



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 (ASVi) 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

There are now proactive efforts to create and develop area for important oilseed crops in Iran; 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 2005-06. However, Genotype x environment (GE) interaction is a major importance to the plant breeders for developing safflower cultivars in rain-fed conditions of Iran. 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). 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. 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; 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 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 (ASVi).



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

Materials and Methods

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 Diñçer (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 Ababd, 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). At each environment the genotypes were planted in a randomized complete block design with three replications. Sowing was done by hand. Plot size was 6m² (4m length, 5rows, and 30 cm between adjacent rows). Plants were spaced 10 cm apart within rows. The area harvested was 3.6m², however, only the middle three rows were harvested. Fertilizer application was 50 kg N ha⁻¹ and 50 kg P₂O₅ 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 methods of Finlay and Wilkinson (1963), coefficient of determination (R^2_i) (Pinthus, 1973) and environmental variance (S^2_i) (Roemer, 1917) were computed. 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.

Result

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 (Tables 1 and 2). 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 1) and the ranks of genotypes according to this parameter are given in Table 2. According to IPCA1 and 2, G7 was the highest stable genotype with the mean yield (647kg/ha) lower than grand mean (700kg/ha). 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 (773kg/ha) followed by G15 (733 kg/ha) 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). 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.

In keeping Wricke's (1962) stability parameter, W^2_i , 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 (b_i) 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 b_i (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 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 1). 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 1). The undesirable genotypes identified by this method were G12 and G7. According to Francis and Kanenberg'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.

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 3. The means of genotype yield were positive correlated with the genotypic parameters of TOP $_i$ ($P<0.01$) and b_i ($P<0.05$) but in negative correlated with S^2_i and IPCA2 $_i$ ($P<0.05$) (Table 3). The b_i was strongly negative correlated with S^2_i , CV $_i$ and W^2_i .

Discussion and conclusion

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; Purchase, 1997).

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. In major problem of safflower improvement program in Iran has been the lack of genotypes consistently perform well across different safflower growing environments. 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) 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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Table 1. Mean yield and genotypic stability parameters for 17 safflower genotypes across 26 environments

Genotype	Mean Yield (Kg/ha)	IPCA1	IPCA2	ASV	W ²	W ² % ^a	bi	R ²	S ²	CV	TOP	MID	LOW
G1	773	-9.4	-14.8	22.3	381064.7	12.2	0.7	0.82	83989	37.5	65	27	8
G15	733	-6	11.2	15.4	178438.9	5.7	0.84	0.92	81054	38.8	50	46	4
G2	723	-12	-5	21.9	234555.3	7.5	0.81	0.9	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	0.9	54224	32.5	62	19	19
G6	716	-1	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	-6.2	9.5	149426.8	4.8	1.0	0.9	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	1.0	0.91	56561	35.3	31	23	46
G8	671	5	-2.3	9.2	121243.8	3.9	1.0	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	3.1	17.9	137905	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	0.9	61382	38.3	15	23	62

^a contribution of each genotype to GE interaction



Table 2. Ranks of 17 genotypes based on mean yield and parametric measures derived from yield across 26 environments

Genotype	Mean yield	IPCA1	IPCA2	ASVi	W2i	R ²	S2i	TOPi	bi	Cvi
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 3. Spearman's rank correlation between mean yield and stability parameters

	Yield	IPCA1	IPCA2	ASV	W ²	S ²	TOP	bi	CV
IPCA1	-0.14								
IPCA2	-0.51*	0.10							
ASV	-0.30	0.93**	0.37						
W²	-0.23	0.39	0.53*	0.53*					
S²	-0.57*	0.36	0.33	0.33	0.51*				
TOP	0.78**	-0.09	-0.43	-0.31	-0.30	-0.18			
bi	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**	
R²	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