

GGE BIPLLOT ANALYSIS OF GENOTYPE × ENVIRONMENT INTERACTION IN SOYBEAN GROWN AS A SECOND CROP

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Received: 25.04.2019

ABSTRACT

The study was aimed to evaluate the adaptability and stability of the soybean genotypes based on the seed yield and the other observed characteristics in the sites cultivated second crop soybean of Turkey which have Mediterranean climate conditions using the GGE biplot analysis method. The experiments were performed under irrigated conditions in 2014, 2015 and 2016 in four different locations (Adana, Antalya, Izmir and Sanliurfa) of Turkey. Fourteen soybean genotypes consisting of 10 advanced soybean lines and four standard varieties were analyzed by a randomized complete block design with 4 replications. The combined analysis of variance revealed significant ($P < 0.01$) effects for all sources of variation (environment, genotype, and $G \times E$ interaction) for the seed yield and yield components. Genotype and environment accounted for about 2.59% and 51.04% of the total variation for seed yield, respectively, while the GE interaction explained 20.84% of the total variation. According to the GGE principle, five mega-environments were formed in the present study. Results of the research revealed that genotypes G8 (KANA), G9 (KASM 02), G11 (ARISOY), G3 (BATEM 306), G1 (BATEM 207) and G12 (ATAEM 7) were found as stable. According to GGE Biplot analysis for all traits and genotypes, G4 (BATEM 317) had the largest values for plant height, first pod height, days to 50% flowering, days to maturity and seed yield.

Keywords: Soybean, $G \times E$ interaction, GGE biplot, seed yield, yield components

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is a crop that is affected by environmental factors. Although, precipitation, temperature, and relative humidity are uncontrollable environmental conditions, it is relatively possible to control factors such as soil type, sowing time, row spacing, plant density. Therefore, the adaptability and stability of a genotype grown should be known. When genotypes are tested for yield performance in different environmental conditions, the effect of genotype by environment interaction is revealed in terms of seed yield, so that the stability status, general and specific adaptabilities of the genotypes are tried to determine.

Soybean is grown widely, as a second crop especially in the southern regions of Turkey. In general, the second crop soybean cultivation, where the main crop is winter cereals is carried out in late sowing. Delayed sowing time

and unfavorable environmental conditions have a negative effect on growth, development and consequent yield of soybean (Hu and Wiatrak, 2012). Changes in photoperiod, temperature and precipitation with delayed planting affect the duration of vegetative and reproductive stages, a number of branches and pods, plant height, leaf area index and grain yield (Bakal et al., 2017). Seed yield reduction in late-planted soybean was attributed to shorter day length (Caliskan et al., 2007). Late maturing cultivars are more sensitive to photoperiod than early maturing cultivars (Bakal et al., 2017). Therefore, the varieties to be grown in the second crop agriculture should be early varieties with a short period of vegetation.

Besides, it has been well known that double cropping systems have very benefits such as increasing the profit, improving soil productivity and reducing erosion, providing for more intensive use of land, equipment, labor and capital, also of course, getting more production from

the unit area (Ilker et al., 2018a). Experiments conducted in several sites are needed to determine high yielding and early maturing genotypes suitable for the second crop conditions. Multi-environment trials (MET) are conducted to evaluate yield stability performance of genetic materials under varying environmental conditions (Delacy et al., 1996; Farshadfar et al., 2012). Consequently, genotype x environment interaction effects can be revealed by this type of experiments. The presence of a significant genotype×environment (G×E) interaction for quantitative traits such as seed yield can lead to the failure of genotypes to achieve the same relative performance in different environments (Gurmu et al., 2009). Typically, there are two types of MET data, one is genotype by environment (GGE) data, and the other is genotype by trait (GT) data in an individual environment or across environments (Zhang et al., 2006). Yan et al. (2000) and Yan (2001) developed GGE biplot to visually analyze these two types of MET data. They reported that GGE biplot was originally designed for graphical analysis of MET data and it was later extended to graphical analysis of other types of two-way data, such as genotype by trait data and other types of two-way data. GGE biplot analysis results can discriminate between expected and realized responses of genotypes through multi-environment trials (Akcura et al., 2017). Essentially, several methodologies have been utilized to evaluate the performance of soybean lines and their interaction with the environment to direct the selection of the most productive, adapted, and stable lines for particular locations, regions, or growing seasons. Currently, the additive main effects and multiplicative interaction analysis (AMMI), genotype main effects and genotype x environment interaction (GGE) biplots, and factor analysis methodologies have been widely used to quantify the genotypic effects of the GxE interaction (Sousa et al., 2015).

There has been only limited studies on use of GGE biplot and GT biplot techniques for soybean cultivars adaptability evaluation in Mediterranean environments. In these areas, more studies are needed to help soybean producers to choose the right varieties. Therefore, the purpose of the present study was to evaluate the stability and GxE interaction effects of soybean genotypes based on observed characteristics of second crop soybean in Mediterranean climate conditions of Turkey using the GGE biplot analysis method.

