EVALUATION OF PERFORMANCE AND STABILITY OF SUNFLOWER GENOTYPES AGAINST SALINITY STRESS

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ABSTRACT

The performance of four sunflower cultivars along with their six F_1 hybrids, was evaluated over three salinity levels at Agricultural University, Faisalabad during 1998-1999. The mean values of oil yield per plant, oil and protein percentage of the genotypes were examined for which significant genotype-environment interactions were detected. Stability statistics based on Eberhart and Russell approach were estimated for all the varieties and traits. KNI possessed maximum mean oil yield per plant and oil percentage but low protein percentage whereas Suncom 110 showed high mean protein percentage. The results indicated that cultivars Suncom 90 and Suncom 110 were stable for oil percentage whereas genotypes KNI showed stability in its performance for oil yield per plant and protein percentage due to the mean above the grand mean and values of b1 and S^2d non-significantly different from 1.0 and 0.0, respectively. The antagonistic relationship between mean yield of the genotypes and their stability statistics was observed, reconciliation is not need to made between yield and stability statistics.

Key words: Stability; oil yield; *Hellianthus annuus*; salinity.

INTRODUCTION

Soil salinity is a common problem in irrigated areas of world. Out of the total land area of the earth (149.6 x 10^6 Km^2), about 62 x 10^6 Km^2 lies in the arid and semi-arid regions of which upto 15 percent is salt affected (Massoud, 1974). Irrigated land is estimated to the extent of 230 x 10 hectares, of which about one third is believed to be affected by salinity (Mass and Hoffman, 1977). Soil salinity problem is seriously affecting the economy of Pakistan by limiting crop productivity to a large extent over 6.67 mha. All phases of plant growth from germination to maturity are affected by the environment in which the plant grows. Saline soils contain excessive amount of salts to impair growth of plants. Salt tolerance is the ability of crops to produce an economical yield under adverse soil conditions in the presence of excessive salts in the root zone (Bresler *et al*., 1982 and Waqas *et al* 2004).

Salt affected soils are normally dominated by NaCI and may contain other salts such as Na_2SO_4, Na_2CO_3, $CaSO_4$, $CaCl_2$, $MgCl_2$, $MgSO_4$, KC1 and K-borates, etc.(Flower, 1975). Plants with heigh K^+ concentration and low Na^+ concentration are salinity tolerant (Waqas *et al*., 2004). Saline soils contain sufficient salts to impair the growth of the crop plants. Changes in the plant behavior induced by salinity have been found in water uptake and water balance, gas exchange, transpiration, photosynthesis and respiration, optical properties of leaves, ion uptake, metabolic pathways, growth morphology and anatomy of the plant and balance of the hormones (Poljakoff and Gale, 1975; Ashraf, 1999 and Ibrahim, 2003).

The oils and fats are necessary ingredients of the human diet being rich in calories per gram and vitamin A and D. To meet the edible oil requirements of the country some non-conventional oilseed crops were introduced. Sunflower (*Helianthus annuus L.*) being one of them. It belongs to the family Asteraceae. Sunflower seedlings have shown severe reduction in shoot length and shoot dry matter (Cheng, 1984) while root growth was comparatively less affected (Charsalli and Cherif, 1979). However, root dry matter yield was reduced when sunflower was grown in soils with high salinity (Heikal *et al*., 1980).

In recent years considerable importance is being given to genotype x environment (salinity levels) interactions in the crop breeding programme. Pakistan has varying agroclimatic (high mountainous valleys and irrigated plains) distribution therefore, relative performance of different genotypes changes in different environments when there is a genotype x environment interaction (Aslam *et al*.1988). In other words, large genotype-environment interactions will effectively reduce progress from selection because worth of the genotypes/ lines with improved quantitative characters like yield, oil and protein percentage depend to a considerable extent, on their repeatability in performance when they are grown over varied environments (Cheng, 1984 and Chan, 1985). This is the major challenge being faced by plant breeders today. Scott (1966) showed that yield stability is genetically controlled and thus suitable for selection. Finlay and Wilkinson (1963) used regression coefficient

as a measure of stability. Eberhart and Russell (1966) used regression coefficient as well as the deviations from linear response as stability statistics. Tai (1971) proposed a slightly modified mathematical model using essentially the two similar statistics of Eberhart and Russell (1966) in determining of stability of potato genotypes. Ali et. el. (1992) observed a differential response in mean paddy yield of the genotypes and their stability statistics.

