Journal of Applied Sciences 5 (1): 118-121, 2005
ISSN 1607-8926

Stability and Adaptability Analysis in Sunflower from Eight Locations in Pakistan

[1]A. Ghafoor, [2]I.A. Arshad and [2]F. Muhammad
[1]Department of Statistics, Government College Farooka District, Sargodha, Pakistan
[2]Department of Mathematics and Statistics, Allama Iqbal Open University, Islamabad, Pakistan

Abstract: Stability of fifteen selected sunflower genotypes across eight environments (locations) in Pakistan with respect to oil yield was tested. On the basis of six different stability measures, genotypes such as SF-187, SMH-269, SC-110 and PSH-21 were found as stable genotypes with respect to oil yield (kg ha^{-1}). Further to group the genotypes having similar response pattern over all environments and to group similar environments over all sunflower genotypes, Ward's fusion strategy of hierarchical clustering technique was used on sunflower genotypes x environments (G x E) data. It was observed that genotypes SMH-32 and SMH-112 are different from remaining genotypes over all environments, but in the largest group-7 genotypes, Hysun-33, SF-270 and SMH-269 have similar response pattern (w.r.t. oil yield) over all environments. Similarly, it was observed that among eight environments, NARC and Sariab were similar, Kot. Diji and Dunya Pur were similar, Tando Jam and Faisalabad were similar and D.I.K. and Tarnab were found similar with respect to oil yield in sunflower over all genotypes. Performance plots used to illustrate each genotype group's performance (w.r.t. oil yield) in a series of environment groups. The results showed that genotypes group-1 (Hysun-341 and NK-265) and genotypes group-2 (SF-187 and NK-277) consistently performed well over Kot Diji, Dunya Pur, Tando Jam and Faisalabad environments. Genotype SMH-32 was found to be better in performance at NARC and Sariab.

Key words: Stability, cluster, genotypes, dendrogram

INTRODUCTION

Sunflower (*Helianthus annuus* L) is one of the oldest oilseed crop grown for edible oil. During the last two decades local production of edible oil has not increased at the rate needed to cope with increasing domestic consumption. Its per hectare yield in Pakistan is far lower than the other countries. The consequent gap between production and consumption is met through the import of edible oil. An increase in the yield of sunflower, being an important source of edible oil, can contribute in tilting the balance of trade favorably.

The goal of the plant breeders is to develop genotypes, which are widely adapted over a wide variety of environmental conditions. The breeders, therefore, select those genotypes, which, to some extent, show stability across environments. These stable genotypes provide a stock from which superior genotypes may be selected. Gwanama *et al.*[1] discussed the cluster and stability analysis for different wheat cultivars. Seaver *et al.*[2] used fuzzy clustering to identify subset of influential observations in regression. The present study was initiated to achieve the following objectives:

- To observe genotypic stability (with respect to oil yield) of 15 selected sunflower genotypes across eight environments (locations) in Pakistan.
- To group the genotypes having similar response pattern over all environments.
- To group the similar environments over all sunflower genotypes.
- To make comparison between different genotype groups, with respect to oil yield (kg ha^{-1}) performance, over different environment groups.
- Finally to make recommendations about sunflower genotype in well adapted environments.

MATERIALS AND METHODS

Sunflower data was obtained from National Oil Seed Development Institute, at National Agricultural Research Center, Islamabad. The trials were laid in RCBD with four replications at each location. The set of treatment consists of fifteen sunflower genotypes. This experiment was conducted in eight different locations of Pakistan, which were NARC, Faisalabad, Dera Ismail Khan, Tando Jam, Kot Diji, Tarnab, Sariab and Dunya Pur.

Corresponding Author: Dr. Irshad Ahmad Arshad, Department of Mathematics and Statistics, Allama Iqbal Open University, Sector H-8, Islamabad, Pakistan
E-mail: irshad_arshad@hotmail.com

A number of statistics have been proposed to measure the genotypic stability. Several of these have been summarized and compared by Lin *et al.*[3]. In the present study several stability statistics have been evaluated on two-way genotypes x environment data. Stability statistics that involves the variation within genotype across environments purposed by Francis and Kannenberg[4] that is independent of the other genotypes. These statistics are within genotype mean square (S_i^2) and genotypic coefficients of variation (CV_i). Wricke[5] suggested ecovalance stability statistics and stability variance, σ_i^2, an estimate of the variance of genotype I across environments, to observe the genotypic stability. Finaly and Wilkinson[6] pointed out that the slope b_i of the linear regression of the yield y_{ij}, of ith genotype and jth environment, on the mean yields, y_j of all the genotypes in j^{th} environment was also helpful to test genotypic stability. They pointed out that a genotype, which has a slop $b_i = 1$ is most stable but genotypes which have slope significantly greater than 1 and less than 1 are specifically adapted to high yielding environments and better adapted to low yielding environments, respectively.

