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Statistics/ Original Article

Relative efficiency of the alpha lattice and randomized complete block designs in maize trials

Abstract – The objective of this work was to compare the relative efficiency of the alpha lattice design (ALD) with that of the randomized complete block design (RCBD) in maize (*Zea mays*) genotype trials. For this, data from 627 trials were used. In each trial, variance components were estimated for grain yield under both designs. The statistical parameters coefficient of variation (CV), heritability, range, least significant difference (LSD), standard error, and coefficient of determination (R^2) were calculated for various sources of variation and the residual. The LSD/range ratio was used as a measure of experimental precision. The analysis of the trials in the ALD not only improved the R^2 of the design (0.62 in the ALD versus 0.42 in the RCBD) and of the genotypes, but also reduced experimental error (0.38 in the ALD versus 0.58 in the RCBD) in more trials than the RCBD. Overall efficiency (RCBD/ALD) varied by statistic, but generally favored the ALD analysis. Specifically, heritability increased from 0.72 in the RCBD to 0.77 in the ALD, while CV decreased from 12.7% in the RCBD to 11.0% in the ALD. The ALD shows a higher relative efficiency than the RCBD in the analysis of maize genotype trials.

Index terms: *Zea mays*, experimental error, experimental precision, heritability.

Eficiência relativa dos delineamentos alfa látice e em blocos ao acaso em ensaios de milho

Resumo – O objetivo deste trabalho foi comparar a eficiência relativa do delineamento em alfa látice (DAL) com a do delineamento em blocos ao acaso (DBC), em ensaios de genótipos de milho (*Zea mays*). Para tanto, dados de 627 ensaios foram utilizados. Em cada ensaio, os componentes de variância foram estimados para rendimento de grãos em ambos os delineamentos. Calcularam-se os parâmetros estatísticos coeficiente de variação (CV), herdabilidade, amplitude, diferença mínima significativa (DMS), erro padrão e coeficiente de determinação (R^2) para várias fontes de variação e o resíduo. Utilizou-se a razão DMS/amplitude como medida de precisão experimental. A análise dos ensaios em DAL não apenas melhorou o R^2 do delineamento (0,62 em DAL contra 0,42 em DBC) e dos genótipos, mas também reduziu o R^2 do erro experimental (0,38 em DAL contra 0,58 em DBC) em mais ensaios que o DBC. A eficiência geral (DBC/DAL) variou com a estatística, mas, geralmente, favoreceu a análise no DAL. Especificamente, a herdabilidade aumentou de 0,72 no DBC para 0,77 no DAL, enquanto o CV diminuiu de 12,7% no DBC para 11,0% no DAL. O DAL apresenta maior eficiência relativa do que o DBC na análise de ensaios de genótipos de milho.

Termos para indexação: *Zea mays*, erro experimental, precisão experimental, herdabilidade.

Román Gordón Mendoza
Instituto de Innovación Agropecuaria de Panamá, Ciudad del Saber, Clayton, Panama.
E-mail: gordon.roman@gmail.com

Ismael Camargo Buitrago
Instituto de Innovación Agropecuaria de Panamá, Ciudad del Saber, Clayton, Panama.
E-mail: camargo.ismael@gmail.com

Jaime Espinosa-Tasón (✉)
Instituto de Innovación Agropecuaria de Panamá, Ciudad del Saber, Clayton, Panama.
E-mail: jaime.espinosa@idiap.gob.pa

✉ Corresponding author

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Introduction

An efficient field trial design is fundamental for the success of plant breeding programs, particularly in minimizing experimental error and improving the precision of varietal comparisons. Traditionally, the randomized complete block design (RCBD) has been widely used due to its simplicity and ability to control variation caused by field heterogeneity (Khan et al., 2015). However, its efficiency diminishes when evaluating a large number of genotypes, as the design struggles to account for increasing variability across plots (Kashif et al., 2011; Anwaar et al., 2019).

