

Analysis of genotype × environment interaction for seed yield in spineless safflower (*Carthamus tinctorius* L.) genotypes

M. Jamshid Moghaddam^{a*}, M. Eskandari Torbaghan^b and A. Mirzaee^c

^aDryland Agricultural Research Institute, Kermanshah, Iran.

^bAgricultural and Natural Resources Station of North Khorasan, Shiravan, Iran.

^cAgricultural and Natural Resource Research Center of Ilam, Ilam, Iran.

*Corresponding author's email: m_jmoghaddam@yahoo.com

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ABSTRACT

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Evaluating cultivars in the presence of unpredictable genotype × environment interaction (GEI) is a major problem in crop breeding programs. This study was conducted to: (1) evaluate seed yield stability of 15 safflower genotypes grown in three consecutive seasons (2005-08) at three locations in Iran; and (2) investigate the inter-relationships among eight agronomic traits using the genotype × trait (GT) biplot technique. The additive main effect and multiplicative interaction (AMMI) analysis, the stability parameters derived from the AMMI model, Shukla's analysis, genotype plus GE (mean performance + stability) distance (GGED), yield-stability (YS) statistic, and several common stability procedures were used to analyze GEI. Results of the AMMI analysis showed that main effects due to genotype (G), environment (E), and GEI, as well as the first six interaction principal component axes (IPCA1 to 6), were significant ($P < 0.01$). The partitioning of GEI also revealed that both heterogeneity caused by the environmental index and heterogeneity caused by residual GEI were important sources of variation. According to rank correlation analysis, stability parameters can be categorized into three distinct sections related to static and dynamic concepts of stability. The parameters of the three groups ranked the genotypes in different ways. Genotypes G12, G9, G11 and G8 were superior in terms of both stability and high yield. The GT biplot revealed that seed yield was positively and significantly associated with seed weight and heads per plant, but oil content was not correlated with seed yield.

Keywords: AMMI model, genotype plus GE distance, genotype × trait (GT) biplot, stability parameters, yield-stability statistic

INTRODUCTION

Safflower (*Carthamus tinctorius* L.) has been grown for many years for its flowers, which are used for coloring food, making dyes, and as medication (Knowles, 1989). Today, the main plant part used is the seed, which produces high quality edible oil and industrial oil and bird feed (Johnston *et al.*, 2002). Seed oil of this plant possesses the highest amount of linoleic acid among the world's 10 major vegetable oil crops (Hamdan *et al.*, 2008).

Safflower is adapted to relatively low rainfall areas where it rains in winter and spring but is dry during flowering and maturation (Yau, 2007). Control of grassy weeds in safflower can benefit subsequent small grain crops grown in rotation (Johnston *et al.*, 2002). Safflower is a suitable crop for rotating with wheat and chickpea in cold and semi-cold drylands of Iran (Pourdad and Beg, 2003), and with barley (Yau, 2005) under Mediterranean rainfed conditions. Fall-sown safflower presents

earlier spring growth and development, and produces higher yield than spring-sown safflower (Johnson and Dajue, 2008).

Many statistical methods have been developed to analyze data from multi-environment trials (MET) in order to better understand and interpret G × E interaction (GEI) patterns (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Tai, 1971; Shukla, 1972; Zobel *et al.*, 1988; Hühn, 1990). Two different concepts of stability are used to characterize a genotype in METs. According to the concept of biological or static stability, a stable genotype presents minimal variance for yield across different environments. This concept has received little attention from breeders and agronomists as they prefer genotypes with high mean yields and the potential to respond to increased agronomic inputs and favorable environmental conditions (Becker and Leon, 1988).

In analyzing data from MET, Zobel *et al.* (1988)

proposed the additive main effects and multiplicative interaction (AMMI) analysis model constructed from principal component (PC) axes to explain GEI patterns, which provides a multiplicative model. The AMMI model used by many researchers exhibits more complex interaction, which requires a maximum of two PC axes to account for the considerable amount of GEI variation. Therefore, for further description of GEI, several AMMI-derived stability statistics have been used to identify stability performance of widely adapted genotypes in METs (Zobel, 1994; Gauch and Zobel, 1996; Sneller *et al.*, 1997; Zhang *et al.*, 1998; Purchase *et al.*, 2000).

The biplot has been used in MET data analysis based on the AMMI model (Zobel *et al.*, 1988) and the GGE (G and GE) biplot model (Yan, 2001). The GGE biplot is similar to the AMMI biplot but differs in that the genotype main effect is included as a multiplicative effect rather than as an additive main effect (Yan and Kang, 2003). Yan and Rajcan (2002) used a genotype \times trait (GT) biplot (an application of the GGE biplot technique) to study genotype \times trait data. They demonstrated that the GT biplot was an excellent tool for visualizing genotype \times trait data.

