



**Full Length Article**

## Adaptability and Stability Analysis of Different Soybean Genotypes using Biplot Model

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### Abstract

Genotype and environment interaction has always been considered as challenging issue in developing desirable traits. Therefore, this study was conducted to evaluate the performance of ten soybean genotypes under five different environments and regions of Saudi Arabia using GGE-Biplot model during 2015 and 2016 growing seasons. There were significant differences among the tested genotypes, environments, and genotype  $\times$  environment interactions (GEI) for the plant height, yield and related traits, and water use efficiency (WUE). However, the difference among environments for plant height and seeds per pod, and GEI for seeds per pod and seed index was not significant. Giza 21 and Giza 111 produced the highest seed yield per plant and WUE ranged from 0.40 to 0.60 g L<sup>-1</sup> in genotypes, respectively. The ideotypes for seed yield per plant were Giza 22 and Giza 83, whereas the ideal ideotypes for WUE were X2 L12 and X 32. GGE-biplot of the ten genotypes based on seed yield per plant indicated that Giza 21 and Giza 111 were the best performing genotypes for the eastern region and Giza 111 was the most suitable for the central region. Thus overall, genotype Giza 111 was the most stable, for seed yield, across regions. Comparison of the tested environments suggested that the western region had the most suitable environment for the selection of widely adaptable soybean genotypes across the regions. © 2018 Friends Science Publishers

**Keywords:** Biplot; Mega-environment; Soybean; Stability; Water use efficiency

### Introduction

Soybean [*Glycine max* (L.) Merr.] is one of the most widely grown leguminous crops in the world. It is being cultivated on about 121 million hectares across 104 countries with total grain production of 334 million mt (FAOSTAT, 2016). It is a pretty good source of proteins and vegetable oil (Lim, 2012) and is used as human food as well as animal feed (Lee *et al.*, 2013). Soybean has a wide variability grouped into 13 maturity classes including both determinate and indeterminate growth types. Early-maturing groups are adapted to the short summer growing seasons whereas the late-maturing groups are suitable for regions with medium and/or long summer season (Acquaah, 2007).

Water-use efficiency (WUE) refers to the capacity of plant to convert used water into plant biomass or economic yield. Optimizing WUE is an urgent need (Hamdy *et al.*, 2003), and the implementation of several strategies is required for improving WUE (Wang *et al.*, 2002), among these breeding new cultivars with high WUE is an important strategy (Condon *et al.*, 2004). Improving WUE may prove a useful method of selecting genotypes better able to adapt

under limited water conditions (Bunce, 2016; Hussain *et al.*, 2018). However, little research had been conducted measuring the variability in WUE between soybean genotypes (Naylor and Fritschi, 2015).

Substantial difference exists among soybean genotypes and genotype  $\times$  environment interactions (GEI), suggest that novel genotypes should be evaluated across diverse environments to select the highest and most stable yielded genotypes (Alghamdi, 2004). Introduction and evaluating of novel genotypes under diverse environments is one of the major breeding methods used to select high yielding and stable genotypes. Genetic and environmental variations could explain the phenotypic variation, whereas the role of GEI is usually small (Yan and Rajcan, 2002), particularly when it is identified as repeatable (Cooper and Hammer, 1996). However, high GEI impairs the precision of trait estimation and reduces the relationship between phenotypic and genotypic characteristics (Ssemakula and Dixon, 2007). Significant GEI can reduce the usefulness of subsequent analysis, restrict the significance of inferences that would otherwise be valid, and limits the feasibility of identifying the elite genotypes (Flores *et al.*, 1998).

Numerous statistical methods have been developed and applied for analysing, perception and prediction of IGE (Malosetti *et al.*, 2013). Additive main effects and multiplicative interaction (AMMI) proposed by Gauch (1993) and genotype main effect and genotype-environment interaction (GGE-biplot) developed by Yan *et al.* (2000) are used for analyzing multi-environment trial data. Both AMMI and GGE-biplot are based on principal component analysis (PCA) and can be used to fully explore multi-environment trials, and relationship among the tested environments, genotypes and the genotype-environment interactions ( $G \times E$  interaction). However, the GGE model was better than AMMI owing to greater retention of GE and G-GE (Balestre *et al.*, 2009). Several authors (Yan *et al.*, 2007; Gauch *et al.*, 2008; Balestre *et al.*, 2009) inferred that the quantity of GE or  $G + GE$  retained is not a good parameter for estimating stability. Incorporation of uncertainty in biplots is a key tool for selecting stable genotypes and defining mega-environments (De Oliveira *et al.*, 2016). GGE-biplot is a useful tool for evaluating the performance of plants under diverse environments (Ukalski and Klisz, 2016), because it helps in the analysis of mega-environment (e.g., “which-won-where” pattern), that indicates the suitability of specific genotypes for specific mega-environments. This also analyzes the mean performance and stability of genotypes and helps in the evaluation of environmental variations (the power to discriminate among genotypes in target environments).

