

AN EVALUATION OF MODIFIED AUGMENTED DESIGNS FOR SINGLE-REPLICATION YIELD TESTING IN COTTON

D. S. Calhoun

Delta Research and Extension Center
Mississippi Agricultural and Forestry Experiment
Station
Stoneville, MS

Abstract

At early stages in cultivar development, genotypes are usually evaluated in a single replication because: 1) seed supplies are too limited, and 2) the number of genotypes to evaluate is too large to permit replicated evaluation. One method that has been proposed for conducting unreplicated tests is the Modified Augmented Design (MAD) which utilizes repeated check genotypes to measure and adjust for field variability and to estimate error variance. Use of MAD has not been reported in cotton (*Gossypium hirsutum* L.), and it is uncertain how effective the approach is in practice in removing the effects of field non-uniformity. Two types of experiments were conducted to evaluate the utility of MAD. Experiment 1 consisted of a MAD superimposed on a randomized complete block design (RCBD) at three Mississippi locations. This allowed the comparison, on a replicated basis, of unadjusted yields and yields adjusted by MAD. In uniform sites, MAD was not effective in reducing error or improving the ratio of genetic and error variances; in a non-uniform site, MAD was effective in this regard. Experiment 2 consisted of four large (360 to 540 entries) tests using MAD. Based on standard deviation of appropriate check plots, error variance was reduced in all four of these tests. The reduction in error variance was generally sufficient to justify the commitment of 10-20% of plots to checks.

Introduction

At early stages in cultivar development, genotypes are usually evaluated in a single replication because: 1) seed supplies are too limited, and 2) the number of genotypes to evaluate is too large to permit replicated evaluation. For convenience, material at this stage of cultivar development will be referred to as progeny rows. Many breeders rely exclusively on visual assessment to decide which progeny rows to harvest and carry forward for replicated yield testing; however, most cotton breeders are familiar with the difficulty of visually identifying the highest yielding genotypes in field trials. Many times, genotypes that appear to have the most cotton will, when harvested, be among the lowest yielding entries. Conversely, some genotypes that are not particularly "showy" will consistently be among the highest yielding entries.

An alternative to visual assessment would be to harvest all progeny rows, determine, at a minimum, seed cotton yields, and then make selections based on this objective yield assessment. There are two objections to this approach: 1) the perceived logistical difficulty of harvesting a large number of progeny rows, and 2) the possibility that field variability will mask any genetic differences. The question of logistics will be addressed first.

If only selected progeny rows are to be harvested, they normally must be harvested by hand. Usually, only quantities sufficient to supply seed for replicated tests the subsequent year (1 to 2 lb. of seed cotton) are harvested. If all progeny rows are to be harvested, they can be harvested mechanically and a sub-sample obtained for use as planting seed. Mechanical mixtures occur in seed from mechanical harvest, but the purity is considered adequate for yield assessment. Reserve seed can be used for pure seed increase of genotypes found to be promising after replicated testing. In our program, if 15 to 20% of progeny rows are to be harvested, fewer man-hours are spent in mechanically harvesting all plots rather than hand-harvesting enough seed for replicated testing from selected plots. If we plan to re-test approximately 10% of genotypes in progeny rows, we will harvest at least 20% and make further discards based on lint fraction and fiber quality.

The issue of field variability masking genetic differences will be the primary focus of this paper. One method that has been proposed to adjust for field non-uniformity is the Modified Augmented Design (MAD) (Lin and Poushiksky, 1985). This approach has been used in barley (*Hordeum vulgare* L.) (May et al., 1989) and soybean (*Glycine max* L. Merr.) (Lin and Voldeng, 1989).