MATERIALS AND METHODS

The experiments were performed under irrigated conditions using randomized complete block design with 4 replications during 2014, 2015 and 2016 growing seasons in four different locations (Adana, Antalya, Izmir and Sanliurfa) of Turkey. Fourteen soybean genotypes consisting of 10 advanced soybean lines and four standard varieties included in 3rd and 4th maturity groups were used as genetic material (Table 1). Characteristics of the locations where the research was conducted are also given Table 2. It can be seen from the table that climate characteristics vary according to the environment. The genotypes were sown by using a plot drill in the plots of 5 m in length consisting of 4 rows in each plot, in a distance of 70 cm and contains 45 plants in the m². Sowings of the trials were generally completed from the second half of June until the beginning of July. The 180 kg ha⁻¹ diammonium phosphate was applied at the sowing time in the experiments. Prior to sowing, seeds were inoculated with *Rhizobium* bacteria culture where necessary. Weed control was made by hand or by the herbicide. Disease and pest control was performed at required locations. All the experimental fields were irrigated at three growth stages (V5, R2, and R5 stages) with a rotary sprinkler to near field capacity.

Table 1. Code, pedigree, maturity group and breeding organization or variety owner of genotypes

Code	Pedigree	Maturity group	Breeding organization/ variety owner
<i>Lines</i>			
BATEM 207	Macon x Defiance	3	BATEM
BATEM 223	Macon x Defiance	3	BATEM
BATEM 306	Ataem 07 x Etae 08	4	BATEM
BATEM 317	J-357 x 9392	4	BATEM
BDSA 05	Sprite 87 x Apollo	3	BDUTAE
BDUS 04	Umut 2002 x Sprite 87	3	BDUTAE
KAMA	Macon x Apollo	4	KTAE
KANA	NE 3297 x AP 2292	4	KTAE
KASM 02	Sprite 87 x Macon	3	KTAE
KASM 03	Sprite 87 x Macon	3	KTAE
<i>Standards</i>			
ARISOY		3	Cukurova University
ATAEM 07		4	BATEM
BRAVO		3	PROGEN Seed Co.
NOVA		3	MAY Agro Co.

Table 2. Data on the experiment, soil properties and climate for environments where the experiments were conducted

Code	Growing seasons	Environments	Soil properties	Mean temperatures at the growing season (°C)	Rain-fall (mm)	Irrigation (mm)	Mean yield (t ha ⁻¹)
E1	2014	Adana	pH= 7.5, clay-loam	24.0	239.1	460	3.32
E2	2015	Adana	pH= 7.5, clay-loam	24.1	194.2	505	3.95
E3	2014	Sanliurfa	pH= 7.8, sandy clay	26.0	116.2	633	4.15
E4	2015	Sanliurfa	pH= 7.8, sandy clay	26.1	94.4	655	3.93
E5	2016	Sanliurfa	pH= 7.8, sandy clay	26.9	57.8	692	3.16
E6	2014	Antalya	pH=8.6, clay-silt	23.8	302.3	347	2.63
E7	2015	Antalya	pH=8.5, clay-silt	23.7	197.9	452	3.07
E8	2016	Antalya	pH=8.6, clay-silt	24.5	97.3	553	3.61
E9	2014	Izmir	pH=7.4, clay-silt	23.3	241.5	408	3.68
E10	2015	Izmir	pH=7.4, clay-silt	23.7	210.3	440	3.49
E11	2016	Izmir	pH=7.5, clay-silt	24.5	61.7	588	3.09

Seven agronomical traits such as plant height (cm), first pod height (cm), number of pods per plant, days to 50% flowering, days to maturity, 1000 seed weight (g) and seed yield per hectare (kg ha⁻¹) were investigated. Plant height, first pod height, number of pods per plant, were measured on twenty plants selected randomly from all plots, and days to 50% flowering and days to maturity were recorded as flowering and maturing dates of more than 50% of plants in each location and year. The seed yield was weighed as mature seed harvested and threshed from 5 m lengths of the four rows. Seed weight has recorded as the weight of 1000 randomly selected seeds from bulk at each plot.

Data from all locations were pooled and tested for the presence of significant G×E by using analysis of variance. To evaluate the stability and adaptability, the GGE biplot analysis was performed, considering the simplified model for two main components. The GGE biplot multiplicative model is similar to the AMMI multiplicative model (Sousa et al., 2015) and was carried out considering the simplified model for two principal components centered on the environment (Yan, 2011):

$$Y_{ij} - \mu_j = \lambda_1 \gamma_{i1} \alpha_{j1} + \lambda_2 \gamma_{i2} \alpha_{j2} + \bar{\epsilon}_{ij}$$

where: \bar{Y}_{ij} : average of genotype i in location j; μ_j : average of all genotypes in a location; $\lambda_1 \gamma_{i1} \alpha_{j1}$: the first principal component (PC1) of the genotype effect + G×E interaction, result of the principal components analysis applied to the matrix of interactions; $\lambda_2 \gamma_{i2} \alpha_{j2}$: is the second principal component (PC2) of the genotype effect + G×E interaction, result of the principal component analysis applied to the matrix of interactions; λ_1 and λ_2 : are the auto values associated with PC1 and PC2; γ_{i1} and γ_{i2} : are the scores of PC1 and PC2, respectively, for the genotypes; α_{j1} and α_{j2} : are the scores of PC1 and PC2, respectively, for the environments; $\bar{\epsilon}_{ij}$ is the residual of the model with NID (0, σ^2/r), in which σ^2 is the variance of the error among plots and r is the number of replicates.