This study was conducted to: (1) evaluate the agronomic characteristics of spineless safflower

breeding lines and improved cultivars under different variable environments; (2) determine the nature and magnitude of GEI effects on seed yield in diverse environments using the AMMI technique; (3) evaluate safflower genotypes based on different stability parameters; and (4) study the interrelationships among safflower traits using the GT biplot technique.

MATERIALS AND METHODS

Experimental data

The 15 safflower spineless genotypes were evaluated in nine environments (a combination of three locations and three consecutive cropping seasons, 2005-08). The trials were conducted at moderately cold locations under rainfed conditions (see climatic characteristics of trial locations in Table 1). A randomized complete block design with three replications was used in each environment. Plot size was 6 m² (5 rows, 4 m in length, and 30-cm row spacing). At sowing, 50 kg N ha⁻¹ and 50 kg P₂O₅ ha⁻¹ were applied. In each experimental unit, agronomic traits days to flowering and maturity, plant height (cm), number of heads per plant, number of seeds per head, seed weight (g), oil content (%), and seed yield (kg ha⁻¹) were measured.

Table 1. Climatic characteristics of the environments included in this study.

Environments			Latitude longitude	Altitude (m)	Rainfall (mm)	Temperature (°C)		No. of days < 0°C	EM †
Location	Year	Code				Min.	Max.		
Sararood	2005-06	E1	34°19'N 47°07'E	1351	515.0	3.7	19.3	80	1213.8
	2006-07	E2			551.8	3.8	17.0	90	813.7
	2007-08	E3			159.1	3.0	18.6	95	314.5
Ham	2005-06	E4	33°41'N 46°35'E	975	574.5	9.2	15.5	39	1245.5
	2006-07	E5			470.3	7.3	19.4	41	942.2
	2007-08	E6			217.3	7.6	21.8	43	763.4
Shirvan	2005-06	E7	37°14'N 58°07'E	1131	214.2	4.4	19.3	76	350.2
	2006-07	E8			551.8	3.3	15.6	103	701.8
	2007-08	E9			172.0	2.2	15.8	85	364.8

†EM, environmental mean.

Statistical analysis

The GEI for seed yield was first analyzed according to the AMMI model (Zobel *et al.*, 1988). From this analysis, the distance of each genotype and environment from the origin as defined by the first two IPCAs was used to generate a biplot. To further describe the stability using AMMI analysis, several stability statistics derived from AMMI analysis were used. The value of first IPCA scores represents the simplest measure of stability provided by AMMI (Annicchiarico, 1997). A genotype can be considered more reactive to different environments when its IPCA1 score is high, either positive or negative.

The next parameter derived from the AMMI

model is the AMMI stability value (ASV), as suggested by Purchase *et al.* (2000). The ASV was reported to produce a balanced measurement between the two IPCA scores. Because the IPCA1 score contributes more to the GEI sum of squares (SS), a weighted value is needed. It was calculated using the following formula:

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1)^2 + (IPCA2)^2}$$

where SS_{IPCA1}/SS_{IPCA2} is the weight given to the IPCA1 value by dividing IPCA1 SS by IPCA2 SS; IPCA1 and IPCA2 scores are the genotypic scores in the AMMI model.

The next two AMMI statistics (SIPC1 and

SIPC6, which are the sums of the absolute values of the IPCA scores) were calculated as follows:

$$SIPC = \left| \sum_{n=1}^N \lambda_n^{0.5} \gamma_{in} \right|$$

For the i th genotype for SIPC1, $N = 1$; for SIPC6, N was the number of IPCA that were retained in the AMMI model using the F ratio test. Genotypes with low SIPC should be more stable across environments (Gauch and Zobel, 1996; Purchase, 1997).

The next two AMMI statistics (AMGE1 and AMGE6, which are the sums across environments of the GEI modeled by AMMI) were calculated as follows:

$$AMGE = \left| \sum_{j=1}^M \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} \right|$$

where M is the number of environments: for AMGE1, N was one; for AMGE6, N was the number of IPCA that were retained in the AMMI model using the F ratio test (Sneller *et al.*, 1997).

The sites regression model analysis was also used to generate a GGE biplot. With this model, genotypes are evaluated for their combined G and GE interaction effects. A GGE distance (GGED) (i.e., the distance of each genotype from the ideal genotype) was calculated as outlined by Yan (2001). The more desirable genotypes are identified in terms of both mean performance and stability. The following common stability procedures were also calculated: environmental variance (S^2_{Ei}) (Becker and Leon, 1988); stability variance (σ^2 and s^2) (Shukla, 1972); regression methods (b and S^2_d) (Eberhart and Russell, 1966) and (α and λ) (Tai, 1971); measure of genotypic stability (D^2) (Hanson, 1970); nonparametric measures ($S^{(1)}$ and $S^{(2)}$) (Hühn, 1990); and yield stability (Y_s) statistic (Kang, 1993).