The MAD utilizes a repeated check genotype to measure and adjust for field variability. The design is described in terms of a split-plot. Entries are arranged in whole-plots consisting of an odd number of sub-plots (usually 5, 7, 9, or 11), the central one of which is occupied by the repeated check genotype (termed the "central control plot" or "control plot"). Whole plots are arranged in any number of rows and columns to accommodate the desired number of test entries. For estimating sub-plot error, an arbitrary number of whole-plots are randomly chosen and additional check genotype(s) are assigned to random sub-plots. These additional checks are termed "control sub-plots". The statistical basis and calculations for MAD have been presented by Lin and Poushiksky (1983 and 1985). A SAS program for analyzing MAD is given by Scott and Milliken (1993). The analysis computes effects due to rows, columns, row x column interaction (i.e. whole plots), and sub-plot error. In addition, two adjusted values for test entries and control sub-plots are calculated. Method 1 adjustment is based on the assumption that row and column effects are additive and is recommended if rows and/or columns effects are significant. Method 3 adjustment is

based on a regression procedure and is recommended if the row x column interaction is significant.

Although MAD have been used in other crops, at least two questions remain, particularly with regard to its use in cotton. First, are the adjustments made using the MAD analysis effective in removing field variability and revealing true genetic differences? Second, if adjusted values are better than unadjusted values, are they enough better to justify investing the 10-20% of space required for check plots? The objective of this study was to answer these questions.

Material and Methods

Experiment 1. Twenty-five cultivars in the early maturing group of the 1995 Mississippi cotton cultivar trials (Calhoun et al., 1996) were planted in a randomized complete block design (RCBD) with 6 replications at three Mississippi locations (Tunica, Elizabeth, and Tribbett). Site descriptions and methods used for these trials are given by Calhoun et al. (1996).

A MAD was superimposed on the RCBD by inserting extra plots of 'DES 119' as central control plots. Whole plots for the MAD consisted of 9 sub-plots, the central one of which was DES 119. Three whole plots made up 1 row of the MAD (and 1 block of the RCBD). The entire MAD thus consisted of 6 rows and 3 columns. Plots of 'Deltapine 50' and 'Stoneville LA887' were used as control sub-plots in the MAD analysis. All plots not assigned to central control plots or control sub-plots (i.e. all entries other than DES 119, Deltapine 50, or Stoneville LA887) were assumed to be 132 non-replicated entries for the MAD analysis.

The MAD and RCBD analyses of seed cotton yields were performed using Agrobases 4.0 software (Mulltze, 1990). The seed cotton yields adjusted by Method 1 and Method 3 in the MAD analysis were stored and subjected to various analyses. Analysis of variance (ANOVA) for an RCBD was performed on the unadjusted values and values adjusted by Method 1 and Method 3 and results compared. All data from DES 119 were excluded from the RCBD analyses, since these values were not adjusted in the MAD analysis.

One desirable attribute of yield adjustments is that they move observed values closer to the "true" value for a given environment. It was assumed that the mean seed cotton yield at each location was the best estimate of the "true" value that should be obtained at that location. Simple correlation coefficients between individual plot measurements (adjusted and unadjusted) and mean values were therefore calculated.

Another desirable characteristic of a yield adjustment is that it removes a portion of the environmental variance, while preserving genetic variance. Broad-sense heritabilities were

calculated from variance estimates in ANOVA tables for unadjusted and adjusted yields.

Experiment 2. Yield trials using MAD were conducted at Stoneville, MS on a Bosket very fine sandy loam in 1995 and 1996. In 1995, two tests were conducted, each consisting of 60 whole plots (10 rows x 6 columns) each consisting of 9 sub-plots. 'Suregrow 125' was used in central control plots and DES 119 and Deltapine 50 were used in control sub-plots in 15 of the whole plots. Each MAD test in 1995, thus consisted of 540 total plots, with 60 (11%) devoted to central control plots and 30 (6%) devoted to control sub-plots. In 1996, MAD yield trials consisted of 40 whole plots each consisting of 9 subplots. 'Stoneville 474' was used in central control plots and Suregrow 125 and Deltapine 5415 were used in 8 control sub-plots in each test. Each MAD test in 1996, thus consisted of 360 total plots, with 40 (11%) devoted to central control plots and 16 (4%) devoted to control sub-plots. In both years, sub-plots were 1 row (40 in) x 40 ft. Plots were harvested by spindle picker and seed cotton yields calculated and analyzed using Agrobases 4.0 software for MAD analysis.

