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# Use of Stability Parameters for Comparing Safflower Genotypes in Multi-Environment Trials

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**Abstract:** In this study, some phenotypic stability parameters; ecovalence ($W^2_i$), regression coefficient ($b_i$), coefficient of determination ($R^2_i$), coefficient of variation ($CV_i$), stability variance ($S^2_i$) AMMI stability value ($ASV_i$) and TOP (proportion of environments in which a genotype ranked in the top third), were used to select among 17 spring safflower genotypes for yield performance and stability simultaneously across 26 environments under rain-fed conditions of Iran during growing seasons 2004-06. The results of AMMI analysis showed that 83.78% of the total sum squares (SS) was attributable to environment effects, only 1.37 and 14.85% to genotype and GE interaction effects, respectively. The results showed none of the parametric statistics *per se* was useful for selecting high yielding and stable genotypes. By simultaneous selection for yield and stability the genotypes G9, G10 and G11 were the best whereas the G1 and G17 with the highest yield performance were the most instable. In conclusion, both of yield and stability should be considered simultaneously to exploit the useful effect of GE interaction and to make selection of the genotypes more precise and refined.

**Key words:** Safflower, phenotypic stability, rank correlation

## INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is a multi-purpose plant cultivated since ancient times not only for the dye contained in its flowers, the oil in its achenes and its medicinal properties, but also for the ornamental value of its colorful inflorescence. In 2005, there area of safflower production in the world was estimated to be about 814,000 ha (FAO, 2006). More than 20 countries grow safflower and Mexico and India produce over half, with 212,765 and 210,000 Million tonnes, respectively. There are now proactive efforts to create and develop area for important oilseed crops; in line with this government is now encouraging safflower cultivation for edible oil purpose. In the last few years safflower area has increased and was 15,000 ha in 2005-2006. However, genotype×environment (GE) interaction is a major importance to the plant breeders for developing safflower cultivars in rain-fed conditions of Iran. GE interaction can be an outcome of genotype rank changes from one environment to another, a difference in scale among environments, or a combination of these phenomena (Mohammadi *et al*., 2007). If relative performances of the entries grown in different environments are highly different, then GE interaction becomes a major challenging factor to crop breeding programs (Zobel and Talbert, 1984). In such cases, the breeder is faced either with developing specific breeding populations for each environment and/or with selecting genotypes that generally perform well across many environments (Isik and Kleinschmit, 2005). Some genotypes are adapted to a broad range of environmental conditions, while others are more limited in their potential distribution and have specific adaptation.

The patterns of genotypes response to environmental change can be summarized in the form of the regression of genotype means on environmental index. The joint regression stability analyses of Finlay and Wilkinson (1963) and Eberhart and Russell (1966) have been widely used. Genotypes with low coefficients ($b_i$) either show specific adaptation or little variation with environment; those genotypes with high slopes ($b_i$) are more responsive to improvements in the environment and generally more adapted to favorable environments (Lin *et al*., 1986; Simmonds, 1991). When different genotypes are tested in a range of specific environments, generally the contribution of each genotype (ecovalence) to the total interaction sum of squares is estimated (Wricke, 1962; Becker and Leon, 1988; Karlsson *et al*., 2001; Isik and Kleinschmit, 2003).

The proportion of sites at which the genotype occurred in the top, middle and bottom third of the ranks was computed to form the parameters $TOP_i$, $MID_i$ and $LOW_i$, respectively (Fox *et al*., 1990). A genotype that

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occurred mostly in the top third (high value of $TOP_i$) was considered to be a widely adapted genotype. Some other univariate parameters are: environmental variance ($S^2_i$) (Roemer, 1917), coefficient of determination ($R^2_i$) proposed by Pinthus (1973) and Francis and Kannenberg's (1978) coefficient of variation ($CV_i$) which suggested for each genotype. More recently, Purchase (1997) developed the AMMI Stability Value (ASV) based on the AMMI model's IPCA1 and IPCA2 (Interaction Principle Components axes 1 and 2, respectively) scores for each genotype ($ASV_i$).