Soybean is a promising crop to introduce it in the Kingdom of Saudi Arabia crop cultivation. Hence, there is a need to evaluate the elite genotypes under diverse environments for adaptability. In this study, different introduced soybean genotypes were evaluated for their adaptability under multi-environments in the Kingdom to select the best-performing soybean genotype related to seed yield and WUE across different environments and to assess the IGE in the tested environments.

## Materials and Methods

### Plant Materials and Trial Protocol

Ten soybean genotypes (Table 1), selected based on pre-experiments data, were evaluated under different environmental conditions of the Kingdom of Saudi Arabia. These genotypes were evaluated at three locations during the growing seasons of 2015 and 2016 using a randomized complete block design (RCBD) replicated three times. The seeds were sown in the first week of April at all locations during both years of study in 10 cm spaced hills. Each experimental plot consisted 3 m long 50 cm spaced three rows. Fertilizers were applied at 120:120:60 NPK kg ha<sup>-1</sup> using di-ammonium phosphate, urea and sulfate of potash as a source. Whole P was applied before sowing whereas, N and K was applied in three equal doses at monthly intervals starting three weeks from seedling

emergence. For micronutrients, the plants received 3 kg ha<sup>-1</sup> Fe, 0.6 kg ha<sup>-1</sup> each of Zn, Cu, and Mn and 0.2 kg ha<sup>-1</sup> Mo. Irrigation was applied, after 50 mm evaporation of ‘class A pan’. Water meter counters were used to record the amount of applied water. Just before the harvesting, plant height was measured with a meter rod. At the time of harvest, five plants were randomly selected from each plot to record number of branches per plant, number of pods per plant and number of seeds per pod. Number of seeds per plant was recorded as a product of number of pods per plant and number of seeds per pod. Ten, randomly selected plants from each plot, were harvested and threshed to separate seeds from the straw to record seed yield per plant. Seed samples, of hundred seeds were taken from each plot and weight to record seed index. The WUE was calculated as ratio of seed yield to water applied (Viets, 1962).

### Experimental Site

The experiments were conducted at three locations *viz.*, Dirab Agriculture Research Station (24°25'49.2"N & 46°22'12.5"E), Riyadh (central Saudi Arabia), Palms and Dates Research Center (25°17'59.7"N & 49°22'36.8"E), Al-Ahsa (eastern Saudi Arabia) and a private farm at Al-Aqiq (20°16'24.2"N & 41°41'36.2"E), Al-Baha (western Saudi Arabia) during 2015 and 2016. Environment code and summery information related to five environments is given in the Table 2.

### Statistical Analysis

The normality of the collected data, from individual environments, was estimated following the Anderson-Darling normality test and the homogeneity of variances for data from individual environments was assessed by Levene's test using statistical software STAR v. 2.0.1 (IRRI, 2013a). Combined analysis of variance was performed on the original dataset to partition the variation into environment (E), genotype (G), and their interactions (GEI). Least significant difference test was used for mean separation at 5% probability. The seed yield and WUE data were analyzed by GGE-biplot analysis using the software PBTtools (IRRI, 2013b).

## Results

### Plant Height, Seed Yield and Related Traits

Analysis of variance indicated that environment significantly ( $p \leq 0.01$  or  $p \leq 0.05$ ) affected the branches per plant, pods per plant, seeds per plant, seed index, seed yield per plant and WUE; whereas there was no difference, among the environments, for plant height and number of seeds per pod (Table 3). Soybean genotypes significantly ( $p \leq 0.01$ ) differed for plant height, seed yield, yield related attributes and WUE. Genotype by environment interaction effects was also significant for plant height, seed yield and

**Table 1:** Name and source of the soybean genotypes used in the study

Genotype code	Genotype name	Source/origin	Genotype code	Genotype name	Source / origin
G1	X 32	Egypt	G6	Giza 35	Egypt
G2	Giza 22	Egypt	G7	X 30	Egypt
G3	Giza 21	Egypt	G8	Giza 111	Egypt
G4	X2 L 12	Egypt	G9	Clark	USA
G5	Giza 83	Egypt	G10	A3803	Syria

**Table 2:** Soil and weather information of the experimental sites

Environment code	Location					
	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	E <sub>5</sub>	
Region	Central	West	Central	East	West	
Season	2015	2015	2016	2016	2016	
Soil texture	Sandy loam	Loam	Sandy loam	Sandy loam	Loam	
Latitude	24°25'	20°16'	24°25'	25°17'	20°16'	
Longitude	46°22'	41°41'	46°22'	49°22'	41°41'	
Altitude (m)	638	1380	638	9.0	1380	
Temperature (°C)	Max	40.4	34.2	41.2	43.6	33.75
	Min	32.4	22	23.8	26.4	21.5
Humidity (%)	Max	16.6	46	19.2	38.4	50.25
	Min	10	8.8	4.4	4.8	11.25

**Table 3:** Analysis of variance summary for plant height, seed yield, related traits and water use efficiency (WUE) of tested soybean genotypes across five environments

