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GGE-BIPLOT ANALYSIS FOR GENOTYPE ENVIRONMENT INTERACTIONS IN SOME QUALITY TRAITS OF SILAGE MAIZE GENOTYPES

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ABSTRACT

Silage maize quality is crucial for yield parameter. However, there is little unknown regarding to GGE-biplot analysis for Genotype-Environment Interactions. For this purpose, experiments were conducted in 6 different environments in randomized blocks design with 3 replications. Effects of genotypes, environments and genotype x environment interactions (GEI) on dry hay yield (DHY) and 8 other quality traits of dry hay [crude protein content (CPC), crude protein yield (CPY), crude ash content (CAC), relative feed value (RFV), dry matter digestibility (DMD), dry matter intake (DMI), acid detergent fiber (ADF) and neutral detergent fiber (NDF)] of 25 silage maize genotypes were investigated. GGE-biplot analysis was used for GEI analysis of 9 traits. Biplot graph axes of the traits were able to explain the least 40.08% of the total variation in CPC and the most 69.6% of the total variation in DHY. It was observed through assessing all traits together that the genotypes of SAFAK and BURAK were placed in ideal genotype section and the genotypes of WAYNE and 30B74 were placed in the stable portion of desirable genotype section for DHY, which is the most significant quality trait in silage maize culture. Besides them, the genotypes, SEME KUKURUZA 877, SEME KUKURUZA 873, DKC 6589 and DKC 7211 were identified as stable genotypes. Furthermore, the genotype 6 was identified as a stable genotype with the best adaptation for ADF, NDF and DMD, the genotype BURAK for crude ash content, the genotype ADV 2898 for crude protein content, the genotype SAFAK for crude protein yield and the genotypes DKC 6590 and DIAN for RFV.

Keywords: crude protein, dry hay yield, GGE-biplot, nutritive quality, silage maize.

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INTRODUCTION

Silage is a common means of preservation and used in animal nutrition worldwide (Wilkinson and Toivonen, 2003; Wilkinson and Davies, 2012; Kaplan *et al.,* 2017). Although several crops can be ensiled (Pisphar-Komleh *et al.,* 2011), maize is the greatest silage crop because of high yields, palatability, and digestibility. Therefore, maize is ensiled as a better source of feed for ruminants (Schroede, 2004; Kaplan *et al.,* 2016). In line with this, the genotypes, environmental and ecological conditions, and cultural practices have great impacts on yield and quality of maize crop (Budakli Carpici *et al.,* 2010).

The greatest objective in multi-environment trials is to investigate several traits and regarding investigated traits to identify the most appropriate genotype for the target environments (Yan and Rajcan, 2002). However, efficient and accurate assessment of numerous traits of several genotypes grown in multi-environments is a great challenge for researchers. Therefore, different statistical analyses were developed for the assessment of traits in multi-environment trails (1988; Flores *et al.,* 1998; Yan, 2001; Akcura *et al.,* 2006). Among these methods, biplot analysis is the most common one (Yang *et al.,* 2009; Kokten *et al.,* 2017; Kokten *et al.,* 2018). Biplot analysis is composed of single and dual linear models with slight differences in between (Cornelius and Seyedsadr, 1997). The additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype × environment interaction effects (GGE) model (fitted to residuals after removal of environment main effects) are two most common models used in biplot analysis (Yang *et al.,* 2009; Akcura *et al.,* 2019). GGE biplot method provides significant advantages for visual assessment of two-way data (both the genotypes and the environments) of multi-environment trials. Because of conveniences in the assessment and interpretation of the graphs, the GGE biplot method is commonly preferred by several researchers (Yan, 2014).

The present study was conducted to assess genotype × environment interactions for 9 traits of 25 silage maize genotypes grown in 6 environments with biplot analysis.

MATERIALS AND METHODS

Experiments were conducted with 25 different maize genotypes (31P41, 30B74, 31Y43, 31A34, 12-219, 12-218, 12-231HO, DKC 955, DKC 6903, DKC 6589, DKC 7211, DKC 6590, DIAN, MARVIN, ELDORA,

WAYNE, SAFAK, BATEM EFE, BURAK, SEME KUKURUZA 877, SEME KUKURUZA 873, ADV 2898, R.U 4 H.D, TUONO and TRUVA) grown in 6 different environments.

Experiments were setup in Diyarbakir-Bismil, (altitude of 535 m), Bingol (altitude of 1153 m) and Elazig (altitude of 1070 m) provinces. Experiments were conducted in 2014 and 2015 growing seasons using a randomized blocks design with 3 replications. Seeds were sown in 5 × 2.8 m plots with 70 × 15 cm spacing. Based on pre-sowing soil analyses, 80 kg ha^{-1} N, 80 kg ha^{-1} P_2O_5 and 80 kg ha^{-1} K_2O were supplied to soils. Two more nitrogen fertilizer doses (150 kg ha^{-1} N in total) were applied, one with inter-row hoeing, when the plants reached to a height of 50-60 cm, and the other one at top tassel formation period. Throughout the growing season, two hoeings and one earthing up were performed. Plants were irrigated once a week based on field capacity.

Climate and soil data for experimental sites are provided in Table 1. Amount of precipitation was higher in the first year of the experiments than in the second year in all three provinces. Experimental soils were loamy in texture. Soil pH was slightly alkaline in Diyarbakır and Elazig provinces (7.73 and 7.78, respectively) and slightly acidic in Bingol province (6.37). Soil lime content was medium in Diyarbakır and Elazig and low in Bingol province.

