 62.15% and the second component 18.33% and more than 80% of the variance of the data. SC307, KSC707, KSC703, KSC705, KSC706, SC301, SC302 and SC604 genotypes had the greatest distance from the graph's origin and were selected as the superior genotypes. Also, SC307 hybrid in terms of Y × GT and KSC707 hybrid in terms of Y × GL, Y × GW and Y × PH combinations and KSC705 and KSC703 genotypes in terms of Y × NRE combination were more favorable than other hybrids (Figure 6C). The multidimensional diagram obtained on the data of the Arak region also indicated that the first and second components explained 50.85% and 20.71%, respectively, and a total of 71.56% of the total variance of the data. Due to the greater distance of genotypes from the chart's origin, KSC260, KSC705, KSC706, KSC704 and SC604 hybrids were identified as desirable hybrids. SC604 genotype in terms of Y × GT composition, KSC260 genotype in terms of Y × NRE and Y × ED composition and KSC705 genotype in terms of Y × GW, Y × NRE and Y × GL combinations were more desirable than other hybrids (Figure 6D). According to the four regions' diagrams, the two hybrids KSC705 and KSC604 were identified as desirable hybrids in all regions. Various researchers have used polygon diagrams to evaluate the genotypes of different plants, including sunflower (Ansarifard et al., 2020), corn (Shojaei et al., 2021; Szabó et al., 2022; Illés et al., 2022; Mahrokh et al., 2023), and cowpea (Araújo et al., 2021), sweet corn (Mousavi et al., 2024) sorghum (Khazaei et al., 2022).

3.5. Ranking of genotypes based on yield × trait

Genotype ranking diagram is used to rank genotypes based on genotype × yield × trait (GYT) combinations. This axis diagram, marked with an arrowhead, determines the balance of genotypes in terms of combination and examines the strengths and weaknesses of hybrids in terms of combination. Genotypes located at the positive end of this axis are selected as superior genotypes based on yield × trait combinations, and genotypes close to the axis are more balanced than these combinations (Figure 7). Based on the ranking diagram of genotypes in Karaj region, KSC707, KSC701 and KSC704 hybrids were identified as superior genotypes and SC301, SC302 and SC307 hybrids as unfavorable hybrids. This diagram selected SC301 and SC302 genotypes as balanced hybrids in relation to yield ×

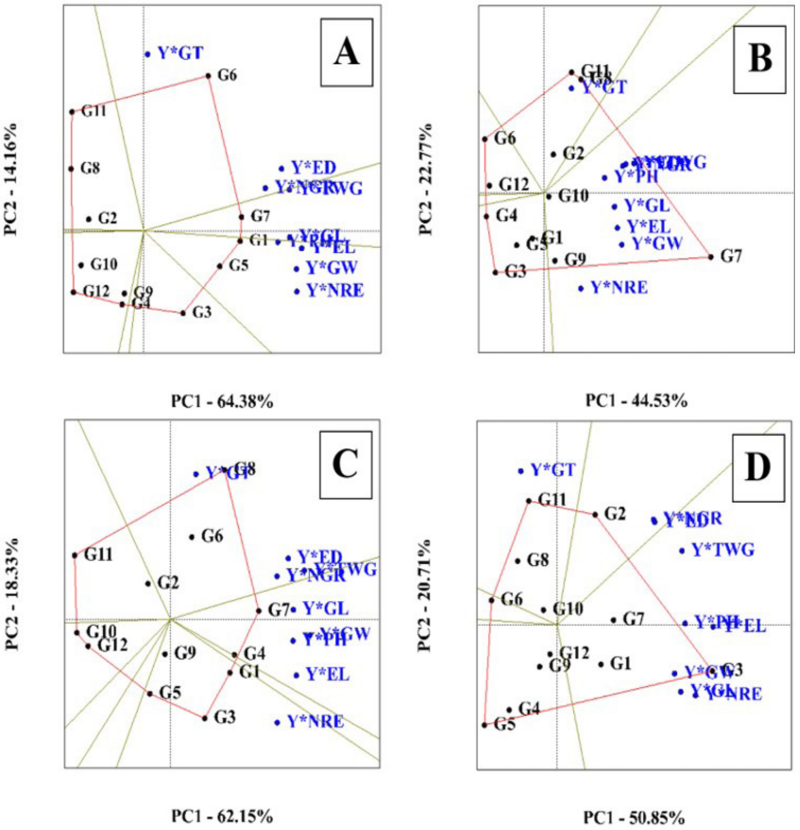

Figure 6. The polygon diagram based on GYT of genotypes in the four regions tested. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

trait combinations. The ranking of hybrids from favorable to unfavorable is as follows (Figure 7A).

