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SPATIAL VARIABILITY MODELS TO IMPROVE DRYLAND FIELD TRIALS

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SUMMARY

Spatial variability in field trials is a reality. A proportion of this is accounted for as inter-block variability by using block (complete or incomplete) designs. A large amount of spatial variability still remains unaccounted for, however, and this may lead to erroneous conclusions. To capture this inexplicable variation (which is mainly due to intra-block variation), yield data from a series of variety yield trials, using cereals and legumes, were analysed using various spatial models. The most suitable of these, selected on the basis of the Akaike Information Criterion, were used to assess the relative performance of genotypes. Although incomplete-block designs have been found to be effective in variety trials, spatial models have added considerable value to trials with legumes and cereals. The 'best' spatial models gave efficiency values of over 330% in winter-sown chickpea (*Cicer arietinum*), 140% in lentil (*Lens esculenta*), and 150% in barley (*Hordeum* spp.) trials. Furthermore, the use of these best models resulted in a change in the ranking of genotypes (on the basis of mean yield), which resulted, therefore, in a different set of genotypes being selected for high yield. It is recommended that: (i) incomplete block designs be used in variety trials; (ii) the Akaike Information Criterion be used to select the best spatial model; and (iii) genotypes be selected after the use of this model. The selected model would account most effectively for spatial variability in the field trials, improve selection of the most desirable genotypes and, therefore, improve the efficiency of breeding programmes.

INTRODUCTION

Field trials are conducted on lands that may be quite variable in terms of, for example, topography, soil fertility and soil structure. In order to account for such variation, and to reduce experimental error, many trial designs have been used over the years. To control systematic variation in field trials, various block designs (complete or incomplete) were introduced (Pearce, 1984; Hinkelmann and Kempthorne, 1994). Among these, incomplete-block designs, such as square lattices and α-designs (Patterson and Williams, 1976; John and Williams, 1995), are in frequent use in crop yield trials conducted by the Germplasm Program of the International Center for Agricultural Research in the Dry Areas (ICARDA) for internationally mandated crops such as kabuli chickpea (*Cicer arietinum*), lentil (*Lens esculenta*) and barley (*Hordeum* spp.). Appropriate designs, however, need to be supplemented with appropriate methods of statistical analysis. Although incomplete blocks usually account for a large amount of

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heterogeneity in the field, a considerable amount of variation within the block often remains unaccounted for by traditional methods of analysis. Modern methods of analysis can help to reduce further this unaccounted-for component of variability. There is a need to identify which combination of experiment design and method of analysis is best for some variety yield trials (for chickpea, lentil and barley) over a range of environments. The optimal combination would be that which is best able to explain the yield data according to a standard statistical criterion; this could be used to identify suitable genotypes with high yields. Changes in the ranking of genotypes based on estimated mean yields could result, and this has important consequences for the selection of genotypes that should be used in further trials. No method of analysis is 'best' in a unique sense, so every trial should be examined separately for genotype evaluation.

Spatial variability arises from variation in soil properties and in biotic and abiotic factors (Sabbe and Marx, 1987; Cressie, 1991). Often, experiment plots are a fixed distance apart in a two dimensional layout. Thus, plots in close proximity to each other are more similar than are plots that are further apart. It is unrealistic, therefore, to assume the independence of errors, which is a basic assumption of classical analyses. Nearest-neighbour methods have been devised to overcome these problems (Wilkinson *et al*., 1983; Besag and Kempton, 1986). Spatial methods of analysis for modelling local fertility trends using nearest-neighbour residuals are given in Wilkinson *et al*. (1983). An effective evaluation of cultivars can be made by identifying the underlying spatial pattern in soil characteristics and by incorporating this pattern into the statistical analysis.

Variation in soil depth, water availability and fertility can be reasonably well modelled using mathematical functions and stochastic errors to describe smooth trends in the field. To describe smooth trends along rows, cubic smoothing splines in column numbers can be used. Cubic smoothing splines are functions derived from 'segments of cubic polynomials between the distinct values' of a variable, such as column numbers, and that are 'constrained to be "smooth" at the junctions' (Genstat 5 Committee, 1997). In a spatially fixed layout, dependence among the plot errors can be accounted for by using random errors that are auto-correlated (Cullis and Gleeson, 1991). For example, one simple structure of dependence in one direction can be represented by considering first-order auto-correlated errors along rows, where the random error in a given plot position can be linearly regressed (i.e. predicted using a linear regression) against the error from the plot in the next position along the row. The use of auto-regressive error structures and local trends to model spatial variability has been reported for cereal (Grondona *et al*., 1996; Gilmour *et al*., 1997) and lentil (Sarker *et al*., 2001) trials.