Silage maize hay samples were ground in a mill with 1 mm sieve and made ready for chemical analysis. NDF and ADF analyses were carried out in accordance with the methods specified in Van Soest (1994), respectively by using an ANKOM 200 Fiber Analyzer (ANKOM Technology Corp. Fairport, NY, USA). The crude ash content of samples was determined by burning at 550 °C for 8 hours. The Kjeldahl method was used to determine the nitrogen (N) content of dried samples taken from the plots. Crude protein content was calculated by using the equation of N × 6.25 (AOAC, 1990). Relative feed value (RFV) of silage maize hay samples was calculated from the estimates of dry matter digestibility (DDM) and dry matter intake (DMI) (Morrison, 2003). DMD % = 88.9 - (0.779 × ADF %); DMI % of BW = 120 / NDF %; RFV = (DDM % × DMI %) /1.29

Resultant data were initially subjected to variance analysis and GGE biplot analysis method was used for data assessment (Yan and Kang, 2003; Yan, 2014). Genotype-focused biplot graphs created for each traits were used to assess genotype × environment interactions. The statistical theory of GGE biplot methodology was explained in detail by Yan (2014). The mathematical model of GGE biplot analysis used separately for each trait are provided below: $Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon ij$

where; Yij = Expected value for cultivar $_i$ in environment $_j$; μ = Grand mean of cultivar– environment combinations; βj= Main effect of environment j; λ1 and λ2 are singular values of the first and the second largest principal components, PC1 and PC2, respectively; ξi1 and ξi2 are eigenvectors of cultivar i for PC1 and PC2, respectively; η_{1j} and η_{2j} are eigenvectors of year j for PC1 and PC2, respectively, and εij = Residue for each cultivar–environment combination not explained by PC1 and PC2.

In order to assess the stability of genotypes, the average environment axis (AEA) was plotted by taking the mean of PC1 and PC2 scores for environments. A performance line passing through the origin of the biplot was used to determine the mean performance of the genotype. The circles created as taking the Average Environment Axis (AEA) as the focus improved the efficiency of the biplot graph in selecting the ideal cultivars. Based on the performance of the cultivars and variations in each trait, the location of cultivars on the graph either moved close to or away from the AEA. In GGE biplot analysis performed separately for each trait, instability index, distance from the ideal genotype and order numbers designating the position of genotypes over the graph were also calculated in GGE biplot program (Yan, 2014).

RESULTS

Variance analysis results for dry hay yield and 8 quality traits are provided in Table 2. Effects of genotype and genotype × environment interactions on all traits were found to be significant (P<0.01). The expression levels of GGE biplot axis values of each trait, statistical terms, and axis expiation ratios were also provided in Table 2. Genotype averages of each trait over the environments and GGE biplot analysis parameters are provided in Tables 3 and 4.

Dry hay yield is the most significant trait investigated in this study. Dry hay yields of the genotypes at different environments varied between 1929.6-2797.3 kg da^{-1} (Table 3). The genotypes SAFAK and 30B74 had the greatest dry hay yields. Genotype-focused GGE biplot created for dry hay yield is presented in Figure 1. GGE biplot axes explained 69.6% total variation in dry hay yields. The genotypes BURAK and SAFAK were placed in ideal genotype section. The genotypes 30B74 and WAYNE were placed at the closest position to ideal genotypes. The genotypes DKC 6903, 31A34 and 12-231HO were placed at the furthest position to ideal genotype. Considering the stability, the genotypes WAYNE, SEME KUKURUZA 873 and SEME KUKURUZA 877 were identified as the most stable genotypes and the genotypes SAFAK, BURAK and 30B74 with high PC1 values had higher hay yields than the stable genotypes. Thus, they were considered as genotypes well complied with good environments (Figure 1).

Hay crude protein contents, crude protein yields and GGE biplot graph for these traits are presented in Figure 2a and b. Crude protein contents of the genotypes in different environments varied between 6.2-7.4% and crude protein yields varied between 122.7-185.8 kg da^{-1}. GGE biplot axes were able to explain 40.8% of the total variation in protein contents and 57.8% of the total variation in crude protein yields. There were not any genotypes in the innermost circle of Figure 2a. Regarding crude protein contents, the genotypes ADV 2898, ELDORA and DKC 955 were identified as the most stable genotypes and the genotypes SAFAK and BURAK had the lowest values. Regarding crude protein yield, the genotype SAFAK was identified as the best genotype and the genotype DKC 6903 was identified as the most undesired genotype. The genotypes SAFAK, WAYNE and 31Y43 were identified as the most stable genotypes and the genotypes BURAK and 12-231HO placed the furthest from average environment axis was identified as the least stable genotypes (Figure 2b).

Crude ash contents of the genotypes in six different environments varied between 4.2-6.2% (Table 3). GGE biplot axes were able to explain 50.5% of the total variation in crude ash contents (Figure 2c). There were not any genotypes within the ideal genotype section. The genotype BURAK was placed at the closest position to the ideal section. The genotypes BATEM EFE and SAFAK had high crude ash contents, but they were still identified as unstable genotypes (Figure 2c).

Regarding ADF and NDF ratios, the genotypes with the lowest values are preferred. ADF and NDF ratios of genotypes varied respectively between 22.8-34.8% and between 45.2-57.1% (Table 4). As can be seen in Figure 2g and h, PC1 and PC2 axes of the biplot graph explained 63.3% of the total variation in ADF and 62.0% of the total variation in NDF ratios. The genotypes 12-218, TOUNO, DKC 6590, DIAN and MARVIN were identified as the best genotypes with regard to ADF ratios and the genotypes 12-218, 12-219, DKC 7211, DKC 6903, 31Y43, 31A34 and WAYNE were identified as the best genotypes with regard to NDF ratios. The genotype 12-218 was identified as the most stable genotype for both traits and the genotype 12-231HO was identified as the most unstable genotype for ADF and genotypes 31P41 for NDF (Figure 2g and h).