The genotype \times trait (GT) biplot method outlined in Yan and Rajcan (2002) was used to display the genotype \times trait data in a biplot. In this biplot constructed by plotting PC1 against PC2, vectors were drawn from the origin of the biplot to each trait to visualize relationships among traits.

Factor analysis based on rank values of parameters was performed for grouping all stability parameters. The analyses were performed by the GENSTAT software program (version 15.0) (GENSTAT, 2012).

RESULTS

Agronomic traits

Mean values of traits across environments are shown in Table 2. Genotypes G10, G11, G12 and

G15 showed fewer days to flowering and maturity than other genotypes. Time to maturity ranged from 196 days (G15) to 204 days (G2). Genotypes G15, G10, G14, G12, G11 and G5 had the shortest plant height, while genotypes G2 and G7 had the tallest. Plants had an average 12.7 heads per plant, with a range of 11 to 14.5 heads per plant with the highest in G11. Seeds per head ranged from 22 to 34.5, with an average of 29.4 seeds. Genotype G12 had the highest number of seeds per plant, while G7 had the lowest. There was variation for seed weight among genotypes (an average of 36.7 g and a range of 28-51 g), and G10 had the highest seed weight. Seed oil content among genotypes ranged from 25.8 to 31.6%, with an average of 28.8%. Genotypes G7, G6, G3 and G13 had the highest seed oil content. Mean yield varied from 609.3 kg ha⁻¹ for genotype G7 to 951.8 kg ha⁻¹ for genotype G11, with an average of 745.5 kg ha⁻¹.

Combined AMMI analysis

The AMMI analysis of variance on seed yield showed that 73.2% of the total sum of squares was attributable to environmental effects, 7.6% to genotypic effects, and 13.5% to GEI effects (Table 3). AMMI analysis revealed that six multiplicative terms would be necessary to account for the considerable amount of GEI variation. Results of the AMMI analysis also indicated that the first PC axis (IPCA1) of the interaction captured 38.0% of the interaction sum of squares. Similarly, the second PC axis (IPCA2) explained a further 29.5% of the GEI sum of squares. The six IPCAs accounted for a total of 98.2% of the interaction, the remaining 1.8% being the residual or noise.

To understand the relationships between particular genotypes and environments in safflower yield trials, an AMMI biplot was constructed, where IPCA1 scores were plotted against IPCA2 scores of the AMMI analysis (Fig. 1). The AMMI biplot accounted for 67.6% of total sum of squares of GEI. The results of this biplot showed that E9 tended to be separated from the other environments and was an effective discrimination environment for selecting G7. The high yielding environment, E4, with a high GEI contribution, was tightly grouped with genotypes G10 and G15, while E6 with high interaction tended to group with G8 and G12; E1 tended to separate from the other environments and grouped with G11. Therefore, environments E1, E4, E6 and E9 helped to identify with high specific adaptation. According to the biplot analysis, genotypes that tended to be close to the origin of the biplot are more stable; therefore G5 and G9 are highly adapted to most environments.

Table 2. Names, origins and means of agronomic characteristics of 15 safflower genotypes grown in nine environments

Cultivar/Line	Code	Origin	Flower color	Agronomic characteristics					
				Days to flowering	Days to maturity	Plant height (cm)	Heads per plant	Seeds per head	Seed weight (g)
Local Marand	G1	Iran	Yellow	162.6	201.4	82.8	13.2	28.3	30.3
Local Arak	G2	Iran	Orange	166.7	204.0	86.2	13.2	28.1	28.1
Local Esfahan	G3	Iran	Red	164.0	201.9	81.7	11.3	32.7	30.9
Almaneh	G4	Iran	Red	163.8	200.0	82.1	11.7	34.4	29.4
Yanghijeh	G5	Iran	Red	163.4	199.0	77.2	13.0	25.5	32.7
Esfahan 8	G6	Iran	Orange	161.3	199.3	80.4	13.0	32.4	32.4
Esfahan 24	G7	Iran	Red	166.4	203.2	85.4	11.7	34.5	28.5
Darab 2	G8	Iran	Yellow	162.6	199.6	80.5	13.3	25.9	37.7
Darab 4	G9	Iran	Red	163.3	200.3	80.8	12.1	33.7	36.2
Darab 7	G10	Iran	Red	159.9	196.4	76.4	12.2	26.6	51.1
47	G11	Iran	Red	159.9	196.3	77.1	14.5	28.3	47.3
Faraman	G12	Iran	Red	159.3	196.7	76.9	13.8	22.0	48.2
Dincer	G13	Turkey	Red	163.2	199.5	79.9	13.2	27.5	32.7
Syrian	G14	Syria	Red	160.1	196.7	76.4	12.4	27.9	40.7
Goldasht	G15	Iran	Red	159.2	196.1	75.1	11.3	33.8	44.8
LSD _{0.05}				0.73	0.77	2.38	0.90	1.96	1.32

*, ** indicate significance at the 5% and 1% probability levels, respectively.