Results and Discussion

Experiment 1. The tests conducted at Tunica and Elizabeth were relatively uniform (CV < 10%), while the test at Tribbett was dramatically affected by soil heterogeneity (CV = 22.4%). The top soil at the Tribbett location is naturally thin and recent field leveling had removed most of the top soil from one corner of the test site. The wide divergence in soil type and field uniformity provided an excellent opportunity to evaluate adjustments made in the MAD analysis.

Results of the MAD analyses from tests conducted at Tunica, Elizabeth, and Tribbett are given in Table 1. The effect of rows was significant only at Elizabeth, the effect of columns was significant at Tunica and Tribbett, and the row x column interaction (whole-plot error) was significant only at Tribbett. At Tunica, adjustment Method 1 would be recommended based on ANOVA, and was confirmed by estimates of relative efficiency (RE). At Elizabeth, ANOVA indicated that Method 1 was the preferred adjustment, but RE was higher for Method 3; however, improvements in efficiency were relatively modest in both cases. At Tribbett, significant row x column interaction indicated Method 3 would be the preferred adjustment, but RE was higher for Method 1. The conflict between ANOVA and RE is fairly common in reports on the use of MAD in other crops.

In the analysis of MAD experiments with soybean, Lin and Voldeng (1989) found disagreement between ANOVA and RE in 18 of 33 cases. Working with barley, May et al. (1989) found disagreement between ANOVA and RE in 9 of 19 cases. In almost all cases in these two studies, RE of Method 3 was higher than Method 1. Lin and Voldeng

(1989) made the general recommendation to use ANOVA to decide whether or not data should be adjusted and to use RE to choose the adjustment method. They also suggested examining the effects of adjustments on control sub-plots. Adjusted and unadjusted control sub-plot values are presented in Table 2. Using these values, a second RE value (RE2) was calculated as the ratio of the standard deviations (SD) of unadjusted to SD of adjusted yield of control sub-plots, [i.e. $RE2 = (SD_{1U} + SD_{2U}) / (SD_{1A} + SD_{2A})$ where subscript numbers indicate control sub-plot genotype and subscript “U” indicates unadjusted values and subscript “A” indicates adjusted values]. Values for RE2 are presented in Table 1. Based on these values, no adjustment would be recommended for the Tunica location. At Elizabeth, Methods 1 and 3 gave moderate and similar reduction in sub-plot variability. At Tribbett, the reduction in sub-plot variability was dramatic using Method 3. Reduction in sub-plot variability by yield adjustment is assumed to mean that adjustments are removing environmental effects on yield.

We also examined the effect of adjustments by looking at changes in error variances when analyzed as an RCBD. The RCBD ANOVA tables and summary statistics for adjusted and unadjusted seed cotton yields from the three locations are presented in Table 3. At Tunica and Elizabeth, MAD adjustments were not successful in reducing CV or LSD or increasing R-square. In fact, at Tunica, Method 1 (indicated by MAD ANOVA and RE as the preferred adjustment) resulted in higher CV and LSD and lower R-square values compared to unadjusted yields. However, at Tribbett, the most variable test site, both adjustment methods reduced CV and LSD, compared to unadjusted yields, with the greatest improvement found using Method 3 (the method indicated as preferred by MAD ANOVA). Using unadjusted yields, block effects were significant at all locations. Using adjusted data, block effects were removed by Method 1 adjustments. In unreplicated tests, removing at least this source of variability would be beneficial in distinguishing among test entries. However, approaches other than MAD could be used to remove this effect (e.g. moving means, Mak et al., 1978).