SOV	DF	Mean Sum of Squares							
		Plant height	Branches /plant	Pods /plant	Seeds /plant	Seeds/ pod	Seed index	Seed yield /plant	WUE
Environment (E)	4	87.94ns	0.76*	861.0**	4569.3**	0.1ns	110.2**	245.5**	0.39**
Error	10	45.07	0.21	76.09	105.56	0.42	5.0	4.06	0.01
Genotype (G)	9	267.5**	2.4**	901.1**	2835.3**	1.3**	53.7**	34.7**	0.06**
G × E	36	86.5**	0.20*	54.1*	200.2**	0.06ns	9.12ns	21.9**	0.03**
Error	90	24.93	0.12	37.74	94.53	0.09	8.87	6.13	0.01
CV (%)		4.6	16.1	13.5	12.9	13.1	19.1	16.0	15.7

SOV =Source of variation; DF =Degree of freedom; CV =Coefficient of variation; ns =Non-significant; \* = Significant at  $P \leq 0.05$ ; \*\* = Significant at  $P \leq 0.01$

yield related traits except number of seeds per pod and seed index. The highest plant height (119.3 cm) mean values was recorded for genotype Giza 22 grown under E4 (eastern region), and under E5 (western region) conditions. Similarly, genotype Giza 21 produced the highest branches per plant (3.0) when planted under E1 (central region) and E2 (western region) conditions, however, the above genotypes were similar in performance with genotype Giza 111 when grown under E1, E2 and E4 conditions (Table 4).

The highest number of pods per plant (70.3) was recorded for genotype Giza 111 planted under E3 and E1 conditions. Likewise, genotype X 30 had maximum number of seeds per plant under E1 conditions (Table 5). Number of seeds per pod (2.7) was the highest in genotype X 30 and genotype Giza 83, whereas, genotype A3803 had the highest seed index (19.2 g). The highest seed index was recorded in environments E3, E4 and E5 (Table 6). Genotype Giza 21 produced highest seed yield per plant (24 g) when planted under E4 than other genotypes and environmental conditions. Similarly, genotypes Giza 21 and Giza 83 had the highest WUE when grown under E5 (Table 7).

### Winning Genotype and Mega-environment

The GGE-biplot figure for seed yield showed that PC1 and

PC2 accounted for 49.9% and 18.8%, respectively explaining total of 68.7% of the variation. Following the 'which-wins-where' rule, eight sectors were constructed on the biplots with genotypes, i.e., G1 (X32), G3 (Giza 21), G4 (X2 L12), G6 (Giza 35), G7 (X30), G8 (Giza 111), G9 (Clark), G10 (A3803), identified as vertex genotypes for seed yield. The environment E4 (eastern region in 2016 growing season) was in the sector with vertex genotypes G3 and G8 (Giza 21 and Giza 111). The environment E1 (central region in 2015 growing season) was suitable for G8 (Giza 111). No environment fell into sectors where G7 (X30), G9 (Clark), G10 (A3803), and G1(X32) were placed on the vertices, demonstrating that these genotypes did not perform well in any of the studied environments. Moreover, G5 (Giza 83) and G2 (Giza 21), were around the origin, which were less responsive to the environment (Fig. 1A).

Analysis of GGE-biplot for WUE showed that PC1 and PC2 accounted for 39.0% and 27.9%, respectively explaining total of 66.9% variation (Fig. 1B). Eight sectors were present in the biplots with genotypes i.e., G2 (Giza 22), G3 (Giza 21), G5 (Giza 83), G6 (Giza 35), G7 (X30), G8 (Giza 111), G9 (Clark), and G10 (A3803). The environment E5 (western region in 2016 growing season) fell into the sector containing genotypes G3 and G5 (Giza 21 and Giza 83) at the vertex.

**Table 4:** Plant height and number of branches per plant of tested soybean genotypes across five environments

Genotypes	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	E <sub>5</sub>	Mean
Plant height (cm)						
X 32	110.0 e-n	115.0 a-i	120.0 a	101.3 o-r	115.7 a-h	112.0 B
Giza 22	116.0 a-g	116.0 a-g	110.3 d-n	119.3 ab	118.7 abc	116.1 A
Giza 21	111.8 b-k	111.8 b-k	102.3 n-r	116.2 a-f	109.3 e-o	110.3 BC
X2 L 12	108.7 f-p	108.7 f-p	104.0 k-r	111.3 b-l	107.7 h-q	108.1 CD
Giza 83	104.3 k-r	104.3 k-r	100.7 pqr	113.7 a-j	107.2 i-q	106.0 D
Giza 35	100.5 qr	100.5 qr	100.5 qr	108.7 f-p	97.10 r	101.5 E
X 30	109.0 f-o	109.0 f-o	116.0a-g	118.3 a-d	117.2 a-e	113.9 AB
Giza111	108.0 g-q	108.0 g-q	115.7 a-h	104.3 k-r	103.7 l-r	107.9 CD
Clark	116.0 a-g	116.0 a-g	96.3 r	109.0 f-o	96.7 r	106.8 CD
A3803	110.0 e-n	110.0 e-n	103.0 m-r	110.7 c-m	106.8 j-q	108.1 CD
Mean	109.4	109.9	106.9	111.3	108.0	
Branches per plant						
X 32	2.2 c-i	2.2 c-i	1.7 h-n	2.3 c-h	1.9 f-m	2.1 De
Giza 22	2.5 a-e	2.5 a-e	2.2 c-j	2.2 c-j	2.0 e-l	2.3 CD
Giza 21	3.0 a	3.0 a	2.5 a-e	2.7 abc	2.6 a-d	2.8 A
X2 L 12	1.3 n	1.3 n	1.6 j-n	1.7 i-n	1.7 i-n	1.5 F
Giza 83	2.6 a-d	2.6 a-d	2.3 c-h	2.4 b-f	2.3 b-g	2.4 BC
Giza 35	2.5 a-e	2.5 a-e	2.1 d-k	2.8 ab	2.1 d-k	2.4 BC
X 30	1.6 k-n	1.6 k-n	1.5 l-mn	1.9 f-m	1.4 mn	1.6 F
Giza111	3.0 a	3.0 a	2.1 d-k	3.0 a	1.7 i-n	2.6 AB
Clark	2.0 e-l	2.0 e-l	2.0 e-l	2.1 c-k	1.8 g-n	2.0 E
A3803	1.9 f-m	1.9 f-m	2.3 c-h	2.5 a-e	2.4 b-f	2.1 CDE
Mean	2.3 AB	2.3 AB	2.0 BC	2.4 A	2.0 C	