Table 3. AMMI analysis of seed yield of 15 genotypes grown in nine environments, and the partitioning of GEI into heterogeneity due to the linear effect of the environmental index and residual GEI.

Sources of variation	df	MS	% (G + E + GEI)	% GEI
Genotype (G)	14	335616**	7.63	
Environment (E)	8	5636260**	73.22	
Block(E)	18	56233**	1.64	
GEI	112	74237**	13.50	
1.				
IPCA1	21	150623**	5.14	38.04
IPCA2	19	129266**	3.99	29.54
IPCA3	17	75024**	2.07	15.34
IPCA4	15	50194**	1.22	9.06
IPCA5	13	23077**	0.49	3.61
IPCA6	11	19517*	0.35	2.58
Residual	16	9528	0.25	1.83
2.				
Heterogeneity†	14	435803**	9.91	73.38
Residual	98	22585**	3.59	26.62
Error	252	9788	4.01	

*, ** indicate significance at the 5% and 1% probability levels, respectively.

† Heterogeneity is a linear effect of the environmental index (see Shukla, 1972; Kang and Magari, 1996).

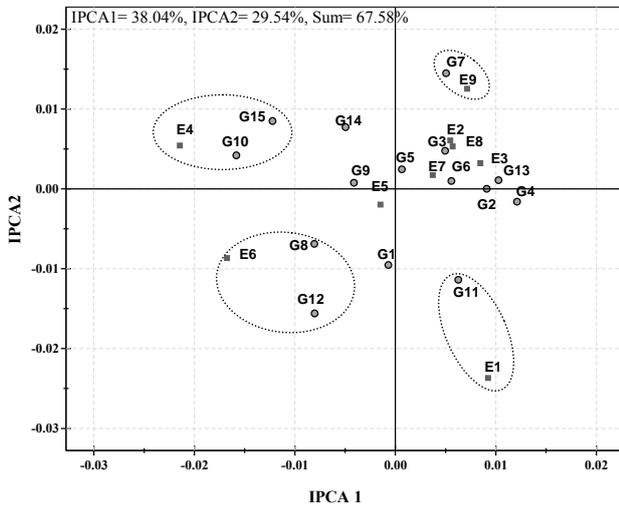


Fig. 1. Plot of the first two genotype × environment interaction principal component axes for 15 safflower genotypes grown in nine environments.

AMMI-based stability parameters

Estimates of six stability parameters for seed yields of safflower genotypes are given in Table 4.

According to IPCA1, G5 and G1 were the most stable genotypes, whereas G10, G15 and G4 were found to be unstable. The lowest ASV was observed for G5 and G1, whose mean yield was lower than the grand mean, whereas the highest ASV scores were achieved by G10, G15 and G4.

The AMMI model used in this research exhibited more complex interaction, which required a maximum of two PC axes to account for the considerable amount of GEI variation. The four AMMI-based stability statistics calculated used the first IPCA or six IPCAs that were retained in the

AMMI model via the F test. According to the SIPC1 score, G5 and G1, which had lower values of SIPC1, were the most stable genotypes. According to the SIPC6 parameter, genotype G9 was stable, but genotypes G11 and G7 were unstable. The largest absolute values of AMGE1 were recorded for genotypes G12 and G7, which are thus considered the least stable genotypes. Using this method, the most stable genotypes were G2 and G9, followed by G6 and G13. Based on AMGE6, G3, G4 and G6 had lower values and were considered stable.

Common stability parameters

To further describe GEI, several stability parameters for seed yield are given in Table 4. According to across-environment variance (S^2_E), genotypes G7, G4 and G5 with lower mean yields than the grand mean were more stable and had biological stability. Genotypes G8, G11 and G12, which produced the highest yields, were considered unstable. The partitioning of GEI into heterogeneity by the environmental index and residual GEI revealed that the linear effect of the environmental index had significant effect on GEI across environments, accounting for 26.6-73.4% of total GEI variation (Table 3).

When heterogeneity is significant, it means that the linear effect of the environmental index influences genotype stability. In such cases, comparing the significance of Shukla’s (1972) stability variance statistics, σ^2 and s^2 , is desirable. According to the σ^2 stability parameter, genotypes G12, G10, G11, G7, G15, G8, and G4 were identified as being less stable ($P < 0.01$) than the others (non-significant σ^2_i). A comparison of the significance of σ^2 and s^2 revealed that genotype G8 was unstable due to the linear effect of the environmental index because after heterogeneity was removed by the environmental index, this genotype was judged to be more stable.