Broad sense heritability [$H = \sigma_g^2 / (\sigma_g^2 + \sigma_e^2)$] estimates are also presented in Table 3. The highest H was observed at Tunica, the site with the lowest CV and highest R-square from unadjusted yield. Estimates of H from adjusted yields were similar to H from unadjusted yields at Tunica and Elizabeth. Only at Tribbett did there appear to be an improvement in H using adjusted yields.

In addition to a CV for the entire test, ANOVA also provides a CV value for each test entry. The average of these CV values for adjusted and unadjusted yields are presented in Table 3. These data support the view that adjustments at Tunica and Elizabeth were of little value in removing experimental error, but of great value in removing experimental error at Tribbett.

The mean unadjusted yield of an entry at a location was assumed to be the best estimate of the true yield of that entry at that location. Thus, a high correlation between individual plot yields (IPY) and the corresponding entry mean yields would indicate that IPY closely approximate true yield. Properly adjusted IPY should have a higher correlation with entry mean yield than should unadjusted IPY. Simple correlation coefficients among adjusted and unadjusted individual plot yields (IPY) and entry mean yields are presented in Table 4. In no case was the correlation of entry mean yield with adjusted IPY substantially higher than its correlation with unadjusted IPY. It should be noted that entry mean yield and unadjusted IPY were somewhat auto-correlated since unadjusted IPY made up 1 of 6 values used to calculate entry means. In addition it should be noted that entry means at Tribbett had large variances and may not represent the “true” values of genotypes at that location.

In summary, it appeared from this experiment that when conditions were fairly uniform, MAD adjustments did little to remove non-genetic variance other than to sometimes remove the effect of block. When test conditions were non-uniform, it appeared, based on test precision (CV and LSD) and estimates of H, that MAD adjustments would improve the chances of correctly distinguishing among genotypes in non-replicated tests. There was no evidence from correlation analyses that MAD adjustments brought IPY closer to entry mean yields.

Experiment 2. Table 5 gives the MAD ANOVA from non-replicated tests in 1995 and 1996. In all four cases, the row and/or column effects were significant and the row x column interaction was not, which would suggest Method 1 adjustments. In all cases, RE for Method 1, which ranged from 189 to 328%, were higher than for Method 3.

Past experience with the field where these tests were conducted has shown a distinct and consistent gradient that would be accounted for by rows and a less obvious gradient that would be accounted for by columns. In the test 96PR1, a distinct gradient that would be accounted for by columns was noted due to insect pest migration from an adjacent field. Therefore, ANOVA results are consistent with the known properties of the test site.

Examination of control sub-plot yields (adjusted and unadjusted) indicated that adjustments consistently reduced standard deviation of these yield values (Table 6). This would suggest that adjustments of unreplicated entries are also removing error components. In 3 of 4 cases, SD was reduced more by Method 3 than by Method 1.

Chandra (1994) has outlined some criteria for evaluating whether or not to use check plots (as is done in MAD) in unreplicated tests. The argument for not using check plots is based on the fact that in check-plot designs, a portion of available testing resources must be devoted to check plots

which reduces the number of available test entries and therefore reduces selection intensity. Chandra (1994) uses decision criteria based on several parameters: 1) $w_o = \sigma_o^2 / \sigma_g^2$, where σ_o^2 is the error variance of unadjusted values and σ_g^2 is the genetic variance of unadjusted values (i.e. a measure of field variability in relation to genetic variability); 2) σ_c^2 / σ_o^2 , where σ_c^2 is the error variance of adjusted values (i.e. a measure of the improvement obtained by use of checks), 3) f_c , the fraction of plots occupied by checks, and 4) k , the fraction of genotypes that will be selected from the population under evaluation. In Experiment 1, w_o can be estimated for each location from variance estimates in ANOVA of unadjusted values. Values for w_o ranged from 0.92 at Tunica to 3.5 at Tribbett. In Experiment 2, σ_c^2 / σ_o^2 can be estimated from the standard deviation of adjusted and unadjusted yields of control sub-plots. These values are given in Table 6. With 20% of plots occupied by checks ($f_c = 0.2$) and fairly uniform test sites ($w_o = 1.0$), the value of σ_c^2 / σ_o^2 must be < 0.76 to justify use of check plots (Chandra, 1994). With $f_c = 0.1$, the value of σ_c^2 / σ_o^2 must be < 0.89 to justify use of check plots in test sites with $w_o = 1.0$. In Experiment 2, approximately 15% of plots were occupied by checks and most estimates of σ_c^2 / σ_o^2 were near the critical point for uniform test sites. In less uniform sites (eg. $w_o = 2.0$), the critical values for σ_c^2 / σ_o^2 are 0.91 and 0.82 for $f_c = 0.1$ and $f_c = 0.2$, respectively.