At the University of Agriculture, Faisalabad (UAF), several promising lines of sunflower have been developed after a period of systematic breeding and selection efforts (Waqas *et al* 2004). Stable and promising lines with low genotype-environment interactions assure repeatability of yield and performance over a wide range of environments (salinity levels). This paper evaluates the performance of these genotypes over three different salinity levels and discusses their merits in the light of the nature and significance of their genotypic stability.

MATERIALS AND METHODS

The experiment was conducted in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 1998-1999. Four sunflower cultivars namely Suncom 90, Suncom 110, Romania and KN1 were crossed in all possible combinations (excluding reciprocals) during 1998. Four parents alongwith their six F_1 hybrids were sown in pots using completely randomizes design in factorial fashion with three repeats, during spring 1999. For pot sowing, soil was passed through 2 mm sieve, air dried and six Kg of soil (clay loam) was transferred to each pot. Polythene lining was used inside the pots to check the salt leaching.

Saturation percentage and electrical conductivity (EC) of the soil were used to know the basic amount of soluble salts present in the soil and to develop different salinity levels on the basis of electrical conductivity (EC) of soil. The EC of the soil (control) was 2.3 mmhos /cm. Higher salinity levels of EC 5.0 mmhos /cm and EC 10.0 mmhos /cm were produced by the addition of calculated amount of mixture of salts viz; NaCI, Na_2SO_4 , $CaCI_2$ and $MgSO_4$ in the ratio of 5 : 9 : 5 : 1 , respectively. Similarly, amount of Urea and Single Super Phosphate (SSP) required for 6 Kg soil / pot were calculated. Different salt concentrations thus developed were mixed in six Kg weight of soil /pot alongwith measured quantity of fertilizers. Second and third doses of urea were applied at two reproductive phases i.e. at bud stage (R_1) and at flowering stage (R_5) (Schneiter and Miller, 1981). Two seeds per pot were sown at the depth of 4 cm and one plant per pot was retained after thinning at four leaf stage (V_4). Irrigation was applied on alternate days and also with respect to the water condition of the pots. All other cultural and agronomic operations were identical.

Data were taken from five randomly selected plants / genotype/ repeat. The characters measured were oil yield per plant (g), Oil and Protein percentages. Random seed samples of five grams from each genotype and repeat were taken after oven drying, grounded to powder form and its oil percentage was determined by Soxhelt extraction method (A.O.A.C., 1970) at P.C.S.I.R. Laboratories Lahore. Protein percentage was determined from each genotype and repeat by Kjeldhal method (A.O.A.C., 1970) at P.C.S.I.R. Laboratories, Lahore after digestion, distillation and titration of the sample.

Analysis of variance over three salinity levels (environments) were carried out for each of the character measured. In the analysis, genotypes were treated as fixed effects while salinity levels and repeats within salinity levels were considered random effects (Eberhart and Russell 1966).

Stability analysis was done by applying Duncan's new multiple range test for all the characters as they showed significant genotype-environment interactions (Steel and Torrie, 1984). Two statistics were used in the description of stability i.e., b_1 which measures the linear response of a variety to environmental index and S^2d, which estimates the deviation from the linear response. Genotypes having mean above the grand mean and values of b_1 and S^2d not significantly different from unity and 0.0 respectively wi11 be considered stable for the traits under study.

RESULTS AND DISCUSSION

The mean square values derived from the combined analysis of variance (across three salinity levels) for oil yield per plant, oil percentage and protein percentage indicated that highly significant differences exist among salinity levels for all the traits evaluated (Table 1). The table 1 indicates that all the characters have variation, arises from differences between genotypes except oil yield/ plant. The genotype-environment interaction was highly significant in all traits under study, thus indicated that genotypes and salinity levels were not independent of one another.

Table 2 shows the genotype and environment means for oil yield / plant, oil and protein percentages. Mean values for these traits of ten sunflower genotypes evaluated across three salinity levels (S_0 = EC, 2.3 mmhos/cm, S_1 = EC, 5.0 mmhos/cm and S_2 = EC, 10.0 mmhos/cm) were compared by using Duncan's new multiple range test.

The performance of the genotypes in terms of oil yield / plant, oil and protein percentage was inconsistent over the environments examined. Therefore, no generalization can be permitted with regards to the superiority of genotypes over three environments; indeed, the significant interactions of these traits argue that valid

comparisons between genotypes may only be made in each environment separately.

Since the analysis of variance did not provide further information about the genotype-environment interactions other than elucidating its existence, the stability of each genotype step by step was examined for each trait using Eberhart and Russell (1966) approach.

Oil yield per plant (gram): The stability analysis of variance for oil yield / plant (Table 3) indicated non-significant differences among sunflower genotypes. The genetic differences does not exist among genotypes for their regression in the environmental index. The pooled deviation mean square was found to be highly significant when tested against pooled error.

