USE OF GGE BIPLOT TO EVALUATE INTERACTION OF COTTON VARIETIES WITH

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Introduction

Plant breeding programs conduct multi-environment trials (MET) to identify genotypes that are superior either across a broad range of environments or within a more narrowly defined subset of environments. To this end, PhytoGen has conducted uniform testing of advanced and elite Upland strains across both the early/mid and the late maturity breeding programs in the Mid-South and Southeast regions of USA.

Since 2003, GGE Biplot (GGE) software has been used to gain some understanding of the primary interactions between genotypes and environments. Like the AMMI model, GGE uses principal component analysis to digest the GxE into components attributable to genotypes and environments that subsequently indicate relative magnitudes of both negative and positive interactions. A significant difference between GGE and AMMI is that GGE first removes the environmental main effects which, though invariably the largest source of variation in MET, are not useful in identifying superior genotypes. GGE graphically displays both the genotypic main effects (G) and GxE interaction (GE), which are the two sources of variation that must be considered in cultivar and test environment evaluation.

Materials and Methods

Yield trials were conducted with 15 experimental elite strains and 4 commercial checks at 9 locations in 2006 and at 15 locations in 2007. The entries were replicated 3 or 4 times and the plot size was 2 rows X 40 ft. Maturity was indicated in 2006 by a visual estimation of percent open bolls at Elko, SC and Leland, MS and in 2007 by a visual estimation of percent open bolls at Elko, NC and by percent first harvest at Leland, MS.

The data within each environment were analyzed by using the nearest neighbor analysis (NNA) procedure of Agrobase 21 software. The NNA-adjusted means were then subjected to the GXE procedure of Agrobase 21 to analyze the data over environments and to calculate Shukla's stability variance. The two-way data matrix of genotype and environment (year + location) means was used to generate a biplot using GGE Biplot software. The data were first scaled by the environmental standard deviation and the tester-centered (G + GE) model was selected. The Average Tester Coordination (ATC) view of GGE was printed and distances in mm from the lowest yielding entry (DP 444 BR) and perpendicular from the ATC were used to reflect the portion of each genotype's mean and instability, respectively, that was explained by the biplot (Figure 1).

Results and Discussion

The ANOVA for yield indicated that the environment, genotype and GxE interaction terms were all highly significant and that the variance due to genotypes was 3.3 times as large as that due to the GxE interaction (Table 1). The yield ranks are listed in Table 2 with the top 5 (T5) entries highlighted in green and the bottom 5 (B5) entries in pink. The two-way data matrix of 456 data points is difficult to visually digest even with ranks, but a few entries stand out. Strain X35 had the highest mean rank and it was in the T5 ten times, but in the B5 once. Strain X51 was in the T5 twelve times, but in the B5 four times. Strain X34 was in the T5 at all of the North Delta environments while X53 and X52 were in the B5 at six of these seven environments.

The development of GGE has been very beneficial to digesting the complex interactions between genotypes and environments that had previously been ignored. The Average Tester Coordination (ATC) view of GGE (Figure 1) displays both the mean and stability of genotypes in addition to indicating the nature and magnitude of GxE interactions. Projection along the red ATC-abscissa indicates relative mean performance with the highest yielding

genotype being displayed farthest to the upper-right. Distance along the blue ATC-ordinate indicates the relative contribution that each entry made to the overall GxE with the most stable genotype contributing the least to GxE as indicated by being closest to the ATC. As also reflected by the mean ranks in Table 2, GGE indicated that DP 555 BR, X34, X51 and X35 were the highest yielding genotypes. The correlation between mean yield and the GGE Mean Distance (mm) from the lowest yielding line, DP 444 BR, was 0.93 (Table 3). According to GGE, X35 and DP 555 BR were the more stable of the best lines with X51 and X34 interacting significantly, but oppositely, with environments. The correlation between Shukla's stability variance and the GGE Instability Distance (mm) from the ATC was 0.41 (Table 3).

Even though the GGE biplot accounted for only 42.2% of the total GxE interaction, it still led to significant understanding of this interaction. The rank differences pointed out in Table 2 for X34 and X52 were also reflected by GGE in their falling on opposite sides of the ATC. Since 2003, the relative maturity of genotypes has been a primary factor of GxE. The GGE Maturity Distance (mm) from the late maturing line X53 was correlated with the % open bolls of the entries at 0.67 (Table 3). The grouping of environments by GGE biplot into "north" or "south" regions as delineated by the ATC yielded better correlations between mean rank over those respective subsets of environments and maturity than did the grouping by geographical latitude along a line through the border of Arkansas and Louisiana. The negative correlation between the average rank across the subset of "north" environments above the ATC and maturity reflects the fact that the earlier maturing entries had a numerically lower rank (higher mean yield) in those environments. The GGE groupings identified X34 as having the best mean rank in the "north" and it identified X51 as the best in the "south". These results indicate that GGE was effective in conveying a biological understanding of the nature of the GxE in this cotton data set.

Figure 1. Average Tester Coordination view of GGE Biplot.



The Average Tester Coordination for entry evaluation

Table 1. Analysis of variance over environments.

Source	df	Mean Sq.	F-value
Total	1367		
Environment	23	3,766,305	141.31
Rep(Env)	48	26,653	
Genotype	18	171,329	3.35
GxE	414	51,192	3.67
Residual	864	13,948	

Table 2. Lint yield ranks of genotypes within each environment with the top 5 in green highlight and the bottom 5 in pink highlight.