Conclusions

Tests designed specifically to evaluate the utility of MAD (i.e. Experiment 1) indicated that when conditions are fairly uniform, adjustments to yield by MAD were not beneficial and could be harmful. When conditions were not uniform, as in the case at Tribbett, such adjustments could be very useful in removing field variability. These tests were relatively small (162 total plots for MAD analysis) compared to those where MAD would normally be used (in our case > 350 plots) and, except for Tribbett, test sites were in use largely because of their proven uniformity. In larger tests, such as those in Experiment 2, it is more difficult to control field variability by site selection. In these cases, MAD adjustments consistently reduced SD of control sub-plots and presumably accurately removed at least a portion of field variability effects from unreplicated entries.

Did MAD remove enough field variability effect to justify the use of checks? According to criteria established by Chandra (1994), the answer was in most cases, yes. There are other compelling reasons to include checks in unreplicated trials. Even when soil variability is known to be minimal, other conditions, such as non-uniform insect infestation, can occur to cause location-specific changes in yield. The use of check-plot designs such as MAD can detect and adjust for those changes.

The MAD did not prove to be a panacea for unreplicated testing. Yield adjustments did not always reduce error variance or improve heritability, particularly in the smaller

tests in Experiment 1; however, when tests were large, or sites were variable, MAD did appear to improve test precision. A more definitive evaluation of yield testing progeny rows (with or without MAD) would require a selection experiment wherein a large number progeny rows selected for both high and low yield and for high and low visual appeal were subsequently evaluated in replicated tests.

Using the Agrobases software, tests were relatively easy to set up and data were relatively easy to analyze. The interpretation of results is somewhat more difficult and may require separate examination of control sub-plot data.

References

- Calhoun, D.S., T.P. Wallace, J.R. Johnson, D.M. Ingram, G.L. Sciumbato, N.W. Buehring, W.S. Anthony, and B.W. White. 1996. 1995 Mississippi cotton variety trials. Miss. Agric. Forestry Exp. Stn. Info. Bull. 294.
- Chandra, S. 1994. Efficiency of check-plot designs in unreplicated field trials. *Theor. Appl. Genet.* 88:618-620.
- Lin, C.S., and G. Pouskinsky. 1983. A modified augmented design (type 2) for rectangular plots. *Can. J. Plant Sci.* 65:743-749.
- Lin, C.S., and G. Pouskinsky. 1983. A modified augmented design (type 2) for an early stage of plant selection including a large number of test lines without replication. *Biometrics* 39:553-561.
- Lin, C.S., and H.D. Voldeng. 1989. Efficiency of type 2 modified augmented designs in soybean variety trials. *Agron. J.* 81:512-517.
- Mak, C., B.L. Harvey, and J.D. Berdahl. 1978. An evaluation of control plots and moving means for error control in barley nurseries. *Crop Sci.* 18:870-873.
- May, K.W., G.C. Kozub, and G.B. Schaalje. 1989. Field evaluation of a modified augmented design (type 2) for screening barley lines. *Can. J. Plant Sci.* 69:9-15.
- Mulitze, D.K. 1990. AGROBASE/4: A microcomputer database management and analysis system for plant breeding and agronomy. *Agron. J.* 82:1016-1021.
- Scott, R.A., and G.A. Milliken. 1993. A SAS program for analyzing augmented randomized complete-block designs. *Crop Sci.* 33:865-867.