The goals of this study were to identify safflower genotypes by simultaneously selecting for yield performance and stability, to estimate the contribution of each test environment to total GE interaction and to study interrelationships among studied stability parameters.

## MATERIALS AND METHODS

**Data collection:** This study was carried out with 16 advanced spring safflower genotypes, PI-537589 (G1), Syrian (G2), PI-537636 (G3), CW-4440 (G4), Lesaf (G5), Cyprus bregon (G6), CW-74 (G7), Kino-76 (G8), S-541 (G9), PI-250536 (G10), PI-250537 (G11), Hartman (G12), Gila (G13), PI-537636-s (G15), PI-198290 (G16) and Dinçer (G17) and Mahali Isfahan (G14) as standard check at nine locations i.e., Sararood, Maragheh, Gachsaran, Shirvan-e-Khorasan, Ghamlo, Khodabandeh, Ardabil, Shirvan Chardavel, Khoram Abad, which are representative of different safflower growing areas under rain-fed conditions of Iran in the three growing seasons of 2003-04 to 2005-06 (data of location of Khoram Abad in 2005-2006 was not available). The descriptive of the trial sites is shown in Table 1. At each environment the genotypes were planted in a randomized complete block design with three replications. Sowing was done by hand. Plot size was 6 $m^2$ (4 m length, 5 rows and 30 cm between adjacent rows). Plants were spaced 10 cm apart within rows. The area harvested was 3.6 $m^2$, however, only the middle three rows were harvested. Fertilizer application was 50 kg N $ha^{-1}$ and 50 kg $P_2O_5$ $ha^{-1}$ at planting. Seed yield (kg $ha^{-1}$) was obtained by converting the grain yields obtained from plots to hectare. In this study some stability parameters were applied to the data chosen so that they cover a wide range of philosophies in stability analysis.

The method of Finlay and Wilkinson (1963) was used to estimate regression coefficient ($b_i$). The stability of grain yield was calculated by regression the mean yields of individual genotypes on environmental index. Coefficient of determination ($R^2_i$) (Pinthus, 1973) and environmental variance ($S^2_i$) (Roemer, 1917) was also computed, where a genotype with the maximum $R^2_i$ value and minimum variance is considered to be stable. The stratified ranking technique of Fox *et al.* (1990) was considered to form the measures $TOP_i$, $MID_i$ and $LOW_i$. A genotype that occurred mostly in the top third (high value of TOP) was considered to be a widely adapted genotype. The stability was measured by combining use of coefficient of variation ($CV_i$) and mean yield (Francis and Kannenberg, 1978). Ecovalence ($W^2_i$) as suggested by Wricke (1962) was computed to further describe stability. A low $W^2_i$ value indicates high relative stability. The AMMI Stability Value (ASV) (Purchase, 1997) based on the AMMI model's IPCA1 and IPCA2 scores for each genotype. ASV is in effect the distance from the coordinate point to the origin in a two dimensional scattergram of IPCA1 scores against IPCA2 scores. The largest the IPCA scores, either negative or positive, the more specific adapted a genotype is to certain environments, the smallest IPCA scores, there more stable the genotype is over all environments sampled.

Table 1: Description of the experimental sites and their overall agro-climatic conditions, like total annual rain fall and average minimum and maximum temperature

| Sites | Locations | Altitude (m) | Rainfall (mm) | Soil type | Mean seasonal temperature in °C | |
|---|---|---|---|---|---|---|
| | | | | | Min. | Max. |
| Sararood | 34°19'N 47°07'E | 1351 | 455 | Clay-loam | -15 | 44 |
| Maragheh | 26°52'N 45°30'E | 1400 | 365 | Clay-loam | -27 | 39 |
| Gachsaran | 50°50'N 30°20'E | 710 | 460 | Silt-loam | -2 | 46 |
| Shirvan-e-Khorasan | 37°14'N 58°07'E | 1131 | 267 | Clay-loam | -15 | 38 |
| Ghamlo | 35°23'N 47°14'E | 1850 | 350 | Clay-loam | -23 | 40 |
| Khodabandeh | 48°49'N 36°09'E | 1875 | 320 | Clay-loam | -15 | 30 |
| Ardabil | 48°20'N 38°15'E | 1350 | 380 | Silt-loam | -25 | 35 |
| Shirvan Chardavel | 33°41'N 46°35'E | 975 | 520 | Loam | -5 | 47 |
| Khoram Ababd | 48°18'N 29°33'E | 1171 | 520 | Silt-loam | -11 | 26 |

