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Error Variation in Multienvironment Peanut Trials: Within-Trial Spatial Correlation and Between-Trial Heterogeneity

F. Casanoves,* R. Macchiavelli, and M. Balzarini

ABSTRACT

Multienvironment Trials (MET) are used to make cultivar recommendations about genotypes in plant breeding programs. Because of the presence of genotype × environment interaction, METs are usually conducted in multiple environments using designs that involve several replications per environment. Blocking of plots within each trial enables one to account for between plot variation. To improve the comparison of genotype means, taking into account within-trial spatial correlation as well as between-trial residual variance heterogeneity, alternative mixed models can be used. The objective of this study was to compare several spatial models, including or excluding heterogeneity of residual variances for cultivar evaluation in a set of independent peanut (*Arachis hypogaea* L.) METs. The modeling impact was evaluated by comparing genotype means from each trial. A series of 18 METs from a peanut breeding program, as according to a randomized complete block design (RCBD) at each location, were simultaneously fitted by (i) a classic analysis of variance model for an RCBD with blocks random and (ii) mixed models incorporating spatial correlation through isotropic and anisotropic covariance structures for the error terms (power correlation function) and including homogenous and heterogeneous residual variances to take into account the different environments having different precision. Results suggest that the model with stationary anisotropic error structure AR1×AR1 within each environment and heterogeneous residual variances constitutes a good alternative analysis for METs, but it was not always better than the RCBD models for peanut. Differences were found between long- and short-cycle peanut cultivars with respect to the best model.

The comparison of genotype performance in METs requires the ability to make reliable mean yield comparisons. Commonly METs are conducted with multiple replications at each location. The stratification or blocking of plots is a technique used to reduce the effect of variation among plots. The blocks are groups of experimental units aligned in such a way that the plots within the blocks are as homogeneous as possible. The RCBD is commonly used. This design is more efficient than the completely randomized design when differences between plots in the same block are minimal and differences among blocks are substantial (Gusmao, 1986). Heterogeneity within blocks may result in imprecise estimation of the genotype effects because of a large error variance (Stroup et al., 1994). Since METs often include a large number of genotypes, the block sizes are usually large, and it is difficult to assure within block homogeneity. Plots close together may be more similar than distant ones. Spatial variability refers to the tendency of genotype responses, such as yield trends, to follow the spatial arrangement of plots on the ground (Mercer and Hall, 1911). Variation from plot to plot within the same block may be due to competition between genotypes (Kempton and Lockwood, 1984), heterogeneity in soil fertility (Pearce, 1980), insect dispersion, weeds, crop disease, or cultural aspects (Smith et al., 2001). Because of the spatial variability between and within blocks, the standard analysis of variance for an RCBD does not always produce the most efficient comparison of genotype effects.

Statistical procedures that account for spatial variation among plots within trials have been proposed (Papadakis, 1937; Mead, 1971; Besag, 1974, 1977; Ripley, 1981; Wilkinson et al., 1983; Besag and Kempton, 1986). Brownie et al. (1993) addressed the topic of modeling spatial variation in crop evaluation trials by using polynomial trend analysis, nearest neighbor analysis, and a model with correlated errors. They compared these methods in a set of independent maize (*Zea mays* L.) yield trials and in a soybean [*Glycine max* (L.) Merr.] yield trial, with a single trial in each set. Stroup et al. (1994) also compared methods using one-location trials and made conclusions about the benefits associated with the spatial variation modeling in a wheat (*Triticum aestivum* L.) MET conducted in the central region of the USA. For yield trials at a single location, Gleeson and Cullis (1987), Cullis and Gleeson (1991), and Cullis et al. (1996) obtained more precise estimates of the cultivar means by modeling spatial variation with a correlated error structure compared with estimates obtained under the classical analysis for an RCBD. Gilmour et al. (1997) partitioned the spatial variability between plots at a single-location trial into local, global, and extraneous spatial variability. The local spatial variability refers to the differences between plots on a small scale, and the global spatial variation represents nonstationary tendencies

