COTTON REGIONAL BREEDERS TESTING NETWORK - GGE BIPLOT ANALYSIS

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Abstract

The Regional Breeders Testing Network (RBTN) is a multi-environment yield trial for the public cotton breeder community. Through a cooperative effort among State and Federal breeders, advanced breeding lines were evaluated in replicated yield trials at twelve locations stretching across the cotton belt from South Carolina to Arizona. To determine relationships among RBTN environments, compare environments for ability to discriminate among breeding lines, and identify mega-environments for lint yield, genotype main effects (G) and genotype x environment interactions (GE) from the 2006 RBTN were subjected to GGE biplot analysis. The Stoneville, MS (MSSTV) location was correlated with eight of eleven locations. Two locations were identified for doing a good job of discriminating among breeding lines. Mega-environments were identified that could be divided roughly into higher and lower latitudes. Defining relationships among RBTN locations will aid in identifying the most useful sites for trials and help characterize breeding lines for regions of adaptation.

Introduction

Public cotton breeders have many of the same goals and face some of the same challenges as breeders in the commercial sector. Most public breeders, however, face the additional challenge of operating on very limited resources. While commercial seed companies have numerous test sites scattered across the cotton belt for evaluating advanced breeding lines, public breeders are typically limited to two or three on-station locations. The RBTN was conceived to facilitate public breeder cooperation in establishment of multi-environment trials (MET) for testing advanced breeding lines. Established in 2002, the RBTN utilizes the combined resources of University and Federal breeding programs for evaluating public breeding lines in MET ranging from South Carolina to Arizona. The MET of the RBTN allows for increased precision in measurement of quantitative traits and can provide an indication of areas of adaptation (Fehr, 1987). RBTN trials are typically located at sites of participating public breeding institutions and have not been chosen to represent specific environmental parameters. However, RBTN test sites do represent the most important cotton growing states in the cotton belt. To determine relationships among RBTN environments and compare environments for ability to discriminate among breeding lines for lint yield, genotype main effects (G) and genotype x environment interactions (GE) were subjected to GGE biplot analysis (Yan, 2001). The existence of mega-environments (ME), defined by a group of environments consistently sharing the best breeding line, were also determined (Yan, et al., 2001).

Materials and Methods

Yield data from the 2006 RBTN were subjected to analysis of variance and GGE biplot analysis. Analysis of variance was conducted to determine percent contribution of G, E, and GE to total variation (G+E+GE). Significant G and GE components were prerequisite to biplot analysis. The “relationship among testers” (environments) and “which-won-where” routines of the GGE biplot software developed by Yan (2001) were employed to generate biplots. Biplots were examined to compare environments for ability to discriminate among breeding lines, relationships among environments, and existence of ME among 12 locations (Fig. 1) of the 2006 RBTN.