E<sub>1</sub> and E<sub>2</sub> represent Central and West regions during 2015 whereas E<sub>3</sub>, E<sub>4</sub> and E<sub>5</sub> represent Central, East and West regions during 2016 growing season. Figures sharing the same case letter, for a parameter, do not differ significantly at P ≤ 0.05

**Table 5:** Number of pods per plant and seeds per pod of tested soybean genotypes across five environments

Genotypes	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	E <sub>5</sub>	Mean
Pods per plant						
X 32	50.7 d-h	38.0 j-r	37.0 k-r	46.3 e-l	44.8 f-m	43.4 B
Giza 22	53.0 c-g	39.8 i-r	46.3e-k	47.1e-j	48.0d-i	46.8 B
Giza 21	62.0 abc	46.5 e-k	54.3 c-f	54.8 cde	54.6 c-f	54.4 A
X2 L 12	55.3 cde	36.4 l-r	44.7 f-n	47.4 e-j	46.0 e-l	46.0 B
Giza 83	41.8 h-p	31.4 qrs	34.8 n-r	42.4 h-p	38.6 i-r	37.8 C
Giza 35	61.3 abc	46.0 e-l	50.7 d-h	39.9 i-r	40.3 i-q	47.6 B
X 30	51.0 d-h	38.3 i-r	41.7 h-p	43.4 g-n	42.6 h-p	43.4 B
Giza111	67.0 ab	40.3 i-r	70.3 a	55.7 cde	57.7 bcd	58.2 A
Clark	55.0 cde	41.3 h-q	46.0 e-l	47.8 d-j	43.0 h-o	46.6 B
A3803	33.3 o-r	21.4 s	30.3 rs	35.0 m-r	32.7 pqr	30.6 D
Mean	53.0 A	37.9 C	45.6 B	46.0 B	44.8 B	
Seeds per pod						
X 32	2.4	2.4	2.0	2.0	2.0	2.2 C
Giza 22	2.4	2.4	2.3	2.1	2.2	2.3 BC
Giza 21	1.8	1.8	2.0	1.8	1.8	1.8 D
X2 L 12	2.4	2.5	2.5	2.4	2.4	2.4 AB
Giza 83	2.8	2.8	2.7	2.3	2.5	2.6 A
Giza 35	1.8	1.8	1.8	2.1	1.9	1.9 D
X 30	2.7	2.7	2.8	2.4	2.6	2.7 A
Giza111	1.8	1.8	1.9	1.8	1.8	1.8 D
Clark	2.3	2.3	2.2	2.3	2.1	2.3 BC
A3803	2.4	1.9	2.4	2.2	2.3	2.2 BC
Mean	2.3	2.2	2.3	2.2	2.2	

E<sub>1</sub> and E<sub>2</sub> represents Central and West regions during 2015 whereas E<sub>3</sub>, E<sub>4</sub> and E<sub>5</sub> represents Central, East and West regions during 2016 growing season. Figures sharing the same case letter, for a parameter, do not differ significantly at P ≤ 0.05

This indicated that these genotypes were the best performed genotypes in this environment. No environment was classified into sectors where genotypes G7 (X30), G6 (Giza 35), G10 (A3803), and G2 (Giza 22) were placed on the vertices, suggesting that these

