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# Adaptation of Safflower Genotypes *Carthamus tinctorius* L.

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Summary. Adaptation reactions of 33 genotypes of safflower *Carthamus tinctorius* L. were studied under 7 different climatic conditions. The genotpyes were divided into two sets. Set I consisted of 15 genotpyes selected from the local populations. Set II had 15 introduced and local varieties. Three control genotpyes, Ute, Ferio, and Local Arak, were common to both sets.

Genotpye-environment interaction was not significant for Set I but it was highly significant for Set II. Three environmental indices were obtained and used in the adaptation analyses of the genotpyes in Set II. One of the environmental indices, designated EI, was dependent on the genotypes of Set II. The other two indices, designated EI-1 and EI-2, were independent of the genotpyes of Set II. The methods of Eberhart and Russell (1966) were used in analyses of adaptation by Index EI and the methods of Freeman and Perkins (1971) for Indices EI-1 and EI-2.

The mean square associated with genotype-environment interaction was partitioned into two components, heterogeneity of regression and its residual, under EI-1 and EI-2. Both components were highly significant for both cases. However, the mean square of heterogeneity of regression was equal to its residual under EI-1 and even smaller than its residual under EI-2. These observations indicate that a major part of genotpye-environment interaction can not be accounted for by differences in the regressions of the individual genotypes. As well as this overall test, individual regression analyses for single genotypes were also considered. None of the genotypes had significant regression mean square under EI-1. Only two introduced genotypes had significant regression mean squares when EI-2 was used. The overall test of equality of the slopes of the regression for the genotypes of Set II was rejected at the 1% level under EI. This test indicated that genotypes of Set II were significantly different in their association with the EI. The significant differences among the genotypes of Set II were also shown by an F test of the pooled deviation mean square divided by the pooled error mean square. Individual regression analyses for single genotpyes of Set II were considered under EI. Mixed adaptation reactions were observed for different genotypes. Among 18 genotypes of Set II, regression mean squares were significant for only 10 genotpyes. Therefore, it appeared that the dependent environmental indices are more useful than the independent environmental indices when statistical theory of regression is used in the analysis of adaptation. Observations in the present study were not in agreement with the hypothesis that the relation between the performance of different genotypes in the various environments and some measure of these environments is linear or nearly so.

Among the 12 introduced genotypes, only one, Ute, was identified as stable and high-yielding. Among the 15 selected from the locally adapted populations, eleven did not differ significantly from Ute in mean yield but four exceeded Ute significantly in mean productivity. The present study thus indicates that the Iranian safflower breeding project has been successful in identifying genotpyes which give high and stable yields under diverse environmental conditions. It does not indicate that introduced and exotic germplasms are unimportant in the breeding projects; it is quite possible that still more desirable genotypes can be developed by incorporating introduced genetic variability into the local germplasm.

## Introduction

Genotype-environment interaction (GE), i.e., the failure of genotpyes to perform consistently relative to each other under different environments, has long been recognized. Different methods have been suggested to measure the components of GE and their implications in applied plant breeding in terms of genotype × location, genotype × year, and genotype × location × year (e.g., Allard and Bradshaw 1964, Hanson 1964, Knight 1970, Proceddu 1970).

These methods, i.e., conventional analysis of variance, do not provide information about the individual contribution of genotypes to components of GE. However, they provide an indication of overall importance of GE and its components. Plaisted and Peterson (1959) suggested a technique for estimating the contribution of individual genotypes to GE. However, when large numbers of genotpyes are involved, this technique becomes tedious.

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Several methods have been developed to estimate GE in terms of parameters responsible for phenotypic stability and adaptation reactions of individual genotypes. These methods have been reviewed in a comprehensive article by Freeman (1973).

Yates and Cochran (1938), Finlay and Wilkinson (1963), Eberhart and Russell (1966), and Perkins and Jinks (1968) observed that the relation between performance of different genotypes in various environments and some measure of these environments is frequently linear. Attention has thus been paid to the measurement of environmental response for different genotypes. For this purpose, statistical theory of regression has been employed and different suggestions have been made for measuring environments.

This paper reports a study of adaptation of two different sets of safflower genotpyes, including 33 local and introduced cultivars. Also, the adaptation reactions of individual genotpyes in one of the sets are compared when one dependent and two independent environmental indices are employed. These environmental indices were measured biologically.