Cluster analysis purposed by Sneath and Sokal[7] is one technique used to simplify the data set by grouping the individuals with similar response for all attributes without making any assumption concerning the number of groups or the group structure. To achieve the objective, Agglomerative Hierarchical technique with Ward's fusion strategy has been used so that minimum loss of information may occur during clustering of objects.

RESULTS AND DISCUSSION

Stability analysis: By analyzing the G x E oil yield data, it was observed that G x E interaction contributed about 85.45% in total variation of G x E oil yield data, which is the indication that a stability analysis of genotypes with respect to oil yield based on location index is important. Within genotype mean square and coefficient of variation stability measures are listed in column 1 of Table 1. Genotypes such as SF-270, SMH-269 and SC-110 look stable with respect to oil yield (kg ha^{-1}) because they have comparatively low values for both the stability statistics. The genotypes SF-270 and SMH-269 have mean oil yield 754.79 and 742.65 kg ha^{-1}, respectively, which are approximately equal to the average genotypes mean oil yield i.e. 750.23 (kg ha^{-1}).

The next two measures of stability namely ecovalance (W_i^2) and interaction variance (σ_i^2) are important measures of stability as they compare the genotypes in relation to the environments, which are given in column 6 and 7 of Table 1. Now based on these two statistics, it was observed that the genotypes, which were recommended before for stability, cannot be chosen for stability. Here the contribution to the interaction variance is quite variable for different genotypes. Based on these two stability statistics, it can be recommend that genotypes PSH-21 and Hysun-33 are stable because of having low values of ecovalance and interaction variance. Also the genotypes PSH-21 and Hysun-33 do not satisfy the criterion of within genotype mean square and CV as they have comparatively large values.

According to slope of the regression of genotype mean on site mean yield, b_i, as a measure of stability, it is clear from Table 1 that genotypes PARC-92E, SF-187, NK-265 and PSH-21 have slopes closest to 1.00 among the 15 genotypes in the data set. On this basis the said genotypes can be recommended as most stable genotypes with respect to oil yield (kg ha^{-1}) of the 15 genotypes over 8 environments represented in this trial. Further, these genotypes contributed least to the genotypes x environment interaction as, measured by ecovalance, W_i^2 and the interaction variance, σ_i^2. The genotypes on the basis of regression model can be further

Table 1: Stability Statistics for fifteen genotypes of sunflower grown at eight locations in Pakistan, w.r.t. oil yield

Genotypes	Mean Y_i (kg ha^{-1})	S_i^2 (kg ha^{-1})^2	Cv_i (%)	Genotypes	W_i^2	σ_i^2	b_i
SF-270	754.79	37441.88	25.64	SF-270	167362.21	19986.77	0.61
SMH-269	742.65	54007.39	31.29	PHS-85	250666.40	33718.22	0.65
SC-110	716.04	51089.78	31.57	PHS-35	365423.78	52634.28	0.76
PHS-85	725.01	54375.54	32.16	NK-277	218010.99	28335.47	0.77
SF-187	836.03	72918.34	32.30	PSH-2	119453.31	12089.69	0.77
NK-277	772.23	64907.65	32.99	SC-110	86394.86	6640.50	0.81
Hysun-341	763.33	63484.56	33.01	SMH-269	90178.34	7264.15	0.83
PSH-2	676.80	50970.91	33.36	Hysun-341	103965.54	9536.76	0.89
NK-265	796.36	84449.16	36.49	PARC-92E	70861.18	4080.00	0.96
PARC-92E	707.38	67647.77	36.77	SF-187	104511.07	9626.69	0.96
PSH-21	747.65	78129.90	37.39	NK-265	102416.41	9281.41	1.06
Hysun-33	809.78	96416.02	38.35	PSH-21	51563.49	899.06	1.06
PHS-35	740.91	85130.93	39.38	SMH-112	111326.19	10750.06	1.12
SMH-112	688.56	94086.55	44.55	Hysun-33	64535.39	3037.29	1.19
SMH-32	1126.7	1370310	103.9	SMH-32	7776256.11	1274200.05	2.57

divided into two mutually exclusive groups. The first group consists of three genotypes, which have slopes, significantly greater than one are SMH-112, Hysun-33 and SMH-32 appears to be better adapted to better environment.