Table 1. Results from analysis of modified augmented designs superimposed on randomized complete block designs using the 1995 Early Maturing Cotton Variety Trials at 3 Mississippi locations (seed cotton yield, lbs/A).

Source	df	Tunica	Elizabeth	Tribbett
<u>Mean squares/1000</u>				
Rows (R)	5	35.94 NS	56.38 *	195.82 NS
Columns (C)	2	400.49 **	11.24 NS	1162.31 **
R x C	10	16.79 NS	14.56 NS	146.01 **
Sub-plot error	12	47.63	29.65	25.28
<u>Summary Statistics</u>				
Grand mean (lbs/A)		2600	3076	2137
R-squared (%)		99	97	97
C.V. (%)		5.0	3.9	17.9
RE (%)				
Method 1		172	120	421
Method 3		96	161	213
RE2 (%) ¹				
Method 1		75	140	139
Method 3		100	159	200

*, ** Significant F at P = 0.05 and 0.01, respectively; NS indicates not significant at P = 0.05.

¹RE2 = Ratio of standard deviation of unadjusted control sub-plot values divided by standard deviation of adjusted control sub-plot values.

Table 2. Comparison of adjusted and unadjusted seed cotton yields of control sub-plots in a modified augmented design analysis at three Mississippi locations in 1995.

Row	Col.	Deltapine 50			Stoneville LA887		
		Unadj.	M1 ¹	M3 ¹	Unadj.	M1	M3
-----lb/A-----							
<u>Tunica</u>							
1	3	3216	3111	3218	2425	2320	2427
2	2	2889	2813	2890	2425	2349	2426
3	2	2838	2767	2844	2304	2234	2310
4	1	3061	3284	3047	2390	2613	2377
5	3	2648	2483	2663	2691	2526	2705
6	1	2769	2963	2760	2442	2636	2433
Mean		2904	2904	2904	2446	2446	2446
SD		205	281	201	130	168	135
<u>Elizabeth</u>							
1	3	3597	3342	3210	3450	3194	3063
2	2	3270	3284	3224	2894	2908	2848
3	2	2862	2953	3131	2796	2887	3066
4	1	3270	3381	3451	2812	2923	2993
5	3	2804	2890	2889	3270	3356	3355
6	1	3344	3299	3289	3344	3299	3289
Mean		3191	3191	3199	3095	3095	3102
SD		303	213	186	293	213	189
<u>Tribbett</u>							
1	3	2273	2869	2335	1570	2166	1632
2	2	2060	2422	2241	2028	2389	2209
3	2	2534	2673	2544	1799	1937	1808
4	1	2976	2354	2392	2633	2010	2048
5	3	2175	2367	2131	1962	2155	1919
6	1	2616	1950	2375	2436	1770	2195
Mean		2439	2439	2336	2071	2071	1969
SD		338	313	140	397	214	227

¹M1 = Method 1; M3 = Method 3

Table 3. Analysis of variance of unadjusted seed cotton yields and seed cotton yields adjusted by Methods 1 and 3 from a modified augmented design superimposed on the 1995 Early Maturing Cotton Variety Trial at 3 Mississippi locations.