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Abbreviations: AIC, Akaike Information Criterion; AR1, first order autoregressive; BIC, Schwarz Bayesian Information Criterion; BLUE, best linear unbiased estimator; BLUP, best linear unbiased predictor; EEA, Estación Experimental Agropecuaria; G, genotype main effect; GL, genotype by location interaction effect; INTA, Instituto Nacional de Tecnología Agropecuaria; L, location main effect; MET, multienvironment trials; PBP, Peanut breeding program; Pow, isotropic power spatial correlation; Powa, anisotropic power spatial correlation; PowaH, anisotropic power spatial correlation and heterogeneous residual variances; PowH, isotropic power spatial correlation and heterogeneous residual variances; PowRB, isotropic power spatial correlation and heterogeneous random block; RB, random block; RBH, random block with heterogeneous residual variances; RBHBH, random block with heterogeneous block variances and heterogeneous residual variances; RCBD, randomized complete block design; REML, restricted maximum likelihood; SAV, square root of average variances of mean differences.

throughout the field trial. Extraneous variation is frequently associated with the management of the trials and includes intra- and interblock variation. One example is the effect of serpentine harvesting, where alternating groups of rows are harvested in opposite directions and reflect a consistently greater or lower yield in one direction than in the other. The global and extraneous spatial variations are handled by including appropriate model terms such as design factors and polynomial functions.

In METs, the local spatial tendency within trials and the residual heterogeneity between trials can be jointly modeled. By using a two-dimensional coordinate system at each trial, it is possible to define the plot location in a field, for example, from latitude and longitude of the plot centers. These coordinates allow for the distance between plots to be calculated and later used to express the correlation between observations from different plots as a function of their Euclidean distance. Modeling the spatial structure of the plots as distance functions can be done in the context of mixed linear models (Zimmerman and Harville, 1991; Gilmour et al., 1997; Cullis et al., 1998; Smith et al., 2002a, 2002b). In the mixed model approach, it is not only possible to consider the correlation structure among yield data obtained from different plots but also to model residual variance heterogeneity between the trials conducted in different environments with different levels of precision. The correlation functions for stationary models, in which the correlation function depends only on the Euclidean distance vectors, can be isotropic (identical in any direction) or anisotropic (different parameter values in different directions). For separable two-dimensional processes, it is common to consider the dependence between plots with an exponential anisotropic correlation model, which is expressed as:

$$\mathrm{Corr}_{ij} = \exp\left[-\delta_r(d_{ij}^r)^{p_r} - \delta_c(d_{ij}^c)^{p_c}\right],$$

where d_{ij}^r and d_{ij}^c are the distances between plot i and plot j in the direction of the field rows and columns, respectively, p_r and p_c are the corresponding unknown powers, and δ_r and δ_c are unknown correlation parameters. Another spatial correlation function commonly used is the power function. The isotropic power model depends on a single parameter (ρ) which, when raised to the distance between two plots (in any direction), provides the correlation between them. The power function is a reparameterization of the exponential function (with $p = 1$). The anisotropic power correlation model, i.e., $\rho_r^{d_{ij}^r}\,\rho_c^{d_{ij}^c}$, usually named AR1 $\times$ AR1, is a recommended approach (Smith et al., 2002a). The AR1$\times$AR1 model depends on two parameters: one that represents the correlation between plots in the direction of rows (ρ_r) and the other that represents the correlation in the direction of columns (ρ_c). The vector parameter elements ρ_r and ρ_c, are called autoregressive coefficients. Cullis and Gleeson (1991) consider the AR1$\times$AR1 and AR1 $\times$ **I** models (autoregressive correlation only in one direction) as the most plausible for modeling spatial correlation in single-location yield trials. Smith et al. (2002b) used ASREML (Gilmour et al., 1999) to analyze wheat MET data, adjusting for spatial field trends at each trial with an AR1$\times$AR1 model for the error terms and random genotype effects to simultaneously incorporate genotypic correlations. They also simulated variety–environment data to investigate the impact on variety predictions (variety effects were regarded as random) when ignoring spatial variation within trials and error variance heterogeneity between trials. The results showed the gains in accuracy and precision of spatial analysis compared with RCBD analysis (fixed block effects), and provided evidence about the impact of ignoring these effects. Since they worked with random genotype effects, the effects were predicted with best linear unbiased predictors (BLUPs) obtained from a Factor Analytic model (Litell et al., 1996) for the covariance structure of the random effects.