PC1 values are placed in the horizontal plane (X) of the GGE Biplot graphical plane by expressing the mean of the genotypes examined, whereas PC2 values are the stability state of the studied parameter and are in the vertical plane (Y) of the graph plane. Where genotypes or genotype-environment interaction or both were significant, GGE biplot analysis was used to obtain information on which genotypes were suitable for which environment and to investigate the stability of genotypes for seed yield. In addition, genotype-by-trait biplots were generated to determine which genotypes were best suited for which specific trait (e.g., plant height, first pod height, number of pod per plant, days to 50 % flowering, days to maturity, 1000-seed weight and seed yield). The GGE Biplot were carried out with the help of the GenStat computer package program (GenStat, version 12) according to Yan and Tinker (2006).

RESULTS AND DISCUSSION

The combined analysis of variance revealed significant (P<0.01) effects for all sources of variation (environment, genotype, and G×E interaction) for the seed yield and yield components (Table 3). The interaction between genotype and environment indicates that the genotypes do not have to be a constant for all evaluation environments; in this way, it is important to determine the G×E interaction (Silveira et al., 2016; Ilker et al., 2018b). Genotype and environment accounted for about 2.59% and 51.04% of the total variation for seed yield, respectively, while the GE interaction explained 20.84% of the total variation. Similar ratios were also revealed for the other traits. The coefficient of variation (CV) for the other traits except for the number of pods per plant and first pod height was low level (1.38% - 9.89%), indicating experimental precision. Genotype by environment interaction is the change in the relative performance of a character of two or more genotypes measured in two or more environments (Haldane, 1946; Bowman, 1972). Therefore, multi-environment trials (MET) are widely used by plant breeders for evaluating the relative

performance of genotypes over the target environments and to quantify adaptability and stability of genotypes (Zhang et al., 2006; Jha et al., 2013). Similar results of our findings were obtained by earlier researchers (Silva and Duarte, 2006; Pelúzio et al., 2008; Karasu et al., 2009; Kumar et al., 2014; Edugbo et al., 2015; Sousa et al., 2015; Cheelo et al., 2017) which also observed the presence of a GxE interaction for soybean yield and some yield components in different regions of the world. In a previous study, Kumar et al. (2014) reported that the GE interaction effect accounted for 27.77% and 15.71% of the total variation for grain yield and number of branches respectively, indicating that the GE interaction is more complex. Bhartiya et al. (2017) found that environment,

genotypes and genotype by environment interactions had significantly affected soybean seed yield and accounted for 9.76, 28.97 and 47.55% of the total variation, respectively. On the other hand, in the genotype x environment interaction analysis of observed traits, the coefficients of variation which found relatively low levels indicated that experimental precision was high. Certainly, high experimental precision expands the field of application of the findings. Our findings were similar to those of Yan (2001), who reported that the coefficient of variation for grain yield was 15.92%. However, the coefficient of variation in our study was lower than that obtained in soybean for grain yield (Zhang et al., 2006; Santi et al., 2012; Cavalcanti et al., 2014).

Table 3. Results of analysis of variance for seed yield and yield components observed from trials conducted with 14 soybean genotypes in 11 environments under second crop conditions (mean square).

Source	df	No.of pods/plant	Days to 50% flowering	Days to maturity	Plant height (cm)	First pod height (cm)	1000 seed weight (g)	Seed yield (t ha ⁻¹)
Model	186	1540.1	99.1	242.6	980.4	49.6	40760.2	9609.8
Environment (E)	10	22972.1**	1523.5**	4014.6**	10625.7**	545.6**	40760.2**	116948.0**
Rep.[Env.]&Rand.	33	70.3	2.15**	22.1**	60.3*	12.3**	177.9**	2458.0**
Genotype (G)	13	391.4**	102.6**	91.1**	3501.8**	137.5**	8526.4**	4562.5**
G x E Int	130	379.4**	13.7**	23.6**	219.8**	12.1**	482.9**	3673.3**
Error	429	54.2	0.69	930.9	35.8	3.39	95.8	1174.5
C.V. (%)		13.6	2.43	1.38	6.33	20.60	5.89	9.89
R ²		0.92	0.98	0.98	0.92	0.86	0.93	0.78

The significance of the GEI effects in terms of observed characters indicated that there were significant differences in responses of genotypes to environments. As seen from Table 4, the BATEM 223, BDUS 04 and KASM 03 lines gave the best results in terms of seed yield and some important yield components over eleven environments. GGE Biplot which is formed by means of genotypes; PC1 (1st main component) and PC2 (2nd main component) are the two main components used to create the biplot. PC1 values have expressed the mean of the trait examined of the genotypes and are expressed in the horizontal plane (X) of the graphical plane, whereas PC2 values are the stability state of the studied parameter and are in the vertical plane (Y) of the graph plane. Stability increases as the PC2 value approach zero (0), while the stability decreases as the values move away from zero

