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Assessment of suitable designs for field experiments involving airborne diseases

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SUMMARY

The suitability was assessed of various designs for field experiments investigating plant diseases caused by airborne pathogens that can be subject to interplot interference. Use of a model to describe such interference showed that the treatments with the most dissimilar effects on controlling the disease should be allocated to experimental plots furthest apart in each block, in order to minimize the interplot interference within a block. When using large square plots, rectangular blocks were more efficient than square blocks in minimizing treatment-comparison biases due to interference between neighbours. For rectangular blocks with the square plots side by side, less biased treatment comparisons were obtained from designs with complete blocks than from designs with incomplete blocks, especially when larger numbers of treatments were included in the experiment. However, when interplot variance is taken into account, incomplete blocks may give better treatment comparisons. Similarly, unbalanced designs composed only of incomplete blocks that yield less biased treatment comparisons may be better than balanced incomplete block designs when interplot variance is low. For high levels of variation, balanced incomplete block designs may be more appropriate, as increasing the precision of the treatment comparisons becomes more important than reducing the bias.

INTRODUCTION

The problem of correlated observations between adjacent plots resulting from interplot interference has been approached either by using special data analysis techniques or by constructing experimental designs that minimize the interference from neighbouring plots. Some recent field experiments conducted at Horticulture Research International (HRI) to study airborne transmitted fungal diseases have used square blocks, each consisting of four large square plots. This seemed appropriate when studying fungal diseases, as their pattern of spread is usually around the foci of infection, which in the experiments at HRI were the plot centres. In these experiments, the plots are kept free of disease until a certain time when the centre of each plot is inoculated with the specific disease. Large square plots mean that plot boundaries are kept at a reasonable distance from the foci of infection. Van der Plank (1963, Chapter 23) concluded that square plots were safer than rectangular plots when considering interference. By using small blocks of large plots it is possible to ensure that each plot is subject to infection from only a few sources and that these sources are not too close together. The objective of the work described in this paper was to assess these designs and find out whether and how they could be improved.

HRI does work on several diseases and on several vegetable species. The treatments of current interest are either spraying regimes or cultivars with different levels of resistance, the overall objective being to control diseases with minimal amounts of fungicide. Interplot interference may occur because of localized spread of disease, although the effect of movement of inoculum between plots is kept to a minimum by the use of large guard areas. The interference is likely to be uneven because plots in which sprays are not used or are ineffective, or plots containing susceptible cultivars, may exert more disease pressure on neighbouring plots than plots with effective treatments do. The treatments are such that the scientists have some prior knowledge of how effective they are and certainly which are likely to be the most effective and which the least effective.

The disease may appear in patches because of the

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way in which fungal spores move from plot to plot due to variation in dispersal conditions. There is no reason to believe that, in general, there will be a directional effect of the wind, since the strongest winds are often in stormy weather when the wind swirls around. In particular, it would be very risky to plan an experiment assuming that interference will be mainly in the direction of the prevailing wind. We will assume that disease from a particular source is equally likely to spread in any direction. According to Ainsley *et al*. (1995) this is the simplest form of interference.

Ainsley *et al*. (1995) and Azaïs *et al*. (1995) showed that randomization on its own and nearest-neighbour analyses are often ineffective when tackling interplot interference and showed how these methods could lead to very biased estimates of treatment effects. For further discussion of the problems of interference see Ainsley *et al*. (1995), Jenkyn *et al*. (1996) and the references contained in these papers. Besag & Kempton (1986) presented a thorough summary of nearest-neighbour analysis and related techniques. As these techniques do not solve the problem of interplot interference, experiments should be designed to ensure that such interference is minimized. Van der Plank (1963, Chapter 23) advised experimenters to avoid having treatments with very different effects in neighbouring plots. David & Kempton (1996) and David *et al*. (1996) proposed the use of prior information on the relative magnitudes of treatment effects in order to control interplot interference due to competition in variety trials. This should be done by ensuring that treatments in neighbouring plots are similar, so that interplot interference can safely be ignored in the subsequent analysis.