An evaluation of genotypic effects in the presence of spatial variability requires the estimation of variance and covariance parameters using the restricted maximum likelihood (REML) algorithm (Patterson and Thompson, 1971). Sarker *et al*. (2001) give a procedure that can be used to select a spatial model in relation to a standard model using the REML command (Genstat 5 Committee, 1997). In order to compare the goodness of fit of the models involving different number of parameters, Akaike (1974)

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described an index, called the Akaike Information Criterion (AIC), for evaluating a general statistical distribution. Since the maximum log-likelihood value is expected to increase with the number of parameters, this criterion decreases this value by introducing a penalty in terms of the number of unknown parameters of the variance–covariance of the error components. Thus the AIC is based on a penalized log-likelihood where the penalty increases with the number of variance–covariance parameters in the fitted spatial structure.

The objectives of the present study are: (i) to examine different models that describe a diversity of spatial patterns in terms of blocks, trends along the row direction of the plot layout, random cubic smoothing splines, and auto-correlated errors; (ii) to present a method, based on the AIC, which can be used to select the model most suited to the task of accounting for spatial patterns based on crop yield responses; (iii) to compare, in terms of efficiency, the most suitable model against the classical approach for crop cultivar comparisons; and (iv) to use the most suitable model in the selection of high-yielding genotypes.

MATERIALS AND METHODS

Chickpea

A total of 138 Elite chickpea lines in F_7 and F_8 generations developed at ICARDA and planted during the winter season (December 1996), were evaluated in seven trials at Tel Hadya in Syria, the main research site of ICARDA. The site is at 36° 01′ N, 36° 56′ E, at an altitude of 284 m asl, and with a long-term average annual rainfall 334 mm. The trials were conducted in square lattice (Lat) designs, with two to three replications, in order to evaluate 25, 49 and 64 genotypes or elite lines. Each genotype was grown in plots containing four rows of plants, with a row length of 4 m and a spacing of 0.35 m between the rows. The plant rows within a plot were used to compute plot yield. Hereafter, however, the term 'row' will refer to the rows of plots in the rectangular layout of the experiment and in the statistical analysis. The term column is used in the same context.

The trials, which used 25 genotypes, were evaluated in a layout of three rows and 25 columns, where each row was a complete replicate and comprised all five incomplete blocks of five plots each. In the case of the trials which used 49 genotypes, the design was a 7×7 simple lattice, in a layout of four rows and 25 columns. Two adjacent rows represented one replicate. The seven incomplete blocks (of seven plots each) were formed using plots along the rows in sequence and in a serpentine order, leaving the last plot in each replication sown with a filler genotype. The design of those trials that used 64 genotypes was an 8×8 simple lattice, arranged in four rows and 32 columns. Each plot was harvested leaving 0.25 m at each end of each row, and the seed yield was recorded.

Lentil

Advanced and preliminary yield trials for lentil (47 trials and 25 genotypes) were conducted over three years at three locations. The sites were Breda (35° 56′ N,

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37° 10′ E) which has an elevation of 300 m asl and a long-term average annual rainfall of 266 mm; Terbol (33° 49′ N, 35° 59′ E), in the Beqqa valley in Lebanon, which has an elevation of 950 m asl and a long-term average annual rainfall of 515 mm; and Tel Hadya in Syria. All the trials were 5 × 5 square lattice designs with two to four replications. Each row comprised a replicate and contained all the incomplete blocks. The number of the rows corresponded to the number of the replicates, and the columns to the number of genotypes. The areas that were harvested in order to assess yields were the central 4.8 m^2 (2 m × 8 rows × 0.3 inter-row distance) of each plot in the advanced trials, and 3 m^2 (2 m × 5 rows × 0.3 inter-row distance) in the preliminary trials.

Barley

Yield trials in barley (four trials) were conducted at Tel Hadya and Breda, Syria during the 1993/94 cropping season. They included either advanced lines (in the F_5–F_7 generations) or, F_2-derived, F_3 lines. Each trial used 360 genotypes or derived lines, with eight of these being common to all trials. They were evaluated using an α-lattice, with18 blocks of 20 plots each in two replications, and which used a rectangular layout of 12 rows and 60 columns.