Mean oil yield and estimates of stability parameters for ten sunflower genotypes combined over three salinity levels (Table 4) depicted that range in oil yield was from 0.62 g (Suncom 110 x Romania) to 1.34 g (KN1) with an average of 0.99 g. Four genotypes namely Suncom 90, Suncom 110, KN1 and Suncom 90 x Suncom 110, had oil yield/ plant above the mean value. The regression coefficients (b-value) for this trait ranged from 0.47 to 1.57. The regression coefficient values were significant for Suncom 90 and Suncom 110. The deviation from regression mean squares (S^2d) were significant for all the genotypes except KN1 indicating that this genotype differed non-significantly from 0.0 for the deviation from regression mean square. The coefficient of determination (R^2) were small for all the genotypes. Genotype KN1 was stable in its oil yield per plant because values of b_1 and S^2d were non-significantly different from 1.0 and 0.0 respectively.

Oil percentage: The stability analysis of variance for oil percentage combined over three salinity levels (Table 3) depicts highly significant differences among sunflower genotypes. The F-test for genotype x environment (linear) was highly significant showing that genetic differences exist among genotypes for their regression in the environmental index. The pooled deviation mean squares were found to be non-significant when tested against pooled error.

Mean oil percentage and estimates of stability parameters for ten sunflower genotypes combined over three salinity levels reveals that mean oil percentage ranged from 12.42 % to 18.10 % with an average of 14.55 % (Table 4). Four genotypes namely KN1, Suncom 90 x Suncom 110, Suncom 90 and Suncom 110 had oil percentage above the mean value. The regression coefficient (b_1) for this trait ranged from 0.65 to 2.01. It was significant for KN1, Suncom 90 x Suncom 110 and Suncom 110 x KN1. The deviation mean squares (S^2d) were non-significant for all the genotypes, indicating that all these genotypes do not differ significantly from 0.0 for the S^2d. Coefficient of determination (R^2) were low for all the genotypes. Sunflower genotypes Suncom 90 and Suncom 110, due to mean above the grand mean and non-significant values (close to unity and 0.0, respectively) for coefficient of regression (b_1) and deviation from regression mean squares (S^2d) were stable for oil percentage.

Table 1: Mean square values for characters examined from combined analysis of variance of 10 genotypes across three salinity levels.

Character	MS(E) df=2	MS(G) Df =9	MS (Gx E)df =18	Error df =60
Oil Percentage	506.41515 **	34.96663 **	84.37984 **	5.23332
Protien Percentage	824.3894 **	41.42172 **	117.8360 **	10.3684 **
Oil Yield per plant (g)	3.09036 **	0.07663 NS	0.4442 **	0.05381 **

Evaluated at 3 environments (salinity levels)
E = Environment G = Genotype
*, ** = Significant at ($P \leq 0.05$) & ($P \leq 0.01$)
NS = Non significant

Table 2: Mean values of genotype for oil yield per plant, oil and protein percentage over salinity levels

Genotype	S0 (Control)			S1 (5.0 EC)			S2 (10.0 EC)		
	Oil yield/ Plant (g)	Oil % age	Protein % age	Oil yield/ Plant (g)	Oil % age	Protein % age	Oil yield/ Plant (g)	Oil % age	Protein % age
Suncon 90	2.92a	19.89c	9.6bc	0.64a	15.86a	5.82ab	0.29a	11.28a	23.41a
Suncon 110	2.87a	19.11d	10.04b	0.73a	14.91ab	17.49a	0.13a	11.40a	23.16a
Romania	1.88a	16.68e	11.37a	0.49a	13.17abc	16.14ab	0.19a	10.17a	19.33d
KNI	2.56a	24.50b	10.03b	1.28a	16.71abc	15.68ab	0.19a	13.10a	19.58cd
Suncon 90 X Suncon 110	2.91a	26.93a	6.97e	0.70a	14.64abc	13.43ab	0.22a	10.89a	17.83e
Suncon 90 X Romania	1.48a	16.45fg	7.79de	0.67a	13.99abc	13.42ab	0.18a	9.83a	21.00b
Suncon 90 X KNI	2.15a	15.92h	8.67cd	0.41a	14.10abc	14.46ab	0.18a	10.42a	19.96c
Suncon 110 X Romania	1.05a	16.32g	8.73c	0.63a	11.59abc	13.71ab	0.18a	9.34a	17.68e
Suncon 110 X KNI	1.04a	16.57ef	7.70e	0.57a	12.72abc	10.43bb	0.32a	10.61a	16.37f
Romania X KNI	1.75a	16.99d	6.08e	0.87a	11.45c	12.12ab	0.13a	10.88a	19.46cd