In this paper we show how this general advice can be most usefully applied to experiments of the type performed at HRI, using small blocks, either square or rectangular, of large square plots which are inoculated at their centres. The designs are applicable to a wide range of diseases and plant species. Semi-systematic designs with a small number of replicates of between four and eight treatments were studied. By studying situations involving several ranges of treatment effectiveness and degrees of airborne mobility to represent the way in which different diseases may affect crops, designs were sought that estimated treatment differences with low bias, but acceptable precision.

METHODS

A model for interplot interference

A treatment that successfully controls a disease will reduce the probability of inoculum production and this in turn will reduce the probability of disease dispersal and hence disease development. The responses measured from field experiments are usually the proportion of infected plants in a plot and the number of lesions per plant in a plot. When treatments are close together in a field experiment, the observed proportion of infected plants in a particular plot may be the result both of the treatment applied to that plot and of the interference from the neighbouring plots. The amount of interference may follow any number of different patterns, but we decided to compare designs by using one particular model for interference. This model accounts only for within-block interference as we are assuming that the blocks are kept far enough apart to minimize interblock interference so that it can be safely ignored.

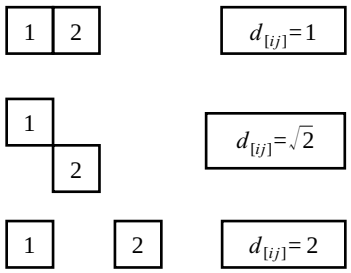

Fig. 1. Values of the distance, $d_{[ij]}$, for three possible allocations of treatments labelled 1 and 2.

We assume that the response observed in each plot is the proportion of plants infected (or some similar proportion). Let $p^*_{[i]}$ be the expected proportion of infected plants observed in plot i, given that plot i is subject to interference. Let $p_{[i]}$ be the expected proportion of infected plants in plot i if plot i were free from interference from neighbouring plots. Then our model for the expected proportion of infected plants observed is

$$p^*_{[i]} = p_{[i]} \prod_{j \neq i} \left(\frac{p_{[j]}}{p_{[i]}} \right)^{\eta(d_{[ij]})}.$$

The ratio $p_{[j]}/p_{[i]}$ increases the expected proportion, $p^*_{[i]}$, infected in plot i, if a less effective treatment is applied to plot j, as $p_{[j]} > p_{[i]}$. The effect is reversed when a better treatment is applied to plot j. Use of $p^*_{[j]}/p_{[i]}$ would be more logical, but we would then have to use simulations to compare different designs. The formula used gives similar results and allows direct calculations to be performed.

The neighbour exponent function, $\eta(d_{[ij]})$, depends on $d_{[ij]}$, the distance between the centres of plot i and plot j relative to the shortest distance between any two plot centres, so that $d_{[ij]} \geqslant 1$. Figure 1 illustrates different values of $d_{[ij]}$ according to three different allocations of two treatments labelled 1 and 2.

If treatments 1 and 2 are applied to adjoining square plots, $d_{[ij]}$ will take its lowest value of 1. If they are applied to diagonally neighbouring plots, $d_{[ij]} = \sqrt{2}$, and if they have a third plot in between, $d_{[ij]} = 2$. The exponent $\eta(d_{[ij]})$ determines the magnitude of the

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increase or decrease to $p_{[i]}$, due to the treatment applied to the neighbouring plot j. It depends on the distance between plot centres and on the degree of airborne mobility of the disease, i.e. how far the spores typically travel in a given time. The ratios $(p_{[j]}/p_{[i]})^{\eta(d_{[ij]})}$ for every plot in the same block as plot i are then multiplied together to determine the adjustment to $p_{[i]}$ to allow for interference.