**Table 6:** Number of seeds per plant and seed index of tested soybean genotypes across five environments

Genotypes	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	E <sub>5</sub>	Mean
Seeds per plant						
X 32	120.3 b-f	90.3 m-r	75.7 rs	94.10 k-q	90.9 m-r	94.3 D
Giza 22	121.7 b-f	91.3 m-r	103.3 g-n	100.5 h-n	103.3 g-n	104.0 BC
Giza 21	111.3 d-h	83.5 o-s	103.7 g-n	95.8 h-p	99.7 h-n	98.8 CD
X2 L 12	133.0 ab	90.4 m-r	110.3 e-j	109.4 e-l	109.9 e-k	110.6 AB
Giza 83	111.0 e-i	83.3 o-s	94.0 l-q	95.8 h-p	94.9 j-q	95.8 D
Giza 35	106.0 f-m	79.5 qrs	88.7 n-r	80.8 o-s	80.7 p-s	87.1 E
X 30	139.3 a	104.5 g-m	117.0 c-g	102.5 g-n	109.8 e-l	114.6 A
Giza111	123.3 b-e	72.5 s	131.3 abc	102.3 g-n	109.2 e-l	107.7 AB
Clark	127.0 a-d	95.3 i-q	100.3 h-n	110.3 e-j	96.5 h-o	105.9 B
A3803	81.3 o-s	39.0 t	72.3 s	72.0 s	72.2 s	67.4 F
Mean	117.4 A	83.0 C	99.7 B	96.4 B	96.7 B	
Seed index (g)						
X 32	14.0	12.6	18.6	14.6	16.6	15.3 BCD
Giza 22	14.6	13.2	13.1	13.8	13.4	13.6 DE
Giza 21	14.5	13.3	18.7	18.5	18.6	16.7 BC
X2 L 12	15.5	12.2	15.6	12.4	14.0	14.0 DE
Giza 83	12.7	11.5	20.8	16.9	18.8	16.2 BC
Giza 35	13.1	11.8	18.7	19.3	19.0	16.4 BC
X 30	13.4	12.0	12.3	14.1	13.2	13.0 E
Giza111	15.9	14.3	16.5	20.6	18.6	17.2 AB
Clark	13.0	11.7	18.8	14.6	14.6	14.5 CDE
A3803	17.7	15.9	21.3	20.3	20.9	19.2 A
Mean	14.4 b	12.8 c	17.4 a	16.5 a	16.8 a	

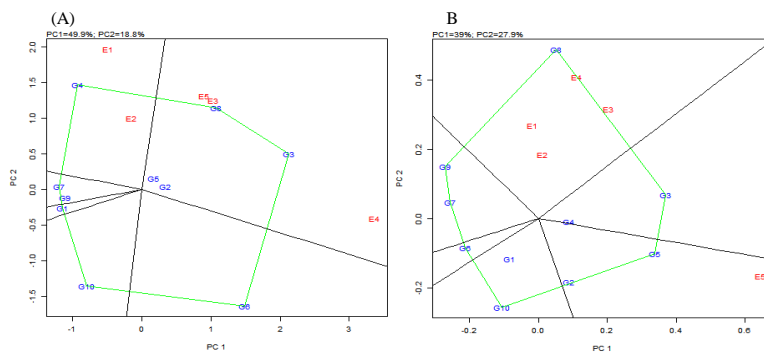
E<sub>1</sub> and E<sub>2</sub> represent Central and West regions during 2015 whereas E<sub>3</sub>, E<sub>4</sub> and E<sub>5</sub> represent Central, East and West regions during 2016 growing season. Figures sharing the same case letter, for a parameter, do not differ significantly at P ≤ 0.05

**Table 7:** Seed yield and water use efficiency of tested soybean genotypes across five environments

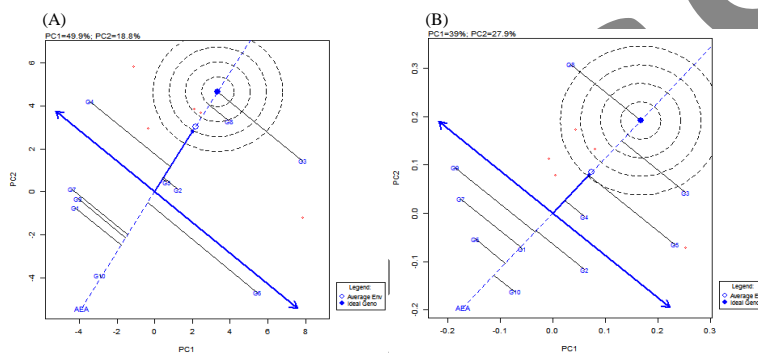
Genotypes	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	E <sub>5</sub>	Mean
Seed yield per plant (g)						
X 32	16.7 e-l	11.3 p-s	14.0 i-q	13.8 j-q	15.4 g-o	14.2 CD
Giza 22	17.4 c-k	11.9 o-s	13.4 k-r	19.3 c-g	18.0 c-i	16.0 BC
Giza 21	16.0 f-n	10.8 qrs	19.3 c-g	24.0 a	19.8 b-f	18.0 A
X2 L 12	20.5 a-e	11.0 p-s	17.2 d-l	13.6 j-q	17.6 c-j	16.0 BC
Giza 83	14.0 i-q	9.5 rst	18.7 c-h	16.0 f-n	19.7 b-f	15.6 C
Giza 35	13.8 j-q	9.3 st	16.3 f-m	23.7 ab	13.3 l-s	15.3 C
X 30	18.6 c-h	12.6 m-s	14.0 i-q	14.4 i-q	13.6 k-q	14.6 CD
Giza111	19.7 b-f	10.4 qrs	21.3 abc	20.8 a-d	15.6 g-o	17.6 AB
Clark	16.5 f-m	11.1 p-s	18.5 c-h	13.3 l-s	12.3 n-s	14.4 CD
A3803	14.3 i-q	6.2 t	15.3 g-o	14.3 i-q	14.8 h-p	13.0 D
Mean	16.7 AB	10.4 C	16.8 AB	17.3 A	16.0 B	
Water use efficiency (g L <sup>-1</sup> )						
X 32	0.47 f-j	0.33 j	0.43 g-j	0.47 f-j	0.67 bcd	0.47 BC
Giza 22	0.50 e-i	0.33 j	0.43 g-j	0.43 g-j	0.78 ab	0.50 B
Giza 21	0.43 g-j	0.57 d-g	0.40 hij	0.60 def	0.79 a	0.58 A
X2 L 12	0.63 cde	0.47 f-j	0.43 g-j	0.40 hij	0.77 abc	0.54 AB
Giza 83	0.37 ij	0.53 d-h	0.33 j	0.53 d-h	0.79 a	0.53 AB
Giza 35	0.33 j	0.43 g-j	0.33 j	0.50 e-i	0.53 d-h	0.43 CD
X 30	0.57 d-g	0.37 ij	0.47 f-j	0.47 f-j	0.53 d-h	0.48 BC
Giza111	0.60 def	0.60 def	0.40 hij	0.77 abc	0.63 cde	0.60 A
Clark	0.47 f-j	0.50 e-i	0.40 hij	0.53 d-h	0.47 f-j	0.47 BC
A3803	0.37 ij	0.40 hij	0.13 k	0.47 f-j	0.63 cde	0.40 D
Mean	0.47 BC	0.45 C	0.38 D	0.52 B	0.68 A	

