ASSESSMENT OF SUITABILITY OF SOME SUNFLOWER INBREDS IN SODIC TRACTS OF INDIA

D. Sassi Kumar, Research Associate, Department of Pulses, Tamil Nadu Agricultural University, Coimbatore-641 003,Tamil Nadu, India
E-mail: sassi_kumar2003@yahoo.com
E-mail: sassiku@rediffmail.com

A. Gopalan, Professor and Head, Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India

Abstract

Twenty-five sunflower (*Helianthus annuus* L.), genotypes were tested over eight environments (sodic soils/normal soils in two seasons) of Tamil Nadu, India. Grain yield data were subjected to the additive main effects and multiplicative interaction (AMMI) analyses. Results indicated a significant G x E interaction of about 31.92% compared to the total variance suggesting the existence of a broad range of diversity among genotypes and environments. The highly significant G x E interaction was further partitioned into three PCA axes (IPCA) with a contribution of 44.98, 24.66 and 14.16 percent respectively to the total G x E interaction variance. The biplot graph identified the genotypes GP86, CO4, GP255, GP161, SF83 and GP336 as high yielding and the most adaptable inbreds. Surya and Morden are the varieties highly suitable to a normal and responsive environment and inbred SF54 is especially adapted to the sodic soil. Further, two environments in TNAU, Coimbatore in both Kharif and Rabi were found ideal for stable performance of the sunflower genotypes.

Introduction

Sunflower (*Helianthus annuus* L.) the crop that gained momentum for its quality oil content, reached static levels in area of cultivation in recent years. The climate and soil factors are the main notable causes for such a decline in area. The premier among the androgenic problems is sodic soils that are capable of reducing the yield potential of the crops grown in them. The reclamation cost of sodic soil as such is expensive. The pragmatic solution to improve the amount of area under sunflower is the exploitation of these sodic soils by release of suitable plant ideotypes. Even then, the salt tolerant plant types released for the one targeted environment may not perform better in other sodic tracts, as a range of salt stress environments exists with varying intensity and nature. Thus breeding for salt tolerance is impeded by large G x E interactions that result from a combination of differences in genotypic adaptation and the heterogeneity of the soil among and within the target environments (Fukai and Cooper, 1995). So it is imperative to conduct a study that gives a detailed account of the G x E interactions before releasing of the variety to the targeted environments.

To study this important G x E interaction, many advanced statistical techniques are relied on such as ANOVA (analysis of variance), PCA (principle component analysis), etc. The AMMI model is a hybrid model involving both additive and multiplicative components of two-way data structure. The AMMI model separates the additive variance and then applies PCA to the interaction portion to extract a new set of coordinate axes, which explain in more detail the interaction pattern. The effectiveness of the AMMI procedure has been clearly demonstrated by various authors, viz., in soybean Zobel et al., (1998); in maize Crossa et al., (1990); Nichit et al. (1992) in wheat, Sharma et al. (1998), Vijayakumar et al. (2001), and Ashok (2000) in pearl millet, rice and sunflower, respectively, using multilocational trial data. Using this AMMI analysis and biplot facility, the sunflower yield trial data were analyzed to determine the nature and magnitude of G x E interaction effects on grain yield in diverse production environments to identify high-yielding stable genotypes adapted to sodic environments.

Materials and Methods

Twenty-five sunflower inbreds comprising six CMS counterpart lines, five high-yielding varieties and the germplasm accessions of different origin were evaluated in different environments. The locations are listed in Table 1.

Table 1. List of environments and nature of soil in which the study materials were raised.

Env.	Location	Season	Soil condition EC	pH
E1	Department of oil seeds, TNAU, Coimbatore	Kharif, 2000	1.58	7.68
E2	Eastern Block, Department of Agronomy, TNAU, Coimbatore	Kharif, 2000	2.69	7.30
E3	Partially reclaimed soil, Anbil Dharmalingam College of Agriculture, Navalur Kuttapattu, Trichy	Kharif, 2000	1.59	8.20
E4	Unreclaimed soil, Anbil Dharmalingam College of Agriculture, Navalur Kuttapattu, Trichy	Kharif, 2000	1.76	8.89
E5	Western Block, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal	Kharif, 2000	1.79	8.50
E6	Department of oil seeds, TNAU, Coimbatore	Rabi 2000-2001	0.02	7.60
E7	Eastern Block, Partially reclaimed soil, Anbil Dharmalingam College of Agriculture, Navalur Kuttapattu, Trichy	Rabi 2000-2001	0.16	8.10
E8	Western Block, Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal	Rabi 2000-2001	1.20	8.90