## RESULTS

**AMMI analysis:** The analysis of variance (additive main effects) showed significant effects for genotype (G), environment (E) and GE interaction (Table 2). These results showed that 83.78% of the treatment Sum of Squares (SS) (G+E+GE) was attributable to environment effects, only 1.37 and 14.85% to genotype and GE interaction effects, respectively. Results from analysis of multiplicative effects also showed that the first Interaction Principle Component Axis (IPCA1) captured 27.34% of the

interaction SS in 10.0% of the interaction degrees of freedom (df). Similarly, the IPCA2, IPCA3 and IPCA4 explained a further 15.42, 13.61 and 9.9% of the GE interaction SS, respectively. In total, AMMI2 model (G+E+IPCA1 and IPCA2) contained 91.51% of the treatment SS, while the residual contained only 8.49%. These results indicate that the AMMI model fits the data well and justifies the use of AMMI2.

**Analysis of stability performance:** The genotypes showed significant differences in grain yield. Taking mean yield as a first parameter for evaluating the genotypes, G1, G15, G2, G5 and G4 gave the best mean yields while G7, G12, G14, G8 and G16 had the lowest mean yields across environments (Table 3, 4). The IPCA scores of a genotype in the AMMI analysis are an indicator of the stability of a genotype over environments (Purchase, 1997). The lowest IPCA1 was observed for the genotypes G7 followed by G6 and G3 and IPCA2 was in the lowest for the genotypes G4, G13 and G7 (Table 3) and the ranks of genotypes according to this parameter are given in Table 4. According to IPCA1 and 2, G7 was the highest stable genotype with the mean yield (647 kg $ha^{-1}$) lower than grand mean (700 kg $ha^{-1}$). The highest IPCA1 was belonging to G17 followed by G13 and G2 with the higher grain yield than grand mean and the lowest IPCA2 was belonging to G1 (773 kg $ha^{-1}$) followed by G15 (733 kg $ha^{-1}$) which had the highest mean yield. The AMMI stability value ($ASV_i$) confirms the results of IPCA 1 and 2 scores. However, $ASV_i$ ranked the genotype G7 with the lowest $ASV_i$, as the most stable genotype, although it had the lowest yield performance (647 kg $ha^{-1}$). Corresponding to $ASV_i$ the G1 was instable although had the highest yield performance. G17 was as the most instable genotype but of high adapted to the testing environments.

Table 2: Additive main effects and multiplicative interactions analysis of variance for grain yield of the 17 genotypes in 26 environments

| Source | df | Mean² | Variance explained (%) |
|---|---|---|---|
| Total | 1325 | 197369 | - |
| Treatments | 441 | 215168** | 36.3 |
| Genotypes | 16 | 81407** | 1.4 |
| Environments@ | 25 | 3179894** | 83.8 |
| Interactions | 400 | 35223** | 14.9 |
| IPCA1 | 40 | 96308** | 27.3 |
| IPCA2 | 38 | 57155** | 15.4 |
| IPCA3 | 36 | 53276** | 13.6 |
| IPCA4 | 34 | 40949** | 9.9 |
| Residuals | 252 | 18869** | 33.8 |
| Block | 52 | 2645936** | 52.6 |
| Error | 832 | 34898 | 11.1 |

Note: The block source of variation refers to blocks within environments, **: Significant at 1% level of probability, @: The data of one the environments (Location of Khoram Abad in 2005-06) was not available