E<sub>1</sub> and E<sub>2</sub> represent Central and West regions during 2015 whereas E<sub>3</sub>, E<sub>4</sub> and E<sub>5</sub> represent Central, East and West regions during 2016 growing season. Figures sharing the same case letter, for a parameter, do not differ significantly at P ≤ 0.05

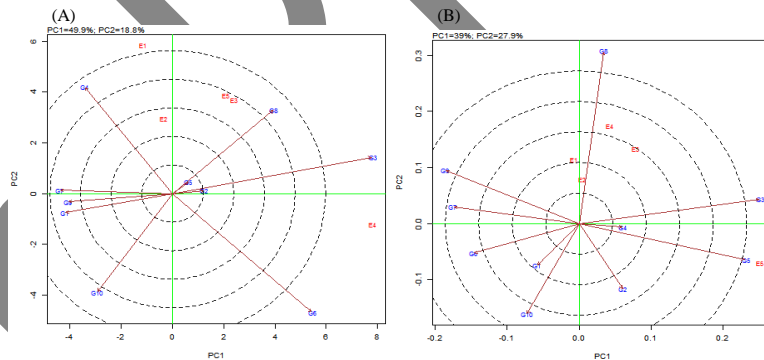
genotypes did not perform well in any of the studied environments. Genotypes G4 (X2 L12) and G1 (X32), located around the origin, which were less responsive to the environment.



**Fig. 1:** Polygon view of GGE Biplot (which–won–where) showing the G×G×E interaction effect of tested soybean genotypes across five environments for (A) seed yield and (B) water use efficiency



**Fig. 2:** The performance and stability of tested soybean genotypes based on (A) seed yield and (B) water use efficiency



**Fig. 3:** GEE biplot for genotypes ranking relative to the center of the concentric circles based on (A) seed yield and (B) water use efficiency

### Stability and Mean Performance of the Ten Genotypes

Circles at the end of average environment Axes (AEA) indicate the highest performing genotypes, whereas the perpendicular line on AEA with a double arrow represents stability (Fig. 2). On the other hand, genotype closeness to AEA indicated higher stable genotypes and the center of the circle points to the ideal genotype (stable genotype with high mean value). The ideal genotypes are close to the origin and have the shortest vector from the average environment axis. The position of genotypes G3 and G8 on top of AEA suggested that their

yield was higher than other genotypes; on the other side G10 (A3803) was down which produced the lowest seed yield. Stable soybean genotypes for seed yield were different than for WUE. The position of genotype G8 (Giza 111) on AEA was opposite to that of genotype G10 (A3803) indicating that genotype G8 had the highest mean WUE. The position of genotypes G9 (Clark), G8 (Giza 111), and G5 (Giza 83) were away from AEA indicating that these genotypes were the most variable (least stable), whereas genotypes G1 (X32), G4 (X2 L12) and G10 (A3803) were highly stable for WUE (Fig. 2B).