$$KSC707 > KSC703 > KSC704 > KSC706 >$$
$$KSC705 > SC647 > KSC400 > KSC260 >$$
$$SC604 > SC307 > SC302 > SC301$$

In the genotype ranking chart in the Birjand region, KSC707 hybrid was identified as the superior hybrid and KSC704 and KSC400 hybrids were identified as undesirable hybrids. Two genotypes SC301 and SC302 were also selected as balanced hybrids compared to the studied compounds. The order of the hybrids from the most desirable hybrid to the most undesirable is as follows: (Figure 7B).

$$KSC707 > SC307 > SC604 > KSC260 >$$
$$SC647 > SC302 > KSC703 > KSC706 >$$
$$KSC705 > SC301 > KSC400 > KSC704$$

The graph obtained in the data of Shiraz region also indicated that KSC707 and SC307 hybrids were identified as superior hybrids and SC302 and SC604 genotypes were identified as unfavorable hybrids. Also, SC301, SC302 and KSC707 genotypes were selected as balanced genotypes based on yield × traits. The order of hybrids from the most desirable to the most unfavorable hybrids is as follows: (Figure 7C).

$$KSC707 > SC307 > KSC400 > KSC703 >$$
$$KSC704 > KSC705 > SC647 > KSC260 >$$
$$KSC706 > SC301 > SC604 > SC302$$

Based on the diagram obtained in Arak region, KSC705, KSC260 and KSC707 hybrids were identified as superior hybrids and KSC706, KSC400 and KSC704 genotypes were identified as unfavorable hybrids. Also SC302 and KSC707 genotypes were selected as balanced genotypes. The order of ranking of genotypes from favorable to unfavorable is as follows: (Figure 7D).

$$KSC705 > KSC260 > KSC707 > KSC703 >$$
$$SC604 > SC302 > SC301 > SC307 >$$
$$SC647 > KSC704 > KSC400 > KSC706$$

By examining the diagrams drawn in all regions, KSC707 and KSC703 hybrids can be selected as top-ranked hybrids and SC301 hybrid as low-ranking hybrids compared to other genotypes.

3.6. Grouping genotypes based on ideal genotype

Genotype ranking diagram based on the ideal genotype is used to identify the best hybrid based on the best point where the center of the dwarf is concentric, indicated by an arrow on the chart, and the rest of the hybrids are ranked based on this point. This diagram defines the

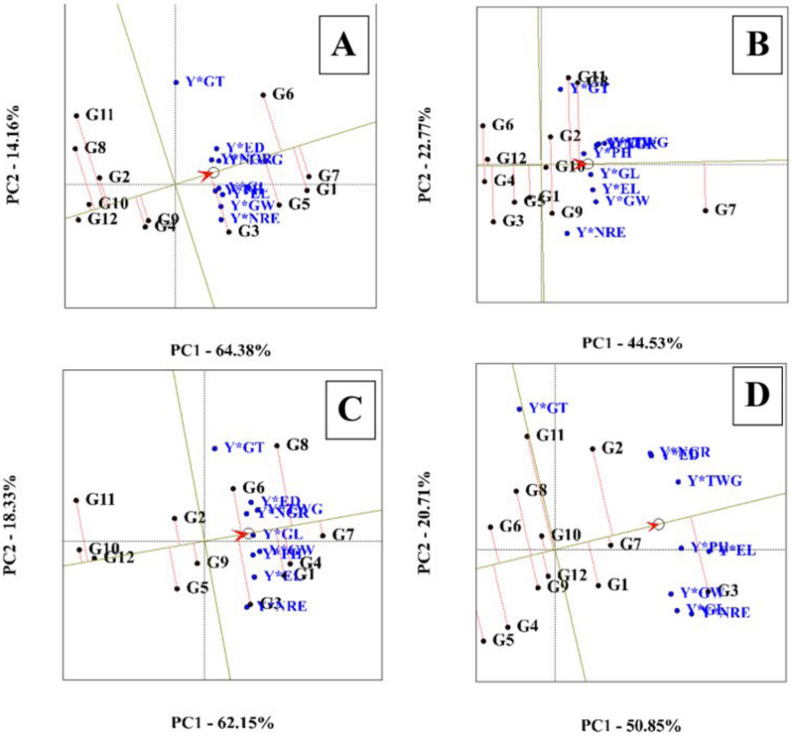

Figure 7. Ranking diagram of genotypes based on GYT compounds in the four regions. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