Of these environments the locations E1, E2 and E6 are normal soil and the rest of the environments had different degrees of sodicity. The genotypes were raised in a randomized block design with three replications in each environment. A spacing of 60 x 45 cm was adopted in 5-meter length ridge. Each genotype occupied 5 ridges in each replication thus forming a plot. The plot yield was recorded in each replication for each genotype and the data was used for statistical analysis.
The AMMI model is:

$$Y_{ge} = \mu + \alpha_g + \sigma_e + \Sigma_{1\text{-}n} + \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge}$$

Where Yge is the yield of the gth genotype in eth environment; αg is the mean of the gth genotype as a deviation from grand mean μ; σe is the environment mean deviations from μ; n is the number of IPCA^s retained in the model; λ_n is the singular value for IPCA axis 'n'; δen is the environmental eign vector values for IPCA axis and ρge is the residual value. The GE interaction sum of squares was subdivided into the PCA axis, where axis 'n' is regarded as having p+q-1-2n degrees of freedom and p and q are the number of genotypes and environments respectively. The data was analyzed by using INDOSTAT statistical computer package.

Results and Discussion

The AMMI analysis of variances is presented in the Table 2. From this ANOVA table it is clearly understood that the mean sum of squares for genotypes, environments and G x E interactions was found to have significant effect on total variance. This suggested that a broad range of diversity existed among genotypes and among environments and that the performance of genotypes was differential over the environments.

Table 2. AMMI analysis of variance of seed yield of 25 sunflower genotypes tested at eight locations.

Source	d. f.	Sum of squares	Mean squares	Percentage SS
Treatment combinations	199	7791.04	39.15**	100
Genotypes	24	901.78	37.57**	11.574
Environment	7	4402.31	628.90**	56.50
GE interaction	168	2486.94	14.80**	31.92
PCA 1	30	1118.63	37.28**	§ 44.98
PCA 2	28	613.21	21.90**	§ 24.657
PCA 3	26	352.27	13.54*	§ 14.16
Residual	84	402.81	4.79	§ 16.197
Error	200	1650.00	8.25	
Total (g x c x r)-1	399	9441.05	23.66	

*, ** = Significant at 5% and 1% level of significance respectively.
§ = As percent of G x E interaction SS.

Out of the total treatment variation, the proportion of variance due to differences in environments was largest (56.50 per cent) followed by the variance due to G x E interaction (31.92%) and the variance due to genotypes (11.57%). Thus the ordinary ANOVA model accounted for only 68.07% of the treatment combination sum of squares attained by genotypes and environment effects.

The G x E interaction that was highly significant was further partitioned into three PCA axes (IPCA) with a contribution of 44.98, 24.66 and 14.16 per cent to the total G x E interaction variance. All the three IPCA axes representing the interaction pattern were highly significant and jointly accounted for 83.8% of the interaction component and the rest of interactions' variance is left as residues. Hence the above analysis seems to suggest the presence of complex, multidimensional variation in genotype by environment data as the first three axes were demonstrated to be highly significant. In the present study the AMMI model with first the IPCA axis was considered for interaction. The second and third ICPA axes despite significance were pooled into the residual; this is because the AMMI models with many ICPA axes are expected to involve rather more noise than explained by high complex interactions among genotypes and environments. Further if the AMMI model includes more than one PCA axis, assessment and presentation of genetic stability are simple (Nitch et al., 1992; Crossa et al., 1991; Sharma et al., 1998; Vijayakumar et al., 2001).

The mean performance of the ICPA 1 score for both the genotypes and environments used to construct the biplot is presented in Table 3. The AMMI biplot is developed by placing both genotype and environment values of the X axis and the respective PCA axes and vectors in the Y axis. The usual interpretation of such a biplot assay is that if a genotype or an environment has a PCA score nearing zero, it has small interaction effects and when the genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their interaction is negative (Zobel et al., 1998; Kempton, 1984; Zobel and Wallace, 1991 and Shinde et al., 2002). In this way the biplot helps in a visual interpretation of the G x E patterns and in identifying genotypes or locations that manifest low, medium and high levels of interaction effects.