### Comparison Plot for Genotypes based on the Concentric Circles

To assess the discrimination and representativeness of the tested environments GGE-biplots were drawn based on seed yield and WUE (Fig. 3A and B). An ideal environment is the one that is present in the innermost circle. Thus, E2 (western region in 2015 growing season) was considered an ideal environment for the selection of adaptable genotypes and high seed yield for all the whole regions studied; however, E1 and E4 (central region in 2015 growing season and East region in 2016 growing season, respectively) could not be ideal environments. Therefore, genotype G2 (Giza 22) and genotype G5 (Giza 83) were the most stable genotypes with good seed yield per plant as compared to other genotypes (Fig. 3A). Regarding WUE, the most and the least discrimination environments were the western region during 2015 growing season and 2016 growing season (E2 and E5), which indicated that the seasonal variations strongly influence this trait. The genotypes G4 (X2 L12) and G1 (X 32) are the ideal genotypes in terms of WUE, as shown by their positions.

### Discussion

In this study, soybean genotypes were evaluated for adaptability and stability in different parts of the Kingdom of Saudi Arabia. The tested genotypes varied in their performance when planted under different environmental conditions. The best performance, in terms of seed yield and WUE, was record from the genotypes Giza 111 and X 30 in the central Saudi Arabia during 2015 growing season (E1). Genotype  $\times$  environment interactions modulate the success of any breeding programs for development of genetic materials adapted to diverse set of environments (Alghamdi, 2004). This indicates that general stability, across regions/environments, should be considered in breeding programs aimed at developing high yielding genotypes (Radi *et al.*, 1993). The high yielding genotype may not necessarily have the highest level of stability. Therefore, the selection of the best genotypes should be not based upon the means of the trait alone, but the stability of these genotypes should be examined and seed yield may not be the only selection criteria (Alghamdi, 2004). Environments usually have strong influence than the genotypes alone and the GEI (Alghamdi, 2004; EL-Harty *et al.*, 2010). However, the presence of significant GEI may complicate selection for the selection traits under different environments. In this study, GEI showed significance for all studied traits except number of seeds per pod and seed index. Magnitude of the IGE effect was two and four times more than that of environment and genotype separately, respectively. Water use efficiency varied among the ten tested genotypes and the genotype Giza 21 and Giza 111 had the maximum WUE.

Development of adaptable genotypes, for a wide range of environments, has been the main goal for breeders;

however, selecting a genotype for a target environment could be the best choice in the breeding programs (EL-Harty, 2016). In this study, GGE-Biplot was effective for analyzing and visualizing the patterns of IGE with respect to test environment and genotype evaluations. In this study, the genotype G10 (A3803) was close to AEA suggesting that it is the most stable genotype, followed by G5 (Giza 83) and G2 (Giza 22). The polygon view of GGE Biplot analysis is the best way to visualize and evaluate the GEI patterns (Yan and Kang, 2003). This helps in establishing the presence/absence of cross over interactions and possible existence of mega environments (Yan and Tinker, 2006). The concept of ideal test environment is characterized by its ability to discriminate genotypes and be representative of other tested environments (Yan and Kang, 2003). Discrimination ability refers to the ability of an environment to portray the variance among the tested genotypes in a study (Blanche and Myers, 2006).

This study indicated that the environments, based on certain traits may offer an opportunity for effective selection approach. Identification of mega-environment would help to reduce the number of total test environments, and may save the time and resources. GGE biplot was not only efficient in interpreting GEI but was also helpful in scrutinizing genotypes in various testing environments. Identification of ideal genotype is important while testing genotypes across locations. However, such an ideal genotype may not exist in reality but it can be used as a reference to identify the most suitable genotype across environments (Yan and Kang, 2003; Mitrovic *et al.*, 2012). The ideal genotype is expected to perform well across tested environments and shows stability as well (Yan *et al.*, 2007).

In this study, the ideotypes for seed yield per plant were Giza 22 and Giza 83, whereas X2 L12 and X 32 were the ideal ideotypes for WUE. GGE-Biplot of the ten soybean genotypes, based on seed yield per plant, indicated that Giza 21 and Giza 111 were the best performing genotypes for the eastern region and Giza 111 was the most suitable for the central region.

### Conclusion

In conclusion, genotypes Giza 21 and Giza 111 were best performing for the eastern region and Giza 111 was the suitable for the central region. Comparison of the tested environments suggested that the western region had the most suitable environment for the selection of widely adaptable genotypes across the regions.