Dry matter digestibility (DMD) values of the genotype varied between 61.8-71.1% (Table 4). The greatest values were observed in genotypes DIAN, 12-218 and TUONO. GGE-biplot axes were able to explain 63.3% of the total variation in DMD values (Figure 2e). The genotypes 12-218, TUONO, DKC 6590, MARVIN and DIAN were placed in ideal genotype section. The genotypes TUONO and 12-218 were identified as the most stable genotypes, the genotype BATEM EFE was identified as the most unstable genotype and the genotype BURAK had the least values (Figure 2e).

Dry matter intake (DMI) values of the genotypes grown in different environments varied between 2.2-2.8%. The biplot axes explained 59.0% of the total variation in DMI values. There were not any genotypes within the ideal genotype section. The genotype DKC 6590 was the most stable and genotype 31P41 was the most unstable genotype. The genotypes DIAN and WAYNE were identified as stable genotypes (Figure 2f).

Relative feed value (RFV) of the genotypes varied between 106.6 and 154.0. The biplot graph created with genotype and environment data was able to explain 56.0% of the total variation in RFVs. While the genotype DIAN was placed right over the ideal genotype line, the genotypes DKC 6589, DKC 7211 and DKC 6590 were identified as the most stable and the genotype 31P41 was identified as the most unstable genotype (Figure 2d).

It was observed through assessing all traits together that the genotypes SAFAK and BURAK were placed in ideal genotype section and the genotypes WAYNE and 30B74 were placed in the stable portion of desirable genotype section for dry matter yield, which is the most significant quality trait in silage maize culture. Besides them, the genotypes, SEME KUKURUZA 877, SEME KUKURUZA 873, DKC 6589 and DKC 7211 were identified as the most stable ones for dry matter yield. The genotype 12-218 was identified as a stable genotype with the best adaptation for ADF, NDF, and DMD, the genotype BURAK for crude ash content, the genotype ADV 2898 for crude protein content, the genotype SAFAK for crude protein yield and the genotypes DKC 6590 and DIAN for RFV.

Table 1. Data for experimental sites.

Code	Environments / seasons		Altitude (m.a.s.l.)	Annual precipitation (mm)	Irrigation*	Soil
DIY14	Diyarbakir	2014	535	110.7	100 x 4	pH= 7.73 Loamy, medium lime
EL14	Elazig	2014	1070	121.5	100 x 4	pH= 7.78 Loamy, medium lime
BIN14	Bingol	2014	1153	135.8	100 x 4	pH= 6.37 Loamy, low lime
DIY15	Diyarbakir	2015	535	67.2	100 x 4	pH= 7.73 Loamy, medium lime
EL15	Elazig	2015	1070	64.8	100 x 4	pH= 7.78 Loamy, medium lime
EL15	Bingol	2015	1153	96.6	100 x 4	pH= 6.37 Loamy, low lime

* – experiments were irrigated using flood irrigation 4 times at required periods. m.a.s.l: Meters above sea level

Table 2. Variance analysis and GGE biplot axis values for silage maize traits.

Source of variation	DF	Mean Square DHY	CPC	CPY	CAC	ADF	DMI	CPC	NDF	DMD	RFV
BLK(ENV)	12	521849.757	0.148	2121.187	0.487	1.646	0.004	0.148	1.281	1	16.632
GEN (G)	24	944450.894**	2.205**	4462.811**	4.235**	124.026**	0.389**	2.205**	140.665**	75.260**	2302.580**
ENV (E)	5	2461558.692**	48.686**	23959.810**	11.255**	2334.914**	11.216**	48.686**	3597.604**	1416.986**	66056.868**
G x E	120	304068.833**	2.135**	2350.974**	3.960**	50.712**	0.275**	2.135**	98.129**	30.776**	1157.469**
Error	288	151077.043	0.176	775.572	0.161	1.625	0.016	0.176	3.025	0.986	74.663
% of Total Sum of Squares											
PC1		49.9^{a}	20.5^{a}	37.1^{a}	28.3^{a}	47.6^{a}	34.7^{a}	20.5^{a}	38.2^{a}	47.6^{a}	35.8^{a}
PC2		19.7^{a}	20.3^{a}	20.7^{a}	22.2^{a}	15.7^{a}	24.3^{a}	20.3^{a}	23.8^{a}	15.7	20.2^{a}
PC3		15.5	17.5^{a}	15.4	20.8^{a}	13.8	15.4	17.5^{a}	15.5	13.8	15.8
Simple Statistics											
Grand Mean		2223.958	6.744	149.285	5.072	26.78	2.508	6.744	49.465	68.039	133.877
Std Error		388.686	0.42	27.849	0.401	1.275	0.125	0.42	1.739	0.993	8.641
CV%		17.48	6.22	18.65	7.91	4.76	4.99	6.22	3.52	1.46	6.45
G/GGE		0.38	0.17	0.28	0.18	0.33	0.22	0.17	0.22	0.33	0.28

DHY: Dry hay yield; CPC: Crude protein content; CPY: Crude protein yield; CAC: Crude ash content; RFV: Relative feed value; DMD: Dry matter digestibility; DMI: dry matter intake; ADF: Acid detergent fiber; NDF: Neutral detergent fiber; **: P<0.01 a: Information ratio > 1

Table 3. Averages over environments for dry hay yield (DHY), crude protein content (CPC), crude protein yield (CPY) and crude ash content (CAC) of 25 maize genotypes and some stability parameters.