Statistical methods

Models (18 in total), covering a range of spatial patterns, were used for analysing seed yields from each of the trials and crops. The components of spatial patterns (Table 1) comprised factorial combinations of: (i) two block structures – which either took account of row and column variability (using lattices) or ignored this variability (using randomized complete blocks, RCB); (ii) three ways of taking account of trends in the direction of columns – either using linear-trend (L) or L with random cubic smoothing spline (CS); or, assuming no trend, (iii) three structures for plot errors, of which two spatial error structures are (a) first-order auto-regressive (AR) errors in columns, and (b) AR errors in columns as well as in row directions (ARAR); the third structure assumes no spatial errors (i.e. independence of plot errors (I)).

A GENSTAT directive facilitates the fitting of a linear trend and random cubic smoothing splines by specifying a variable that consists of column numbers. The 'best' of these models is taken as being that which is most appropriate for modelling the data from a specific trial. These best models can include the classical models, which are based on complete blocks or incomplete blocks alone, and those that assume independent plot errors.

Genotype effects were assumed to be fixed parameters, while replication and block effects within replications were assumed to be random variables. Parameters were estimated using the residual maximum likelihood (REML) method and commands used in GENSTAT 5.4.1. The variance components, or the block structures, comprised terms for replication effects, incomplete blocks within replications, and plot errors, and were described using the directive VCOMPONENTS of GENSTAT. The REML directive produced a statistic, called the deviance, which facilitated the computation

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Table 1. List of models used to describe spatial variability and analyses.

Model number	Block	Trend	Errors	Abbreviation
1	Complete		I	RCB
2	Complete		AR	RCBAr
3	Complete		ARAR	RCBArAr
4	Incomplete		I	Lat
5	Incomplete		AR	LatAr
6	Incomplete		ARAR	LatArAr
7	Complete	L	I	RCBL
8	Complete	L	AR	RCBLAr
9	Complete	L	ARAR	RCBLArAr
10	Incomplete	L	I	LatL
11	Incomplete	L	AR	LatLAr
12	Incomplete	L	ARAR	LatLArAr
13	Complete	LCS	I	RCBLCS
14	Complete	LCS	AR	RCBLCSAr
15	Complete	LCS	ARAR	RCBLCSArAr
16	Incomplete	LCS	I	LatLCS
17	Incomplete	LCS	AR	LatLCSAr
18	Incomplete	LCS	ARAR	LatLCSArAr

I: independent plot errors. L: fixed linear trend along rows. CS: random cubic smoothing spline in column number. AR: first order auto-regressive errors along rows; ARAR: first order auto-regressive error along rows and along columns. Lat: Lattice block model. RCB: randomized complete blocks model (non-spatial).

of the AIC. The deviance is minus twice the REML log-likelihood ignoring a constant depending on the fixed terms.

A comparison of models with the same set of fixed effects was carried out using the AIC. When expressed in terms of the deviance values, this can be defined as AICD = deviance + twice the number of linear and non-linear variance components of the models. The AICD values can then be used to compare models with the same fixed-effect terms; the model with the lowest AICD value is considered to be better than the other models.

Using the AICD values, Models 1 to 6 (first group), as well as Models 7 to 18 (second group), can be compared within each group. Models in different groups (e.g. Model 1 vs. Model 7), however, cannot be compared using the AICD because they differ in their fixed effects. Models in the second group have a linear trend in column number, while those in the first group do not. Therefore, the authors selected the best model within each group. In the second group, the significance of the linear trend was tested using the Wald statistic (Genstat 5 Committee, 1997). This is computed as the ratio of the squared estimate of the linear trend to its estimated variance, and follows a chi-square distribution in the absence of a trend. If the trend is statistically significant at $p < 0.05$, then the best model is chosen from the second group of models, otherwise the best of the first group is chosen.

For each trial, the best model was used to compute the efficiency of the method of analysis. This was assessed by comparing the average variance of pair-wise genotype comparisons with that of an RCB design with independent errors (i.e. no spatial errors).

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Table 2. Akaike Information Criterion based on the deviance (AICD) values for a lentil trial, and used to select the 'best' model.

Number	Model	Deviance	*d.f.*	q	AICD	Wald[$]
1	RCB	564.2	49	2	568.2	*
2	RCBAr	554.2	48	3	560.2	*
3	RCBArAr	538.3	47	4	546.3	*
4	Lat	556.4	48	3	562.4	*
5	LatAr	555.0	47	4	563.0	*
6	LatArAr	539.0	46	5	549.0	*
7	RCBL	551.9	48	2	555.9	11.6
8	RCBLAr	546.3	47	3	552.3	5.5
9	RCBLArAr	531.6	46	4	539.6	3.4
10	LatL	547.9	47	3	553.9	6.5
11	LatLAr	547.0	46	4	555.0	4.5
12	LatLArAr	532.4	45	5	542.4	3.1
13	RCBLCS	534.2	47	3	540.2	21.7
14	RCBLCSAr	534.1	46	4	542.1	25.1
15	RCBLCSArAr	527.9	45	5	537.9	8.5
16	LatLCS	534.6	46	4	542.6	19.5
17	LatLCSAr	534.2	45	5	544.2	24.9
18	LatLCSArAr	528.5	44	6	540.5	6.9