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## Reference

- Acquaah, G., 2007. Breeding soybean. In: *Principles of Plant Genetics and Breeding*, pp: 521-528. Acquaah, G. (ed.). Blackwell Publishing, Malden, Oxford
- Alghamdi, S.S., 2004. Yield stability of some soybean genotypes across diverse environments. *Pak. J. Biol. Sci.*, 12: 2109-2114
- Balestre, M., R.G. Von Pinho, J.C. Souza and R.L. Oliveira, 2009. Genotypic stability and adaptability in tropical maize based on AMMI and GGE biplot analysis. *Genet. Mol. Res.*, 8: 1311-1322
- Blanche, S.B. and G.O. Myers, 2006. Identifying discriminating locations for cultivar selection in Louisiana. *Crop Sci.*, 46: 946-949
- Bunce, J., 2016. Variation among Soybean Cultivars in Mesophyll Conductance and Leaf Water Use Efficiency. *Plants*, 5: 44
- Condon, A.G., R.A. Richards, G.J. Rebetzke and G.D. Farquhar, 2004. Breeding for high water-use efficiency. *J. Exp. Bot.*, 55: 2447-2460
- Cooper, M. and G.L. Hammer, 1996. "Plant Adaptation and Crop Improvement". CAB International, Wallingford
- De Oliveira, L.A., C.P. da Silva, J.J. Nuvunga, A.Q. da Silva and M. Balestre, 2016. Bayesian GGE biplot models applied to maize multi-environments trials. *Gene. Mol. Res.*, 15: DOI.10.4238/gmr.15028612
- EL-Harty, E.H., 2016. Selection of some faba bean segregation genotypes in contrasting environments. *Ann. Agric. Sci.*, 54: 15-24
- EL-Harty, E.H., A.M.A. Rizk, E.K. Gendy and H.T. Abd El-Aal, 2010. Performance of twelve soybean genotypes under four sowing dates at middle Egypt. *Egypt. J. Plant Breed.*, 14: 283-293
- FAOSTAT, 2016. www.fao.org/faostat (Accessed on March 10, 2018)
- Flores, F., M.T. Moreno and J.I. Cubero, 1998. A comparison of univariate and multivariate methods to analyze G×E interaction. *Field Crops Res.*, 56: 271-286
- Gauch, H.G., Jr., H.P. Piepho and P. Annicchiarico, 2008. Statistical analysis of yield trials by AMMI and GGE: further considerations. *Crop Sci.*, 48: 866-889
- Gauch, H.G., 1993. *Matmodel Version 2.0: AMMI and Related Analysis for Two-way Data Matrices*. Micro Computer Power, Ithaca, New York, USA
- Handy, A., R. Ragab and E. Scarascia-Mugnozza, 2003. Coping with water scarcity: water saving and increasing water productivity. *Irrig. Drain.*, 52: 3-20
- Hussain, M., S. Farooq, W. Hasan, S. Ul-Allah, M. Tanveer, M. Farooq and A. Nawaz, 2018. Drought stress in sunflower: Physiological effects and its management through breeding and agronomic alternatives. *Agric. Water Manage.*, 201: 152-167
- IRRI, 2013a. *Plant Breeding Tools (PBTtools) Version 1.3*. International Rice Research Institute, Los Baños, Philippines
- IRRI, 2013b. *Statistical Tool for Agricultural Research (STAR) Version: 2.0.1*. International Rice Research Institute, Los Baños, Philippines
- Lee, W.K., N. Kim, J. Kim, J.K. Moon, N. Jeong, I.Y. Choi, S.C. Kim, W.H. Chung, H.S. Kim, S.H. Lee and S.C. Jeong, 2013. Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. *Theor. Appl. Genet.*, 126: 1103-1119
- Lim., T.K., 2012. *Edible Medicinal and Non-Medicinal Plants*, Vol. 2, pp: 634-714. Fruits, Springer Science
- Malosetti, M., J.M. Ribaut and F.A. Van Eeuwijk, 2013. The statistical analysis of multi-environment data: Modeling genotype-by-environment interaction and its genetic basis. *Front. Physiol.*, 4: 44. <https://doi.org/10.3389/fphys.2013.00044>
- Mitrovic, B., D. Stanisavljevic, S. Treski, M. Stojakovic, M. Ivanovic, G. Bekavac and M. Rajkovic, 2012. Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analyses. *Turk. J. Field Crops*, 17: 35-40
- Naylor, B. and F.B. Fritsch, 2015. *Water-use Efficiency of Soybean (Glycine max) Genotypes Contrasting for Carbon Isotope Discrimination*. Presentation in: Synergy in Science: Partnering for Solution. Annual meeting of Crop Society of America, held on 15-18 Nov. Minneapolis, MN
- Radi, M.M., M.A. El-Borai, Safia, T. Abdalla, A.E. Sharaf and E.F. Desouki, 1993. Estimates of stability parameters of yield of some soybean cultivars. *Tanta J. Agric. Res.*, 11: 86-91
- Ssemakula, G. and A. Dixon, 2007. Genotype × environment interaction, stability and agronomic performance of carotenoid-rich cassava clones. *Sci. Res.*, 2: 390-399
- Ukalski, K. and M. Klisz, 2016. Application of GGE biplot graphs in multi-environment trials on selection of forest trees. *Folia Forestalia Polonica, Series A-For.*, 58: 228-239
- Viets, F.G., 1962. Fertilizers and the efficient use of water. *Adv. Agron.*, 14: 233-264
- Wang, H.X., C.M. Liu and L. Zhang, 2002. Water-saving agriculture in China: an overview. *Adv. Agron.*, 75: 135-171
- Yan, W. and I.R. Rajcan, 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. *Can. J. Plant Sci.*, 42: 11-20
- Yan, W. and M.S. Kang, 2003. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. CRC Press, Boca Raton, FL
- Yan, W. and N.A. Tinker, 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.*, 86: 623-645
- Yan, W., L.A. Hunt, Q. Sheng and Z. Szlavnic, 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.*, 40: 597-605
- Yan, W., M.S. Kang Ma B and B. Woods, 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.*, 47: 643-653

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