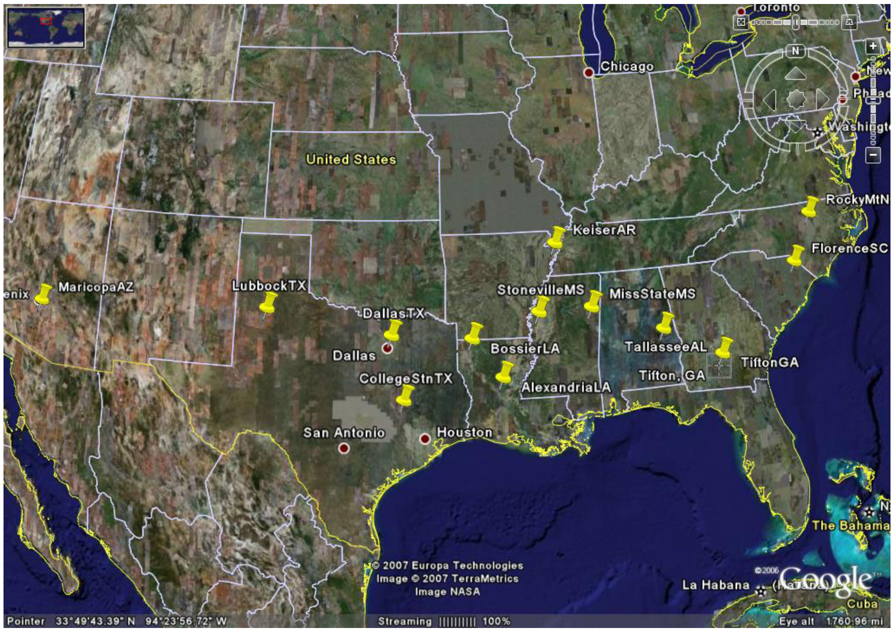

Figure 1. Locations of the 2006 Regional Breeders Testing Network.

Results and Discussion

Although significant, the proportion of total variation in lint yield attributed to G and GE was only 4.4 and 10.9%, respectively. Environment (E), which is known to have a much greater impact on yield compared to G and GE, accounted for 84.7% of observed variation. Relationships among RBTN environments with respect to yield are shown in Fig. 2. A correlation coefficient is approximated by the cosine of the angle between any two environments. The Stoneville, MS (MSSTV) location was significantly correlated with RBTN environments located in Georgia, Louisiana (2), North Carolina, South Carolina, Texas, and Mississippi. Stoneville has long been recognized as a desirable location for breeding. Cultivars developed in this area tend to have a wide area of adaptation so it is not surprising that more locations were correlated with Stoneville than any other location. Correlation coefficients among the 12 environments are provided in Table 1. With the exception of Stoneville, there does not appear to be a pattern of redundancy among environments. Vector lengths in Fig. 2 provide an indication how well an environment performed in discriminating among breeding lines. Trials in Arizona (AZMAR) and Mississippi (MSSTV and MSMSU) were best for discriminating among breeding lines for yield. Although AZMAR discriminated among breeding lines, this site was unlike any other location. The wide angle between AZMAR and remaining locations indicated a strong GE interaction and explains why no other locations were correlated with AZMAR (Table 1). The Lubbock, TX (TXLUB) location (biplot origin) did not discriminate among breeding lines in 2006. Remaining environments were similar in ability to discriminate among breeding lines.