(Yan, 2001; Yan and Hunt, 2001; Yan, 2002; Kaya et al., 2006). Biplot in Figure 1 displays 14 genotypes as well as 11 environments on the two-dimensional biplot. Principal component 1 (PC1) explained 33.14% of total variation and principal component 2 (PC2) explained 18.76% of the total variation. Thus, PC1 and PC2 together explained 51.89% of the total variation for yield. In the GGE biplot analysis, although the variation of 51.89% for the first two principal components was lower than the ideal limit (66%), this was an expected result because there was a great variation between the soil and climate conditions of the environments and genotype x environment interaction had a complex effect. However, this result is lower than that obtained by Edugbo et al. (2015) (93.74%) and Cheelo et al. (2017) (86.01%) and similar to that found by Sousa et al. (2015) (57.9%).

Table 4. Mean of agronomical traits for fourteen soybean genotypes tested (over eleven environments) at three locations in second crop conditions during 2014 to 2016.

Code	Genotypes	No.of pods/plant	Days to 50% flowering	Days to maturity	Plant height (cm)	First pod height (cm)	1000 seed weight (g)	Seed yield (t ha ⁻¹)
G1	BATEM 207	54.3 c-f	34.1 d	108.0 b	106.4 b	10.0 b	165.9 d	3.47 b-d
G2	BATEM 223	54.8 c-e	34.7 bc	107.2 c	90.3 ef	9.0 c	138.2 f	3.63 a
G3	BATEM 306	54.5 c-f	35.0 b	107.0 c	107.0 b	12.5 a	165.3 d	3.55 ab
G4	BATEM 317	51.1 gh	39.1 a	110.5 a	109.9 a	12.2 a	154.8 f	3.54 ab
G5	BDSA 05	52.3 e-h	34.9 bc	105.8 ef	97.1 d	7.9 de	181.0 b	3.50 a-c
G6	BDUS 04	49.5 h	34.6 c	105.8 ef	89.9 ef	9.1 c	196.3 a	3.55 ab
G7	KAMA	55.9 b-d	33.0 ef	106.6 cd	89.1 f	7.6 d-f	178.3 bc	3.50 a-c
G8	KANA	51.1 gh	34.0 d	108.7 b	96.5 d	8.9 c	167.1 d	3.44 b-e
G9	KASM 02	55.3 c-e	33.9 d	106.1 d-f	83.8 h	7.5 d-f	163.7 d	3.50 a-c
G10	KASM03	59.6 a	34.1 d	106.1 d-f	84.1 h	7.6 d-f	165.8 d	3.50 a-c
G11	ARISOY	53.2 d-g	32.8 f	105.4 f	92.4 e	8.3 cd	154.3 f	3.40 c-f
G12	ATAEM 7	51.6 f-h	33.1 ef	105.9 ef	103.1 c	10.3 b	174.1 c	3.27 f
G13	BRAVO	58.8 ab	34.1 d	106.1 d-f	87.7 fg	7.4 ef	159.4 e	3.34 d-f
G14	NOVA	56.9 a-c	33.3 e	105.7 ef	86.1 gh	6.8 f	157.5 ef	3.31 ef
LSD (0.05)		3.10	0.36	0.77	2.55	0.83	4.22	1.48

In the GGE biplot (Figure 1), the vectors from the biplot center divided the graph into six sectors. Then the highest yielding genotypes were identified for each sector. Similar results were observed by Bhartiya et al. (2017) and Ramos et al. (2017), who reported that the GGE biplot created for soybean genotypes in seed yield was divided into six or eight sectors. When using the first two principal components, five clusters of environments (mega-environments) were formed using the GGE biplot methodology. A polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon. The genotypes located on vertices of polygon performed either best or poorest in one or more environments. The rays in Figure 1 are lines that are perpendicular to the sides of the polygon and ray 1 and ray

2 is perpendicular to the side that connects genotypes G8 (KANA) and G10 (KASM 03); ray 3 is perpendicular to side G10 (KASM 03)-G14 (NOVA); ray 4 is perpendicular to side G14 (NOVA)-G12 (ATAEM 7), ray 5 to side G12 (ATAEM 7)-G6 (BDUS 04), ray 6 to side G6 (BDUS 04)- G7 (KAMA). The G7 (KAMA) was winning genotype at E3 (Sanliurfa in 2014) and E4 (Sanliurfa in 2015), G8 (KANA) was the best genotype at E10 (Izmir in 2015), genotype G10 (KASM 03) was the best performer at E9 (Izmir in 2014) and E11 (Izmir in 2016), G2 (BATEM 223) was winning genotype at E6 (Antalya in 2014). Genotype G6 (BDUS 04) was the winner at E1 (Adana in 2014), E4 (Sanliurfa in 2015) and E8 (Antalya in 2016) while G12 (ATAEM 7) was the best performer at E7 (Antalya in 2015) (Table 5, Figure 1).