In keeping Wricke's (1962) stability parameter, $W^2i$, the genotypes G13 followed by G4 and G3 with the lowest ecovalence and were considered to be stable which being responsible for 1.5, 1.7 and 1.8% of the total interaction sum of squares, respectively, whereas the G17 followed by G1 with the highest $W^2_i$ were instable and had the most contribution to GE interaction. The regression coefficients for the seventeen genotypes examined was ranged from 0.70 to 1.02. Corresponding to Finlay and Wilkinson's (1963) method, the genotypes G8, G10 and G16 had coefficient regression (bi) value equal to one and the genotypes G3, G7, G12, G9 and G13 with values closer to one were more stable. The genotypes with the lowest bi (especially, G2, G6 and G15) were adapted to marginal environments.

The coefficient of determination ($R^2_i$) represent agronomic stability (Becker, 1981), which is the predictability of estimated response ($R^2$ = 1.0). The predictability of genotypes for the yield was varied. The values ranged from 0.82 (for G1) to 0.98 (for G4) which indicated that 82.0 to 98.0% of the mean yield variation

Table 3: Mean yield and genotypic stability parameters for 17 safflower genotypes across 26 environments

| Genotype | Mean yield (kg $ha^{-1}$) | IPCA1 | IPCA2 | $ASV_i$ | $W^2_i$ | $W^2$%[a] | bi | $R^2_i$ | $S^2_i$ | $CV_i$ | TOP | MID | LOW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 773 | -9.4 | -14.8 | 22.3 | 381064.7 | 12.2 | 0.70 | 0.82 | 83989 | 37.5 | 65 | 27 | 8 |
| G15 | 733 | -6.0 | 11.2 | 15.4 | 178438.9 | 5.7 | 0.84 | 0.92 | 81054 | 38.8 | 50 | 46 | 4 |
| G2 | 723 | -12.0 | -5.0 | 21.9 | 234555.3 | 7.5 | 0.81 | 0.90 | 86616 | 40.7 | 38 | 46 | 15 |
| G5 | 719 | -5.2 | 9.7 | 13.4 | 113167.5 | 3.6 | 0.86 | 0.95 | 79652 | 39.3 | 35 | 58 | 8 |
| G4 | 718 | -4.8 | 0.5 | 8.5 | 52405.3 | 1.7 | 0.92 | 0.98 | 72477 | 37.5 | 31 | 65 | 4 |
| G9 | 717 | 2.5 | -10.2 | 11.2 | 161265.2 | 5.2 | 1.02 | 0.90 | 54224 | 32.5 | 62 | 19 | 19 |
| G6 | 716 | -1.0 | 7.2 | 7.4 | 260714.4 | 8.4 | 0.81 | 0.88 | 84027 | 40.5 | 42 | 23 | 35 |
| G17 | 713 | -16.8 | 7.8 | 30.8 | 417574.1 | 13.4 | 0.73 | 0.85 | 100966 | 44.6 | 31 | 23 | 46 |
| G11 | 704 | 13.1 | 2.1 | 23.3 | 240858.7 | 7.7 | 0.93 | 0.85 | 61663 | 35.3 | 58 | 15 | 27 |
| G13 | 702 | 5.8 | 0.5 | 10.3 | 47435.3 | 1.5 | 1.02 | 0.97 | 58125 | 34.3 | 46 | 54 | 0 |
| G10 | 693 | 4.0 | -6.2 | 9.5 | 149426.8 | 4.8 | 1.00 | 0.90 | 56364 | 34.3 | 35 | 54 | 12 |
| G3 | 686 | -2.9 | -5.5 | 7.5 | 55411.7 | 1.8 | 0.98 | 0.96 | 62947 | 36.6 | 23 | 38 | 38 |
| G16 | 673 | 7.7 | -4.8 | 14.5 | 138772.8 | 4.5 | 1.00 | 0.91 | 56561 | 35.3 | 31 | 23 | 46 |
| G8 | 671 | 5.0 | -2.3 | 9.2 | 121243.8 | 3.9 | 1.00 | 0.92 | 56813 | 35.5 | 23 | 31 | 46 |
| G14 | 661 | 10.6 | 7.6 | 20.2 | 256206.6 | 8.2 | 0.87 | 0.85 | 69581 | 39.9 | 23 | 27 | 50 |
| G12 | 654 | 10.0 | 3.1 | 17.9 | 137905.0 | 4.4 | 0.99 | 0.91 | 57955 | 36.8 | 12 | 50 | 38 |
| G7 | 647 | -0.8 | -0.9 | 1.6 | 165143.6 | 5.3 | 0.95 | 0.90 | 61382 | 38.3 | 15 | 23 | 62 |