To address this limitation, more complex designs such as the Latin square and lattice designs have been proposed. While these offer improved control over field heterogeneity, their practical use is constrained by rigid structural requirements and inefficiency when dealing with large genotype sets (Sewenet, 2019). In this context, alpha lattice designs (ALDs), introduced by Patterson & Williams (1976), offer a flexible and resolvable incomplete block structure suited for trials involving many treatments. These designs have shown superior statistical properties, such as lower coefficients of variation and improved accuracy in genotype comparisons across a wide range of crops and environments (Masood et al., 2008; Mona et al., 2018; Kumar et al., 2020). However, to evaluate the wider applicability of these designs, more trials should be conducted.

Considering both cited designs, Kashif et al. (2011) and Anwaar et al. (2019) found that, to control variability in field trials, a RCBD could be replaced by an ALD when the number of varieties in the trial exceeds 10. In this line, Khan et al. (2015) suggested that the use of the RCBD is not suitable when the number of genotypes reaches 16.

In this scenario, the adaptability and statistical efficiency of the alpha design have led to its widespread adoption in countries with robust plant breeding programs, mainly in Asia, Africa, parts of Latin America, and Mesoamerica (Sierra-Macías et al., 2005; Khan et al., 2015; Sanadya et al., 2022; Akinwale et al., 2021; Morales et al. 2025); in the latter, Centro Internacional de Mejoramiento de Maiz y Trigo (CIMMYT), an international maize and wheat improvement center, stands out. However, despite its proven advantages, the application of the design in Central American breeding programs remains undocumented. As a result, the decision to continue using the RCBD in this region may stem more from convention than from an empirical assessment of alternatives.

As no single design is considered universally optimal, the choice between complete and incomplete block designs, such as the RCBD and ALD, depends on specific research objectives and conditions (Sewenet, 2019), aiming an efficient data collection and accurate parameter estimates in agronomic and genetic research.

The objective of this work was to compare the relative efficiency of the ALD with that of the RCBD in maize (*Zea mays* L.) genotype trials.

Materials and Methods

For this study, the trial database from 2000 to 2021 of the project for the generation of maize varieties and hybrids of Instituto de Innovación Agropecuaria de Panamá was used. These trials include the evaluation, by the project, of genotypes, hybrids, and synthetic varieties from CIMMYT and commercial companies, both at the El Ejido experimental station and at commercial plots of maize producers in the Azuero region of Panama. The analyzed data correspond to the variable grain yield (Mg ha^{-1}) of all trials.

From the total of 692 trials between 2000 and 2021, 627 were used in the analysis of the present work. These trials were selected because their experimental unit was two furrows, not one and four like the remaining 65 trials. From the selected trials, 254 were planted in the El Ejido experimental station (41%) and 373 in fields of producers collaborating with the project (59%). The number of genotypes in the trials ranged from 6 to 102, and all trials with more than 30 genotypes were only planted at the experimental station.

The analyzed trials had different numbers of replicates: three, four, and two for 538, 12, and 77 trials, respectively. All trials were planted using the ALD (Vargas et al., 2013), and the number of genotypes per block varied between 2 and 9, although most of the lattice trials had 3 and 4 genotypes per block.

In each trial, the different variance components of the linear model were calculated for the grain yield variable using the analyses for the ALD and RCBD, through the following equations:

ALD: $Y_{ijk} = \mu + \text{Replicate}_i + \text{Block}_j\,(\text{Replicate}_i) + \text{Genotype}_k + \varepsilon_{ijk}$

RCBD: $Y_{ijk} = \mu + \text{Replicate}_i + \text{Genotype}_k + \varepsilon_{ijk}$

For both analyses, the restricted (or residual) maximum likelihood method implemented in the MIXED procedure of the SAS software (SAS Institute Inc., Cary, NC, USA) was used. In addition to the variances or the mean square (MS) of the design (MS replicate, MS block x replicate, MS genotypes, and MS error), the following statistics were calculated: coefficient of variation (CV), heritability (H^2), range, least significant difference (LSD), coefficient of determination (R^2) of the models and of the sources of variation (genotypes, replicate, and block nested in the replicate), as well as the R^2 of the fraction not explained by each of the designs (R^2 error, residual) and the standard error of difference (SED). The ratio or quotient between the LSD and the range of the trial (LSD/range) was calculated as a measure of experimental precision. The respective equations were used to calculate the aforementioned statistics:

$$CV = \frac{\sqrt{\text{MS error}}}{x} \times 100$$

$$H^2 = \frac{\delta^2_{\text{genotypes}}}{\delta^2_{\text{genotypes}} + \dfrac{\delta^2_{\text{error}}}{\text{No replicate}}}$$

$$\text{Range} = \text{Max} - \text{Min}$$

$$LSD_{5\%} = t \times SED_{x1-x2}$$

$$R^2_{ALD} = \frac{\text{MS replicate} + \text{MS block (replicate)} + \text{MS genotypes}}{\text{MS total}}$$

$$R^2_{RCBD} = \frac{\text{MS replicate} + \text{MS genotypes}}{\text{MS total}}$$

$$R^2_{\text{genotypes}} = \frac{\text{MS genotypes}}{\text{MS total}}$$

$$R^2_{\text{replicate}} = \frac{\text{MS replicate}}{\text{MS total}}$$

$$R^2_{\text{block (replicate)}} = \frac{\text{MS block (replicate)}}{\text{MS total}}$$

$$R^2_{\text{error}} = \frac{\text{MS error}}{\text{MS total}}$$

$$SED_{x1-x2} = \sqrt{\frac{2 \times \text{MS error}}{\text{MS total}}}$$

$$\text{LSD / range ratio} = \text{LSD / range}$$

After being calculated, each of the experimental precision statistics (H^2, LSD/range, CV, and SED), as well as the different variance components for both designs (R^2 of the design, R^2 of the genotypes, R^2 of the experimental error, and R^2 of the replicate), were grouped according to the ALD and RCBD. To determine the relative efficiency of the ALD over the RCBD, i.e., the harmonic mean efficiency (HMEF), the value of the statistic calculated with the RCBD was divided by that calculated with the ALD (Masood et al., 2008; Khan et al., 2015).

In both designs, the trials were conducted according to the number of locations in which they were planted, the number of genotypes in the trial, the number of genotypes per block, and the value of variance between replicates and within blocks.

The criteria used for interpreting the precision of the statistics and designs for the analysis of the trials and of the HMEF factor were the values of the ratio (Table 1): if greater than 1.0, the ALD is more efficient than the RCBD; if lower than 1.0, the RCBD is better than the ALD; if equal or very close to 1.0, then both designs are similar for the evaluated statistic.

To determine which design is more efficient, the data were grouped according to the R^2 values from the different components of the design (treatment, replicate, error, and design), as well as to variance, the nest block component within the replicate, and

Table 1. Criteria for the interpretation of the precision statistics in the alpha lattice design (ALD) and randomized complete block design (RCBD), as well as of the harmonic mean efficiency factor (HMEF), used in the analysis of data from 627 maize (*Zea mays*) genotype trials.

Statistics(1)	Better if the value of the statistic is	Better ALD, if HMEF is
H^2	Higher	Lower
LSD/range	Lower	Higher
CV (%)	Lower	Higher
SED	Lower	Higher
MSE	Lower	Higher
LSD	Lower	Higher
R^2 MS error	Lower	Higher
R^2 MS design	Higher	Lower
R^2 MS treatment	Higher	Lower

(1)H^2, heritability; LSD/range, least significant difference/range ratio; CV, coefficient of variation; SED, standard error of difference; MSE, mean square error; LSD, least significant difference; R^2, coefficient of determination; and MS, mean square.

replicate. The data were also grouped into ranges according to the different sources of the designs and then used for the interpretation of the obtained results.

Results and Discussion

The analysis of the statistics calculated for the ALD and RCBD as a function of the variation between replicate and within the block resulted in groups A to D (Table 2). The trials in group A did not show any variation between replicates or within the replicate, i.e., they should have been analyzed as complete randomized treatments. Of all analyzed trials, 63 presented this condition (10%), among which only 6 (10%) were single trials and the remaining 57 were sown in multiple locations. The 167 trials in group B (27% of the total) showed variation within the replicate, but not between the replicate. In group C, 131 trials (21%) exhibited variation between replicates but not within the replicate, meaning they should have been analyzed in the RCBD; however, only 7 trials (5%) were planted in a single location, while the remaining 124 trials were planted in multiple locations and analyzed in a combined manner. In group D, the 266 trials represented the majority (42%), showing variation both between and within the replicate, consequently displaying the greatest advantage under the ALD.