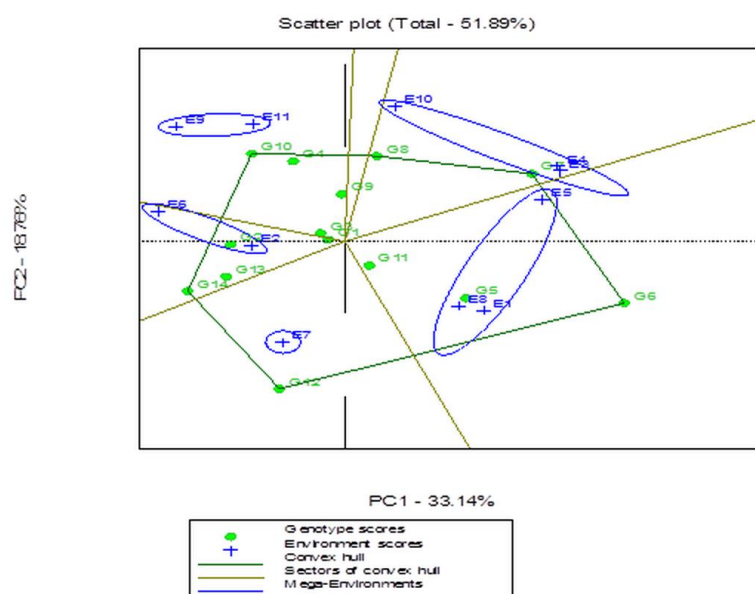


Figure 1. The GGE biplot graph showing the mega-environments and the which-won-where view of the genotype in seed yield

Table 5. Average seed yields of soybean genotypes tested in eleven environments (t ha⁻¹)

Code	Genotypes	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	Mean
G1	BATEM 207	3.57 a-d	3.40	3.91.de	3.83 c-e	3.13	2.70 b-c	3.28 a-d	3.55 b-d	3.66 a-d	3.63b-d	3.46 a	3.47 b-d
G2	BATEM 223	3.70 a-b	4.41	4.21 a-d	3.64 d-f	2.92	3.19 a	3.32 a-c	3.71 a-d	3.83 a-d	3.62 b-d	3.41 a	3.63 a
G3	BATEM 306	3.46 a-d	3.69	3.91 de	3.99 b-d	3.16	2.57 c-d	3.35 a-c	3.70 a-d	3.88 a-c	3.65 bc	3.35 ab	3.55 ab
G4	BATEM 317	2.81 e	4.14	4.20 b-d	4.23 b	3.24	2.77 a-c	3.38 a-b	3.22 d	4.03 ab	3.89 ab	3.04 b-e	3.54 ab
G5	BDSA 05	3.67 a-b	3.99	4.47 a-c	4.15 bc	3.15	2.19 d-e	3.28 a-d	3.84 a-c	3.47 b-e	3.35 c-f	2.91 d-f	3.50 a-c
G6	BDUS 04	3.79 a	3.86	4.59 ab	4.70 a	3.53	2.47 c-d	2.96 b-f	4.17 a	3.02 e	3.27 ef	2.66 fg	3.55 ab
G7	KAMA	3.44 a-d	3.82	4.71 a	4.35 ab	3.49	2.02 e	2.77 d-f	3.45 c-d	3.77 a-d	3.67 a-c	2.98 c-f	3.50 a-c
G8	KANA	2.98 d-e	3.64	4.50 a-c	4.07 bc	2.99	2.60 c-d	2.71 f	3.52 c-d	3.56 b-e	3.99 a	3.25 a-c	3.44 b-e
G9	KASM 02	3.13 b-e	3.78	4.14 b-d	3.82 c-e	3.15	2.65 b-c	2.72 f	4.09 a-b	3.83 a-d	3.62 b-d	3.52 a	3.50 a-c
G10	KASM 03	3.04 c-e	4.08	4.06 cd	4.06 bc	3.14	3.04 a-b	2.75 e-f	3.40 c-d	4.17 a	3.58 b-e	3.23 a-d	3.50 a-c
G11	ARISOY	3.62 a-c	4.17	4.15 b-d	3.66 d-f	3.24	2.56 c-d	2.85 c-f	3.28 d	3.27 de	3.54 c-e	2.97 c-f	3.40 c-f
G12	ATAEM 7	3.20 a-e	3.72	3.79 de	3.45 ef	2.88	2.57 c-d	3.64 a	3.65 a-d	3.35 c-e	3.31 d-f	2.42 g	3.27 f
G13	BRAVO	2.80 e	3.94	3.87 de	3.59 ef	3.15	2.87 a-c	3.24 a-e	3.45 c-d	3.84 a-d	3.13 f	2.85 ef	3.34 d-f
G14	NOVA	3.17 b-e	4.33	3.55 e	3.44 f	3.07	2.59 c-d	2.79 d-f	3.56 b-d	3.94 ab	2.73 g	3.28 a-c	3.31 ef
	Mean	3.32 DE	3.95 B	4.15 A	3.93 B	3.16 EF	2.63 G	3.07 F	3.61 C	3.68 C	3.49 CD	3.09 F	

E1: Adana 2014; E2: Adana 2015; E3: Şanlıurfa 2014; E4: Şanlıurfa 2015; E5: Şanlıurfa 2016; E6: Antalya 2014; E7: Antalya 2015; E8: Antalya 2016; E9: İzmir 2014; E10: İzmir 2015; E11: İzmir 2016.