In this paper, we investigate the performance of the RCBD, the spatial AR1$\times$AR1 and other modeling approaches for the error terms in a set of independent peanut-METs rather than MET for cereals (which have been used in most other papers related to spatial analysis). This paper details the use of spatial analysis and combined analysis of MET in a single model, while permitting the fitting of heterogeneous error variances and spatial parameters in different trials. Models were compared on the basis of model selection criteria and precision of genotype mean comparisons within environments. The equivalence between some spatial models in the particular context of multienvironment MET is discussed, and SAS code for fitting these models is provided.

MATERIALS AND METHODS

Database

At each breeding cycle of the Peanut Breeding Program at EEA-Manfredi, INTA, (PBP-INTA) Argentina, experimental lines of peanut are generated by the pedigree breeding method, with plots bulk harvested at the F6 generation. The METs are conducted using advanced generations of breeding lines by sowing the same genotypes at different locations. We used independent peanut-MET data sets conducted during 9 yr (1984–1985 to 1992–1993) for two types of experimental genotypes. The METs for type 1 genotypes correspond to trials involving short-cycle genotypes, and METs for type 2 genotypes to trials where long-cycle genotypes are compared. A total of 18 independent data sets (two maturity classes within each of nine years) were used in this study to evaluate various statistical models. In each year, the METs were conducted in three locations in the peanut crop area in the Province of Córdoba (Argentina): Manfredi (Lat. S 31°41′, Long. W 63°26′), General Cabrera (Lat. S 32°49′, Long. W 63°51′) and Río Tercero (Lat. S 32°10′, Long. W 64°7′), with the exception of the 1991–1992 and 1992–1993 years when Río Tercero was excluded. The climate and soil characteristics of the three locations are very similar, as the Province at Córdoba crop area is highly homogeneous (Casanoves et al., 2005). In each location and year, approximately 15 genotypes of each maturity class (short and long cycle) were evaluated. The set of genotypes evaluated in each year was the same at each location. In each location, both short-cycle genotype trials and long-cycle genotypes trials were conducted using an RCBD with four replications. The plots were composed of two 10-m-long furrows with 70 cm between furrows. At each site, the blocks were composed of contiguous plots, with one for each assayed genotype. A rect-

angle of four contiguous blocks was planted within each location. Recommended seeding rates (15 seed m^{-2}) and cultural practices were followed in all of the METs. Each plot was harvested manually after eliminating the border areas. Yield data was expressed in kilograms of peanuts per plot at constant moisture (80 g kg^{-1}).

Analysis Procedures

Each of the 18 year-maturity group combinations was treated as an independent MET data set. First we compared different spatial analyses (isotropic and anisotropic power correlation) with the classical RCBD model with random blocks at each location for each MET data set. After comparing these models within locations, we conducted an across-locations analysis within each data set using the following MET models. The first two procedures were based on analysis of variance for an RCBD at each location:

$$y_{ijk} = \mu + L_j + B(L)_{k(j)} + G_i + GL_{(ij)} + \varepsilon_{ijk} \quad [1]$$

where y_{ijk} is the yield of genotype i, in location j, block k; μ is the overall mean; L_j is the effect of location j with $j = 1, \ldots, s$; $B(L)_{k(j)}$ is the random effect of block k within location j with $k = 1, \ldots, n$; G_i is the effect of genotype i with $i = 1, \ldots, g$; $GL_{(ij)}$ is the effect of the interaction of genotype i with location j and ε_{ijk} is the error term associated with observation y_{ijk}. Except for ε_{ijk} and the block effects, all of the model factors were considered as fixed effects. The ε_{ijk} were assumed independent with a constant variance σ^2 in the first method, assuming that local spatial variation and heterogeneous residual variance between locations do not exist. The block effect variances were also assumed to be homogeneous (RB model). The second procedure denoted as an RBH model was also based on Eq. [1], but permitted heterogeneous residual variances across locations.

