Stability Analysis of Yield Performance of Safflower Genotypes

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Abstract—*25 safflower genotypes and 2 checks were evaluated across 16 environments. The experimental layout was a randomized complete block design with three replications. The Additive Main Effects and Multiplicative Interaction (AMMI) analysis of variance identified highly significant effects for environment, genotype and genotype by environment interaction denoting different responses of genotypes across environments. The AMMI1 biplot identified 5 as the most stable genotype.*

Keywords*: AMMI model, Safflower, yield, genotypes*

1. INTRODUCTION

Multiple location trials (MLT) are generally carried out by plant breeders to select and release high yielding and stable genotypes for different environments. The analysis of MLT data reveals genotype*environment interactions which often causes difficulties in the interpretation of data and reduce efficiency in selecting the best genotypes. AMMI analysis method is widely used to overcome these difficulties in data analysis.

The AMMI model uses analysis of variance (ANOVA, an additive model) to characterize genotype and environment main effects and principal component analysis (a multiplicative model) to characterize their interactions (IPCA). The AMMI analysis captures a large portion of the GE sum of squares and separating the main effects and interaction effects and the model provides meaningful interpretation of the data (H.G. Gauch, 1992). AMMI partitions the interaction into individual genotypic and environmental scores (Zobel et al. (1988)). Purchase et al. (2000) developed a quantitative stability value to rank genotypes through the AMMI model. AMMI analysis refers to double centered principle component analysis. Gruneberg et al. (2005) showed that AMMI, the multivariate tool, was highly effective for the analysis of MLT.

The objective of this study was to determine the stable and best genotypes using AMMI analysis.

2. MATERIALS AND METHODS

The data were collected from All India Coordinated Research project on Safflower annual report 2014-15. The data contains 25 safflower genotypes and 2 checks evaluated at 16 locations. In each location the design followed was RBD with three replications. Combined data analysis was done for replicated data for 16 centers. Data was subjected to AMMI model using SAS 9.3 software.

The following model was used for analysis**.**

The AMMI model

$Yge = \mu + \alpha g + \beta e + \Sigma n\lambda n\gamma gn\delta en + \rho ge.$

Yge = yield for genotype (g) in environment (e)

μ = grand mean

αg = genotype deviation

βe = environment deviation

λn = singular value for component n

γgn = eigenvector value for g

δen = eigenvector value for e

ρge = residual term.

3. RESULTS AND DISCUSSION

The combined analysis of variance showed that there are highly significant differences for environment, genotype and their interactions. AMMI analysis is shown in Table 1. showed that safflower yields were significantly affected by the environment because of significant variance at 1% level which explained 51% of the total (G + E + GEI) variation, while G x E interaction captured 14.9% of the total sum of squares. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing variation in the grain yields. The AMMI model demonstrated the presence of G x E interactions, and this has been partitioned among the first and second IPCA. The yield variation is due to genotypic and environment factors. Results from AMMI analysis showed that the first principal component axis accounted for 71.07% and the second accounted for 17.7%. Table 2. shows that AMMI model scores of 25 genotypes.

Table 1: AMMI analysis of variance over sixteen

Source	*DF*	*SS*	*Mean Square*	*F Value*	*Pr > F*
ENV	15	651993410	43466227	444	<.0001
BLK(ENV)	32	11370057	355314	3.64	<.0001
GEN	24	73588768	3066198	31.38	<.0001
EI(GEN)	24	73007600	3041983	31.13	<.0001
*ENV*GEN*	336	97724688	290847	2.98	<.0001

The results indicated that the yield performance of safflower was highly influenced by G*E interaction effects. The magnitude of environment effect was about 8 times that of genotype effect.

Table 2: PCA scores for Genotypes

Genotypes	Mean	PCA1	PCA2	PCA3
PBNS-129	1539.11	-0.11751	0.22461	0.28950
SSF-1307	1846.97	0.15840	0.16434	-0.45171
JSI-117-14	1470.85	-0.29770	0.28057	0.32816
3941-3-6-3-8	1168.50	-0.23916	0.04051	-0.14527
NARI-106	1453.74	-0.03879	-0.09449	0.15845
SSF-1350	1934.11	0.44116	0.09688	0.18347
NARI-107	1607.77	0.11895	-0.12362	-0.02665
SPP-70 (NSP)	1419.37	0.06790	-0.62222	0.08929
NARI-6 (Non-spiny check)	1086.66	-0.18224	-0.13700	-0.03735
PBNS-137	1608.70	0.03312	-0.01551	-0.01777
14-129 (NSP)	1130.11	-0.22735	-0.22340	0.14980
SSF-1369	1868.10	0.32468	0.03765	-0.04859
PBNS-12 (Check)	1716.29	-0.02048	0.17345	-0.13133
JSI-120-1-1	1480.47	-0.20558	0.14694	0.17354
SFS-9943	1195.08	-0.28034	-0.02985	-0.38136
A-1 (National check)	1915.88	0.24187	0.32899	0.04093
SSF-1302	1711.04	-0.02761	0.04254	-0.34453
ASF-1402	1292.75	-0.22640	-0.21667	0.07469
NARI-104	1476.86	-0.13979	0.12878	-0.02240
PBNS-138	1711.53	0.18515	-0.26762	-0.05720
SSF-1305	1866.43	0.31280	-0.05403	0.25688
ASF 1401	1546.70	0.05589	-0.06628	-0.27051
PBNS-130	1543.48	0.02533	-0.08998	0.16255
NARI-105	1520.89	-0.08374	0.13848	0.03507
AKS-330	1874.77	0.12146	0.13691	-0.00765

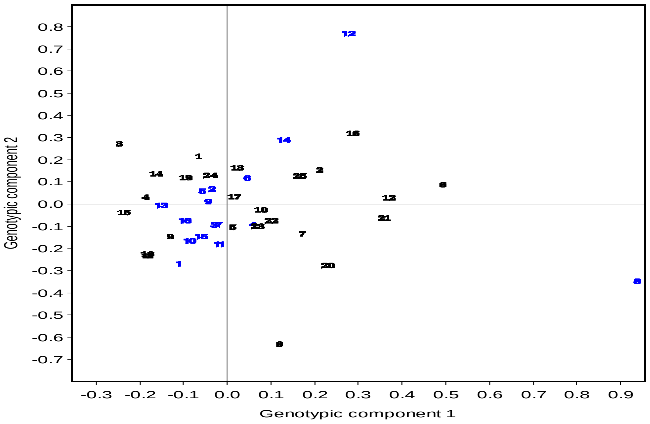

Fig. 1: Biplot of G*E interaction

There were desirable genotypes in terms of high mean yields and stability. Therefore, both yield and stability should be considered simultaneously to exploit the useful effect of G*E interaction and to make selection of genotypes more precise and refined.

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