In theory the model used allows proportions of infected plants > 1. However, in practice, when the plots show near 100% infection, treatment comparisons are based on other variables such as the number of lesions. Therefore this is one reasonably plausible model of interference, although of course there are many others. We would expect that the pattern of results we report will be similar for other models of interference; our method of comparing designs can be applied for any such model.

We studied different levels of airborne mobility of the disease including the extreme cases:

1. Under low levels of airborne mobility, treatments applied to plots would affect only their nearest neighbours. Thus,

$$\eta(d_{[ij]}) = c, \quad \text{for } d_{[ij]} = 1$$
$$\eta(d_{[ij]}) = 0, \quad \text{for } d_{[ij]} > 1$$

2. Under high levels of airborne mobility, treatments applied to a plot affect other plots in the same block in the same way, regardless of the distance between their centres. Thus,

$$\eta(d_{[ij]}) = c, \quad \text{for all values of } d_{[ij]}$$

This was studied as an extreme case, even though in reality such a situation is difficult to envisage, except for very small blocks.

In this paper we present the results from using an intermediate level of airborne mobility, where the amount of interference is reduced as the distance between plot centres increases. Thus,

$$\eta(d_{[ij]}) = c^{d[ij]}, \quad \text{for all values of } d_{[ij]}$$

The constant c is an arbitrary value that balances (i) the decrease in potential infection caused by neighbouring more effective treatments with (ii) the increase due to neighbouring less effective treatments. A value of $c = 0{\cdot}025$ was found to give a plausible description of the neighbour interference on the treatment effects in the experiments described in the Introduction.

Appropriate values of treatment effects when no interplot interference is present were established from previous experimentation. Various patterns of treatment effectiveness were considered and the conclusions were consistent over all patterns studied. The results presented in this paper correspond to a wide range of treatments, from 1% to 90% of infected plants, and an intermediate degree of airborne mobility of the disease.

Assessment of properties of the designs

A good design has to be both efficient and valid. Efficiency is measured by the variances of the estimated treatment differences which depend on the design and the within-block variation, which is estimated by the residual mean square. High within-block variation will lead to high standard errors of the treatment comparisons and imprecise estimation of treatment effects. Validity is concerned with the expected closeness of the estimated treatment effects to the true treatment effects and is measured by the bias of the estimated treatment differences.

A measure of how close the estimated treatment differences are to the true treatment differences is the Mean Square Error (M.S.E.) which is given by

$$\text{M.S.E.} = \text{bias}^2 + \text{variance}$$

where both bias and variance are of the estimated treatment differences. Low values of M.S.E. will indicate good designs. Thus, the bias and standard error of each treatment comparison are the key measures in the assessment of the designs. Ainsley *et al.* (1995) considered only bias, but here it is particularly important to look at the within-experiment variance because the plots are large, in order to reduce the effect of interference, and therefore the total replication is low and the within-block variance may be quite high. This is unlike the usual small plots which allow more replication and are chosen to minimize within-block variance.

The proportion, p, of infected plants, which is often the variable of interest in phytopathology studies, was used as a basis for comparing designs. Because such a response is usually transformed before analysis of the data, a logit transformation, $\log_e [p^*/(1-p^*)]$, was chosen in this study to calculate the biases for each treatment comparison in every design.

Estimates of the differences between the logits for particular pairs of treatments have different biases if the treatments are allocated in different relative positions in various blocks. Thus, the bias obtained from a particular design is the average bias over all the blocks in which this pair of treatments appears. Therefore, for example, in a design comprising six complete blocks where treatments labelled 1 and 2 vary in their neighbour positions, each apparent treatment effect will have six different values according to the treatments allocated to the neighbouring plots. The apparent treatment effect to look at will be the difference in the averages of the respective six values. The bias of the estimated difference between treatments 1 and 2 will be

$$\left\{\frac{1}{6}\prod_{k=1}^{6} \text{logit}\,(p^*_{1k}) - \frac{1}{6}\prod_{k=1}^{6} \text{logit}\,(p^*_{2k})\right\} - \{\text{logit}\,(p_1) - \text{logit}\,(p_2)\}$$

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where k indicates the block from which the apparent proportion of infected plants from the treatments is obtained; p_1 and p_2 are the expected proportions of infected plants from treatments 1 and 2 assuming no interplot interference; and p^*_{1k} and p^*_{2k} are the expected proportions of infected plants from treatments 1 and 2 in the presence of interplot interference in block k.