Source	Unadjusted	Method 1	Method 3
<u>Tunica</u>			
<u>Mean squares/1000</u>			
Entry	157.46**	261.09**	156.12**
Block	349.00**	62.90 NS	372.30**
Error	20.81	41.46	21.36
Grand mean (lbs/A)	2636	2635	2636
R-squared (%)	69	57	69
C.V. (%)	5.47	7.73	5.54
LSD (0.05)	138	195	140
H ¹	52.2	46.9	51.3
Avg. C.V. (%) ²	6.7	7.5	6.9
<u>Elizabeth</u>			
<u>Mean squares/1000</u>			
Entry	180.77**	198.29**	199.48**
Block	551.72**	113.35 NS	111.43 NS
Error	55.17	54.88	60.29
<u>Summary Statistics</u>			
Grand mean (lbs/A)	3001	3001	3000
R-squared	52	45	42
C.V. (%)	7.83	7.80	8.18
LSD (0.05)	225	224	235
H	27.5	30.3	27.8
Avg. C.V. (%)	8.6	7.3	7.8
<u>Tribbett</u>			
<u>Mean squares/1000</u>			
Entry	463.67 **	295.18 **	187.68
Block	1924.70 **	128.84 NS **	213.40
Error	169.62	87.21	49.61
<u>Summary Statistics</u>			
Grand mean (lbs/A)	2182	2183	2184
R-squared	50	42	48
C.V. (%)	18.88	13.53	10.20
LSD (0.05)	394	283	213
H	22.4	28.4	31.7
Avg. C.V. (%)	20.8	12.2	9.4

*** Significant F at P = 0.05 and 0.01, respectively; NS indicates not significant at P = 0.05.

¹H = $\sigma_g^2 / (\sigma_g^2 + \sigma_e^2)$

²Avg. C.V. is the average of CV values from individual test entries.

Table 4. Simple correlation coefficients from analysis of data from a modified augmented design superimposed on a RCBD of the 1995 Early Maturing Cotton Variety Test at 3 Mississippi locations.

	Adjustment method ¹					
	Individual Plot Yield (IPY)			Mean Plot Yield		
	None	M 1	M 3	None	M 1	M 3
<u>Tunica</u>						
M 1 (IPY)	0.61	--	--	--	--	--
M 3 (IPY)	1.00	0.58	--	--	--	--
None (Mean)	0.67	0.63	0.68	--	--	--
M 1 (Mean)	0.59	0.74	0.57	0.86	--	--
M 3 (Mean)	0.69	0.62	0.68	1.00	0.85	--
<u>Elizabeth</u>						
M 1 (IPY)	0.90	--	--	--	--	--
M 3 (IPY)	0.86	0.95	--	--	--	--
None (Mean)	0.56	0.63	0.61	--	--	--
M 1 (Mean)	0.56	0.63	0.61	1.00	--	--
M 3 (Mean)	0.55	0.62	0.62	0.98	0.98	--
<u>Tribbett</u>						
M 1 (IPY)	0.59	--	--	--	--	--
M 3 (IPY)	0.63	0.72	--	--	--	--
None (Mean)	0.52	0.52	0.49	--	--	--
M 1 (Mean)	0.43	0.62	0.54	0.83	--	--
M 3 (Mean)	0.41	0.54	0.63	0.78	0.87	--

¹ Adjustment methods include none (unadjusted), M 1 = Method 1, M 3 = Method 3.

Table 5. Analysis of variance from modified augmented design of 4 tests in Mississippi during 1995 and 1996.

Test	Mean squares/10,000				Relative efficiency (%)	
	Row	Col.	R x C	Sub-plot	M1	M3
95PR1	29.4**	47.1**	5.4 NS	3.6	237	172
95PR2	50.2**	15.9 NS	7.0 NS	4.4	205	188
96PR1	12.5 *	136.1 **	5.1 NS	4.2	328	206
96PR2	15.3 **	22.6 **	4.7 NS	3.3	189	141

*,** Significant F at P = 0.05 and 0.01, respectively; NS indicates not significant at P = 0.05.

Table 6. Standard deviation of yield from control sub-plots in four modified augmented design tests in Mississippi during 1995 and 1996. Values in parenthesis are the ratio of standard deviations of unadjusted to adjusted yields.

Test	Standard Deviation		
	Unadjusted	Adjustment Method 1	Adjustment Method 3
95PR1	305	272 (0.89)	246 (0.81)
95PR2	343	287 (0.84)	248 (0.72)
96PR1	371	301 (0.81)	238 (0.64)
96PR2	240	198 (0.82)	211 (0.87)