The third procedure consisted of fitting an isotropic spatial correlation model within locations with a power correlation function, including block effects and assuming no correlation between plots from different locations (Pow model). The fourth procedure was the same as the previous one, but allowing heterogeneous error variances between locations (PowH model). The other procedures were based on anisotropic spatial correlation models with a power correlation function within locations. These models were fitted assuming homogeneous residual variances (Powa model) as well as heterogeneous residual variances across locations (PowaH model). Two additional models were run to check specific assumptions. The two models are identified as the RBHBH model (like the RBH model, but allowing heterogeneous block variances across trials), and the PowRB model (like the Pow model, but including random block effects). All of the above models were estimated in the context of the mixed linear models using PROC MIXED, SAS, Version 8.2 (SAS Institute, 2001). The program syntax used for each of the analysis models is presented in Table 1.

The models associated with each procedure were evaluated with Akaike's (AIC) criteria, calculated as follows:

$$AIC = -2L + 2d$$

where L is the restricted maximum likelihood value and d is the number of estimated covariance parameters. The best model is the one with the lowest value of AIC. We also used the Schwartz's Bayesian Information Criterion (BIC) to compare models with no random block effects. Variance components were estimated by using the ridge stabilized Newton-Raphson algorithm implemented in SAS PROC MIXED for restricted maximum likelihood (REML) estimation (Wolfinger et al., 1994). We used the adjustment of degrees of freedom proposed by Kenward and Roger (1997). The square root of the average variance of genotype mean differences (SAV) was used to show how the precision of mean differences changes under the different models. This was computed by averaging across trials the variances of the differences between genotype means within each trial. Pearson's correlation coefficients between genotype means (BLUEs) for each genotype at each site were computed for every pair of methods. The estimates of the covariance parameters associated with each model were also obtained to compare procedures.

RESULTS AND DISCUSSION

According to the AIC values (Table 2), spatial models fitted the within trial data better than the RCBD model in 29 of the 50 independent data sets analyzed for peanut. Most of the models selected by the AIC also had the smallest square root of the average variance to compare genotype means (Table 3). This is one of the main impacts of using these models from a practical point of

Table 1. Summarized syntax for the Proc Mixed SAS (Version 8.2) commands to fit eight models for MET.

Syntax used for all models: proc mixed scoring = 200 maxfunc = 2500 maxiter = 5000 method = reml;†	
Model‡	**Syntax**
RB	class block genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; random block(location);
RBH	class block genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; random block(location); repeated/group = location;
Pow	class genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; repeated/subject = location type = sp(pow) (lat long);
PowH	class genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; repeated/subject = location type = sp(pow) (lat long) group = location;
Powa	class genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; repeated/subject = location type = sp(powa) (lat long);
PowaH	class genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; repeated/subject = location type = sp(powa) (lat long) group = location;
RBHBH	class block genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; random block(location)/ group = location; repeated/group = location;
PowRB	class block genotype location; model yield = genotype location genotype*location/ddfm = kenwardroger; random block(location); repeated/subject = location type = sp(pow) (lat long);

† This command is written before the specific commands for each scenario.

‡ RB, random block; RBH, random block with heterogeneous residual variances; Pow, isotropic power spatial correlation; PowH, isotropic power spatial correlation and heterogeneous residual variances; Powa, anisotropic power spatial correlation; PowaH, anisotropic power spatial correlation and heterogeneous residual variances, RBHBH, random block with heterogeneous block variances and heterogeneous residual variances; PowRB, isotropic power spatial correlation and random block.

Table 2. Akaike information criteria (AIC) for three within-location models fitted in 18 peanut-MET data sets (nine years, two types of genotype cycle). Smaller AIC values indicate better fitting models.