	DHY					CPC					CPY					CAC				
GN	Mean	INS	R	DI	DHY	Mean	INS	R	D	CPC	Mean	INS	R	D	CPY	Mean	INS	R	D	CAC
1	2115.2	50.4	21.0	3.3	-S	6.3	0.6	23.0	2.3	UD	135.5	28.3	19.0	2.9	-US	5.0	0.6	22.0	3.2	UD
2	2526.2	97.2	3.0	1.5	D	6.7	-0.2	17.0	2.1	-S	164.2	-27.9	4.0	1.8	DUS	5.3	0.4	6.0	2.2	+S
3	2126.5	24.7	11.0	2.7	-S	7.4	0.2	8.0	1.4	+S	159.9	-0.4	5.0	1.8	DS	4.6	-0.1	12.0	2.6	-S
4	2129.7	-267.8	24.0	3.3	UD	6.5	-0.8	19.0	2.1	-US	132.9	8.2	22.0	3.1	-S	5.7	0.1	4.0	2.0	+S
5	2184.3	-34.7	16.0	3.0	-S	6.9	0.4	22.0	2.2	-US	153.6	26.7	10.0	2.1	+S	4.8	-0.4	19.0	2.9	-US
6	2159.8	43.0	15.0	3.0	-S	7.1	0.3	18.0	2.1	-US	154.1	27.7	11.0	2.1	+S	4.7	-0.7	23.0	3.2	UD
7	2057.9	-334.3	22.0	3.3	UD	6.4	0.8	21.0	2.2	-US	138.8	41.3	24.0	3.2	-S	5.5	0.8	13.0	2.7	-US
8	2059.9	234.1	13.0	2.8	US	6.8	0.1	5.0	1.1	+S	136.9	-24.1	20.0	2.9	-S	5.4	-0.8	8.0	2.3	+US
9	2015.5	-150.2	25.0	3.4	UD	6.2	0.2	10.0	1.4	+S	122.7	2.0	25.0	3.3	-S	4.8	-0.7	18.0	2.9	-US
10	2201.2	-48.3	12.0	2.7	+S	6.3	0.0	12.0	1.6	+S	138.8	3.1	17.0	2.7	-S	4.5	-0.5	15.0	2.7	-US
11	2268.4	-112.6	8.0	2.5	+S	7.2	-0.4	2.0	0.8	DUS	162.6	-12.4	7.0	2.0	DUS	5.3	0.2	16.0	2.7	-S
12	2163.9	159.9	14.0	2.9	US	6.5	0.5	3.0	0.9	DUS	142.0	2.9	18.0	2.8	-S	4.8	-0.5	21.0	3.0	-US
13	2026.2	20.0	20.0	3.3	-S	6.5	-0.6	16.0	2.0	-US	126.9	-7.5	23.0	3.2	-S	5.4	-0.4	17.0	2.8	-US
14	2102.0	5.7	19.0	3.3	-S	7.0	0.3	6.0	1.2	+US	148.7	22.9	13.0	2.5	-US	4.2	0.9	24.0	3.3	UD
15	2067.8	-221.1	18.0	3.1	US	6.8	-0.3	7.0	1.2	+US	141.6	2.4	15.0	2.7	-S	4.8	-0.7	20.0	3.0	-US
16	2062.0	-176.7	17.0	3.0	US	6.9	-0.1	4.0	1.0	DS	142.3	-6.3	16.0	2.7	-S	5.1	0.6	14.0	2.7	-US
17	2415.5	-9.3	4.0	2.0	DS	7.1	-0.2	14.0	1.8	-S	171.7	-3.4	2.0	1.5	DS	5.2	0.7	10.0	2.5	+US
18	2797.3	110.9	1.0	0.9	I	6.6	0.2	24.0	2.4	UD	185.8	-2.1	1.0	0.8	I	5.4	1.0	3.0	1.7	+US

19	2441.7	477.9	7.0	2.4	US	6.5	0.0	20.0	2.1	-S	154.3	-9.1	6.0	1.9	DS	5.8	-0.8	2.0	1.5	+US
20	2146.8	-25.8	10.0	2.6	-S	6.8	0.0	13.0	1.7	-S	155.7	12.8	9.0	2.1	DS	4.9	-0.5	7.0	2.3	+US
21	2726.1	-136.0	2.0	1.2	I	6.3	-1.0	25.0	2.6	UD	165.2	-36.0	8.0	2.0	+US	6.2	-0.2	1.0	0.9	DS
22	2282.8	41.8	6.0	2.4	+S	6.6	0.4	15.0	1.8	-US	143.2	-17.1	14.0	2.5	-US	4.4	-0.2	25.0	3.4	UD
23	2269.6	10.2	5.0	2.3	+S	7.0	-0.6	11.0	1.5	+US	151.9	-21.7	12.0	2.3	+US	5.0	-0.1	11.0	2.6	-S
24	2323.0	347.5	9.0	2.6	US	7.3	0.0	1.0	0.6	DS	166.4	-16.4	3.0	1.8	DUS	5.0	0.8	9.0	2.4	+US
25	1929.6	-106.4	23.0	3.3	-S	6.9	0.2	9.0	1.4	+S	136.5	5.9	21.0	3.0	-S	5.1	0.4	5.0	2.2	+S
Mean	2224.0					6.7					149.3					5.1				
LSD5%	636.1					0.7					45.6					0.7				

INS: Low absolute value genotypes are stable; R: Order number. The genotype with the greatest value has the lowest order number; DI: distance from ideal genotype; -S: Low value stable; +S: High value stable; US: Unstable; UD: Undesirable genotype; DS: Desirable stable genotype; DUS: Desirable unstable genotype

Table 4. Averages over environments for relative feed value (RFV), dry matter digestibility (DMD), dry matter intake (DMI), acid detergent fiber (ADF) and neutral detergent fiber (NDF) of 25 maize genotypes and some stability parameters.