d.f.: residual degrees of freedom. q: number of variance components in the model.
[$] Wald statistic for testing for a linear trend along rows.
Model 15 (RCBLCSArAr) is the 'best' when selection is based on the AIC.
CV (%): 35.1 (for RCB model) and 26.7 (for RCBLCSArAr).
Efficiency of RCBLCSArAr relative to the RCB: 245%.

To illustrate the process by which the best model was selected, the authors present various statistics for one trial with lentil (Table 2). The design was a 5×5 triple lattice with a layout of three rows and 25 columns. The authors found that RCBArAr gave an AIC value of 546.3, which was the lowest found in the first group of models (1 to 6). Similarly, the model RCBLCSArAr gave an AIC value of 537.9, which was the lowest in the second group of models (7 to 18). Furthermore, they found that, for the model RCBLCSArAr, the value of the Wald statistic (8.5) was higher than that of the chi-square statistic (3.84) with one degree of freedom at the 5% level of significance. This indicated the presence of a linear trend along rows. The authors concluded, therefore, that the model RCBLCSArAr was the best for the evaluation of these lentil genotypes in this trial.

The GENSTAT programs for spatial analysis of field data are available from the authors on request.

RESULTS AND DISCUSSION

In chickpea trials, the best models selected using AICD criteria had auto-regressive spatial errors and complete blocks, except in one case where the lattices were also found to be effective in accounting for unexplained variation (Table 3). Of the 47 lentil trials, lattices were found to be best in only eight cases; in the remainder, the best models were those with complete blocks with linear trends and spatial errors (either

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Table 3. Best models, selected on the basis of the AICD criterion.

Crop	Best models (number of trials)
Chickpea	RCBAr (2), RCBArAr (1), RCBLCSAr (2), Lat (1), LatArAr (1)
Lentil	RCB (14), RCBAr (7), RCBArAr (8), RCBL (5), RCBLArAr (2), RCBLCS (2), RCBLCSArAr (1), Lat (7), LatL (1)
Barley	RCBArAr (2), RCBLArAr (1), RCBLCSArAr (1)

RCB: Randomized complete blocks design. RCBAr: RCB with first order auto-correlated (AR) errors along rows. RCBArAr: Randomized complete blocks with first order auto-correlated errors in plots along rows and along columns. RCBL: RCB with linear trend along rows. RCBLCS: Randomized complete blocks with linear trend along rows and random cubic smoothing spline in column numbers. RCBLCSAr: Randomized complete blocks with linear trend along rows, random cubic smoothing spline in column numbers, and AR errors along rows. RCBLCSArAr: Randomized complete blocks with linear trend along rows, random cubic smoothing spline in column numbers, and AR errors along rows and columns. Lat: Lattice design. LatL: Lattice with linear trend along rows. LatArAr: Lattice with first order auto-correlated errors in plots along rows and along columns.

Table 4. Mean and range of efficiencies of best model and lattice designs, relative to RCB designs.

			Efficiency	
Crop	Experiment design	Number of trials	Lattice (%)	Best method (%)
Chickpea	Square lattice, 25–64 genotypes in 2–3 replications	7	213 (126–420)	336 (134–697)
Lentil	Square lattice, 25 genotypes, 2–3 replications	47	120 (100–263)	141 (100–638)
Barley	Alpha lattice, 360 genotypes, 2 replications	4	105 (101–107)	152 (136–171)

AR or ARAR). There were 14 trials in which neither the incomplete blocks (with or without trends), nor the spatial errors were effective. In the barley trials, ARAR with complete blocks, and with and without a linear trend along the rows, were found to be the most suitable.

In Table 4, the average efficiency relative to RCB is presented for the lattice and for the best method for each of the three crops. Except in the case of barley, the use of lattice blocks to account for variability improved the efficiency of genotypic comparisons over RCBs. Lattices gave a gain in efficiency of 20% for lentils and of 113% for winter-sown chickpea over RCBs. The average efficiency values relative to RCB were 336%, 141% and 152% respectively for chickpea, lentil and barley under the best method, while the corresponding average efficiency values were substantially lower under lattices. Thus, in comparison with lattices, the best model, on average, reflected a considerable increase in efficiency in all the crops. For the legume trials, the maximum efficiency was more than twice the value of the mean efficiency.