hypothetical ideal genotype based on the most stable and productive genotype [20]. Based on the diagrams obtained from Karaj region data, KSC707, KSC703 and KSC704 genotypes were selected as superior hybrids and SC301, SC307 and SC604 hybrids as unfavorable hybrids. The order of ranking of hybrids based on this graph from favorable to unfavorable is as follows: (Figure 8A).

$$KSC707 > KSC703 > KSC704 > KSC706 > KSC705 > SC647 > KSC400 > KSC260 > SC302 > SC307 > SC604 > SC301$$

The ranking chart of genotypes based on the ideal genotype in Birjand region showed that KSC707 hybrid was more desirable than other hybrids and KSC704, KSC705 and KSC400 hybrids were introduced as undesirable hybrids. The ranking of genotypes in this region from the most favorable to the most unfavorable is as follows: (Figure 8B).

$$KSC707 > SC604 > KSC260 > SC302 > SC647 > KSC703 > KSC706 > SC301 > KSC705 > KSC400 > KSC704$$

The graph obtained in Shiraz region also showed that KSC707, KSC400 and KSC703 hybrids had better rank than other genotypes and SC604, SC302 and SC301 hybrids had lower rank than other hybrids. The ranking of hybrids in Shiraz region from the most favorable to the most undesirable is as follows: (Figure 8C).

$$KSC707 > KSC400 > KSC703 > KSC705 > KSC704 > SC307 > SC647 > KSC260 > KSC706 > SC301 > SC302 > SC604$$

Based on the diagrams drawn from the data of Arak region, KSC705, KSC707 and KSC260 genotypes were identified as desirable hybrids and KSC706, KSC400 and KSC704 genotypes were identified as unfavorable hybrids. The order of genotypes in Arak region from favorable to desirable is as follows (Figure 8D).

$$KSC705 > KSC707 > KSC260 > KSC703 > SC302 > SC301 > SC604 > SC647 > SC307 > KSC704 > KSC400 > KSC706$$

Considering the ranking of genotypes based on the ideal genotype in all evaluated areas, KSC707 and KSC703 hybrids were identified as desirable hybrids and SC301 genotype as unfavorable hybrids, respectively.

3.7. Cluster analysis

Cluster analysis based on the average yield × trait combinations in two years of experiment, genotypes based on four tested environments, in three different main clusters. Also, yield × traits were grouped into 5 main clusters. The first cluster was divided into three sub-clusters in the genotype grouping, with G7K, G7B, G9S and G9K genotypes located below the first cluster. Under the second cluster,