When grouping the trials according to the presence of variation between replicates, the analysis of the precision statistics (H^2, CV, and the LSD/range ratio) indicated that these were slightly higher in the ALD analysis (Table 2). The differences between the designs were verified when there was no variation within the block, with H^2 and CV showing equal values for both analyses, with a HMEF equal to 1.0. In this scenario, the LSD/range ratio slightly increased from 0.37 to 0.39, performing better in the RCBD analysis. Regarding the sources of variation, a greater representativeness was observed for the genotypes, experimental error calculation, and the model in general when the data analysis was carried out in the ALD, with a HMEF higher than 1.0 for the R^2 of the error and less than 0.75 for the genotypes and the model in general.

Table 2. Statistics calculated in the alpha lattice design (ALD) and randomized complete block design (RCBD) as a function of the variation between the replicate and within the block for data from 627 maize (*Zea mays*) genotype trials⁽¹⁾.

Variation	No. of trials	H^2			CV (%)			LSD/range		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
REP = 0	230	0.72	0.77	0.92	12.8	10.9	1.19	0.41	0.37	1.14
REP > 0	397	0.72	0.76	0.94	12.6	11.0	1.14	0.40	0.37	1.09
BL (REP) = 0	194	0.78	0.78	1.00	10.3	10.3	1.00	0.37	0.39	0.35
BL (REP) > 0	433	0.69	0.76	0.90	13.8	11.3	1.23	0.42	0.36	1.18
A) REP= 0, BL(REP)= 0	63	0.75	0.75	1.00	11.0	11.0	1.00	0.41	0.44	0.95
B) REP= 0, BL(REP)> 0	167	0.70	0.78	0.89	13.5	10.9	1.25	0.41	0.35	1.21
C) REP> 0, BL(REP)= 0	131	0.80	0.80	1.00	10.0	10.0	1.00	0.35	0.37	0.95
D) REP> 0, BL(REP)> 0	266	0.69	0.74	0.91	13.9	11.5	1.21	0.42	0.37	1.16
	%	R^2 GEN			R^2 EE			R^2 design		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
REP = 0	37	0.41	0.54	0.72	0.59	0.38	1.96	0.41	0.62	0.64
REP > 0	63	0.40	0.51	0.76	0.58	0.38	1.79	0.42	0.62	0.66
BL (REP) = 0	31	0.46	0.57	0.78	0.53	0.41	1.36	0.47	0.59	0.78
BL (REP) > 0	69	0.38	0.50	0.73	0.61	0.37	2.07	0.39	0.63	0.60
A) REP= 0, BL(REP)= 0	10	0.43	0.55	0.76	0.57	0.45	1.35	0.43	0.55	0.76
B) REP= 0, BL(REP)> 0	27	0.40	0.53	0.70	0.60	0.35	2.19	0.40	0.65	0.59
C) REP> 0, BL(REP)= 0	21	0.47	0.58	0.78	0.51	0.39	1.36	0.49	0.61	0.78
D) REP> 0, BL(REP)> 0	42	0.37	0.48	0.74	0.61	0.38	2.00	0.39	0.62	0.60

(1)H^2, heritability; CV, coefficient of variation. LSD/range, least significant difference/range ratio; HMEF, harmonic mean efficiency factor; R^2 GEN, coefficient of determination of the genotype; R^2 EE, coefficient of determination of the experimental error; R^2 design, coefficient of determination of the design; REP, replicate; and BL(REP), replicate within the block. A to D represent the groups into which the trials were classified.

When the trials with no variation between replicates were divided into groups A and B, the precision statistics did not show improvements in the 63 trials in group A that also had no variation within the block, but did in the 167 trials in group B analyzed in the ALD (Table 2). In the case of the design statistics, both groups improved when analyzed in the ALD, presenting a HMEF greater than 1.0 for the CV and LSD/range ratio and lower than 1.0 for H^2. The HMEF for the design statistics indicated a reduction greater than the double in error calculation and of 50% in the calculations for the genotypes and model in general. Similar results were obtained for the analysis of the trials that presented differences between replicates (groups C and D), with improvements in both the precision and statistics of the model when there was variation within the replicate.