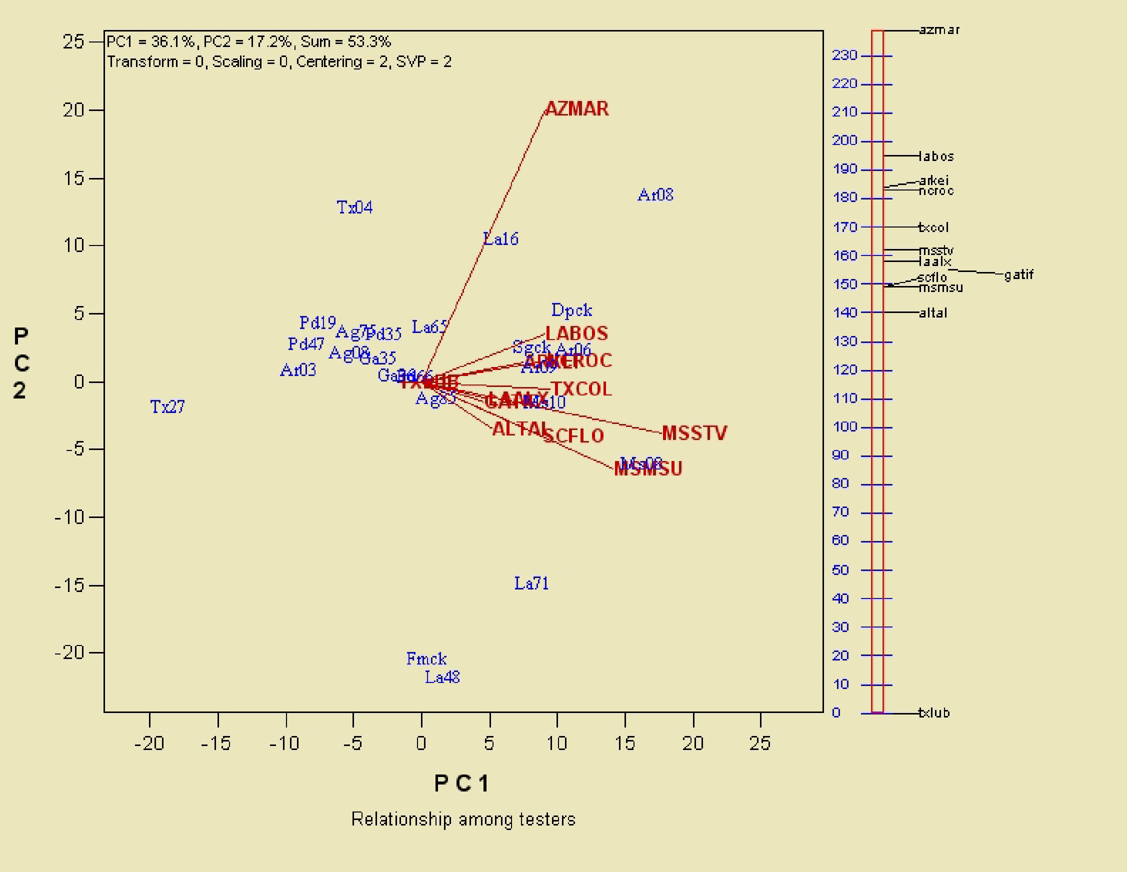

Figure 2. Relationship among testers (environments) view of GGE biplot demonstrating relationships and discriminating ability of environments for lint yield.

Table 1. Correlation matrix among environments for yield in the 2006 RBTN.

Row/Col	ALTAL	ARKEI	AZMAR	GATIF	LAALX	LABOS	MSMSU	MSSTV	NCROC	SCFLO	TXCOL
ALTAL	-	-	-	-	-	-	-	-	-	-	-
ARKEI	-0.160	-	-	-	-	-	-	-	-	-	-
AZMAR	0.046	0.286	-	-	-	-	-	-	-	-	-
GATIF	0.143	0.240	0.112	-	-	-	-	-	-	-	-
LAALX	0.387	0.350	0.105	0.381	-	-	-	-	-	-	-
LABOS	-0.036	0.405	0.382	0.104	0.386	-	-	-	-	-	-
MSMSU	0.182	0.590**	0.028	0.297	0.403	0.276	-	-	-	-	-
MSSTV	0.302	0.440*	0.191	0.473*	0.509*	0.520**	0.743**	-	-	-	-
NCROC	0.221	0.336	0.357	0.206	0.390	0.346	0.363	0.492*	-	-	-
SCFLO	0.682**	-0.010	0.068	0.238	0.403	0.251	0.393	0.579**	0.413*	-	-
TXCOL	0.124	0.299	0.074	0.037	0.442*	0.737**	0.214	0.490*	0.420*	0.288	-
TXLUB	-0.250	-0.124	-0.071	0.262	-0.269	-0.214	-0.135	0.116	0.202	-0.136	-0.120

*,**Correlation (r) significant a the 0.05 and 0.01 level of probability, respectively.

Two mega-environments were identified for yield (Fig. 3). Breeding line Ms08 defined one ME (lower right sector of biplot) having the highest yield in half of all environments: GATIF, LAALX, ALTAL, SCFLO, MSSTV, and MSMSU. These environments were similar in that Ms08 was consistently the best performer. A second ME was defined by Ar08, the highest yielding breeding line in AZMAR, LABOS, ARKEI, TXLUB and NCROC. Breeding lines La16, Ar06, Ar09, along with check varieties DPck and Sgck were also consistent performers in this ME. With the exception of LABOS, this ME is delineated geographically by higher latitudes compared to remaining locations.