Different neighbour positions for pairs of treatments in designs with complete blocks do not affect the design matrix from which the standard error of the treatment comparison is obtained. However, the within-block variation may vary in blocks of different shapes and sizes and this will affect the precision of the estimated treatment comparisons.

The results in the next section compare blocks of different shapes and sizes for square plots; with one exception, only square and rectangular blocks are considered. As stated in the Introduction, square plots have been recommended for experiments on plant pathogens and are used at HRI. The same method could be used to compare blocks of plots of other shapes, such as long, narrow, rectangular plots. Calculations based on designs with complete blocks of four plots established the principles for minimizing biases. Biases from comparisons amongst treatments allocated in all possible relative neighbour positions into square and rectangular blocks were obtained. For simplicity, the within-block variance was assumed to be the same regardless of the block shape. Studies of more complex designs, comprising a larger number of treatments, were primarily concerned with offsetting bias against variability.

For more than four treatments, designs with complete blocks of several shapes were compared with incomplete balanced or near balanced designs and with designs where treatments were allocated only in the optimal relative neighbour positions for minimizing biases.

RESULTS

Throughout this section, treatments will be labelled 1, 2, … in order of effectiveness, where treatment 1 is the least effective.

Designs for four treatments – principles for minimizing bias

The square block that was found to have the least biased treatment comparisons was the one that allocates treatments ranked 1–4 in the following neighbour positions:

1 2
3 4

Such a block can be randomized in eight different ways by interchanging diagonally adjacent treatments and rotating through 90°.

The rectangular block with the least biased treatment comparisons was:

1 2 3 4

The only alternative arrangement for maintaining neighbour structure under randomization is:

4 3 2 1

The preliminary investigation that looked at four treatments, with $\eta(d_{[ij]}) = 0{\cdot}025^{d[ij]}$ and $p_1 = 0{\cdot}90$, $p_2 = 0{\cdot}50$, $p_3 = 0{\cdot}10$ and $p_4 = 0{\cdot}01$, allocated to complete blocks, established the following principles for minimizing biases:

1. Designs in which extreme treatments are allocated to more distant plots give the lowest biases in the estimation of treatment comparisons. For instance, block 1 2 3 4 had a mean squared bias of 0·015 and block 2 3 4 1 had a mean squared bias of 0·357.
2. Less biased treatment comparisons are obtained from rectangular blocks than from square blocks when the experimenter is certain of the order of the treatments. The least squared bias from a square block was 0·281 against 0·015 for the rectangle with least bias.
3. The magnitude of the biases increases as the level of airborne mobility increases and the interplot interference becomes less controllable.
4. When treatments with similar effects are considered in the same experiment, less biased treatment comparisons are obtained than when considering a wide range of treatments.
5. Combinations of block types with lower biases are advantageous over neighbour balanced designs and over completely randomized designs.