The values of regression coefficients (b) for genotypes ranged from 0.70 (G7) to 1.39 (G8). Genotypes G14, G1 and G15, with b values closer to 1, were more stable, genotypes G7 and G4, with the lowest b values, were adapted to marginal environments, while G8, G11 and G12, with the highest b values, were adapted to favorable environments. Most of the studied genotypes had a non-significant deviation mean square from linear regression (S^2_d), implying that they were stable across environments, although genotypes G12, G10, G15, G11, and G7 had the highest S^2_d value and were significantly unstable. Based on Eberhart and Russell’s (1966) definition of stability ($b = 1, S^2_d = 0$), G14 and G1 can be considered the most stable of

Table 4. Estimates of stability parameters for seed yield of 15 safflower genotypes grown in nine environments

G	AMMI parameters						S^2_E †	Stability variance		Joint regression		Tai's parameters	
	IPCA1	ASV	SIPC1	SIPC6	AMGE1	AMGE6		σ^2	s^2	b	S^2_d	α	λ
G1	0.7	1	30	537	0.15	0.08	160861	14289	15539	1.09	14971	0.08	4.3**
G2	9	14	383	749	0.00	0.06	109198	16677	16779	0.87	16048	-0.13	4.6**
G3	5	8	209	789	0.08	0.00	98091	10249	8416	0.85	8802	-0.16	2.5**
G4	12	18	511	488	0.03	0.01	93982	25201**	21352*	0.78	20011	-0.22	5.7**
G5	0.6	1	27	238	0.04	0.17	93744	13432	10512	0.82	10615	-0.18	3.0**
G6	6	9	235	311	0.02	0.02	97725	9181	7305	0.85	7839	-0.15	2.2*
G7	5	8	213	855	0.23	0.23	81585	34638**	25093**	0.70	23248*	-0.30	6.6**
G8	8	12	340	649	0.11	0.17	251119	31487**	11675	1.39*	11631	0.39	3.3**
G9	4	6	174	20	0.01	0.05	163058	9080	8704	1.11	9056	0.11	2.6*
G10	16	24	667	295	0.07	0.06	190042	42524**	47278**	1.10	42562**	0.10	12.2**
G11	6	10	264	873	0.18	0.16	224891	38853**	33941**	1.26	30927**	0.26	8.9**
G12	8	12	339	480	0.24	0.26	234360	59028**	59546**	1.22	53111**	0.23	15.2**
G13	10	16	433	606	0.02	0.03	107277	17505	17260	0.86	16464	-0.14	4.7**
G14	5	8	209	385	0.12	0.18	140942	16235	18992	1.00	17963	0.00	5.2**
G15	12	19	516	321	0.13	0.14	178319	32685**	36386**	1.09	33035**	0.09	9.5**
r v. Seed yield	-0.22	-0.21	-0.21	0.01	-0.38	-0.25	-0.94**	-0.43	-0.40	-0.93**	-0.40	-0.92**	-0.40

*, ** indicate significance at the 5% and 1% probability levels, respectively.

† S^2_E , environmental variance.

‡ D^2 , genotypic stability.

†† Y_s , yield-stability statistic.

** GGED, GGE distance.

the 15 tested genotypes.

Tai (1971) developed two stability parameters similar to parameter b of Finlay and Wilkinson (1963) and parameter S^2_d of Eberhart and Russell (1966), but they were obtained in a manner that is a continuation of ANOVA by using the structural relationship principle. Tai (1971) used parameters α for the linear response of the i th genotype to environmental effects and λ for the deviation from linear response. Genotype G8 with a positive α value had specific adaptability to favorable environments, but genotype G7 with a negative α value had specific adaptability to unfavourable environments. Genotype G14 had average stability because its α value was not different from zero. Tai's (1971) second stability parameter (λ) identified all genotypes significantly different from the mean square from regression (S^2_d).

Hanson (1970) proposed a measure of genotypic stability (D^2) on the regression analysis since it uses the minimum slope from Eberhart and Russell's (1966) analysis. Genotypes G6, G3 and G5 had the lowest D^2 values and thus were stable, but genotypes G12, G8, G11 and G10 had the highest D^2 values and were unstable.

The $S^{(1)}$ and $S^{(2)}$ statistics proposed by Hühn (1990) are based on the ranking of genotypes in each environment and use homeostasis as a measure of stability. According to both $S^{(1)}$ and $S^{(2)}$, G5 and G6 had the smallest change in rank and were thus regarded as the most stable genotypes, although their mean yields were lower than the grand mean. The next most stable genotype was G9, whose mean yield was higher than the grand mean. The most unstable genotype according to these statistics was G7, which had the lowest mean yield.