## Material and Methods

Two sets of 18 genotypes of safflower were planted separately at each of 9 locations in Iran in 1973. Since heavy damage by diseases and insects was observed in two locations, data of 7 locations were considered for analysis. These locations included: 1 - Varamin, 2 - Kermanshah, 3 - Darab, 4 - Zerghan, 5 - Hamadan, 6 - Khoramabad, and 7 - Torogh. Different environmental conditions were evident for each of the locations: altitude ranged from 838 m to 1322 m, latitude differed from 28°45N to 36°12N, longitude ranged from 47°20E to 59°40E, amount of rainfall during experiment ranged from 8 mm to 199 mm, and mean temperature varied from 19°C to 35.5°C.

The two sets had 3 genotypes, Ute, Ferio, and Local Arak, in common. Thus a total number of 33 genotypes were used in this study. In addition to the 3 control genotypes, the following 15 genotypes were included in the first set: V49-236, V49-251, V49-280, V49-287, V49-307, V49-415, V50-63, V50-165, V50-166, V50-167, V50-190, V50-237, V50-241, V50-243, and V49-338. These genotypes are selected lines from different local populations of safflower from Iran.

The genotypes in the second set were Neb. 852, U.S. 10, U.C. 1, Gila, Neb. 10, Local Esfahan, Local Marand, Local Rezaieh, Local Mashad 3150, Local Mashad 3151, Pacific, Lid 41, Dart 45, C.G.L. 88, and C.G.L. 112, plus the 3 control varieties.

A randomized complete block design with 4 replications was used for each set of genotypes at each location. Each experimental plot consisted of four 11.0m rows spaced 0.50 m apart, with 0.10 m spacing of plants within rows. The experiments were irrigated as needed. Before harvesting, 0.50 m was discarded from each end of the rows and only the two middle rows in each experimental plot were harvested. Seed yield was recorded in tons per hectare.

Genotype-environment interaction was not signivicant for the first set of genotypes and analysis of adaptation was thus not carried out; however, the data were used to calculate environmental indices. Three environmental indices were calculated and used in the adaptation analysis of the genotypes in the second set, which showed highly significant GE interactions.

The methods used for measuring the environmental indices were as follows:

1 - The procedure outlined by Eberhart and Russell (1966), using the data of the second set. This set of environmental indices is therefore dependent on the genotypes in the second set. This set is designated EI.

2 - Calculating an environmental index for individual environments from the deviation of mean performance of the control genotypes in a particular environment from the grand mean of the control genotypes over all environments. This set of environmental indices is based on combined data of control varieties over both sets and it is thus independent of the 15 remaining genotypes of the second set. This index is designated EI-1.

3 - This method was similar to the second method except data of the first set of genotypes (excluding the controls) were used. This set of environmental indices is thus independent from the 18 genotypes of the second set and designated EI-2.

In the analysis of adaptation, each environmental index was coded by subtracting the mean of environmental indices from it. Thus, the sum of environmental indices for EI, EI-1, and EI-2 was equal to zero.

## Results and Discussion

Set I: The analysis of variance for the genotypes of Set I, including and excluding the control genotypes, is presented in Table 1. Highly significant differences were observed between environments (locations) over genotypes in both cases. Mean performance of the genotypes over environments was also significantly different in both cases. However, GE interaction was not significant in either case.

Table 1. Analysis of variance for the genotypes of Set I including and excluding the control genotypes

| Source of variation | All genotypes | | Excluding control genotypes | |
|---|---|---|---|---|
| | df | Mean squares | df | Mean squares |
| Environments (E) | 6 | 13.834** | 6 | 11.136** |
| Rep. (E) | 21 | 0.337 | 21 | 0.280 |
| Genotypes (G) | 17 | 0.198** | 14 | 0.196** |
| Interaction (GE) | 102 | 0.077$^{ns}$ | 84 | 0.068$^{ns}$ |
| Error | 357 | 0.073 | 294 | 0.078 |

** Significant at the 1 % level

$^{ns}$ Not significant at the 5 % level

Table 2. Analysis of variance for the genotypes of Set II including and excluding the control genotypes

| Source of variation | All genotypes | | Excluding control genotypes | |
|---|---|---|---|---|
| | df | Mean squares | df | Mean squares |
| Environments (E) | 6 | 3.651** | 6 | 3.054** |
| Rep. | 21 | 0.156 | 21 | 0.154 |
| Genotypes (G) | 17 | 0.304** | 14 | 0.228** |
| Interaction (GE) | 102 | 0.204** | 84 | 0.200** |
| Error | 357 | 0.057 | 294 | 0.055 |

** Significant at the 1 % level

Because GE interaction was not significant for the first set of genotypes, analyses of adaptation were not carried out for these genotypes. However, the data of Set I were used to compute independent environmental indices (EI-1 and EI-2) to be used in the adaptation analysis of the genotypes in Set II. These environmental indices were expected to be valid if similar environmental conditions persisted for both sets of genotypes within each location.