The benefits of the ALD were evident even with three replicates, which is consistent with the design parameters used in most reviewed works (Rebollosa-Hernández et al., 2020; Morales et al. 2025). Despite the limited guidance in the literature on optimal replicate levels, the consistent precision gains across studies using three replicates suggest this number is adequate in trials with a well-structured blocking.

With the ALD, a higher proportion of trials showed an improved design fit and a lower residual. This design also detected a greater genotypic variance, indicating an improved experimental precision.

In the analysis of the two studied designs, a varied HMEF or RCBD/ALD ratio was observed for the different evaluated statistics. However, these statistics were always better under the alpha lattice analysis (Table 3). According to the experimental precision statistics, H^2, the LSD/range ratio, CV, and SED showed better results in the ALD, with respective averages of 0.77, 0.37, 11.0, and 0.51% in the analyzed trials compared with those of 0.72, 0.40, 12.7, and 0.58% under the RCBD. HMEF was higher than 1.0 for the LSD/range ratio, CV, and SED but lower than 1.0 for H^2. Since the latter statistic is better when its value is higher and the HMEF is lower than 1.0, the ALD shows superiority in comparison to the RCBD.

The percentage of trials where the ALD was superior to the RCBD was much higher than the percentage where the RCBD was superior to the ALD (Table 3). The SED decreased from 0.53 in the RCBD analysis to 0.36 in the ALD analysis, presenting a HMEF of 1.47, which indicated an improvement of 47% using the latter design. This represented 53% (HMEF of 1.53) in the reduction of what this value represents in the statistical model. Both the R^2 of the genotypes and of the design showed improvements when the data were analyzed in the ALD, with a ratio or HMEF lower than 1.0, i.e., with values of 0.77 and 0.67, respectively. These differences were not only superior in the ALD analysis but were also observed in most locations (in more than 98%) for the precision statistics and almost in all locations for the model statistics (Table 4).

Regarding the calculation of H^2, a greater number of points was noted above the diagonal of the graph (69%), indicating higher values when the trial was analyzed in the ALD (Figure 1). In relation to the dispersion of the trials, there was a greater number of points above the diagonal line, indicating a higher R^2 under the ALD (Figure 2). For the R^2 for the experimental error, most

Table 3. Average of the calculated statistics in the alpha lattice design (ALD) and randomized complete block design (RCBD) for data from 627 maize (*Zea mays*) genotype trials[1].

Calculated statistics	Better if statistics is	RCBD	ALD	HMEF (ratio)	Better ALD (%)	Best RCBD (%)	Equal
H^2	Higher	0.72	0.77	0.94	77	4	9
LSD/range	Low	0.40	0.37	1.09	59	9	32
CV (%)	Low	12.70	11.00	1.16	71	7	22
SED	Low	0.58	0.51	1.14	71	0	29
MS error	Low	0.53	0.36	1.47	100	0	0
R^2 error	Low	0.58	0.38	1.53	100	0	0
R^2 genotype	Higher	0.40	0.52	0.77	98	1	1
R^2 design	Higher	0.42	0.62	0.67	100	0	0

(1)HMEF, harmonic mean efficiency factor; H^2, heritability; LSD/range, least significant difference/range ratio; CV, coefficient of variation; SED, standard error of difference; MS, mean square; and R^2, coefficient of determination.

of the points were below the diagonal, indicating that the experimental error was higher in the trials analyzed in the RCBD.

When analyzing or grouping the trials according to whether they were conducted in multiple locations or in a single location, the precision statistics were better in the ALD in both types of trials (Table 4). These trials presented a HMEF greater than or very close to 1.0 for three statistics (H^2, CV, and the LSD/range ratio), showing the highest values in the single location. As for the R^2, all values were better in the ALD analysis and very similar for trials in single and multiple locations.

When the trials were grouped according to the number of genotypes, the precision statistics improved in the ALD analysis, since a decrease in the CV and LSD/range ratio was observed, as well as an increase in H^2 (Table 5). An improvement was also verified in the values calculated for HMEF in the case of error, which was almost half in the ALD analysis compared with that in the RCBD (1.94), but higher than 50% for genotypes and the design in general under the ALD analysis, with a HMEF of 0.75 and 0.70, respectively. Therefore, both sets of statistics were better in the ALD analysis as the number of genotypes increased. This result can be explained by the fact that the greater the number of genotypes, the greater the length of the replicate, with a greater variation expected within the block.

