

COMPARISON OF LATTICE DESIGNS, CHECK PLOTS, AND MOVING MEANS IN WHEAT BREEDING TRIALS

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SUMMARY

Efficiencies of lattice designs, check plot designs, and moving means were compared in seven environments for control of error in wheat breeding trials. Lattice analyses of lattice designs and check plot covariance analyses of check plot designs gave similar CV's and intra-site heritabilities and were superior to direct RCBD analyses of these designs. Moving mean covariance analyses were generally only slightly less efficient than lattice analyses or check plot covariance analyses. Differences between designs and methods of analysis, which were evident on an intra-site basis, were not evident from combined analyses indicating that genotype \times environment interaction is much more important than intra-site error in limiting progress from selection. Moving mean covariance analyses with 2 replicates per location and as many locations as feasible is suggested as a useful strategy for early generation wheat breeding trials.

INTRODUCTION

Sound experimental design in plant breeding involves use of the principles of randomization, replication, and local control (FISHER, 1973; LE CLERG, 1966). Randomization allows an unbiased estimate to be made of error variance and the error variance of a variety mean is inversely proportional to the number of replications. Local control may involve restricting the random arrangement to either complete (whole replicate) and incomplete blocks (partial replicate) or the use of systematically placed controls.

Early generation wheat breeding trials are characterised by large numbers of entries and incomplete block designs, particularly lattice designs, have proved useful for local control of error (LE CLERG, 1966; YATES, 1936). Lattice designs, however, have certain disadvantages over complete block designs: (a) the number of treatments is restricted to a multiple of p^n , being the number of plots per block and $n \geq 2$; (b) the nature of the lattice design used restricts the field layout and different lattice designs have different field restrictions, and (c) the analysis is somewhat complex although not a problem for most modern computers. Check plot designs in which a systematic arrangement of checks are superimposed on a randomized complete block design have been proposed as an alternative method of error control in experiments with large numbers of treatments (LE CLERG, 1966). Plot values are generally adjusted for the values of adjacent check plots using covariance methods (MAK et al., 1978). Expressing plot values as a percentage or as a difference of adjacent check plots can lead to inappropriate adjust-

ment if a high correlation does not occur between check and test plots. The check plot method has the disadvantage of requiring many additional plots and WIANCKO et al. (1921) recommended the use of additional replication rather than check plots for error control. TOWNLEY-SMITH & HURD (1973) used a moving-average method in which the mean of a number of adjacent plots is used as a covariate for adjusting plot values, obviating the need to devote plots to checks.

MAK et al. (1978) found that a partially balanced square lattice design achieved superior error control to both check plots and moving means for grain yield and protein content of barley; check plots and moving means gave similar error control. They concluded that each of these designs would be useful in particular circumstances. SCHUTZ & COCKERHAM (1966) suggested that experimental design for control of intra-site error may be relatively unimportant if genotype \times environment interactions are large.

In this study I compared the efficiency of lattice designs, check plot covariates, and moving mean covariates to control intra-site error for several traits in wheat. The experiments involved were grown in seven environments to enable the importance of intra-site error to be compared with that of genotype \times environment interaction.

MATERIALS AND METHODS

Eighty one homozygous wheat lines from a range of crosses were grown in two experimental designs at seven locations in the agricultural areas of Western Australia. The two experimental designs used were a partially balanced 9×9 square lattice and a check plot design. The check plot design consisted of a randomized complete block in which a check plot of the cultivar Gamanya was planted between every three test plots. Each experiment was grown in four replicates and each replicate consisted of three ranges of plots with 27 test plots per range (the check plot design therefore had a total of 37 plots per range). Plots were spaced on 1.25 m centres, contained six rows sown 5 m long with a cone seeder, and were trimmed to 3 m before harvest.

Plant height (cm) was measured before harvest. Plots were harvested with a small plot combine harvester and grain yields recorded and converted to kg/ha. A test weight measurement (g) was taken by weighing the amount of clean grain in a 100 ml beaker. A seed weight measurement (g) was taken by counting 100 seeds at random from the plot.

The locations involved in this study were (1) Merredin, 1976; (2) Mount Barker, 1976; (3) Wongan Hills, 1976; (4) Badgingarra, 1977; (5) Esperance, 1977; (6) Merredin, 1977; and (7) Wongan Hills, 1977. The two experimental designs were grown adjacent to one another at each location.

A randomized complete block design (RCBD) analysis, with no covariates, was performed on each experiment at each location. In addition, lattice analyses were performed on the lattice designs and RCBD analyses with check plot covariates were performed on the check plot designs. Simple averages of performance of the two adjacent checks were used as covariates for the check plot designs. Moving mean covariates were constructed for both designs using means of the nearest eight test plots in the same range as a covariate for each plot. The moving mean covariates were used in a RCBD analysis for each design. Coefficients of variability (CV's) and variance

COMPARING EXPERIMENTAL DESIGN

Table 1. Means of four traits from two experimental designs in seven environments.