	RFV					DMD					DMI					ADF					NDF				
GN	Mean	INS	R	D	RFV	Mean	INS	R	D	DMD	Mean	INS	R	D	DMI	Mean	INS	R	D	ADF	Mean	INS	R	D	NDF
1	133.9	16.6	16.0	1.8	+US	69.1	2.3	6.0	1.5	DUS	2.5	0.3	20.0	1.9	-US	25.4	2.9	20.0	3.8	DUS	49.8	5.0	10.0	2.6	+US
2	106.6	-17.2	25.0	3.2	UD	61.8	-3.3	25.0	3.8	UD	2.2	-0.3	24.0	2.9	UD	34.8	-4.2	1.0	1.7	UD	57.1	-6.1	3.0	1.7	-US
3	134.8	-8.0	11.0	1.6	+S	67.9	-1.6	15.0	1.8	+S	2.5	-0.1	5.0	1.2	DS	27.0	-2.1	10.0	3.4	DUS	48.7	-1.9	18.0	3.0	I
4	130.9	-3.0	10.0	1.5	+S	67.2	-0.8	14.0	1.8	+S	2.5	0.0	6.0	1.2	DS	27.9	-1.0	8.0	3.3	DS	50.3	-1.9	16.0	3.0	I
5	140.8	-15.0	9.0	1.5	DUS	68.3	-1.2	12.0	1.6	+S	2.6	-0.2	11.0	1.4	DUS	26.5	-1.6	15.0	3.5	I	47.4	-4.0	21.0	3.1	I
6	150.6	-17.3	5.0	1.3	DUS	70.7	-0.3	2.0	1.0	DS	2.7	-0.3	10.0	1.4	DUS	23.4	-0.4	24.0	4.1	I	45.6	-4.0	23.0	3.2	I
7	125.3	7.3	19.0	1.9	-S	68.0	4.0	22.0	2.1	-US	2.3	0.1	22.0	2.0	-S	26.9	5.1	11.0	3.5	-US	52.8	2.2	4.0	2.2	-US
8	120.3	-2.2	22.0	2.2	-S	65.2	-1.6	23.0	2.5	-S	2.4	-0.1	19.0	1.8	-S	30.4	-2.1	3.0	2.7	-US	51.9	-1.4	6.0	2.4	-DS
9	134.4	-9.1	15.0	1.8	-S	68.3	-1.6	13.0	1.7	+S	2.5	-0.2	15.0	1.6	+US	26.4	-2.0	13.0	3.5	DUS	48.7	-3.0	11.0	2.7	I
10	142.9	9.1	4.0	1.1	DS	69.4	2.0	8.0	1.5	DUS	2.6	0.2	4.0	1.1	DUS	25.1	2.6	18.0	3.7	DUS	47.8	3.8	22.0	3.2	+US
11	137.2	-7.6	6.0	1.4	DS	67.0	-1.4	20.0	2.0	-S	2.6	-0.2	7.0	1.2	DUS	28.2	-1.9	6.0	3.1	DUS	47.2	-3.5	20.0	3.0	I
12	146.8	-4.2	3.0	1.0	DS	70.2	0.6	4.0	1.1	DS	2.7	0.0	3.0	1.0	DS	24.0	0.7	22.0	4.0	I	46.5	-0.1	19.0	3.0	DUS
13	131.6	9.5	8.0	1.5	DUS	68.0	2.6	11.0	1.6	DUS	2.4	0.1	13.0	1.5	+US	26.8	3.3	19.0	3.7	DUS	50.6	1.9	12.0	2.7	DUS
14	154.0	5.4	1.0	0.7	I	71.1	1.4	1.0	1.0	DS	2.8	0.1	1.0	0.9	DS	22.8	1.8	25.0	4.2	I	45.2	1.8	24.0	3.2	DUS
15	145.7	5.3	2.0	1.0	DS	70.0	1.0	5.0	1.1	DS	2.6	0.2	2.0	1.0	DS	24.2	1.3	21.0	4.0	I	46.9	2.2	25.0	3.2	DUS
16	135.7	13.1	7.0	1.4	DUS	68.5	2.2	9.0	1.6	DUS	2.5	0.2	12.0	1.4	+US	26.2	2.8	17.0	3.6	DUS	49.5	3.8	17.0	3.0	+US
17	135.8	-6.1	14.0	1.8	-S	68.1	-1.9	17.0	1.9	+S	2.6	-0.1	9.0	1.3	DS	26.7	-2.4	9.0	3.4	-DUS	47.8	-1.9	13.0	2.8	I
18	135.5	7.5	23.0	2.5	-S	69.1	0.6	7.0	1.5	DS	2.5	0.1	25.0	3.0	UD	25.4	0.8	16.0	3.6	I	50.7	1.4	1.0	1.4	-US
19	128.5	0.4	21.0	2.2	-S	68.1	-2.4	16.0	1.8	+US	2.4	0.0	21.0	1.9	-S	26.6	-3.1	14.0	3.5	DUS	50.5	0.7	5.0	2.3	-DUS
20	143.1	12.3	12.0	1.6	+US	70.3	-0.1	3.0	1.1	DS	2.6	0.2	14.0	1.6	+US	23.8	-0.1	23.0	4.0	I	47.3	4.1	14.0	2.8	+US
21	116.0	-3.7	24.0	2.7	-S	64.8	0.0	24.0	2.8	-S	2.3	-0.2	23.0	2.7	-US	31.0	0.0	2.0	2.2	-S	53.9	-3.2	2.0	1.5	-S
22	132.7	1.8	13.0	1.7	-S	67.7	-1.2	18.0	1.9	-S	2.5	0.1	8.0	1.3	DS	27.2	-1.6	7.0	3.2	-DUS	48.9	1.6	15.0	2.9	DUS
23	126.2	4.4	17.0	1.8	-S	67.6	0.7	10.0	1.6	DS	2.4	0.1	16.0	1.7	-S	27.3	0.9	12.0	3.5	-DS	51.4	1.6	9.0	2.5	DUS
24	123.9	3.1	20.0	2.0	-S	66.7	-0.1	21.0	2.1	-S	2.4	0.1	17.0	1.7	-S	28.4	-0.2	4.0	3.0	-DS	51.5	1.2	7.0	2.5	-DUS
25	133.8	-2.5	18.0	1.9	-S	67.9	0.2	19.0	1.9	-S	2.5	-0.1	18.0	1.7	-S	27.0	0.3	5.0	3.1	-DS	48.6	-0.4	8.0	2.5	-DUS
Mean	133.9					68.0					2.5					26.8					49.5				
LSD5%	14.1					1.6					0.2					2.1					2.8				