		Models†					
		Short cycle			Long cycle		
Year	Location	RB	Pow	Powa	RB	Pow	Powa
1984–1985	General Cabrera	29.32	33.81	34.28	30.34	31.13	30.88
1984–1985	Manfredi	−3.22	−9.15	−7.89	70.73	68.55	
1984–1985	Río Tercero	34.86	24.31	25.71	46.21	45.30	
1985–1986	General Cabrera	28.14	25.87	27.84	92.41	92.72	94.37
1985–1986	Manfredi	22.52	18.93	18.64	16.82	16.91	18.91
1985–1986	Río Tercero	34.15	33.33	34.09	30.25	31.82	32.76
1986–1987	General Cabrera	18.86	14.96	9.75	92.57	93.71	95.62
1986–1987	Manfredi	51.52	56.63	57.35	56.89	55.76	54.17
1986–1987	Río Tercero	25.85	19.85	21.14	3.18	3.76	
1987–1988	General Cabrera	35.57	39.15	41.11	45.59	44.93	46.61
1987–1988	Manfredi	42.19	44.12	44.75	25.07	25.85	27.85
1987–1988	Río Tercero	3.73	−7.41	−5.58	25.82	26.40	26.99
1988–1989	General Cabrera	45.69	24.67	23.55	54.23	51.47	51.49
1988–1989	Manfredi	44.96	39.60	41.59	9.70	13.50	10.18
1988–1989	Río Tercero	−23.55	−20.73		31.66	31.37	30.68
1989–1990	General Cabrera	69.62	71.55	72.71	21.37	17.75	17.67
1989–1990	Manfredi	61.98	57.22	57.59	38.65	34.34	33.05
1989–1990	Río Tercero	62.65	56.10	55.93	60.88	60.90	62.41
1990–1991	General Cabrera	43.73	39.70	41.44	47.14	47.84	43.28
1990–1991	Manfredi	30.27	30.04	27.84	60.85	61.79	
1990–1991	Río Tercero	24.92	17.78	19.74	21.41	21.70	19.05
1991–1992	General Cabrera	9.68	11.80	12.89	7.97	7.71	9.25
1991–1992	Manfredi	28.81	27.77	29.76	46.39	52.59	51.83
1992–1993	General Cabrera	29.50	29.08		39.93	40.94	42.84
1992–1993	Manfredi	13.16	12.33	9.50	46.39	49.07	50.10

† RB, random block; Pow, isotropic power spatial correlation; Powa, anisotropic power spatial correlation. Empty cells indicate convergence problems during the estimation process.

view, being able to detect smaller differences between genotypes.

When modeling the MET data, the genotype × location interaction was significant in all data sets ($p < 0.0001$). Therefore the genotype mean comparisons were performed within each location using the standard errors obtained from the combined analysis of the three locations (SLICE option in SAS). According to the AIC values, the RB model was the best only in one MET (cycle 2, 1987–1988) and the RBH model was best in only two METs (cycle 2, 1985–1986 and 1986–1987). Furthermore, there are two METs (cycle 2, 1991–1992 and 1992–1993) in which the best model is the RB with heterogeneous residual and block variances. However, fitting models

Table 3. Square root of the average variance of the mean differences for three within-location models fitted in 18 peanut-MET data sets (nine years, two types of genotype cycle).