Similarity of environmental conditions was tested in two steps: (1) homogeneity of the error mean squares for both sets of genotypes within each location was tested by the F test; (2) mean performance of each control genotype in the first set was compared with mean performance of the corresponding control genotypes in the second set. The error mean squares for both sets of genotypes were homogeneous within each location except for location 4. A pooled error mean square was accordingly computed for each location except location 4 and it was used to compare the mean yield of individual control genotypes in both sets. For location 4, both error mean squares were used. Among 21 comparisons (3 control genotypes × 7 locations) only four comparisons were significant. It was therefore concluded that the environmental indices obtained from data of Set I were useful estimates of environmental conditions which persisted for the genotypes of Set II.

Set II: The analysis of variance for the genotypes of Set II, including and excluding the control genotypes, is presented in Table 2. Highly significant differences were observed among environments, among genotypes, and for GE interactions in both cases. Estimates of interaction component of variance ($\hat{\sigma}^2_{GE}$) for the two cases were 0.0363 and 0.0362, respectively. Estimates of genetic component of variance ($\hat{\sigma}^2_G$) for the two cases were 0.0088 and 0.0061, respectively.

Analyses of adaptation were carried out for the genotypes of Set II using EI (dependent environmental indices) and EI-1 and EI-2 (independent environmental indices) for 15 genotpyes and all genotypes, respectively. Environmental means and indices are presented in Table 3.

The methods of Eberhart and Russell (1966) were followed when EI was used in the analysis of adaptation. The ratio of two mean squares ($MS_2$ and $MS_3$) was 7.059 with 17 and 90 degrees of freedom. This value is significant at the 1 % level, indicating large differences between the regression lines of different genotypes. The estimate of the pooled error (the variance of a genotype mean for the jth environment) was

Table 3. Environmental means and indices used in the analysis of adaptation of the genotypes in Set II

| Items | | Environmental means and indices | | | | | | | Mean |
|---|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | |
| EI | mean† | 1.428 | 1.335 | 1.861 | 1.642 | 1.224 | 1.665 | 1.367 | 1.503 |
| | index | -0.075 | -0.168 | 0.358 | 0.139 | -0.279 | 0.162 | -0.136 | 0.0 |
| EI-1 | mean‡ | 1.548 | 1.470 | 2.141 | 2.161 | 1.345 | 1.438 | 1.342 | 1.635 |
| | index | 0.087 | -0.165 | 0.506 | 0.526 | -0.290 | -0.197 | -0.293 | 0.0 |
| EI-2 | mean§ | 1.628 | 1.595 | 2.297 | 2.350 | 1.300 | 1.384 | 1.453 | 1.715 |
| | index | -0.087 | -0.120 | 0.582 | 0.635 | -0.415 | -0.331 | -0.262 | 0.0 |

† Mean of all genotypes in Set II
‡ Mean of control genotypes in both sets
§ Mean of 15 genotypes in Set I (excluding control genotypes)

Table 4. Statistics calculated in adaptation analysis of the genotypes in Set II using dependent environmental indices (EI)

| Genotype no. | Mean (ton/ha) | Regression MS ($10^{-4}$) | Deviation MS ($10^{-4}$) | b | Dev. MS/Pooled error |
|---|---|---|---|---|---|
| 1 | 1.639† | 4194* | 105 | 1.175 | 0.729$^{ns}$ |
| 2 | 1.608† | 3792* | 443 | 1.117 | 3.076** |
| 3 | 1.600† | 3348* | 387 | 1.050 | 2.688* |
| 4 | 1.426 | 5741* | 673 | 1.375 | 4.674** |
| 5 | 1.370 | 5954* | 756 | 1.400 | 5.250** |
| 6 | 1.632† | 5958* | 614 | 1.400 | 4.264** |
| 7 | 1.473 | 2329$^{ns}$ | 923 | 0.875 | 6.410 |
| 8 | 1.448 | 559$^{ns}$ | 286 | 0.429 | 1.986 |
| 9 | 1.354 | 111$^{ns}$ | 248 | 0.191 | 1.722 |
| 10 | 1.452 | 1376$^{ns}$ | 408 | 0.673 | 2.833 |
| 11 | 1.676 | 1884$^{ns}$ | 1139 | 0.787 | 7.910 |
| 12 | 1.614 | 2651$^{ns}$ | 621 | 0.934 | 4.313 |
| 13 | 1.348 | 4450$^{ns}$ | 893 | 1.210 | 6.201 |
| 14 | 1.520 | 4631* | 482 | 1.234 | 3.347** |
| 15 | 1.449 | 2280* | 191 | 0.866 | 1.326$^{ns}$ |
| 16 | 1.501 | 2560$^{ns}$ | 406 | 0.918 | 2.819 |
| 17 | 1.421 | 2747* | 244 | 0.951 | 1.694$^{ns}$ |
| 18 | 1.524 | 6186* | 272 | 1.427 | 1.889$^{ns}$ |