INS: Low absolute value genotypes are stable; R: Order number. The genotype with the greatest value has the lowest order number; DI: distance from ideal genotype; -S: Low value stable; +S: High value stable; US: Unstable; UD: Undesirable genotype; DS: Desirable stable genotype; DUS: Desirable unstable genotype

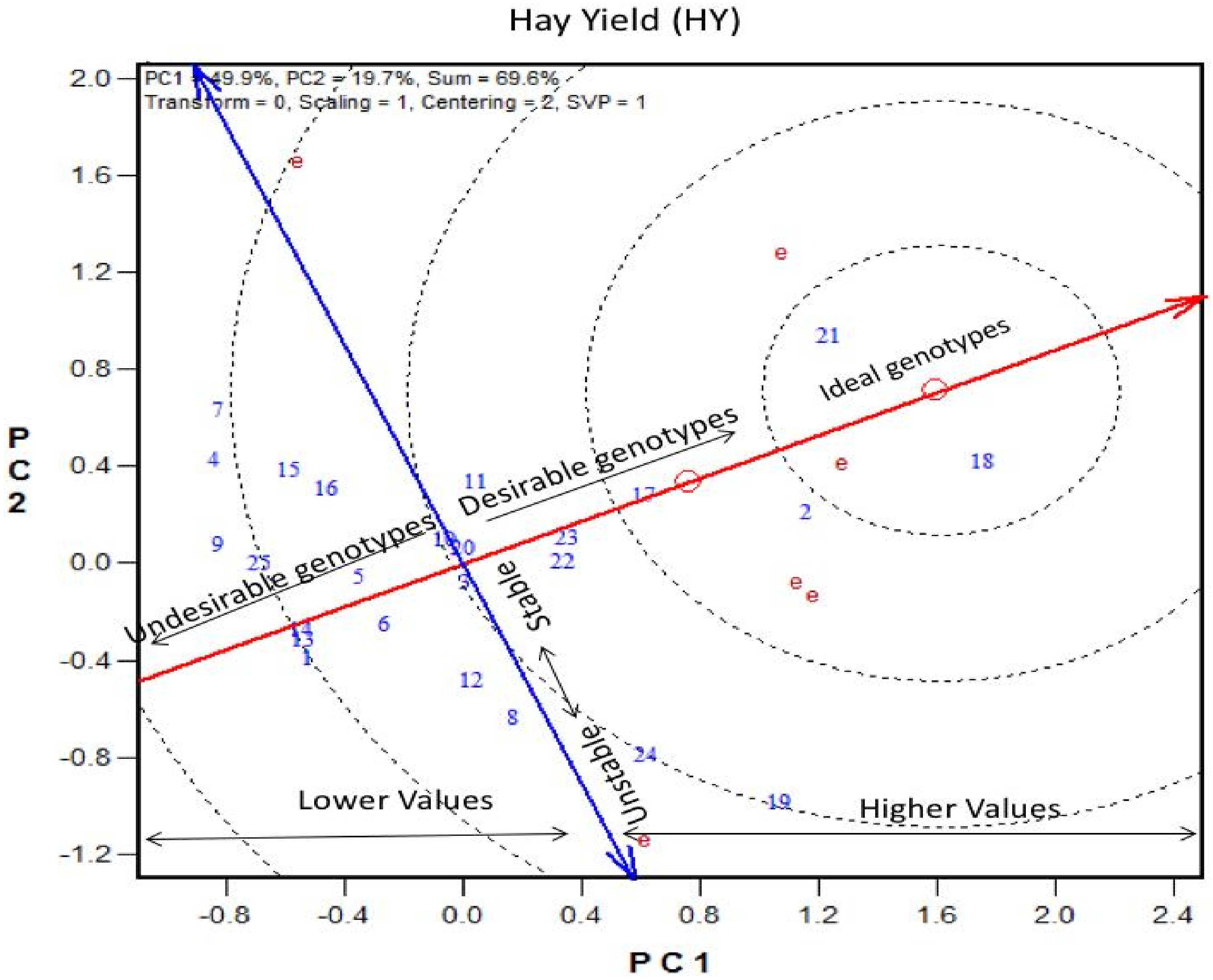

Figure 1. Biplot graph for dry hay yields of 25 silage maize genotypes at 6 environments