GGE biplot

The GGE biplot method (Yan, 2001) was used for visualizing mean seed yield performance and stability of safflower genotypes. The GGE biplot was constructed by two principal components (PCs), PC1 and PC2, derived by subjecting the environment-centered data to singular-value decomposition. The GGE biplot explained 75.3% of total variation, with PC1 and PC2 accounting for 53.4% and 21.9%, respectively (Fig. 2). Genotypes G12 and G8 were the top yielding genotypes as they are located on the far right-hand side of the biplot towards the pointing arrow of the AEC abscissa. In addition, the biplot indicates that genotypes G3, G5 and G8 are highly stable, as they are positioned very close to the AEC abscissa with near zero scores. This indicates that their ranking was highly

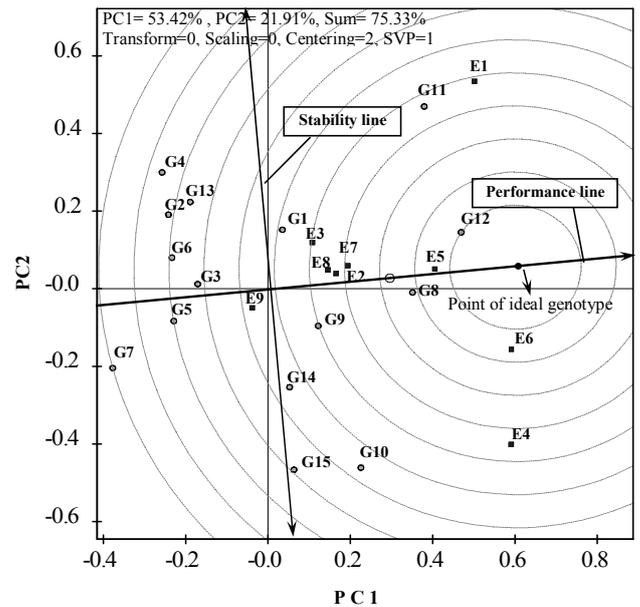


Fig. 2. GGE-biplot showing ranking of 15 safflower genotypes based on yield and stability performance over nine environments.

consistent across environments.

In contrast, genotype G11 (which is high yielding based on its mean yield and its position in the biplot) is deemed to be highly unstable as it has a very high PC2 score and is away from the AEC abscissa. Genotype G7, which is on the far left-hand side of Fig. 2, is regarded consistently as the lowest yielding genotype. According to the GGE biplot, the ideal genotype has a high PC1 value, indicating high yielding capacity, and a low PC2 value, indicating greater stability (Yan, 2001). Fig. 2 shows that G12 was closest to the ideal genotype, followed by G8. A GGED (i.e., the distance between the markers of individual genotypes and the ideal genotype) of the safflower genotypes is also presented in Table 4. Based on the ideal genotype, genotype ranking was G12 > G8 > G11 > G9 > G1 > G10 > G14 > G15 > G3 > G13 > G6 > G5 > G2 > G4 > G7.

The genotypes were also evaluated for yield stability statistic (Y_s), which integrates yield with stability (Kang, 1993). The Y_s identified G9, G11, G12, G14, and G8 as the top 5 genotypes, and G7, G5, G4, G6, and G2 as the bottom 5 genotypes. However, in addition to the top 5 genotypes, genotypes G1, G10, and G3 had Y_s values > $\bar{Y}_s = 3.9$. They were thus selected as desirable genotypes (Table 4).

Rank correlation

The results of rank correlation coefficients between mean yield and stability statistics are presented in

Table 4. Mean yield performance across environments was significantly positively correlated with Ys and GGED ($P \leq 0.01$), but significantly negatively correlated with $S^2_{E_s}$, b, α and D^2 ($P \leq 0.01$). No significant relationship was found between mean yield with AMMI stability parameters and the other statistical methods when ranking genotypes for stability.

To better understand the relationships among stability statistics, a factor analysis based on the rank correlation matrix was performed to group stability parameters. This analysis separated those methods based on an agronomic concept of stability from those based on a biological concept of stability. To determine concepts of stability, environmental variance (S^2_E) and nonparametric stability statistics ($S^{(1)}$ and $S^{(2)}$) were used as symbols of static stability, and mean yield was used as a symbol of dynamic stability. The first and second factors explained 70.5% of the total variance in stability parameters. For better visual presentation, the two first factors were plotted against each other to generate a plot (Fig. 3), in which the first factor separated parameters Ys, GGED and Seed Yield (as section A) from the other methods (as sections B and C), and so had a dynamic concept of stability.