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Table 5. Performance rankings of the highest-yielding genotypes (denoted by numerical codes), obtained when yield data from specific trials were analysed with three different models (RCB, lattice and best models).

		Ranks*														
Crop	Model	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Chickpea		Chickpea trial number 2 (25 genotypes); best model: RCBLCS†														
	RCB	10	15	17	12	18	9	22	5	19	4					
	Lattice	15	18	17	6	19	9	5	4	7	14					
	Best	18	17	6	9	15	4	11	20	14	13					
Lentil		Lentil trial number 10 (25 genotypes); best model: RCBArAr‡														
	RCB	16	6	3	17	20	18	21	14	10	9					
	Lattice	16	21	18	24	17	19	9	6	14	15					
	Best	20	21	16	17	18	6	19	7	24	9					
Barley		Barley trial number 2 (360 genotypes); best model: RCBArAr														
	RCB	85	232	263	164	16	75	342	352	289	193	84	208	194	230	105
	Lattice	85	263	232	164	75	342	16	352	84	289	193	105	279	194	208
	Best	85	16	263	342	289	230	164	319	252	232	12	189	84	104	86

* Rank 1 signifies the highest yield obtained in the trial. NB The top 10 (of 25) genotypes are presented for the chickpea and lentil trials; the top 15 (of 360) genotypes are presented for the barley trial.

† RCBLCS: Randomized complete blocks with linear trend along rows and random cubic smoothing spline in column numbers.

‡ RCBArAr: Randomized complete blocks with first order auto-correlated errors in plots along rows and along columns.

Table 5 lists the ranks of the highest-yielding genotypes when evaluated using RCB, lattice and the best models for one selected trial for each of the crops. There was a considerable change in the ranking of the genotypes when different models were used. The range of models explored here capture spatial variability in the field using various components, including complete or incomplete blocks, linear trends along rows, random effects as a cubic smoothing spline in column number, and auto-regressive errors along rows and/or along columns. The model selection criterion, AICD, is based on the deviance, which is a function of REML log-likelihood values and upon a penalty function based on the number of variance–covariance parameters. This criterion takes into account the maximum amount of information in the data, including the underlying statistical distribution (in terms of the various parameters which express the spatial pattern). Use of this criterion favours simpler models over more complex ones, because the penalty value is lower when the number of parameters is smaller.

Further analysis of a large number of experiments resulted in the identification of the models that were most frequently found to be the best when accounting for variability in field trials. Irrespective of the specific form of the model, and acknowledging that the spatial variability of each field is unique, models which included complete blocks and, in addition, accounted for spatial errors (auto-regressive error structures), were found to be the most frequent. As can be seen from the lentil trials (Table 3), the RCB was the best design in 14 trials, while lattice blocks were the best design in only seven trials. The traditional methods, therefore, proved the most effective, and so should be retained. Thus, the variety trials may continue to be designed in incomplete blocks,

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but analysis must be carried out to account for the spatial patterns, as this is likely to give a higher efficiency when comparing genotypes.

In situations where guard rows are used, competition between the neighbouring plots is assumed to be reflected in the growth of plants in the guard rows and, therefore, the data for these rows are not recorded. However, this precaution does not eliminate the existence of underlying spatial variability. In such cases, one may also use methods for modelling competition as well as spatial variability (Durban *et al.*, 2001).

It is important that the efficiencies of the spatial method analyses be evaluated for different geographical areas. For this reason, the experimental fields used in the study included three different sites which varied, for example, in total rainfall (266–515 mm), altitude (284–950 m asl), soil type, and temperature during the cropping season. The depth of soil, the availability of water and the frequency of storms also varied with the field and year, and so contributed to the spatial variability. In this study, the inclusion of different sites, with varying agro-climatic conditions, was intended to generalize the use of spatial methods and to minimize any specific site and year effects.

CONCLUSIONS

Models covering a range of spatial patterns were assessed regarding their effectiveness in evaluating seed yields from legume and cereal crops grown in field trials. No one model could describe the spatial pattern in all situations. For each trial, the most appropriate model was identified. These 'best' models varied in their efficiencies for genotype comparisons being highest for kabuli chickpea and considerably lower for barley and lentil.

The identification of the best model, and its use, led to different adjusted mean seed yields for the genotypes, which, in turn, changed their ranking. Compared with classical approaches, spatial analysis increased the efficiency of genotype selection for further evaluation.

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