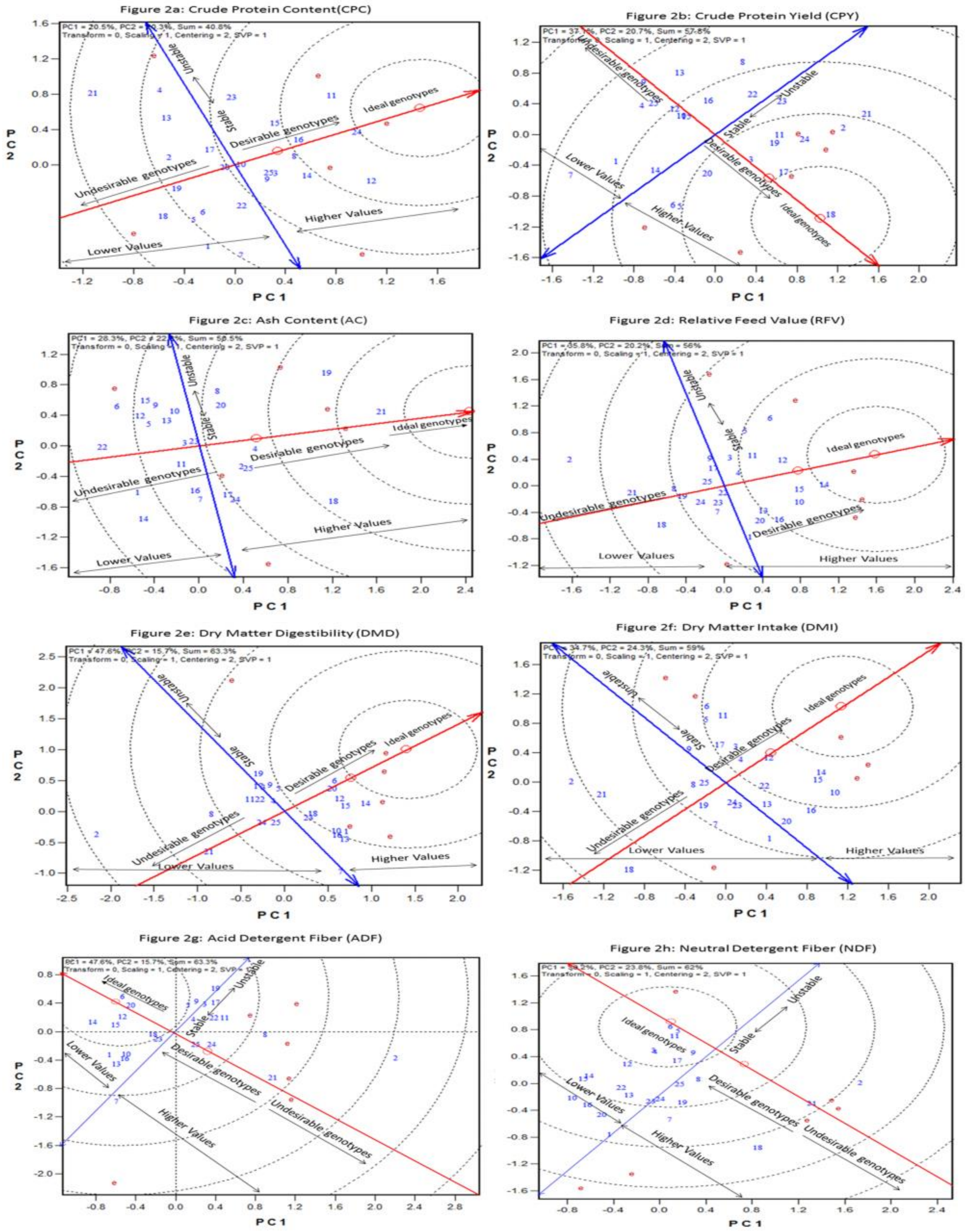
Figure 2a: Crude Protein Content(CPC)

Figure 2b: Crude Protein Yield (CPY)

Figure 2c: Ash Content (AC)

Figure 2d: Relative Feed Value (RFV)

Figure 2e: Dry Matter Digestibility (DMD)

Figure 2f: Dry Matter Intake (DMI)

Figure 2g: Acid Detergent Fiber (ADF)

Figure 2h: Neutral Detergent Fiber (NDF)

Figure 2. Biplot graphs for 8 quality traits [crude protein content (CPC), crude protein yield (CPY), crude ash content (CAC), relative fed value (RFV), dry matter digestibility (DMD), dry matter intake (DMI), acid detergent fiber (ADF), neutral detergent fiber (NDF)] of 25 silage maize genotypes at 6 environments.

DISCUSSION

Green forage production is a serious problem in winter months (Kim *et al.,* 2006). Silage can meet such a need for livestock. In addition, quality attributes and nutritive values of plant materials to be ensiled should be determined to minimize the potential negative impacts when they were used in animal feeding (Gill *et al.,* 2013). In a previous study, effects of genotypes, genotype × environment interactions on dry hay yields and hay quality traits of 25 hybrid silage maize cultivars grown in 6 different environments for 2 years were investigated and the effects on genotypes, environments and genotype × environment interactions on all traits were found to be significant ($P<0.01$). In another study, the effects of genotype × environment interactions on maize kernel yield were investigated and the effects were also found to be significant (Ndhlela *et al.,* 2014). Higher effects of the environments than the other sources of vitiation were reported in previous studies carried out with different plants (Kaya *et al.,* 2006; Jalata, 2011). Maize chemical composition is greatly influenced by climate factors. Mean temperatures, relative humidity, amount of precipitation and sunshine durations have significant impacts on maize chemical composition (Zhang *et al.,* 2016). Such cases than influence maize chemical composition based on the years and locations. Variations in temperature result in variations in leaf area and cell membranes (ADF and NDF), plant growth and development (Galdamez-Cabrera *et al.,* 2002; Mahajan and Tuteja, 2005).