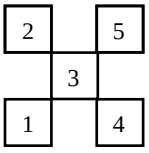
Designs for five treatments

Complete blocks

Two block shapes were investigated, rectangular and star-shaped. The optimal rectangular block in minimizing bias was the one that allocates treatments in a ranked manner, in agreement with results for four treatments:

1 2 3 4 5 or 5 4 3 2 1 (C1)

The star-shaped block that showed the lowest biases was



(C2)

This block allocates intermediate treatments 2, 3 and 4, in rank order, to plots forming one of the diagonals and extreme treatments 1 and 5 to the remaining

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Table 1. *Values of I_i for a wide range of five treatments. I_i is the percentage increase in σ^2 for the design with C2 blocks, over the design in the Table, which would give the same* M.S.E. *from both designs*

Design	σ^2 in designs in Table		
	1	0·1	0·01
C1 blocks	0·3	3·0	30·0
Balanced rectangle	7·8	24·2	188·0
Unbalanced rectangle	28·5	33·0	78·0
Balanced square	41·1	417·4	4120·0
Unbalanced square	51·8	265·6	2404·0

plots. Randomization can be achieved by interchanging pairs of diagonally opposite treatments and treatments within pairs in the non-central plots. This leads to eight different layouts for the same block type.

Incomplete blocks

The optimal neighbour arrangements for all possible incomplete blocks of size four in square and rectangular shapes are shown in Fig. 2.

The designs that were assessed were those comprising four blocks of type C1, four C2 blocks and five blocks in either of these groupings:

1. I1, I2, I3, I4, I5. (Balanced design)
2. I1, I1, I2, I2, I2. (Unbalanced design).

Under the assumption that designs have the same within-block variation, regardless of the shape, the design with lowest M.S.E. was the one comprising blocks of type C2. This was the design with lowest mean squared biases and lowest mean variance of the treatment comparisons.

However, more realistically, when blocks cover a larger area they are expected to show a higher within-block variation. Therefore, the design with C2 blocks was used as a baseline design in order to calculate the minimum increase of within-block variance acceptable without increasing its M.S.E. to that of the other designs. This measure, denoted I_i, is the minimum percentage of increase in within-block variance required when using the design with C2 blocks to get a M.S.E. as large as any design with smaller blocks.

Low values of I_i are likely to occur in experimental conditions when the block area is increased. Hence, designs with smaller blocks, i.e. covering less area, would represent a better option than designs with bigger blocks when I_i is small.

Table 1 shows results for three levels of σ^2, the within block variance, for the designs with smaller blocks. In this case, $\eta(d_{[ij]}) = 0{\cdot}025^{d[ij]}$ and $p_1 = 0{\cdot}90$, $p_2 = 0{\cdot}62$, $p_3 = 0{\cdot}23$, $p_4 = 0{\cdot}05$ and $p_5 = 0{\cdot}01$.

Table 1 shows that a design with C2 blocks and $\sigma^2 \leqslant 1{\cdot}003$ will have a M.S.E. not greater than that of a design with C1 blocks and $\sigma^2 = 1$. As the bigger C2 blocks are likely to have larger σ^2 values than the C1s, designs with complete rectangular blocks are a better option than star-shaped blocks when the within-block variance is expected to be near 1 in the designs with smaller blocks.

Designs of the same size can also be compared against each other by subtracting their I_i values. For instance, when comparing balanced designs with square blocks and balanced designs with rectangular blocks for $\sigma^2 = 1$, the within-block variation of the rectangular blocks would have to be increased by $41{\cdot}1 - 7{\cdot}8 = 33{\cdot}3\,\%$ in order to get the same M.S.E. as the design with square blocks. This is a rather high value, unlikely to occur, so in general the rectangular blocks would give treatment comparisons with lower M.S.E. than square blocks of the same size.

As the within-block variance, σ^2, decreases, the difference between balanced and unbalanced designs with blocks of the same shape is less evident and unbalanced designs comprising blocks which minimize biases may eventually become a better option than balanced designs. To illustrate this, compare across the rows containing results for Balanced rectangle and Unbalanced rectangle in Table 1. The advantage of using unbalanced designs with blocks that minimize biases becomes evident as the value of σ^2 is reduced, because the bias then becomes more important than the variance when calculating the M.S.E. values.

