Prediction of Sesame Yield in the Presence of Genotype x Environment Interaction

Kang-Bo Shim*, Churl-Whan Kang, Jae-Duck Seong, Jung-Dong Whang, Duck-Yong Suh

Yeongnam Agricultural Research Institute, NICS, RDA

Objectives

To evaluate and select sesame line with higher stability to the multi-cultural environments by analyzing interaction of genotype by environment at different sites.

Materials and methods

○ Materials : Yangbaekkae, Ansankkae, Suwon193, Suwon194, Suwon195, Kyeongbuk2,
  Miryang1, Mirynag2, Miryang4, Miryang7, Miryang8, Miryang9, Miryang10

○ Methods
  - ANOVA for the interaction of genotype by environment
  - Gollob's F-test for significance
  - AMMI analysis for quantification of interaction of genotype by environment.

Results and discussion

○ Statistically significant difference to the environment, genotypes and interaction of genotype by environment were showed.

○ The first two AMMI multiplicative components were significant at the 1% probability level.

○ Ansankkae, Miryang1 and Miryang7 scored near the zero of PCA value indicating higher stability by smaller interaction of genotype by environment.

○ Naju and Miryang showed adequate site for sesame regional evaluation in view of higher stability and lower interaction portion of genotype by environment. But Chuncheon and Suwon showed higher PCA1 and lower PCA2 scores respectively indicating higher interaction portion of genotype by environment.

Correspondence : Phone : 055-350-1241, E-mail shimkb@rda.go.kr

Table 1. ANOVA for the yield of thirteen sesame genotypes in eight environments

Source of variation	df	Sum of Squares	Mean Squares	F value
Total	105	109332.83	1041.27	11.01**
Replication	2	196.85	98.42	1.04^{NS}
Environment	7	70413.99	10059.14	106.40**
Genotypes	12	23835.40	1986.28	21.01**
Environment x genotype	84	14886.60	177.22	1.87**

Table 2. Gollob F-test for the AMMI terms of the yield of thirteen sesame genotypes in eight environments.

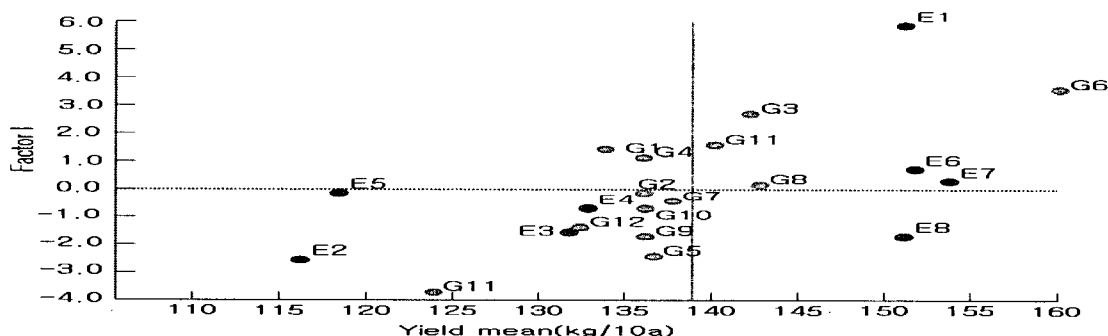| Sum of Squares for each AMMI	Percent of GxE Sum of Squres	Cumulative percent of GxE Sum of Squres	Df of each AMMI	Mean Squares of each AMMI	F value of each AMMI
7998.23	53.727	53.727	18	444.35	4.699**
3368.16	22.626	76.353	16	210.51	2.227**
1427.16	9.587	85.940	12	101.940	1.078^{NS}
655.75	4.405	98.001	10	65.575	1.005^{NS}
189.19	1.271	99.272	8	23.648	0.694^{NS}

Fig. 1. Biplot of interaction principal component axis(PCA1) against mean yield of thirteen genotypes and eight environments. Genotypes and environment codes are G1:Yangbaekkae, G2:Ansankkae, G3:Suwon193, G4:Suwon194, G5:Suwon195, G6:Kyeongbuk2, G7:Miryang1, G8:Miryang2, G81:Miryang4, G9:Miryang7, G10:Miryang8, G11:Miryang10, G12:Miryang12, E1:Chuncheon, E2:Suwon, E3:Cheongwon, E4:Yaesan, E5:Naju, E6:Andong, E7:Jinju, E8:Miryang
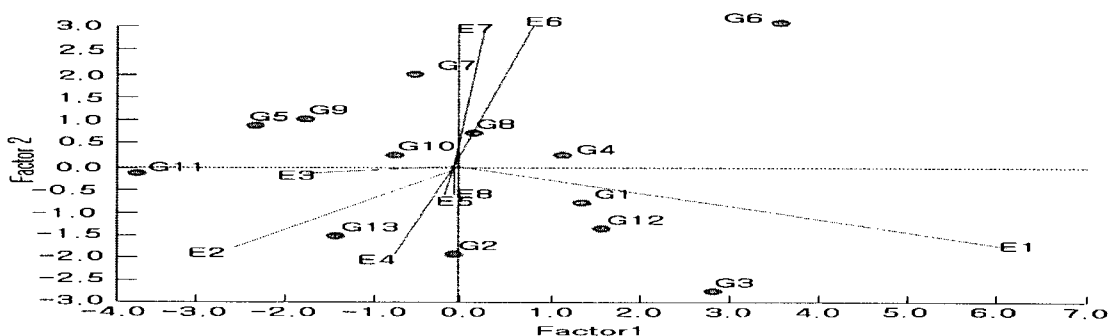

Fig. 2. Biplot of interaction principal component axis(PCA1) against PCA2 for yield of thirteen genotypes(circles) in eight environments(lines)