The second group consists of 8 genotypes which have slopes significantly less than 1 are SF-270, PSH-35, PSH-2 SMH-269, SC-110, PHS-85, NK-277 and Hysun-33 appears to be better adapted to poorer environments.

Finally it was concluded that the genotypes such as SF-187, SMH-269 SC-110 and PSH-21 are stable genotypes according to different stability measure with respect to oil yield (kg ha^{-1}).

Cluster analysis: Ward's fusion strategy of hierarchical clustering technique was used on sunflower G x E data of oil yield (kg ha^{-1}). Fifteen genotypes and eight environments were grouped into 8 genotype clusters and 4 environment clusters, which are given in Table 2 and 3 respectively. Table 2 clearly indicates that genotypes SMH-32 and SMH-112 are different from remaining genotypes over all environments. The group-7 containing maximum genotypes i.e Hysun-33, SF-270 and SMH-269 have similar response pattern (with respect to oil yield) over all environments. Also genotype groups labeled A, B, C, D and E in Table 2 each consists of two genotypes having similar response pattern with respect to oil yield, over all environments.

In Table 3, similar environments are grouped into four clusters namely group-1, group-2, group-3 and group-4 over all genotypes with respect to oil yield (kg ha^{-1}). It is clear from the Table 4 that the environments NARC and Sariab are similar over all genotypes

Similarly, environments in group-4 (i.e. Kot Diji and Dunya Pur) have similar response pattern w.r.t. oil yield over all genotypes. Also Tando Jam and Faisalabad in group-3 and environments in group-1 (D.I.K. and Tarnab) have similar response pattern (with respect to oil yield) over all genotypes. The dendrograms of genotypes and environments are shown in Fig. 1 and 2, respectively.

Table 2: The group members at the specified group level for genotypes oil yield (kg ha^{-1})

Groups	No.	Group members
Indiv-13	1	SMH-32
Indiv-14	1	SMH-112
Group-7	3	Hysun-33, SF-270, SMH-269
Group-2	2	SF-187, NK-277 (A)
Group-3	2	PHS-35, PSH-2 (B)
Group-5	2	PSH-2, PARC-92E ©
Group-4	2	PHS-85, SC-110 (D)
Group-1	2	Hysun-341, NK-265 (E)

Table 3: Groups of similar environments over all genotypes

Groups	No.	Group members
Group-1	2	D.I.K, Tarnab
Group-2	2	NARC, Sariab
Group-3	2	Tando Jam, Faisalabad
Group-4	2	Kot Diji, Dunya Pur