		Models†					
		Short cycle			Long cycle		
Year	Location	RB	Pow	Powa	RB	Pow	Powa
1984–1985	General Cabrera	0.1685	0.1834	0.1834	0.1723	0.1667	0.1609
1984–1985	Manfredi	0.1241	0.1114	0.1135	0.2728	0.2480	
1984–1985	Río Tercero	0.1875	0.1567	0.1616	0.2132	0.2097	
1985–1986	General Cabrera	0.1701	0.1568	0.1628	0.3713	0.3913	0.4007
1985–1986	Manfredi	0.1755	0.1598	0.1578	0.1553	0.1624	0.1691
1985–1986	Río Tercero	0.2064	0.2065	0.2079	0.1875	0.1912	0.1896
1986–1987	General Cabrera	0.1619	0.1472	0.1321	0.3201	0.3352	0.3454
1986–1987	Manfredi	0.2076	0.2263	0.2217	0.2134	0.2054	0.1919
1986–1987	Río Tercero	0.1689	0.1521	0.1547	0.1299	0.1360	
1987–1988	General Cabrera	0.1714	0.1718	0.1768	0.2066	0.2087	0.2144
1987–1988	Manfredi	0.2014	0.2077	0.2076	0.1673	0.1794	0.1855
1987–1988	Río Tercero	0.1300	0.1085	0.1109	0.1687	0.1788	0.1768
1988–1989	General Cabrera	0.1969	0.1488	0.1433	0.2266	0.2092	0.2022
1988–1989	Manfredi	0.2047	0.1929	0.1994	0.1333	0.1343	0.1336
1988–1989	Río Tercero	0.0981	0.1076		0.1771	0.1821	0.1766
1989–1990	General Cabrera	0.2542	0.2686	0.2699	0.1562	0.1483	0.1437
1989–1990	Manfredi	0.2350	0.2220	0.2227	0.2041	0.1828	0.1804
1989–1990	Río Tercero	0.2439	0.2226	0.2199	0.2479	0.2581	0.2623
1990–1991	General Cabrera	0.2098	0.1931	0.1963	0.2422	0.2409	0.2090
1990–1991	Manfredi	0.1781	0.1849	0.1724	0.2735	0.2961	
1990–1991	Río Tercero	0.1634	0.1448	0.1501	0.1627	0.1703	0.1592
1991–1992	General Cabrera	0.1358	0.1444	0.1450	0.1427	0.1492	0.1549
1991–1992	Manfredi	0.1966	0.1973	0.2072	0.2147	0.2429	0.2344
1992–1993	General Cabrera	0.1788	0.1873		0.2209	0.2289	0.2369
1992–1993	Manfredi	0.1442	0.1462	0.1292	0.2154	0.2248	0.2295

† RB, random block; Pow, isotropic power spatial correlation; Powa, anisotropic power spatial correlation. Empty cells indicate convergence problems during the estimation process.

Table 4. Akaike information criteria (AIC) obtained from fitting eight models for 18 peanut-METs. Smaller AIC values indicate better fitting models.

		Models†							
Cycle‡	Year	RB	RBH	Pow	PowH	Powa	PowaH	RBHBH	PowRB
1	1984–1985	63.68	60.25	51.96	48.96	50.52	52.09	60.96	50.83
1	1985–1986	84.31	87.03	76.24	78.13	75.67	80.57	84.81	73.95
1	1986–1987	100.53	100.75	95.02	91.44	90.62	88.24	96.23	97.02
1	1987–1988	90.53	85.05	90.62	75.87	92.56		81.49	88.34
1	1988–1989	87.76	66.19	63.64	43.55	65.39		67.10	60.99
1	1989–1990	187.41	191.12	179.30	184.87	177.07	186.24	194.26	179.04
1	1990–1991	94.19	95.68	85.04	87.51	84.87	89.00	98.93	85.04
1	1991–1992	39.27	38.29	37.58	39.57	39.99	41.71	38.48	37.98
1	1992–1993	40.83	41.08	42.66	41.41	44.64	39.92	42.66	42.63
2	1984–1985	151.05	146.89	149.97	144.98	152.11	147.70	147.28	145.90
2	1985–1986	172.86	137.84	173.26	141.45	174.41	144.04	139.48	170.74
2	1986–1987	183.22	152.69	188.29	153.23	189.96	155.51	152.70	190.28
2	1987–1988	91.90	93.10	95.93	97.18	96.38	99.69	96.48	93.80
2	1988–1989	107.74	98.54	99.76	96.34	100.80	92.35	95.59	99.76
2	1989–1990	126.08	121.43	117.38	113.14	115.46	113.00	120.90	118.83
2	1990–1991	134.13	128.26	134.55	131.34	133.74	123.86	129.40	136.33
2	1991–1992	61.33	57.13	70.75	60.30	71.06	61.08	54.35	55.96
2	1992–1993	87.79	89.77	93.85	90.00	95.30		86.32	93.85

† RB, random block; RBH, random block with heterogeneous residual variances; RBHBH, random block (heterogeneous across environments) with heterogeneous residual variances; Pow, isotropic power spatial correlation; PowRB, isotropic power spatial correlation plus random block; PowH, isotropic power spatial correlation and heterogeneous residual variances; Powa, anisotropic power spatial correlation; PowaH, anisotropic power spatial correlation and heterogeneous residual variances.