According to the GGE principle, any number of environments with the same winning genotype is considered to be a mega-environment. As seen from Figure 1, five mega-environments were formed in the present study. Genotype G7 (KAMA) was the stable and high yielding for mega-environment I, which was composed of the environments E3 (Sanliurfa in 2014), E4 (Sanliurfa in 2015) and E10 (Izmir in 2015). Genotypes G5 (BDSA 05) and G6 (BDUS 04) were high yieldings for mega-environment II, which was composed of the environments E1 (Adana in 2014), E5 (Sanliurfa in 2016) and E8 (Antalya in 2016). For mega-environment III (E9; Izmir in 2014 and E11; Izmir in 2016), genotype G10 (KASM 03) were the most adapted. In mega-environment IV (E2; Adana in 2015 and E6; Antalya in 2014), G2 (BATEM 223) was the highest yielding genotype. In addition, for mega-environment V (E7; Antalya in 2015) G12 (ATAEM 7) was the stable genotype.

environment closest to the center of the concentric circles is the most representatives of the environments. The ideal environments were E3 (Sanliurfa in 2014) and E4 (Sanliurfa in 2015), which had a greater value for CP1, and a value closer to zero for CP2, demonstrating a greater power of discrimination between the genotypes and greater yield in regards to the other environments. On the other hand, E2 (Adana in 2015) and E5 (Sanliurfa in 2015) were stable environments for seed yield. In addition, E7 (Antalya in 2015) and comparatively E6 (Antalya in 2014) were the most unfavorable environment in the study. According to Yang et al. (2009), an ideal environment should have a high PC1 score (greater genotype discriminating power regarding genotype main effects) and zero scores for PC2 (greater representativeness of all other environments). Similar results to our findings were stated by Zhang et al. (2006) and Bhartiya et al. (2017).

The GGE biplot in Figure 2 shows the relative ranking of the environments relative to the ideal. In this biplot, the

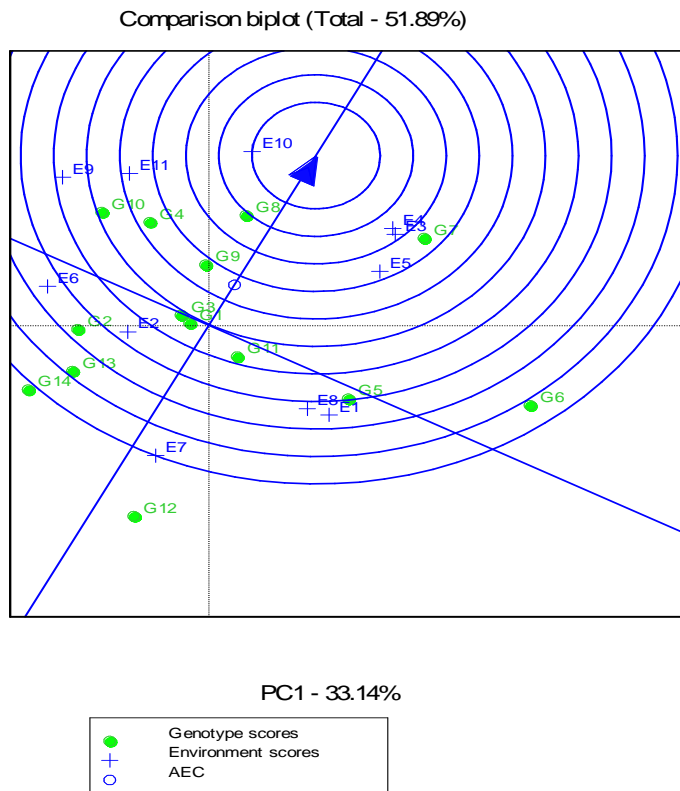


Figure 2. GGE Biplot graph showing stability status of the genotypes, environments and genotype × environment interactions in seed yield

Genotype ranking relative to an ideal genotype is also shown in Figure 2. An ideal genotype should have high mean performance and be absolutely stable across environments. In Figure 2, the arrow direction of the single-headed line indicates the ideal genotype. Genotypes G7 (KAMA), G8 (KANA) and G9 (KASM 02) were closest to the ideal genotypes. In contrast, G12 (ATAEM 7), G13 (BRAVO) and G14 (NOVA) who standard varieties were the below-average in the yield.

The ideal genotype should have high mean performance coupled with high stability to give wide adaptability in the target region (Amira et al., 2013). Our findings were similar to those of Zhang et al. (2006), Bhartiya et al. (2017) and Cheelo et al. (2017) who suggested that ideal soybean genotypes were determined for different regions.