According to the AMMI model, the genotypes that are characterized by mean greater than the grand mean and the PCA scores of nearly zero are considered as generally adaptable to all the environments. However, the genotypes with high mean performance and with a large value of ICPA scores are considered as having specific adaptability to the environments

The biplot presented in Figure 1 thus identified GP86, CO4, GP255, GP161, SF83 and GP336 as the highest yielding and most adaptable inbreds as they were scattered at the right-hand side of the grand mean level and close to the IPCA-1 = 0 line. Surya and Morden are the varieties highly suitable to E6 environment. Similarly the inbred SF54 is specially adapted to the E3 environment. Regarding the suitability of the environments, Figure 1 clearly indicated that environment E1 had good conditions for the yield expression of the inbreds, as the environment was higher than the grand mean as well, and the PCA score was near zero. Environments E5, E4, and even E8 also had a near zero score on the PCA axis but their yield potential was below average. The environments E6 and E2 had great potential for yield levels but were exhibiting high interaction effects and therefore they are most suitable for specially adapted genotypes, *viz*., Surya and Morden for the E6 environment. However, the response of genotypes to the highly interactive environments can be judged more precisely by scattering the genotypes and environments in a biplot between the PCA I and PCA II axes. As per Figure 2 the inbreds GP 324, Morden, CO2 and SF54 had the most scattering indicating their high interaction effects with the environments. This gives the inference that any change in the environment will have a proportional impact on the yield of the above genotypes.

Table 3. Estimates of stability parameters (AMMI) seed yield.

Genotypes	**Mean**	**PCA I**	**PCA II**	**PCA III**	**G x E ResSS**
CO2	22.21	-1.436	-0.912	-0.389	104.67
CO3	22.70	-0.698	-0.276	-0.275	21.31
CO4	24.99	0.279	-0.172	-0.627	16.31
Surya	24.67	2.164	-0.034	-0.431	12.26
Morden	24.03	2.029	-1.377	-1.19	214.88
5B	21.75	1.452	0.604	0.572	39.81
6B	20.39	-1.909	0.038	-0.255	8.37
302 B	20.39	-1.909	0.038	-0.255	8.37
400 B	17.89	-1.089	-0.358	1.041	17.22
336 B	22.23	0.901	0.282	-1.603	24.43
86 B3	19.81	-0.876	0.641	0.533	43.88
GP 161	25.50	-0.285	0.496	-1.193	44.03
GP 255	25.34	-0.136	-1.582	-0.408	255.07
GP 86	25.90	0.155	-1.197	0.714	158.35
GP 336	24.70	0.803	-0.933	0.684	112.60
GP 324	23.60	2.226	1.764	0.326	323.37
GP 93	24.01	0.617	0.944	0.402	95.74
SF 91	22.97	-0.728	2.449	0.296	595.47
SF 54	25.10	-1.867	0.930	-1.587	88.80
SF 45	20.33	-0.440	-0.023	-0.614	14.27
SF 34	21.15	-1.376	0.039	1.517	24.42
SF 83	24.35	-0.531	0.128	0.526	85.76
SF 7	19.99	-0.055	-1.960	0.290	386.33
SF 30	21.16	-0.210	-0.602	0.369	43.62
SF 60	24.90	0.981	0.252	1.839	44.72
E1	27.11	-0.671	3.938	0.411	1558.90
E2	28.18	-1.426	-0.422	-1.292	132.01
E3	17.81	-0.513	1.413	-0.245	268.97
E4	17.81	-0.513	1.413	-0.245	268.97
E5	16.26	-0.267	-1.203	3.766	149.12
E6	29.90	3.945	-0.469	-1.107	56.78
E7	20.79	2.711	-0.604	0.164	99.93
E8	20.48	-1.353	-0.450	-0.824	61.33