Designs for six treatments

Complete blocks

Two designs with complete blocks were assessed, rectangular blocks of six consecutive plots on a 1×6 array and rectangular blocks of 2×3 plots. The behaviour of these 2×3 plots is considered to be

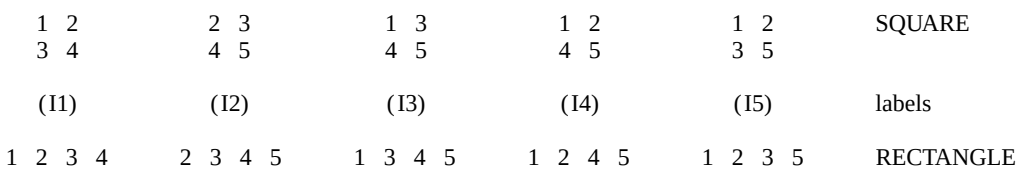

Fig. 2. Optimal neighbour arrangements for incomplete blocks.

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Table 2. *Values of I_i for a wide range of six treatments. I_i is the percentage increase in σ^2 for the design with 1×6 blocks, over the design in the Table, which would give the same* M.S.E. *from both designs*

Design	σ^2 in designs within Table 1	0·1	0·01
2×3	11·0	109·8	1089·0
RECTANGLE			
Near-balanced	13·7	29·4	186·0
Unbalanced	46·1	47·7	60·0
SQUARE			
Near-balanced	36·2	254·4	2436·0
Unbalanced	57·0	156·4	1150·0

equivalent to their corresponding 90° rotations of 3×2 rectangles. The 2×3 layout which minimizes bias is

1 3 5
2 4 6

In this layout, similar treatments are allocated to plots that are as close as they can be. This result is consistent with results for designs with four and five treatments, for which the block types with lower biases were the ones where treatments with similar effects were allocated to closer plots. The optimal 1×6 rectangular block was

1 2 3 4 5 6 or 6 5 4 3 2 1

Incomplete blocks

Near-balanced and unbalanced designs with bias-minimizing blocks of size four were assessed for both square and rectangular shapes. Only the optimal designs with square blocks are presented (Fig. 3), but rectangles can easily be constructed.

The design that showed the lowest M.S.E. is the one with complete 1×6 blocks and this was therefore used as a baseline design. Table 2 shows the values of I_i required in order to make any of the designs as good as the optimal design with 1×6 blocks for $p_1 = 0{\cdot}90$, $p_2 = 0{\cdot}70$, $p_3 = 0{\cdot}37$, $p_4 = 0{\cdot}13$, $p_5 = 0{\cdot}04$ and $p_6 = 0{\cdot}01$.

The design comprising 2×3 blocks appears far from being a better option than the one formed by 1×6 blocks as the required increase in within-block variance is high. For example, if the 2×3 blocks gave a residual mean square of 0·1, the 1×6 blocks would still be as good if they gave a residual mean square of 0·2. The design with 2×3 blocks may be appropriate to more heterogeneous experimental conditions, bearing in mind that the reduction in variance has to be big enough to compensate for the more biased treatment comparisons. An increase to 1·110 for the within-block variance for 1×6 blocks would be needed when the residual mean square for 2×3 blocks is 1.

Unbalanced designs comprising blocks expected to give less biased treatment comparisons are better than near-balanced designs for residual mean squares of 0·01. As for five treatments, this is due to the increase in relative importance of the bias with respect to the variance when the experimental conditions are more homogeneous. On the other hand, near-balanced designs are better when the within-block variance is 1 or 0·1.