[a]: Contribution of each genotype to GE interaction

Table 4: Ranks of 17 genotypes based on mean yield and parametric measures derived from yield across 26 environments

| Genotype | Mean yield | IPCA1 | IPCA2 | $ASV_i$ | $W^2_i$ | $R^2$ | $S^2_i$ | $TOP_i$ | $b_i$ | $CV_i$ |
|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 1 | 12 | 17 | 15 | 16 | 1 | 14 | 1 | 1 | 9 |
| G15 | 2 | 10 | 16 | 11 | 11 | 6 | 13 | 4 | 4 | 12 |
| G2 | 3 | 15 | 8 | 14 | 12 | 11 | 16 | 7 | 3 | 16 |
| G5 | 4 | 8 | 14 | 9 | 4 | 4 | 12 | 8 | 5 | 13 |
| G4 | 5 | 6 | 1 | 4 | 2 | 3 | 11 | 9 | 7 | 10 |
| G9 | 6 | 3 | 15 | 8 | 9 | 8 | 1 | 2 | 13 | 1 |
| G6 | 7 | 2 | 11 | 2 | 15 | 9 | 15 | 6 | 3 | 15 |
| G17 | 8 | 17 | 13 | 17 | 17 | 10 | 17 | 9 | 2 | 17 |
| G11 | 9 | 16 | 4 | 16 | 13 | 10 | 8 | 3 | 8 | 4 |
| G13 | 10 | 9 | 2 | 7 | 1 | 2 | 6 | 5 | 13 | 3 |
| G10 | 11 | 5 | 10 | 6 | 8 | 8 | 2 | 8 | 12 | 2 |
| G3 | 12 | 4 | 9 | 3 | 3 | 8 | 9 | 10 | 10 | 7 |
| G16 | 13 | 11 | 7 | 10 | 7 | 7 | 3 | 9 | 12 | 5 |
| G8 | 14 | 7 | 5 | 5 | 5 | 5 | 4 | 10 | 12 | 6 |
| G14 | 15 | 14 | 12 | 13 | 14 | 10 | 10 | 10 | 6 | 14 |
| G12 | 16 | 13 | 6 | 12 | 6 | 7 | 5 | 12 | 11 | 8 |
| G7 | 17 | 1 | 3 | 1 | 10 | 8 | 7 | 11 | 9 | 11 |

Table 5: Spearman's rank correlation between mean yield and stability parameters

| | Yield | IPCA1 | IPCA2 | $ASV_i$ | $W^2_i$ | $S^2_i$ | TOP | $b_i$ | $CV_i$ |
|---|---|---|---|---|---|---|---|---|---|
| IPCA1 | -0.14 | | | | | | | | |
| IPCA2 | -0.51* | 0.10 | | | | | | | |
| ASV | -0.30 | 0.93** | 0.37 | | | | | | |
| $W^2$ | -0.23 | 0.39 | 0.53* | 0.53* | | | | | |
| $S^2$ | -0.57* | 0.36 | 0.33 | 0.33 | 0.51* | | | | |
| TOP | 0.78** | -0.09 | -0.43 | -0.31 | -0.30 | -0.18 | | | |
| $b_i$ | 0.55* | -0.38 | -0.46 | -0.41 | -0.67** | -0.94** | 0.19 | | |
| CV | -0.25 | 0.28 | 0.27 | 0.21 | 0.48* | 0.87** | 0.20 | -0.84** | |
| $R^2$ | 0.20 | 0.25 | 0.06 | 0.25 | 0.56* | 0.20 | 0.12 | -0.21 | 0.33 |