Figure sharing a common in columns letter do not differ significantly

Table 3: Mean squares from the stability analysis of variance of ten Sunflower genotypes across three salinity levels

SOV	df	Traits		
		Oil yield/ plant (g)	Oil % age	Protein % age
Genotypes (G-1)	9	0.22989 NS	11.64492 **	13.08024 **
Env.+ (Genotype X Env.) G(S-1)	20	1.0965	20.0718	29.1341
Environment (linear)	1	16.4684	337.728	549.5242
Genotype X Env. (linear)(G-1)	9	0.26101 NS	5.82954 **	2.9033 *
Pooled deviation G (S-2)	10	0.31121 **	1.12413 NS	0.7028 NS
Pooled Error S (R-1) (G-1)	60	0.01794	1.74444	3.4561

*, ** = Significant at ($P \leq 0.05$) & ($P \leq 0.01$); NS = Non Significant

Table 4: Mean Oil yield / plant, Oil percentage, Protein percentage and estimates of stability parameters for 10 Sunflower genotypes Across three salinity levels

Genotypes	Oil yield per plant (g)				Oil percentage				Protein percentage			
	X	b	S^2d	R^2	X	b	S^2d	R^2	X	b	S^2d	R^2
Suncom 90	1.28	1.55 *	-0.14 *	0.03	15.68	1.03	-0.83	0.03	16.28	1.32 **	-3.36	0.001
Suncom 110	1.24	1.57 *	-0.19 *	0.04	15.14	0.94	-1.51	0.01	18.90	0.68	-0.69	0.10
Romania	0.85	0.91	0.10 *	0.04	13.34	0.79	-1.55	0.01	15.61	0.75	-2.47	0.03
Suncom 90 *x* Suncoffl 110	1.34	1.17	0.03 **	0.09	18.10	1.41 *	-1.34	0.01	15.10	0.91	-2.68	0.02
Suncom 90 *x* Romania	1.28	1.04	2.08	0.51	17.49	2.01 **	2.06	0.03	12.74	1.05	-3.26	0.003
Suncom 90 x KN1	0.78	0.86	-0.22 **	0.24	13.42	0.78	-0.01	0.08	14.07	1.26 **	-2.98	0.01
Suncom 110 *x* Romania	0.91	1.09	0.18 **	0.04	13.48	0.65	-0.10	0.10	14.36	1.07	-2.90	0.01
Suncom 110 *x* KN1	0.62	0.52	-0.15 **	0.09	12.42	0.86	-1.60	0.01	13.37	0.85	-2.96	0.01
Romania x KN1	0.64	0.47	-0.18 **	0.21	13.30	0.73 *	-1.71	0.002	11.5	0.83	-2.05	0.04
Average	0.99	0.82	0.17 **	0.07	13.11	0.78	0.34	0.09	12.55	1.28 **	-3.45	0.0001
	0.99	1.00			14.55	1.00			14.45	1.00		

*, ** = Indicates genotype differ significantly from 0.0 and 1.0

Protein percentage (%): The stability analysis of variance for protein percentage combined over three salinity levels indicates highly significant genotypic differences (Table 3). Significant genotype-environment interaction (linear) indicates that genetic differences exist among sunflower genotypes for their regression in the environmental index. The pooled deviation mean square was also found to be non-significant when tested against pooled error.

Mean protein percentage and estimates of stability parameters for ten sunflower genotypes combined over three salinity levels (Table 4) depicts that mean protein percentage ranged from 11.50 % to 18.90 % with an average of 14.45 %. All the four parental lines showed protein percentage above the mean value. The egression coefficient for this trait ranged from 0.68 to 1.32. Three sunflower genotypes (Suncom 90, Suncom 90 x Romania and Romania x KN1) showed significant b-values. The deviations from regression mean squares (S^2d) were non-significant for all the genotypes. Values for coefficient of determination (R^2) were small or all the genotypes. KN1, due to the mean above the mean and b value close to unity and non-significant S^2d was stable for protein percentage. This finding is in consistency with results of Tai (1971), Aslam *et al*. (1988), Cheng (1984), Chan (1985) and Eberhart and Russell (1966). These workers observed antagonistic relationship between stability and yield and warrants some form of reconciliation between these two conflicting criteria in selection of varieties for cultivation under different environments and circumstances. In conclusion, the stability statistics gave valuable information for the behavior of the genotypes over salinity environments and can be treated as the sole criteria in selection of genotypes for using in breeding program aiming at the development of salinity tolerant cultivars.

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