‡ 1, short-cycle genotypes; 2, long-cycle genotypes. Empty cells indicate convergence problems during the estimation process. Underscored values indicate the minimum AIC in each row.

with spatial correlation rather than with block effects produced reductions of AIC values in 72% of the METs (13 out of 18 METs).

The reason that the AIC indicated that heterogeneous error models were often superior was that, in many cases, there were large differences between error variances estimated within each environment. In 62% of the METs, the ratio between the highest and lowest within-location residual variances was greater than two (results not shown), which made the model with heterogeneous residual variances a more appropriate choice. The percentage difference between the highest and the lowest within-trial residual variance of an MET varied from 36 to 623%. The largest differences between residual variances between trials were observed in the METs with long-cycle experimental genotypes. These genotypes remain in the ground longer, thus the trials could have greater experimental error and greater differences between locations, because of the impact of climatic factors during a longer period. With the exception of the 1987–1988 and 1992–1993 year, in all of the METs for long-cycle genotypes, the AIC criteria suggested that the models with heteroscedastic residual variance were more appropriate than their homogeneous residual variance versions (Table 4). The two years when the models with heterogeneous residual variance were not superior to the RB were the only years with negligible differences in residual variances between trials. In Table 4, we include the RBHBH model to check whether the assumption of homogeneous block variances was satisfied. Only in two METs (1991–1992 and 1992–1993 for long-cycle genotypes) did the RBHBH have the smallest AIC, and in these cases the differences between the AIC with respect to the RBH model were very small. From these results, we suggest that modeling heterogeneous block variances between trials is unnecessary for these METs.

Table 4 also includes the PowRB model to compare it with the Pow and the Powa models. The model including both the block effects and the spatial correlation (PowRB model) was the selected model in only one of the METs. The value of the spatial correlation parameter was larger in all the METs when the block effect was not included in the model (maximum value $r = 0.75$). This result was expected since, in the PowRB model, part of the correlation for spatial variability was considered in the term related to the blocking. When working with anisotropic models, the inclusion of the block effect seems redundant since, in both cases, the spatial variability is modeled separately in two directions. According to the AIC criteria, the models involving an AR1×AR1 spatial correlation (Powa and PowaH) were the most appropriate ones for 8 of the 18 analyzed METs. The homogeneous (Powa) AR1×AR1 model was superior to the heterogeneous model (PowaH) in the METs involving short-cycle genotypes and conducted in years that correspond to the METs with the smallest difference between residual variances across locations.

The heterogeneous AR1×AR1 model can present computational problems, at least with the estimation algorithm used in SAS. We used the PARMS command, inputting as initial values in the REML process the estimates obtained by using an ML algorithm. This solved convergence problems in three of the six cases that did not converge originally. The convergence troubles could be more frequent in combined analysis of METs when there are only a few trials, since the trial plays the role of replication during the estimation process.

In general, and mainly for short-cycle peanut cultivars, the SAV values were smaller for the combined MET analyses including spatial correlations than those incorporating the block effects (Table 5). We also compared the models with no block effect using the BIC criterion (results not shown) and according to this cri-

Table 5. Square root of the average variance (SAV) of the mean differences obtained from fitting eight models that incorporate spatial correlations for 18 METs.