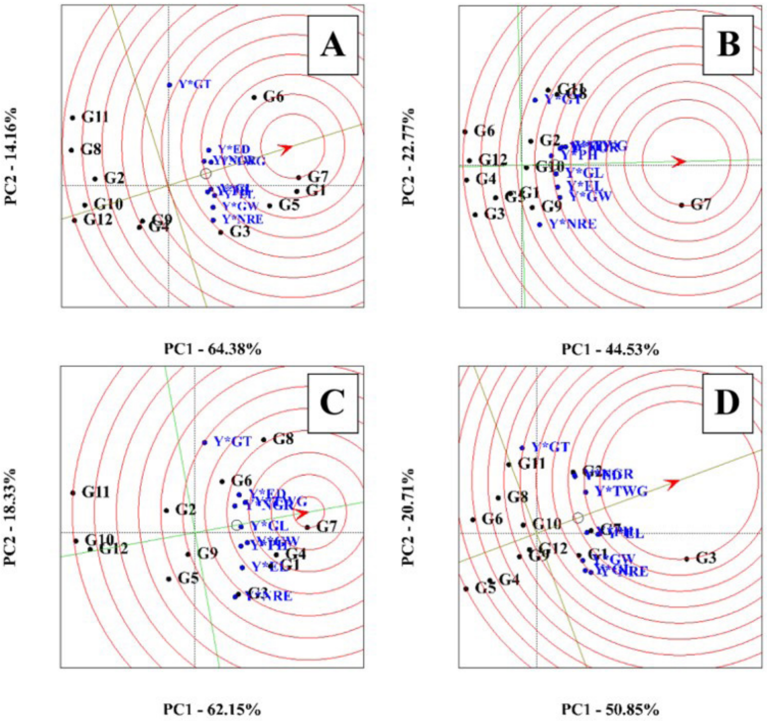

Figure 8. Ranking chart of genotypes based on the ideal genotype in the four regions. A: KARAJ, B: BIRJAND, C: SHIRAZ, D: ARAK.

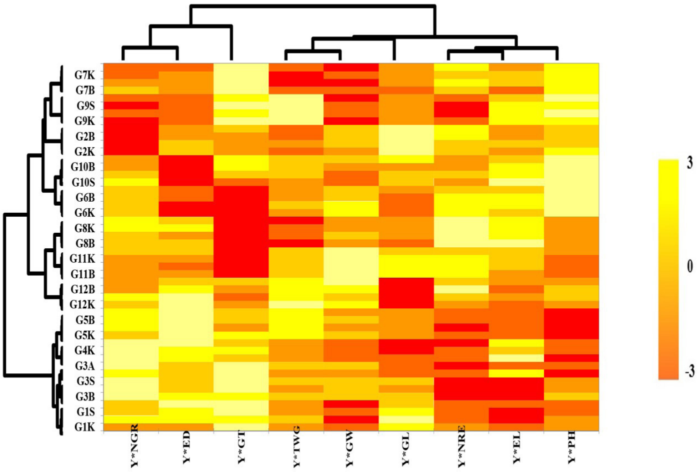

Figure 9. Cluster analysis of maize hybrids in four regions evaluated based on yield composition × trait.

two genotypes G2B and G2K were in the same group and the third sub-cluster included G10B, G10S, G6B and G6K hybrids, which were in good condition in Y × PH, Y × EL and Y × GT combinations. The second cluster was also divided into two sub-clusters. The first sub-cluster included G8K, G8B, G11K and G11B hybrids and the second sub-cluster included G12B and G12K genotypes. This cluster had good performance in terms of Y × GW, Y × NGR and Y × ED compounds. Finally, the third cluster was grouped into two sub-clusters. The first sub-cluster included G5B, G5K, G4K and G3A genotypes and the second sub-cluster included G3A, G3B, G1S and G1K genotypes, which were in good condition in terms of Y × GT, Y × NGR and Y × ED combinations were placed in a group (Figure 9). Yue et al. (2022) Used heat map cluster analysis to evaluate 28 maize genotypes and group them (Yue et al., 2022).

4. Conclusions

The results of combined analysis performed on the data of this study showed a significant difference in genotypes in terms of the studied compounds and considering the significance of the effect of genotype × year × environment, comparison of the average effect of genotype × year in environments variation was performed on the data ($p \leq 0.01$). Comparing the average effect of genotype × year in different places showed that KSC703 and KSC707 hybrids are among the most productive hybrids among the studied genotypes in terms of grain yield. By examining the correlation coefficients between yield × traits in the tested areas, Y × TWG with Y × GW, Y × NRE, Y × NGR and Y × EL, Y × ED with Y × NGR, Y × NRE with Y × GW and the combination of Y × GW with Y × GL had a positive and significant correlation in all regions. The correlation diagrams drawn on the data of the evaluated areas also showed the correlation of most compounds except Y × GT with each other. Based on the analysis of the main components, the first three components explained the greatest diversity in the population and were named as the component of ear grain profile, grain thickness component and plant height profile component, respectively. Polygon diagrams, ranking genotypes based on yield × trait combinations and were used ranking of genotypes based on ideal genotype, a graphical analysis method. Based on the polygon diagrams of KSC705 and KSC604 hybrids, based on genotype ranking diagrams based on yield × trait and genotype ranking based on ideal genotype, two hybrids KSC707 and KSC703 were identified as desirable hybrids. Based on the cluster analysis performed on the average yield compounds × trait in two years of experiment, genotypes were grouped into three main groups in terms of these compounds.

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