Yield performance and stability of genotypes were evaluated by average environment coordination (AEC)

method (Figure 3). The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa indicates greater G×E interaction effect and reduced stability in either direction away from the biplot origin and separates genotypes with below-average means from those with above-average means (Bhartiya et al., 2017). The average yield of a genotype is approximated by the projections of their markers on the AEC x-axis while the stability is determined by the projection onto the AEC ordinate line (y-axis) (Yan and Rajcan, 2002). The results in Figure 3 showed that genotypes G8 (KANA), G9 (KASM 02), G11 (ARISOY), G3 (BATEM 306), G1 (BATEM 207) and G12 (ATAEM 7) were found as stable. Among the stable genotypes, performances of G8 (KANA) and G9 (KASM 02) were above average in generally all the environments while G11 (ARISOY) and

G12 (ATAEM 7) were below average in generally all the of environments. Genotypes G2 (BATEM 223), G5 (BDSA 05), G6 (BDUS 04), G7 (KAMA) and G10 (KASM 03) were unstable. The yield performances of these genotypes significantly changed according to the environments. Generally, G5 (BDSA 05), G6 (BDUS 04) and G7 (KAMA) had adaptive to favorable (ideal) environments while G2 (BATEM 223) was good adaptive to unfavorable (poor) environments (Table 5, Figure 3). A previous study, Cheelo et al. (2017) reported that the best genotype for general adaptability was the variety TGX 1988-22F which was ideal across all the locations as it was high yielding and stable. In many of previous studies conducted in multi-environments, stable and unstable soybean genotypes were identified (Yan, 2001; Amira et al., 2013; Sousa et al., 2015; Ramos et al., 2017).

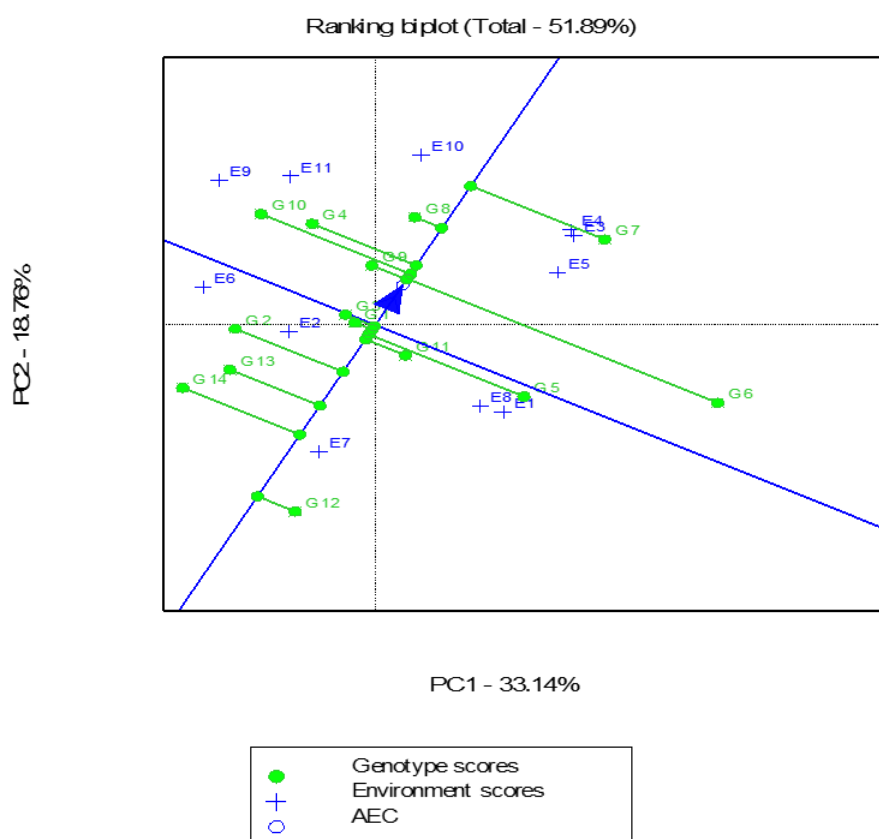


Figure 3. GGE Biplot graph showing the mean performance according to environments and stability of genotypes in seed yield

The relationships between the genotypes and traits by GGE Biplot analysis method in terms of observed traits are illustrated in Figure 4. This figure is the polygon view or “which-won-where” view of the genotype. For each polygon side a line was drawn to start from the biplot origin and to be perpendicular to the polygon side. These lines divided the yield-trait combinations into two sectors; corresponding to each sector there was a polygon vertex. The geometry of the biplot determines that the genotype placed on a vertex has the largest values for the yield-trait combinations placed within the corresponding sector (Yan and J. Frégeau-Reid, 2018). GGE Biplot in Figure 4

indicated that the total variation of PC1 (49.68%) and PC2 (20.56%) values were 70.24%. According to GGE Biplot, G4 (BATEM 317) had the largest values for plant height, first pod height, days to 50% flowering, days to maturity and seed yield. Genotypes G10 (KASM 03), G13 (BRAVO) and G14 (NOVA) were the highest level in terms of the number of pod per plant while genotype G6 (BDUS 04) was the largest value for 1000 seed weight. Genotype G2 (BATEM 223) had high value for only seed yield (Table 4 and Figure 4). Our findings were consistent with the results of Zhang et al. (2006) and Yan and J. Frégeau-Reid (2018).