		Models†					
Cycle‡	Year	RB	RBH	Pow	PowH	Powa	PowaH
1	1984–1985	0.1622	0.1625	0.1631	0.1490	0.1517	0.1536
1	1985–1986	0.1847	0.1844	0.1778	0.1726	0.1682	0.1741
1	1986–1987	0.1808	0.1817	0.1828	0.1769	0.1661	0.1709
1	1987–1988	0.1715	0.1712	0.1700	0.1661	0.1703	
1	1988–1989	0.1735	0.1741	0.1581	0.1510	0.1559	
1	1989–1990	0.2445	0.2445	0.2518	0.2360	0.2300	0.2356
1	1990–1991	0.1849	0.1844	0.1806	0.1741	0.1709	0.1718
1	1991–1992	0.1688	0.1679	0.1622	0.1715	0.1729	0.1783
1	1992–1993	0.1625	0.1622	0.1715	0.1676	0.1735	0.1631
2	1984–1985	0.2232	0.2236	0.2052	0.2015	0.2049	0.2042
2	1985–1986	0.2565	0.2594	0.2629	0.2683	0.2627	0.2724
2	1986–1987	0.2345	0.2347	0.2542	0.2377	0.2400	0.2390
2	1987–1988	0.1817	0.1822	0.1905	0.1889	0.1895	0.1903
2	1988–1989	0.1852	0.1841	0.1913	0.1766	0.1752	0.1712
2	1989–1990	0.2081	0.2078	0.2110	0.2002	0.1942	0.1997
2	1990–1991	0.2317	0.2317	0.2339	0.2408	0.2330	0.2274
2	1991–1992	0.1822	0.1833	0.2083	0.1997	0.2005	0.1960
2	1992–1993	0.2193	0.2193	0.2476	0.2245	0.2425	

† RB, random block; RBH, random block with heterogeneous residual variances; Pow, isotropic power spatial correlation; PowH, isotropic power spatial correlation and heterogeneous residual variances; Powa, anisotropic power spatial correlation; PowaH, anisotropic power spatial correlation and heterogeneous residual variances.

‡ 1, short-cycle genotypes; 2, long-cycle genotypes. Empty cells indicate convergence problems during the estimation process.

terion the heterogeneous AR1×AR1 model (PowaH) was more often the best choice (12 out of 15 trials without convergence troubles). Although the BIC penalizes models with more parameters more than the AIC does, the larger likelihood of the PowaH model made it often the best model.

The previous results show that modeling the local spatial tendencies through an analysis of variance including spatial correlation structures in the error terms increases, in many cases, the ability to identify differences between genotypes. Smith et al. (2001) suggest that in field experiments the plots are generally the same size and are organized in regular continuous arrangements. Since the distance between them can be expressed in terms of row and column numbers, it seems possible to express the distance between plots as distances between rows and columns in which they are located by the quantities $1, \ldots, R - 1$ and $1, \ldots, C - 1$, respectively. For stationary anisotropic models which originated from the exponential model, i.e., $\mathbf{R} = \sigma^2\text{Corr}(\delta) = \sigma^2(\text{Corr}_r(\delta_r) \otimes \text{Corr}_c(\delta_c))$, this recommendation simplifies the analysis since it is not necessary to obtain the latitude and the longitude at the plot centers; the covariance function does not change but the scale of the coefficients δ_r and δ_c changes. If, on the other hand, the proposed model is isotropic, a scale change affecting distances between both rows and columns in different amounts is impossible and hence the use of a two-dimensional coordinate system based on row and column numbers is incorrect for isotropic models.

The modeling impact is clearly reflected on the comparison of genotype means at each trial. These environment specific inferences are of interest in the presence of genotype × location interaction in METs. When estimating genotype means under the mixed models with spatially structured covariance, least squares genotype means (LSMEANS command in SAS) at each trial (SLICE command in SAS) should be computed, since the structure chosen may affect both the mean estimates and their within-trial standard errors.

CONCLUSIONS

The incorporation of spatial dependence can improve the genotype mean comparisons, but it is not always better than traditional models that include block effects. In this paper, we showed that even for the same crop (peanut) the choice of the best model may depend on other features, such as length of the growing season. Long-cycle peanut cultivars are subject to climate variations longer and did not benefit in general from using spatial correlation structures. A possible reason is that local spatial tendencies may be smoothed with longer seasons, and thus the homogeneity within each block favored models with block effects. We conclude that researchers should evaluate different covariance models and select the best models for their specific crops and environments before comparing genotype means. The mixed model procedure with REML estimation provides a general framework to select the best analysis strategy. For METs, the modeling of the between trial residual heterogeneity can greatly improve the combined analysis, both in models with block effects and with a spatial correlation structure.

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