The greater efficiency of the ALD in detecting treatment differences reflects its superior ability to control spatial variability. This advantage becomes especially evident in trials involving a large number of genotypes, as documented by Khan et al. (2015) and Akinwale et al. (2021), who noted an improved precision and statistical power when using this design to test more than 10 genotypes.

According to the number of genotypes per block, all the precision statistics were better under the ALD analysis, with increases in H^2, decreases in CV, and decreases in the LSD/range ratio (Table 6). However, in two of these three statistics (H^2 and the LSD/range ratio), the best values were those obtained in the trials using 3 genotypes per block. For the R^2 of the experimental error, as the number of genotypes per block decreased, its values showed a tendency of reduction, which was almost three times greater (2.96) in the trials using 2 genotypes per block in the ALD. Contrastingly, the HMEF was reduced as the number of genotypes per block increased. In both evaluated designs, the highest values for the R^2 and genotypes were achieved in the analyses using 3 genotypes per block; however, the greatest gain in HMEF was obtained in the trials analyzed in the RCBD and then in the ALD, specifically with more than 4 genotypes per block. By reducing the number of genotypes per block, the variation within the block is expected to decrease, which suggests a more uniform block and, therefore, a greater experimental precision through a better control of the experimental error.

Even though details on block sizes have not been consistently reported across studies, the improved performance when using the ALD in the tested trials suggests that even moderately-sized incomplete blocks can effectively account for local variation. This aligns with the observations by González□Barrios et al. (2019), who emphasized that the ALD

Table 4. Statistics calculated in the alpha lattice design (ALD) and randomized complete block design (RCBD) as a function of the number of experimental locations where each trial was planted for data from 627 maize (*Zea mays*) genotype trials⁽¹⁾.

Experimental locations	H^2			CV (%)			LSD/range		
	RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
Multiple locations	0.73	0.77	0.94	12.7	11.0	1.15	0.40	0.37	1.10
Single location	0.63	0.69	0.88	12.9	10.4	1.20	0.41	0.35	1.18
	R^2 GEN			R^2 EE			R^2 design		
	RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
Multiple locations	0.4	0.52	0.74	0.58	0.38	1.86	0.42	0.62	0.65
Single location	0.41	0.52	0.74	0.59	0.38	1.71	0.41	0.62	0.65

⁽¹⁾H^2, heritability; CV, coefficient of variation; LSD/range, least significant difference/range ratio; HMEF, harmonic mean efficiency factor; R^2 GEN, coefficient of determination of the genotype; R^2 EE, coefficient of determination of the experimental error; and R^2 design, coefficient of determination of the design.

optimizes field layout without compromising the integrity of genotype comparisons.

In relation to the R^2 values from different sources of variation of the design, a reduction in experimental error was observed in all groups, despite being greater (more than double) in those in which the trials showed variation within the replicate. An increase in both the R^2 of genotypes and the model in general was also verified, mainly in the trials in group D, which presented the greatest variability in experimental units in the whole study.

When the significance test was performed under both methods of analysis, a higher F-value, with a higher probability of rejecting the null hypothesis, was observed. This resulted in a HMEF greater than 1.0 as the number of genotypes in the trial and the number of