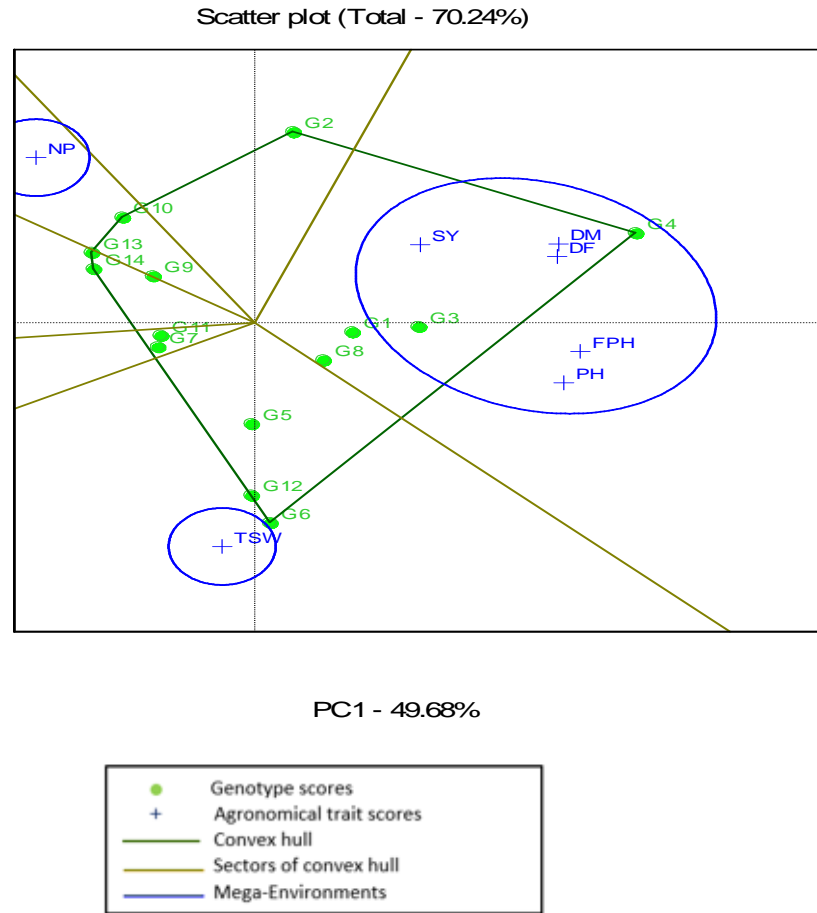


Figure 4. Grouping of the genotypes and traits by GGE Biplot analysis method in terms of observed traits and relationships of genotypes with these traits

CONCLUSIONS

The present study revealed a better expressing of the G×E interaction by GGE biplot model. According to the combined analysis of variance, soybean seed yield and some yield components were significantly affected by G×E interaction followed by genotypic (G) and environment (E) effects, respectively. Results of the research revealed that genotypes G8 (KANA), G9 (KASM 02), G11 (ARISOY), G3 (BATEM 306), G1 (BATEM 207) and G12 (ATAEM 7) were found as stable. Among the stable genotypes, performances of G8 (KANA) and G9 (KASM 02) were above average in generally all the environments while G11(ARISOY) and G12 (ATAEM 7) were below average in generally all the of environments. Genotypes G2 (BATEM 223), G5 (BDSA 05), G6 (BDUS 04), G7 (KAMA) and G10 (KASM 03) were unstable. The ideal environments were E3 (Sanliurfa in 2014) and E4 (Sanliurfa in 2015), which had a greater value for PC1, and a value closer to zero for PC2, demonstrating a greater power of discrimination between the genotypes and greater yield in regards to the other environments. On the other hand, E2 (Adana in 2015) and E5 (Sanliurfa in 2015) were stable environments for seed yield. In addition, E7 (Antalya in 2015) and comparatively E6

(Antalya in 2014) were the most unfavorable environment in the study. Generally, G5 (BDSA 05), G6 (BDUS 04) and G7 (KAMA) had adaptive to favorable (ideal) environments while G2 (BATEM 223) was good adaptive to unfavorable (poor) environments. According to GGE biplot for all traits and genotypes, G4 (BATEM 317) had the largest values for plant height, first pod height, days to 50 % flowering, days to maturity and seed yield. Genotypes G10 (KASM 03), G13 (BRAVO) and G14 (NOVA) were the highest levels in terms of the number of pod per plant while genotype G6 (BDUS 04) was the largest value for 1000 seed weight.

ACKNOWLEDGMENTS

This research was funded by the Scientific and Technological Research Council of Turkey (TUBITAK, project number 113O082). The authors thank TUBITAK for their financial support.

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