Table 3. *Resolvable designs for seven treatments. Each design has four replicates each comprising two rectangular incomplete blocks of three and four plots respectively*

Design number	Block	Blocks with four plots	Block	Blocks with three plots
1	I	1 2 3 4	V	5 6 7
	II	1 2 3 4	VI	5 6 7
	III	4 5 6 7	VII	1 2 3
	IV	4 5 6 7	VIII	1 2 3
2	I	1 2 3 4	V	5 6 7
	II	4 5 6 7	VI	1 2 3
	III	2 5 6 7	VII	1 3 4
	IV	2 3 6 7	VIII	1 4 5
3	I	1 2 3 4	V	5 6 7
	II	4 5 6 7	VI	1 2 3
	III	2 5 6 7	VII	1 3 4
	IV	1 4 5 6	VIII	2 3 7
4	I	1 2 3 4	V	5 6 7
	II	4 5 6 7	VI	1 2 3
	III	1 3 4 5	VII	2 6 7
	IV	1 4 5 6	VIII	2 3 7

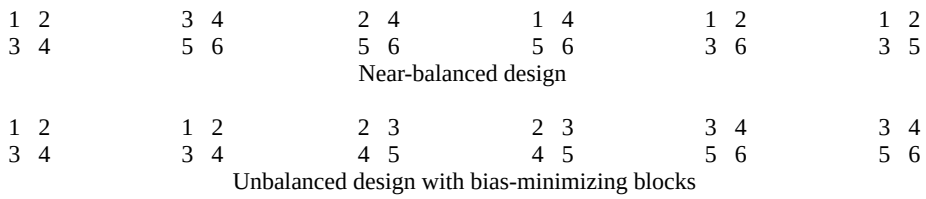

Fig. 3. Optimal near-balanced and unbalanced designs with incomplete square blocks.

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Table 4. *Designs for seven treatments. Each design is made up of incomplete rectangular blocks of four plots*

Design number	Layout of the Designs									
	Block					Block				
1	I	1	2	3	4	V	2	3	4	5
Unbalanced	II	2	3	4	5	VI	3	4	5	6
(least biased)	III	3	4	5	6	VII	4	5	6	7
	IV	4	5	6	7					
2	I	1	2	3	4	V	2	3	4	5
Compromise	II	3	4	5	6	VI	4	5	6	7
	III	1	2	3	5	VII	3	4	5	7
	IV	1	2	4	7					
3	I	1	2	3	4	V	1	3	5	6
Balanced	II	1	2	5	7	VI	1	4	6	7
(least variance)	III	2	3	6	7	VII	2	4	5	6
	IV	3	4	5	7					

Designs for seven treatments

Only designs with rectangular blocks were considered. The optimal complete block design is the one comprising rectangular blocks with treatments allocated in increasing or decreasing order according to their effects. Four complete blocks of seven plots in a 1×7 optimum array were considered,

1 2 3 4 5 6 7 or 7 6 5 4 3 2 1

Four resolvable incomplete block designs, each consisting of four pairs of blocks of size three and four, were assessed (see Table 3). A resolvable design is one in which groups (in this case pairs) of blocks contain complete sets of the treatments. The assumption behind these designs is that the within-block variance is the same for both sizes of block, but the possibility of increased variability for bigger blocks should be borne in mind. Design 1 comprises only blocks with consecutive treatments, which makes it the most unbalanced. The other three designs in Table 3 include also blocks with other pairs of treatments to improve the balance of the design.

Designs with seven incomplete blocks, all of size four, were also considered (see Table 4). Design 1 of Table 4 is an unbalanced design with blocks that achieve less biased treatment comparisons, where the three blocks with more effective treatments are repeated. Design 2 of Table 4 is a compromise design between balance and bias, formed by four blocks with lowest biases and three more that improve the balance. Design 3 of Table 4 is a balanced incomplete block design where the starting block in its construction was a block already known to have low bias, 1 2 3 4.

The baseline design for the construction of Table 5 was the one with complete rectangular blocks, 1×7. Here $p_1 = 0{\cdot}90$, $p_2 = 0{\cdot}74$, $p_3 = 0{\cdot}48$, $p_4 = 0{\cdot}23$, $p_5 = 0{\cdot}09$, $p_6 = 0{\cdot}03$ and $p_7 = 0{\cdot}01$. The values in Table 5 show that the lowest percentage of increase in within-block variance required for preferring compact blocks to blocks of size seven is $> 15\%$. The optimum design with incomplete blocks will vary according to the within block variance of small blocks.