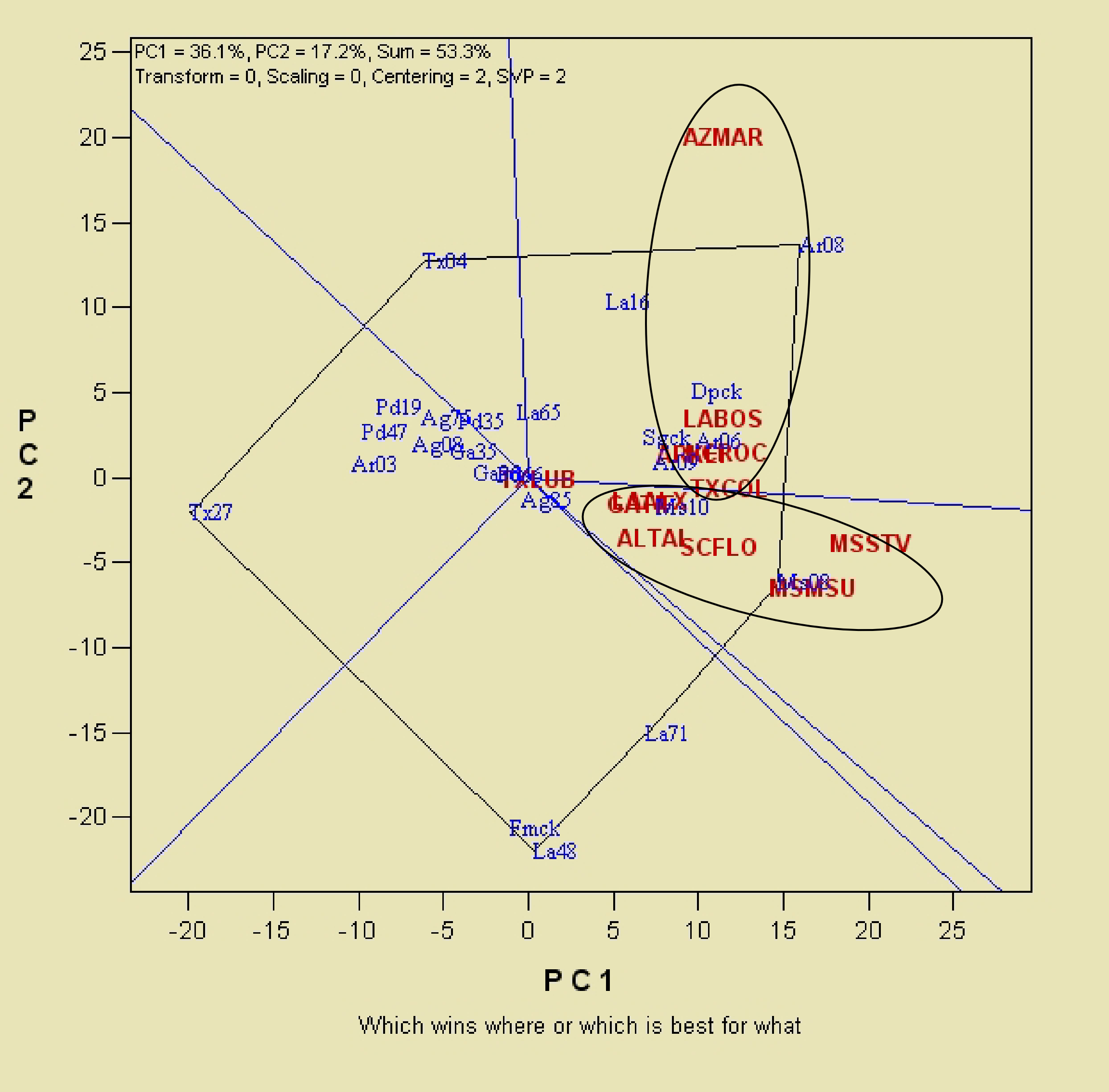

Figure 3. Which-won-where (genotypes) view of GGE biplot for yield in the 2006 RBTN to identify environments of highest yielding genotypes.

Biplot analysis is useful in identifying redundant environments, sites most useful in discriminating among breeding lines, and ME to define areas of adaptation. One of most important advantages of the RBTN to public breeders is the identification of areas of adaptation beyond the confines of local on-station trials. Multi-year data of the RBTN will be collected to confirm observed GE interaction patterns and better define relationships among trial sites. This information will be useful identifying potential deficiencies or duplications in RBTN trial sites.

References

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