	North Delta							North Coastal						South Delta				South Coastal						Avg.	
Name	60CR	70CR	6ALN	7ALN	7MCL	6MLL	7MLL	7VSF	7NCM	6NWS	7NWS	7SFL	6SEL	7SEL	6LCR	7LCR	6LBV	7LBV	7BSH	7GPL	6GCH	7GCH	6GC2	7GC2	Rank
DP444	3	11	15	4	12	19	4	12	19	18	19	4	18	10	19	17	19	-	13	16	19	18	19	17	14.1
DP555	15	5	12	15	17	4	7	6	11	1	2	17	2	15	1	9	1	-	15	4	2	8	10	1	7.8
PHY370	4	1	1	1	6	10	8	2	18	8	8	16	8	6	18	18	16	-	11	7	16	7	12	5	9.0
PHY485	5	8	14	5	19	9	10	3	16	3	17	14	11	19	13	12	12	-	16	13	12	11	3	18	11.4
X31	6	2	16	8	4	17	3	1	15	4	1	10	17	17	5	8	17	9	19	9	18	19	17	9	10.5
X32	1	19	3	14	14	11	6	13	17	14	5	18	19	3	6	19	5	5	18	11	17	17	5	16	11.5
X33	9	9	13	6	8	1	2	8	14	11	4	11	13	8	9	14	3	13	12	1	10	13	16	14	9.3
X34	2	4	4	3	1	2	1	11	9	16	11	19	14	14	8	7	7	11	10	3	13	9	1	6	7.8
X35	13	3	6	7	3	3	9	9	4	9	10	12	4	4	11	10	10	3	4	2	7	3	7	15	7.0
X41	12	16	17	9	2	8	15	5	8	15	18	9	9	7	3	5	8	2	9	5	14	5	11	13	9.4
X42	10	6	10	19	11	5	17	15	7	13	16	1	7	13	12	16	6	10	5	6	8	6	2	4	9.4
X43	16	10	9	12	13	13	5	16	3	19	14	6	16	16	17	3	15	6	3	10	6	16	4	2	10.4
X44	11	15	11	11	15	14	13	19	5	5	9	5	10	18	14	13	18	8	14	17	11	15	9	8	12.0
X45	8	13	8	10	7	12	12	18	10	10	15	7	12	12	10	15	14	12	17	18	4	4	6	12	11.1
X46	14	12	2	18	5	16	14	14	6	12	7	8	15	9	7	11	11	7	6	12	15	10	13	11	10.6
X51	18	14	5	2	10	7	16	4	2	2	12	15	1	1	2	1	13	14	2	8	1	1	8	10	7.0
X52	17	18	7	17	18	18	18	7	1	7	6	3	5	2	15	2	9	1	8	19	3	14	14	19	10.3
X53	19	17	18	13	16	6	19	10	13	17	3	2	3	11	4	4	2	4	1	15	9	12	15	3	9.8
X54	7	7	19	16	9	15	11	17	12	6	13	13	6	5	16	6	4	15	7	14	5	2	18	7	10.4

Table 3. Summary statistics and mean ranks across regions as grouped by latitude or by GGE Biplot

	Yield	Shukla's	% Open	GGE	E Distance	Map A	vg. Rk	GGE Avg. Rk			
Name	Avg.	Stability	Avg.	Mean	Instability	Maturity	North	South	North	South	
DP444	1089	111,935	81.6	0	25	64	12.0	17.4	11.5	16.2	
DP555	1276	142,070	66.6	82	6	32	9.2	5.7	8.7	7.2	
PHY370	1241	62,673	82.9	55	32	71	6.9	12.2	4.8	12.2	
PHY485	1202	66,084	78.8	39	10	48	10.9	12.2	10.3	12.3	
X31	1199	76,544	82.8	42	26	65	8.6	13.0	6.7	13.1	
X32	1170	51,396	85.8	37	21	60	11.2	11.9	9.7	12.8	
X33	1225	44,017	84.5	64	15	53	8.4	10.5	6.1	11.5	
X34	1247	52,994	80.2	80	28	66	7.9	7.5	4.2	10.3	
X35	1249	19,598	84.4	74	1	38	6.9	7.2	6.5	7.4	
X41	1230	30,697	79.3	58	7	31	10.7	7.5	10.7	8.4	
X42	1219	40,372	76.7	57	13	25	10.7	7.5	11.5	7.9	
X43	1180	36,604	82.7	44	6	32	12.0	8.2	11.8	9.4	
X44	1154	22,419	77.9	35	7	31	11.5	12.7	13.5	10.9	
X45	1173	25,149	77.8	45	1	38	11.0	11.2	12.1	10.4	
X46	1176	12,946	76.6	45	6	33	10.9	10.3	11.4	10.1	
X51	1264	62,028	75.5	79	24	14	7.8	6.0	9.6	5.2	
X52	1183	57,432	70.7	35	32	1	10.3	10.4	14.5	7.4	
X53	1185	83,613	74.7	54	38	0	11.9	6.9	13.6	7.1	
X54	1180	51,920	77.2	53	10	28	11.1	9.4	12.8	8.7	
Correlations				0.93	0.41	0.67	-0.17	0.41	-0.47	0.59	
				Yield	Shukla's	Shukla's% Open%					