Dry hay yield, crude protein content and crude protein yield are the most significant parameters looked for in silage maize culture. These parameters are determined to assess the nutritive value of plant material. In the present study, genotype × environment interactions had significant effects on these three parameters. Differences in dry hay yields and protein contents of the genotypes may result from plant genetics, ripening stages, temperatures and fertilization practices (Ball *et al.,* 2001). While increasing ADF ratios reduce the digestibility of the feeds, increasing NDF ratios reduce feed intake, let the animal to have a sense of fullness and, thus, limit feed consumption and availability. Therefore, since increasing ADF and NDF ratios reduce DMD, DMI, and RFVs, feeds are desired to have quite a low ADF and NDF ratios (Kaplan *et al.,* 2015). Different stem and leaf ratios also result in different crude protein, ADF and NDF ratios (Ulger and Kaplan, 2016). Crude ash is composed of the unburnt portion and designates mineral content of the feeds (Genctan, 1998). Since these minerals are not synthesized by animals, they should be supplied externally.

Several methods have been developed to assess multi-environment trails and GGE biplot analysis is the most effective one used to assess the investigated traits (Kaya *et al.,* 2006). GGE biplot axes were able to explain 40.8% of total variation in crude protein contents, 69.6% of the total variation in dry hay yields. The explanation ratios for all traits (except for crude protein ratio) were over 50.0% specified by Yan *et al.* (2001) for reliable interpretation of GGE biplot graphs. However, lower values (less than 50%) were also reported in previous studies for some traits (Yan, 2014).

GGE biplot method allows researchers to do visual assessments for different traits over both the environments and the genotypes (Ilker *et al.,* 2011). In GGE biplot analysis, the genotypes with a high PC1 value (PC1>0) have higher trait values and designated as compatible genotypes and the ones with a low PC1 value (PC1<0) have lower trait values and designated as incompatible genotypes (Yan and Kang, 2003). However, in some cases, lower values are preferred for some traits of multi-environment trials, thus the genotypes with low PC1 values are desired in those cases (Yan, 2014). In present the study, ADF and NDF values, for which low values are desired, were interpreted in a different fashion other than the commonly used one.

In GGE biplot graphs for 9 traits, generally high PC1 values of the investigated traits (except for ADF and NDF for which low values are preferred) indicated the high-performance genotypes in different environments. However, the genotypes DKC 6903 and DKC 6589 for crude protein ratio, 31A34 and SAFAK for relative feed value and 31A34 for dry matter digestibility were located in places in which they were not expected to be placed. For instance, with regard to relative feed value, despite higher values than the general average, the genotype SAFAK was placed in undesirable genotypes section at the furthest left section of the graph. In the GGE biplot method, the origin of the average environment axis (AEA) gives the average of an investigated trait over the entire environments (Yan and Tinker, 2006). The position of genotypes with regard to average environment axis for 9 different traits was used to assess their stability. For each trait, the genotypes with high values and close to AEA were assessed as “+S”, the ones with low values but close to AEA were assessed as “-S”. The abbreviations for the other assessments are provided in Table 3 and 4. Present literature don’t have any studies about the effects of genotype × environment interactions on nutritive values of maize hay. However, some researchers performed similar studies with the other plants and assessed the genotypes moving away from the AEA as unstable genotypes (Kaya *et al.,* 2006; Jalata, 2011; Ndhlela *et al.,* 2014).

In silage maize culture, quality parameters of dry hay are quite important parameters to be considered (Garibay *et al.,* 1997). The assessments made over GGE biplot created for each trait are provided in Tables 3 and 4. GGE biplot method allows researchers to identify the ideal genotypes for investigated traits in each environment (Yan and Kang, 2003; Akcura *et al.,* 2019). In the present study, genotype-focused GGE biplot graphs were used to identify the ideal genotypes. Regarding crude ash, crude protein content, dry matter intake, dry matter digestibility, and relative feed value, none of the genotypes were placed in ideal genotype section of the graph. Ideal genotype assessment is a quite hard job under normal conditions (Yan and Kang, 2003). However, the best genotypes for different traits of multi-environment trails are assessed as ideal genotypes (Yan, 2014). Therefore, such an assessment is not necessarily done in every study (Yan *et al.,* 2000). In the present study, since the biplot graphs were created as to identify the ideal genotype, stability and general performance of genotypes were assessed over the environments. Table 3 and 4 presenting the assessments made over biplot graphs have made the graphs more meaningful (Yan, 2014; Akcura *et al.,* 2019).

Conclusion: We conclude that the genotypes, environments and genotype × environment interactions had significant effects on all investigated traits of silage maize genotypes. Crossed and none-crossed genotype × environment interactions were also found to be significant. GGE biplot method basically developed for G × E interactions was proved to be used efficiently used for nutritive values of silage maize dry hay. Instead of creating different graphs, a single ideal genotype-focused biplot graph was found to be sufficient for assessment of the general performance of the genotypes. In the present study, an ideal genotype for all traits and all environments was not able to be identified. However, the genotype SAFAK with the greatest average dry hay yield was assessed as stable also for crude protein yield and ADF. That is why, this genotype can be grown in different regions to meet dry hay needs of livestock in the winter season.

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