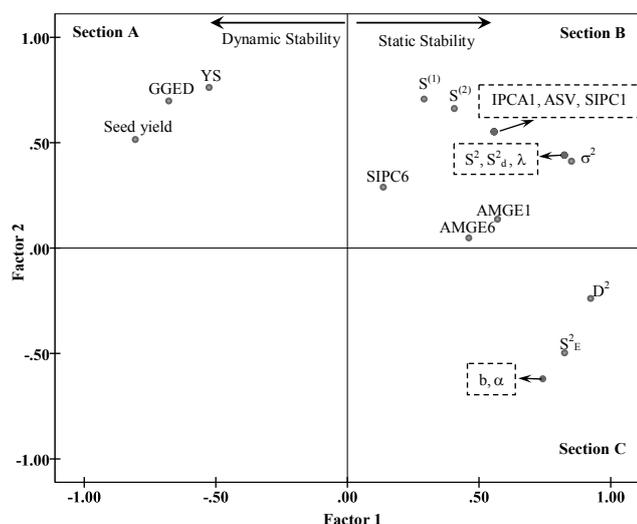


Fig. 3. Plot of the first two factors of ranking values of stability parameters of 15 safflower genotypes grown in nine environments.

Fig. 3 shows, on the right, methods corresponding to the biological concept of stability and, on the left, methods based on the agronomic concept of stability. The second factor separated parameters b, α and D^2 , along with S^2_E , which represents static stability (Becker and Leon, 1988) (as section C) from the other 12 parameters (as section B). Table 5 shows the ranking of genotypes for both the dynamic and static concepts of stability. The top stable genotypes G12, G9 and G11 in

section A were characterized based on dynamic stability, whereas G9, G6, and G5 in section B and G7, G5 and G4 in section C can be characterized the three genotypes with the highest static stability.

Genotype \times traits (GT) biplot

The GT biplot was used to compare genotypes based on multiple traits and to identify genotypes

Table 5. Ranking of safflower genotypes based on static and dynamic concepts of stability.

Dynamic stability (Section A) †		Static Stability (Section B) ‡		Static Stability (Section C) ††	
G	Mean	G	Mean	G	Mean
G12	2.3	G9	2.8	G7	2.5
G9	2.5	G6	3.3	G5	2.8
G11	2.5	G5	3.5	G4	3.3
G8	3.5	G3	5.1	G6	3.6
G14	5.3	G1	6.8	G3	3.9
G1	5.8	G2	7.4	G13	5.5
G10	6.3	G14	7.4	G2	6.5
G3	8.5	G8	8.5	G14	8.0
G15	8.8	G13	8.6	G1	9.4
G13	9.8	G4	10.1	G15	10.4
G6	11.3	G11	10.5	G9	10.8
G2	12.3	G7	11.3	G10	11.5
G5	12.8	G12	11.4	G11	13.5
G4	13.8	G10	11.6	G12	13.8
G7	15.0	G15	11.9	G8	14.8

† Mean of ranks for the two parameters with dynamic stability (GGED and YS).

‡ Mean of ranks for the group of parameters with static stability (IPCA1, SIPC, AMGE, ASV, $S^2_{E_s}$, σ^2 , s^2 , λ , $S^{(1)}$ and $S^{(2)}$).

†† Mean ranking for the group of parameters with static stability ($S^2_{E_s}$, b, α and D^2).

that were particularly desirable relative to several traits. The GT biplot (Fig. 4) displays 82.3% of the information in the standardized data of the 15 genotypes for the eight traits. This biplot can be visualized from two perspectives. First, it shows associations among traits across the 15 genotypes: (1) a strong positive correlation between seed yield and heads per plant, and between seed yield and seed weight, as indicated by the acute angle between them; (2) a near-zero correlation between seed yield and seed oil content, as indicated by the near-perpendicular vectors; (3) negative associations (obtuse angle) between seed yield and flowering, maturity, plant height and seeds per head; and (4) strong positive correlations among traits: flowering, maturity, plant height and seed oil content. Second, it shows the trait profiles of the genotypes, particularly those that are located farther away from the biplot origin. Genotypes G12, G11 and G10 with the largest PC1 negative scores, respectively, were located very close to seed yield and seed weight. Genotypes G7 and G2 had the largest PC1 positive scores and were located very close to flowering, maturity, plant height and seed oil content.