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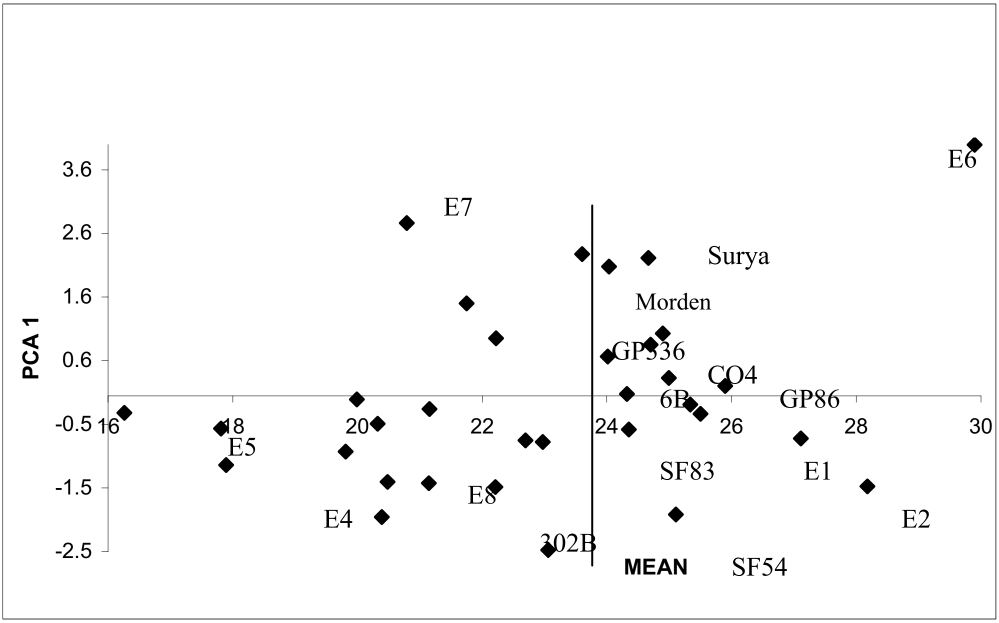

Figure 1. Biplot graph for the mean and PCA 1 per plant yield.

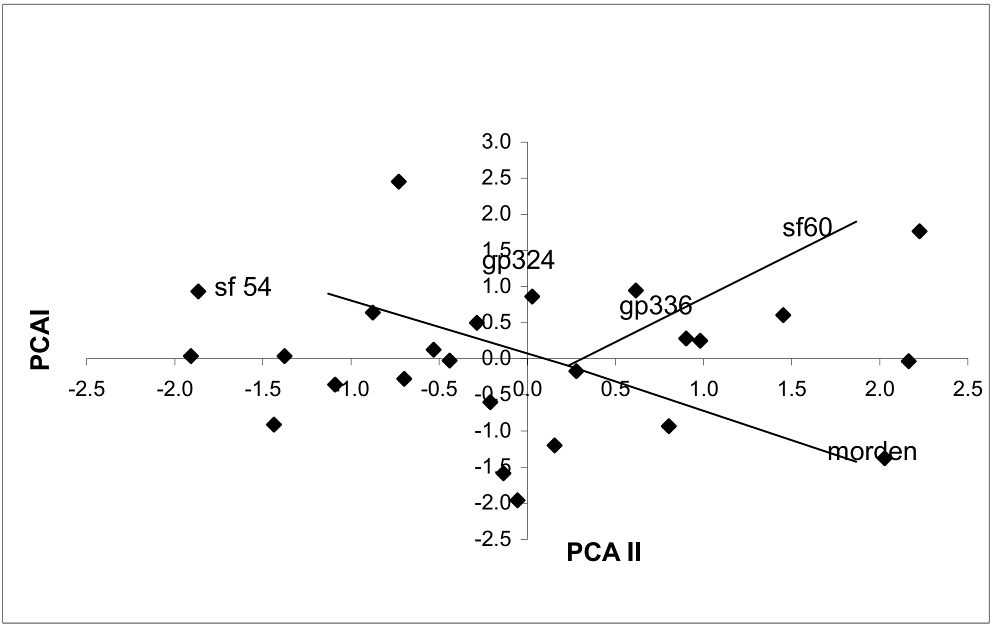

Figure 2. Biplot graph for mean and PCA I and PCA II (per plant yield).

Often the underlying cause of an interaction can be deduced from knowledge about the genetic differences between the cultivars involved and/or the different environments involved. In this study the interactions represented by the biplot (Figure 1) are due to the interaction of the set of genotypes with the nature of the soil in the growing environments. In this study the environments E5, E4, E7 and E8, which have very low mean values with very low interaction of the genotypes, are composed of a high degree of sodic soil, hence these environments are not suited to the inbreds studied. Similarly E3 which is a partially reclaimed soil gave a higher environmental mean yield. The most suitable inbred for the E3 environment is SF54 from a germplasm collection originating in France; this inbred has been proved to be tolerant to sodicity through laboratory experiments (data not shown). Alternatively the environments E6, E1 and E2 have higher mean values and most of the inbreds have positive interaction or less interaction with these environments and have normal soil, especially the environment E6 which may contain high nutrient levels.

Conclusions

The AMMI analysis used for studying the performance and stability of sunflower inbreds in sodic soil has clearly indicated stable and sodic-tolerant lines. It is also useful for characterizing the environments/locations that are suitable for growing a specific genotype or group of genotypes.

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