† Means greater than grand mean by 2s
*, ** Significant at the 5 % and 1 % level, respectively
$^{ns}$ Not significant at the 5 % level

0.0144 with 357 degrees of freedom. Pooled error was used to test the deviations from regression for each of the genotypes.

The statistics computed to determine the adaptation reactions of individual genotypes of Set II when EI was used are presented in Table 4. Among 18 genotypes of Set II, regression mean squares were significant for only 10 genotypes. Therefore, the mean performance of these 10 genotypes was linearly associated with varying environments and could accordingly be predicted. The regression mean square of the remaining 8 genotypes was not significant; thus their performance could not be predicted by a linear relation with the environments. These observations are not in accord with the hypothesis that the relationship between the performance of different genotypes in various environments and measures of these environments is linear.

According to the definition given by Eberhart and Russell (1966), a desirable genotype should have a high mean, unit regression coefficient and the deviation from regression as small as possible. None of the regression coefficients was significantly different from unity for the ten genotypes of Set II. However, among the ten genotypes only four, Ute, Lid 41, C.G. L. 88, and C.G.L. 112, showed non-significant deviations from regression. Thus, the four genotypes mentioned above meet the criteria of high adaptation. The mean performance of Ute was significantly greater than the mean performance of three other adapted genotypes.

The methods of Freeman and Perkins (1971) were followed when the independent environmental indices (EI-1 and EI-2) were used to measure the adaptation reactions of individual genotypes of Set II. Independent environmental indices can be measured either biologically or physically. Because the exact nature of the environmental variables is rarely known, it is not often possible to use physical measures of environments. Biological measures of environments are usually made by including a single or limited number of control genotypes or a set of genotypes closely related to the genotypes under test.

In this study, the mean yields of the three control genotypes were used to measure a set of independent environmental indices (EI-1). The analysis of variance for the remaining 15 genotypes of Set II, using EI-1 as a measure, is given in Table 5. Sources 3, 4, 7, and 8 in Table 5 are significant at the 1 % level when compared with the error. The combined regression mean squares significant at the 10 % level when tested against its residual mean square, indicating that EI-1

Table 5. Analysis of variance for the 15 genotypes of Set II (excluding control genotypes) when independent environmental indices (EI-1) were used

| Source of variation | df | Mean squares | $F^{\dagger}$ | $F^{\dagger}$ |
|---|---|---|---|---|
| 1. Genotypes (G) | 14 | 0.228 | 4.146(9)** | |
| 2. Environments (E) | 6 | 3.054 | 19.831(5)** | |
| 3. Combined regression | 1 | 9.365 | 170.273(9)** | 5.288(4)$^{+}$ |
| 4. Residual | 5 | 1.771 | 32.200(9)** | |
| 5. Rep. | 21 | 0.154 | | |
| 6. Interaction (GE) | 84 | 0.200 | 3.636(9)** | |
| 7. Heterogeneity of regressions | 14 | 0.205 | 3.727(9)** | 1.025(8)$^{ns}$ |
| 8. Residual | 70 | 0.200 | 3.636(9)** | |
| 9. Error | 294 | 0.055 | | |

$^{\dagger}$ Source used as denominator given in parentheses
$^{+}$, ** Significant at the 10 % and 1 % level, respectively
$^{ns}$ Not significant at the 5 % level