DISCUSSION

Analysis of GEI is an important part of crop breeding programs. Variety selection and recommendation based on yield trials may benefit from this type of analysis. In the present study, a large amount of the total sum of squares (13.5%) of data combined over environments was due to GEI. In characterizing GE interaction in spineless safflower MET, AMMI biplots were used to assess the relationships between genotypes and

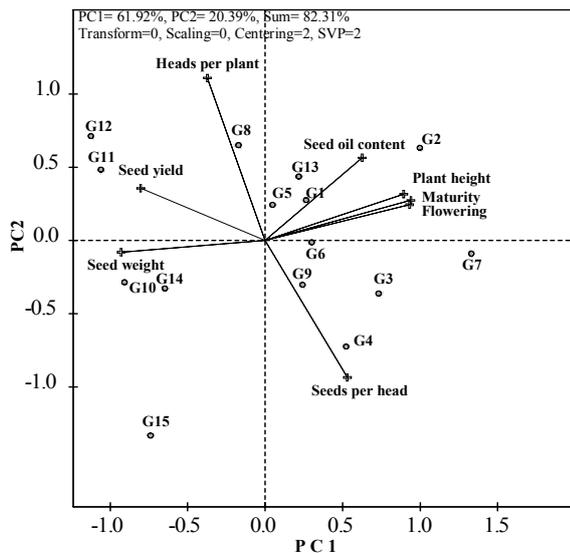


Fig. 4. Vector views of genotype \times trait biplot showing the relationships among traits.

environments and facilitate a visual description of “which wins where” patterns.

As suggested by Zobel *et al.* (1988), only IPCA1 and IPCA2 were included in the biplot, although more complex interactions with six IPCAs were significant in this study. This suggests that parameters (i.e., SIPC, AMGE) that use the number of IPCAs retained in the AMMI model are more useful (Zobel, 1994; Gauch and Zobel, 1996; Sneller *et al.*, 1997; Zhang *et al.*, 1998). Applying AMMI parameters to many MET data revealed their efficiency for analyzing GEIs on different crops, for example, chickpea (*Cicer arietinum* L.) (Dehghani *et al.*, 2010), durum wheat (*Triticum turgidum* L.) (Mohammadi *et al.*, 2010), lentil (*Lens culinaris* L.) (Sabaghnia *et al.*, 2008), and soybean (*Glycine max* L.) (Sneller *et al.*, 1997).

The choice of a particular definition of stability also has a major impact on entry rankings. Stability parameters related to static stability would be useful if selection were based primarily on stability. Stable genotypes based on this group would be suited to unfavorable environments with poor climatic conditions. In contrast, those related to a dynamic

concept of stability would be more useful for breeders interested primarily in yield. According to these statistics, stable genotypes would be recommended for unpredictable and/or favorable environments.

Fig. 3 shows that stability parameters can be classified into three groups related to static and dynamic concepts of stability (Becker and Leon, 1988). Mean yield was included in section A with parameters Ys (Kang, 1993) and GGED (Yan, 2001), suggesting section A comprises methods where yield has an important influence on the ranking across environments. Parameter GGED was highly correlated with the Ysi statistic ($r = 0.91^{**}$), and is in agreement with other reports in maize (*Zea mays* L.) (Yan and Kang, 2003; Fan *et al.*, 2007), cotton (*Gossypium hirsutum* L.) (Blanche *et al.*, 2007), and durum wheat (*Triticum turgidum* L.) (Mohammadi *et al.*, 2010). The YSi statistic and GGE biplot method complemented each other. The YSi statistic identified eight genotypes as potential candidates for selection. GGE biplot analyses revealed genotypes G12 (Faraman) and G8 (Darab 2) to be most suitable for production in rainfed, moderately cold regions. Faraman is an outstanding spineless safflower cultivar recently released for use under both rainfed and supplemental irrigation conditions in Iran, and is well appreciated by farmers.

No significant relationship was found between mean yield with AMMI stability parameters (IPCA1, ASV, SIPC1, SIPC6, AMGE1 and AMGE6) and the other statistical methods (σ^2 , s^2 , S^2_d , λ , $S^{(1)}$ and $S^{(2)}$) in ranking of genotypes for stability in section B. According to stability parameters, the most stable genotype in section B was G9, which had relatively high mean yield performance. The next most stable genotypes were G6 and G5, but they had low seed yield. The parameters in section C (S^2_E , b , α and D^2) had significant but negative correlations with mean yield. The most stable genotypes were G7, G5 and G4, although they had the lowest seed yields.

The GT biplot applied in this investigation on safflower genotypes shows visual interrelationships among safflower traits, providing much more information than other conventional methods such as a correlation table. Trait correlations (Fig. 4) revealed that seed yield was positively and significantly associated with seed weight and heads per plant. However, it is clear that there was no positive and significant correlation between seed yield and seed oil content, which may indicate that these important traits can be improved independently of each other. Similar reports on GT biplots (Egesi *et al.*, 2007; Dehghani *et al.*, 2008) have demonstrated that the GT biplot is an excellent tool for visualizing genotype \times trait data and revealing the interrelationships among crop traits.

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