Table 5. *Values of I_i for a wide range of seven treatments. I_i is the percentage increase in σ^2 for the design with 1×7 blocks, over the design in the Table, which would give the same* M.S.E. *from both designs*

Designs with blocks of	σ^2 in designs in Table		
	1	0·1	0·01
UNEQUAL SIZE			
Design 1	120·0	120·1	121·2
Design 2	33·2	44·3	155·2
Design 3	33·4	45·5	167·2
Design 4	29·6	43·7	185·2
EQUAL SIZE			
Design 1	88·1	89·1	99·2
Design 2	36·4	39·7	73·2
Design 3	15·7	30·9	183·2

For values of residual mean square of 1 or 0·1, the precision of a treatment comparison is a more important issue than its bias. Therefore, balanced or near-balanced designs should be used if the experimenter expects to get values of residual variation within this range.

When the experimental conditions are more homogeneous, with values of residual mean square of 0·01 or less, the biases of the treatment comparisons are more important than their variances, so unbalanced designs comprising blocks that lead to lower biases should be preferred. Amongst designs with incomplete

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blocks of equal size, the most unbalanced design 1 is not better than the compromise design 2, as the reduction in bias does not compensate for the imprecision in treatment comparisons. However, for a residual mean square of 0·001, design 1 behaves better than design 2 with a percentage of increase of 196 against 412.

The behaviour of designs for eight treatments was consistent with the results obtained so far.

DISCUSSION AND CONCLUSIONS

Selection of a good experimental design can reduce interplot interference effects when airborne-transmitted diseases are studied in field experiments, by allocating treatments expected to have similar effects to plots that are close together and extreme treatments to plots that are further apart. We have demonstrated how to apply the principle suggested by Van der Plank (1963, Chapter 23), that treatments in any one experiment should be limited to those that do not differ greatly from each other in the amount of disease that they allow to develop. There is also consistency with the results of David & Kempton (1996) and David *et al*. (1996), where block designs to control interference are chosen such that all treatments in a block belong to the same or a similar treatment group.

Biases due to interplot interference increase as airborne mobility increases and as the difference between extreme treatment effects in an experiment increases. With square plots, rectangular blocks are more effective than square blocks in reducing biases of treatment comparisons due to interplot interference when their within-block variances are nearly the same. This will depend on the experimental conditions but, as the number of treatments increases, the advantage of a rectangular block in reducing these biases is more evident. Because only biases due to interplot interference were investigated, square blocks may still have advantages that are not evident from this study. One of the unknown factors is the effect of neighbouring non-experimental plots. Concern about such effects may make the experimenter favour square blocks of four plots, because each plot then has an equal number of non-experimental neighbours. This requires further investigation.

Complete blocks give lower biases than incomplete blocks. However, as complete blocks may have higher within-block variation than incomplete blocks, there must be a compromise between the relative importance of precision and accuracy when deciding which design to use. When designs with incomplete blocks are used, the level of within-block variance will determine the choice of design. Unbalanced designs comprising blocks that ensure less biased treatment comparisons are preferred when within-block variance is small. Balanced designs are a better option when the residual variation is large enough to make precision more important than bias in a treatment comparison. Differences in M.S.E. amongst designs are higher when the number of treatments increases, making the choice of design a more important issue.

These are general conclusions from calculations that reproduce a wide range of possible diseases and crops. Our results depend on the suitability of the proposed model and on the prior knowledge of the treatment effects. The model gave inherently sensible results and so we consider that it is a good basis for the comparison of designs. For every particular experimental situation it is possible to validate the model used for our calculations and get adequate estimates of the neighbour exponent function, or to use a completely different model. This will enable the experimenter to use our methodology to find good designs in any situation that arises in practice.

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