Table 6. Analysis of variance for the 18 genotypes of Set II when independent environmental indices (EI-2) were used

| Source of variation | df | Mean squares | $F^{\dagger}$ | $F^{\dagger}$ |
|---|---|---|---|---|
| 1. Genotypes (G) | 17 | 0.304 | 5.333(9)** | |
| 2. Environments (E) | 6 | 3.651 | 23.404(5)** | |
| 3. Combined regression | 1 | 11.587 | 203.281(9)** | 5.617(4)$^{+}$ |
| 4. Residual | 5 | 2.063 | 36.193(9)** | |
| 5. Rep. | 21 | 0.156 | | |
| 6. Interaction (GE) | 102 | 0.202 | 3.544(9)** | |
| 7. Heterogeneity of regressions | 17 | 0.150 | 2.632(9)** | 0.708(8)$^{ns}$ |
| 8. Residual | 85 | 0.212 | 3.719(9)** | |
| 9. Error | 357 | 0.057 | | |

$^{\dagger}$ Source used as denominator given in parentheses
$^{+}$, ** Significant at the 10 % and 1 % level, respectively
$^{ns}$ Not significant at the 5 % level

is adequate for assessing the additive environmental component. Significance of sources 7 and 8 in Table 5 indicates the presence of both linear and non-linear components of GE interaction for the data of Set II. The heterogeneity of regression mean square is not greater than its residual (Table 5), indicating that a major part of GE interaction cannot be accounted for by differences in the regressions of the individual genotypes. Despite this overall test, it is possible that there may be a linear change in the behavior of individual genotypes which will become apparent only when individual regression analyses for single genotypes are considered. When mean yield of individual genotypes at each environment were regressed on EI-1 the regression mean square of none of the 15 genotpyes of Set II was significant.

Table 6 shows the analysis of variance for the 18 genotypes of Set II when the environmental indices were determined from the 15 genotypes of Set I (EI-2). The patterns observed in Table 6 are very similar to the patterns seen in Table 5. Thus, this analysis of adaptation leads to the same conclusions. However, when individual regression analyses were performed for the individual genotypes of Set II using EI-2, two genotypes (Ute and Dart 45) had regression mean squares significantly greater than their corresponding deviation mean squares. The regression coefficient, b, for Ute and Dart 45 was 0.513 and 0.484, respectively. When independent environmental indices are used to determine the adaptation reactions of a genotype there is no guarantee that b will have any particular value. However, it will be true that the higher values of b will be associated with lower adaptation, and conversely (Freeman and Perkins 1971). Deviation mean squares for Ute and Dart 45 were 0.0375 and 0.0396, respectively, under EI-2. The regression

coefficients and deviation mean squares of the two genotypes were compared by the t-test and the F-test, respectively (Freeman and Perkins 1971). Ute and Dart 45 were similar with regard to these stability statistics. However, Ute had a mean yield significantly greater than the mean yield of Dart 45.

Adaptation reactions of the safflower genotypes in Set II were similar when measured by two different independent environmental indices (EI-1 and EI-2).

Different adaptation reactions were observed for the same genotypes when dependent environmental indices (EI) were used. The most adequate estimates of environmental indices are obtained by mean performance of the same trial genotypes in each environment. For this reason, Freeman and Perkins (1971) suggested dividing the replicates of each genotype into two groups, using one group to measure the GE interaction and the mean of the second group over genotypes to measure the environment. However, this solution increases the size of the experiment, particularly when a large number of genotypes is being considered and the experiment conducted in the field. These authors also suggested another solution, which involved inclusion of closely related genotypes in the experiment and assessing the environment by these genotypes, i.e. using parental genotypes as assessment genotypes in relation to any generation derived by crosses between them. In practice, trial genotypes come from different crosses and using few or all parental genotypes to assess the environment does not seem to be satisfactory.

In the present study, the level of stability of the introduced safflower genotypes was not satisfactory, except for Ute, which was used as a control. In contrast, GE interactions were not significant for the selected genotypes from different local populations; also 4 of these genotypes had mean yields significantly greater than the best performing introduced genotype, Ute. The mean yield of the 11 remaining genotypes were statistically equal to mean performance of Ute. The top yielding local genotypes were V50-165, V50-63, V49-287, and V49-307 with mean yield 1,926 kg/ha, 1,788 kg/ha, and 1,780 kg/ha, respectively.

This study also demonstrates the importance of locally adapted populations as the base material for developing superior cultivars in breeding projects. These local safflower populations had been exposed to varying environments, and therefore intense natural selection for adaptability, for many years. The present study indicates that our breeding program was successful for developing a few stable high-yielding genotypes from these populations. A great deal of genetic variability still exists within and between these locally adapted populations. Thus, further selection within populations and interpopulation hybridization followed by selection will most probably increase mean performance and adaptation. The present study does not preclude the importance of introduced and exotic germplasms in the breeding projects. It is quite possible to develop still more desirable genotypes by amalgamating local and introduced genetic variability.

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