*, **: Significant at 5 and 1% levels of probability, respectively

was explained by genotype response across environments. Roemer (1917) stability index, $S^2_i$, which describes biological stability (Becker, 1981), quantitatively reflects the yield of a genotype in all environments. Therefore genotypes such as G9, G10 and G16 have low biological stability unlike the genotypes G17, G1 and G6 with the highest $S^2_i$ (Table 3).

Corresponding to parameter of Fox *et al.* (1990), G1 was an adapted genotype, because it ranked in the top third of genotypes in a high percentage of environments (high top value, 65%) and was followed by G9 (62%) and G11 (58%) (Table 3). The undesirable genotypes identified by this method were G12 and G7. According to Francis and Kannenberg's (1978) stability parameter ($CV_i$), the genotypes G9, G10 and G13 were considered to be stable genotypes. These genotypes with the lowest $CV_i$ were medium in yield. The genotypes G17, G2 and G6 with the highest $CV_i$ values had high yield performance.

**Interrelationship among stability parameters:** The ranks of 17 genotypes and 26 environments after applying the method stability analysis were used to rank correlation (the ranks of genotypes and environments are not shown). Spearman's rank correlations coefficient among genotypic mean yields with the parameters are shown in Table 5. The means of genotype yield were positive correlated with the genotypic parameters of $TOP_i$ ($p<0.01$) and bi ($p<0.05$) but in negative correlated with $S^2_i$ and IPCA2i ($p<0.05$) (Table 5). The bi was strongly negative correlated with $S^2_i$, $CV_i$ and $W^2_i$.

## DISCUSSION

Analysis of GE interaction and estimation of phenotypic yield stability have been widely studied and several methods were proposed for its estimation (Wricke, 1962; Eberhart and Russell, 1966; Pinthus, 1973; Francis and Kannenberg, 1978; Lin *et al.*, 1986; Becker and Leon, 1988; Purchase, 1997). One of the reasons for growing genotypes in a range of environments is to estimate their phenotypic stability because of the increasing grower demands for stable varieties especially in areas where climatic conditions are highly unpredictable (Ceccarelli, 1994).

In breeding programs genotypes are tested in numbers of environments. Environmental variations seemed to be of important to in determining performance, so, evaluation based on several years and locations is a good strategy to be pursued in breeding programs (Mohammadi and Amri, 2007). Farmers in developing countries which use no or limited inputs or growing safflower under harsh and unpredictable environments, will need stable varieties. In these cases genotypes with good performance and stability should be recommended. Stability performance of genotypes is the most important factor under rain-fed conditions in Iran, where

environmental conditions vary considerably (Mohammadi and Amri, 2007). In major problem of safflower improvement program in Iran has been the lake of genotypes consistently perform well across different safflower growing environments. Hence, the development of high yielding genotypes and information multi-location stable performance are a paramount importance in Iran where environments vary greatly within short distances.

However, several of stability measures that have been used in this study quantified stability of genotypes with respected to mean yield, stability and the best combination of them. Most of were closely related in sorting out the relative stability of the evaluated safflower genotypes. Some deviations were, however, observed specially for the genotype superiority measure. Purchase (1997) and Adugna and Labuschagne (2003) also reported similar results, indicating that it was more of a performance measurement than a yardstick for stability of genotypes across environments. In summary, according to stability parameters the genotypes G9, G10 and G11 with a good combination of yield and stability can be selected, whereas the genotypes G1 and G17 as unstable ones with high yield performance. The remaining genotypes were intermediate between these two groups.

In conclusion, several of stability statistics that have been used in this study quantified stability of genotypes with respected to yield, stability and both of them. Therefore, both of yield and stability should be considered simultaneously to exploit the useful effect of GE interaction and to make selection of the genotypes more precise and refined.

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