Site	Grain yield (kg/ha)		Height (cm)		Test weight (g)		Seed weight (g)	
	lattice	check plot	lattice	check plot	lattice	check plot	lattice	check plot
1	1107	968	57	54	85	82	3.75	3.67
2	1427	1357	104	104	78	74	2.84	2.97
3	2568	3109	95	96	85	88	3.69	3.72
4	2717	2664	95	93	83	83	3.41	3.52
5	1954	1789	86	83	84	79	3.26	3.12
6	728	877	55	58	87	88	3.32	3.28
7	763	827	57	60	86	83	3.07	3.02
Mean	1609	1656	79	78	84	82	3.33	3.35

component heritabilities on a location basis were determined for each analysis. Combined analyses across the seven locations were performed using means determined from each of the individual analyses. Variance component heritabilities were determined from the combined analyses and expressed on a location basis.

RESULTS AND DISCUSSION

At each site means for the lattice experiments and check plot experiments were similar for all traits (Table 1). Mean grain yields were normal for Western Australia, varying between 728 and 3109 kg/ha.

The highest CV's for each trait were obtained with the check plot experiments when analysed as a RCBD without covariates (Table 2). The check plot experiments had the largest block size and the disadvantage of increased block size can be ascertained by comparing CV's of the lattice experiments with RCBD analysis to those of the check plot experiments with RCBD analysis. Lattice analysis of the lattice experiments and check plot covariance analysis of the check plot experiments gave similar CV's for each trait and CV's were consistently lower than those for the respective RCBD analyses. Moving mean covariance analyses of the lattice and check plot experiments gave

Table 2. Coefficients of variation (%) for four traits from two experimental designs analysed by three methods (results are means for seven experiments).

Trait	Lattice			Check plot		
	RCBD	lattice	moving mean covariates	RCBD	check plot covariates	moving mean covariates
Grain yield	19.8	17.0	17.5	21.4	15.8	17.0
Plant height	6.0	5.9	5.8	6.3	5.6	5.8
Test weight	3.0	2.8	2.8	3.4	3.0	3.1
Seed weight	5.8	5.5	5.7	7.0	6.5	6.7

Table 3. Within location variance component heritabilities (%) for four traits from two experimental designs analysed by three methods (results are means for seven experiments).

Trait	Lattice			Check plot		
	RCBD	lattice	moving mean covariates	RCBD	check plot covariates	moving mean covariates
Grain yield	74	80	79	70	80	77
Plant height	75	76	75	70	75	73
Test weight	64	68	66	63	67	66
Seed weight	86	88	86	74	81	80

similar or slightly higher CV's than lattice and check plot covariance analyses, respectively.

Within location variance component heritabilities (Table 3) reflected the general pattern obtained with CV's. Highest heritabilities were obtained from the lattice experiments with lattice analyses and check plot experiments with check plot covariance analysis, and lowest heritabilities were obtained with the check plot experiments with RCBD analysis. Moving mean covariance analysis of the lattice and check plot experiments gave similar or slightly lower heritabilities to the lattice and check plot covariance analyses, respectively.

Variance component heritabilities determined from a combined analysis of the lattice and check plot experiments showed little consistency (Table 4); the lattice experiments showed higher heritabilities for grain yield, test weight, and seed weight, but the check plot experiments showed the highest heritability for plant height. The advantage the lattice experiments showed for these traits cannot be attributed to the lattice arrangement; combined site heritabilities for lattice analyses and moving mean covariance analyses were only marginally better than those for RCBD analyses of the lattice experiments. Similarly check plot covariates and moving mean covariates made little difference to the heritabilities of traits in the check plot experiments. The gross differences in heritabilities between the lattice and check plot experiments is probably due to differences in the amount of genotype \times environment interaction which occurred for these two sets of experiments. That differences of this magnitude should occur

Table 4. Single location variance component heritabilities (%) for four traits determined from a combined analysis over the seven locations for the two experimental designs analysed by three methods.

Trait	Lattice			Check plot		
	RCBD	lattice	moving mean covariates	RCBD	check plot covariates	moving mean covariates
Grain yield	28	30	30	23	24	23
Plant height	26	27	28	32	31	31
Test weight	33	34	34	30	31	31
Seed weight	55	55	56	47	48	47

between experiments grown adjacent to one another is surprising but consistent with the high genotype \times environment interactions which occurred among the seven sites (compare heritabilities in Table 3 with those in Table 4).

The results suggest that the lattice design is the most efficient for control of intra-site error. However, the difference between a lattice design and a randomized complete block design with moving mean covariates was marginal. Use of RCBD's with moving mean covariates has advantages over lattice designs in that the number of treatments is not restricted to a multiple of p^n and it is easier to standardize field layouts for experiments with different numbers of treatments. Check plot designs appear to have no advantage over moving mean techniques, particularly if it is considered that the plots which were planted to checks could have been used for additional replication. In this study approximately 1/4 of the plots in the check plot design were devoted to controls so that three replicates of a check plot design would have approximately the same number of plots as four replicates of a design without check plots. Results from this study indicate that four replicates of a randomized complete block design with moving mean covariates is more efficient than three replicates of a check plot design. Check plot designs, however, would be useful for error control in situations where entries are discarded before harvest.

It would appear that intra-site error variance is relatively unimportant in comparison to genotype \times environment interaction variance because differences between designs which were evident on an intra-site basis were not evident from combined site analyses. This suggests that replication over environments is a more effective way of increasing progress from selection than intra-site replication. A useful strategy for early generation wheat breeding trials where entry numbers are likely to be large may be the use of moving mean analyses on RCBD's with as many locations as feasible and with only two replicates per location. A minimum of two replicates would be required to adjust data by covariance analyses on an intra-site basis and to provide an estimate of intra-site error.

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