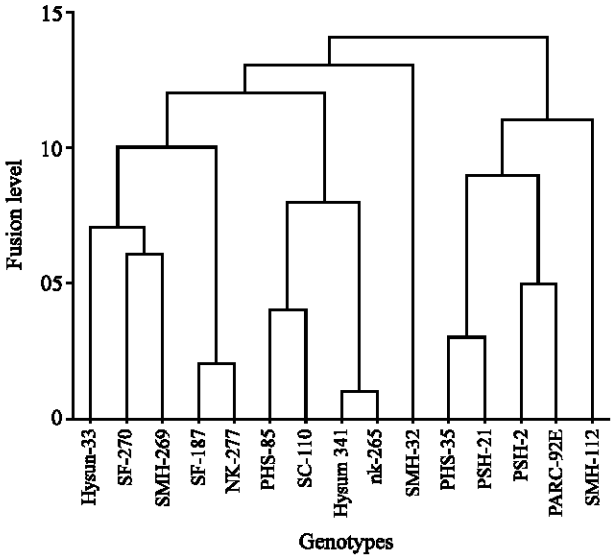

Fig. 1: Genotype dendrogram representing eight genotype clusters

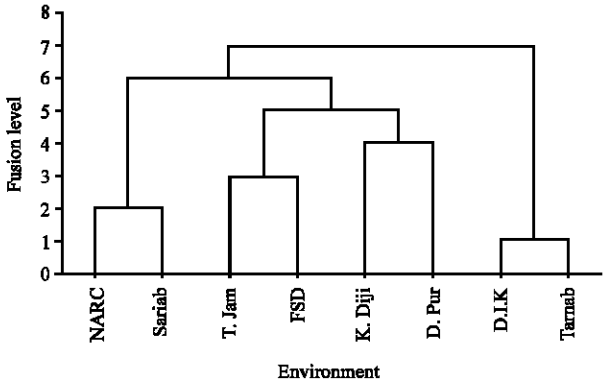

Fig. 2: Environment dendrogram representing four environment clusters

In Fig. 3, four genotype group's performance lines are shown per plot. From the above said plots, it is clear that genotype group-1 (Hysun-341 and Nk-265) and genotype group-2 (SF-187 and NK-277) consistently performed well over all environment groups except in environment group-1 (D.I.K., Tarnab) and environment group-2 (NARC, Sariab), respectively. However, the performance of genotype SMH-32 in Indiv-13 is extra-ordinary well at environment group-2 (NARC and Sariab). On the other hand genotypes SMH-112 in Indiv-14 and genotype group-5 (PSH-2, PARC-92E) performed very poorly, at environment group-3 (Tando Jam, Faisalabad) and group-4 (Kot Diji, Dunya Pur). Performance of

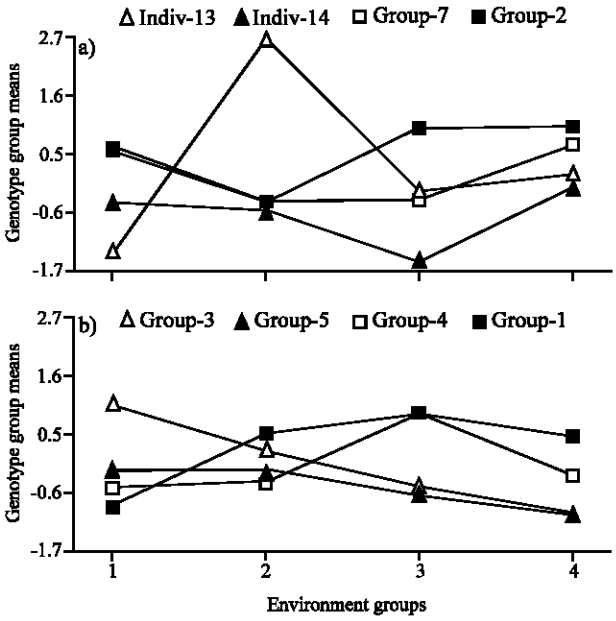

Fig. 3: Performance plot of genotypes group versus environment groups

genotype group-3 (PHS-35, PSH-21) was quite surprising because its performance with respect to oil yield that gradually increased with the decreasing order of environment groups from group-4 to group-1 and maximum at environment group-1. The remaining genotype groups performed variably at different environment groups. So on the basis of the above results, it can be recommended that the sunflower genotypes SF-187, PHS-21, SMH-32 and PSH-35 are better (with respect to oil yield) than the others for wider adaptation.

A comparison with the previously recommended stable genotypes by using stability parametric approach showed that only two genotypes SF-187 and PSH-21 satisfied both the criterion of clustering and Parametric stability approach.

REFERENCES

1. Gwanama, C., M.T. Labuschagne and A.M. Botha, 2000. Analysis of genetic variation in *Cucurbita moschata* by random amplified polymorphic DNA markers. Euphytica, 113: 19-24.
2. Seaver, B., k. Triantis and C. Reeves, 1999. The identification of influential subsets in regression sing a fuzzy clustering strategy. Technometrics, 41: 340-351.
3. Lin, C.S., M.R. Binns and L.P. Lefkovitch, 1986. Stability analysis: Where we do stand. Crop Sci., 26: 894-900.
4. Francis, T.R. and L.W. Kannenberg, 1978. Yield stability studies in short-season maize. A descriptive method of grouping genotypes. Can J. Plant Sci., 58: 1099-1034.
5. Wricke, G., 1962 Ube Eine methode Zut Erfussung Der Okologischen Streubreite in Feldversuchen. Z. Pflanzenzuecht, 47: 92-96.
6. Finlay, K.W. and G.N. Wilkinson, 1963. The analysis of adaptation in the plant breeding programme. J. Agri. Res., 14: 742-754.
7. Sneath, P.H.A. and R.R. Sokal, 1973. Numerical Taxonomy: The Principal and Practice of Numerical Classification, W. H. Freeman and Co., San Francisco.