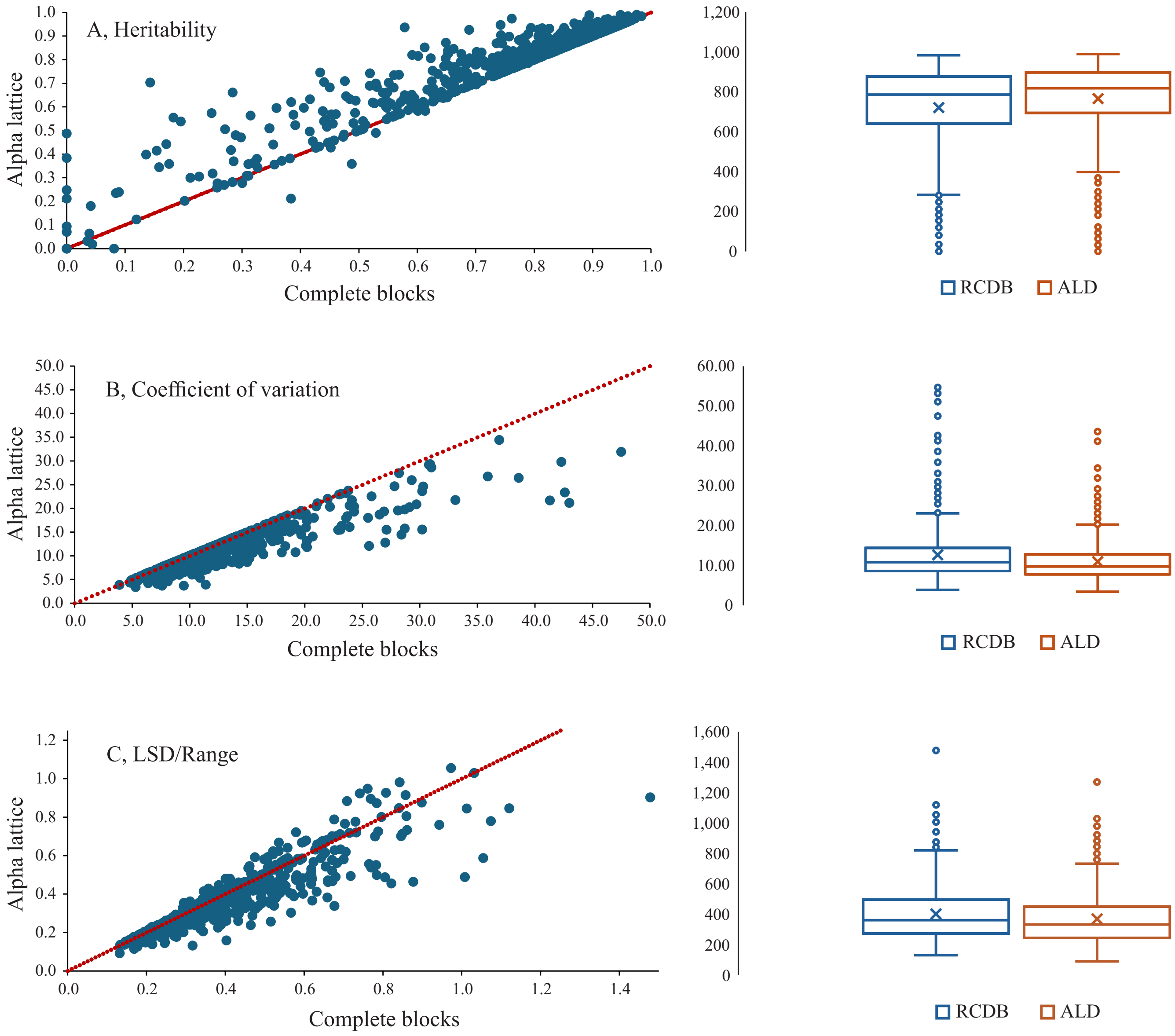

Figure 1. Distribution and Tukey boxes of maize (*Zea mays*) trials for the statistics: A, heritability (H^2); B, coefficient of variation (CV); and C, ratio between the least significant difference and the range of the trial (LSD/range), analyzed in the alpha lattice design (ALD) and randomized complete blocks design (RCBD) for the grain yield variable of 627 maize (*Zea mays*) genotype trials.

genotypes per block increased (Figure 3). In relation to the presence or absence of variation regarding replicates, there was a greater reduction when variation was present between and within replicates. In the RCBD analysis, 199 trials showed a significance of less than 5%, while, in the ALD analysis, 240 trials exhibited a significance of less than 5%, i.e., 41 trials improved precision in detecting statistical differences, as shown by the higher amount of values close to zero (indicated by the bar) of the ALD (y-axis) compared with those of the RCBD (x-axis).

In most studies, the ratio of the mean square error of the RCBD over that of the ALD is used to estimate the HMEF (Referência). However, Kumar et al. (2020) proposed estimating the HMEF considering the CV of the RCBD over that of the ALD, obtaining similar

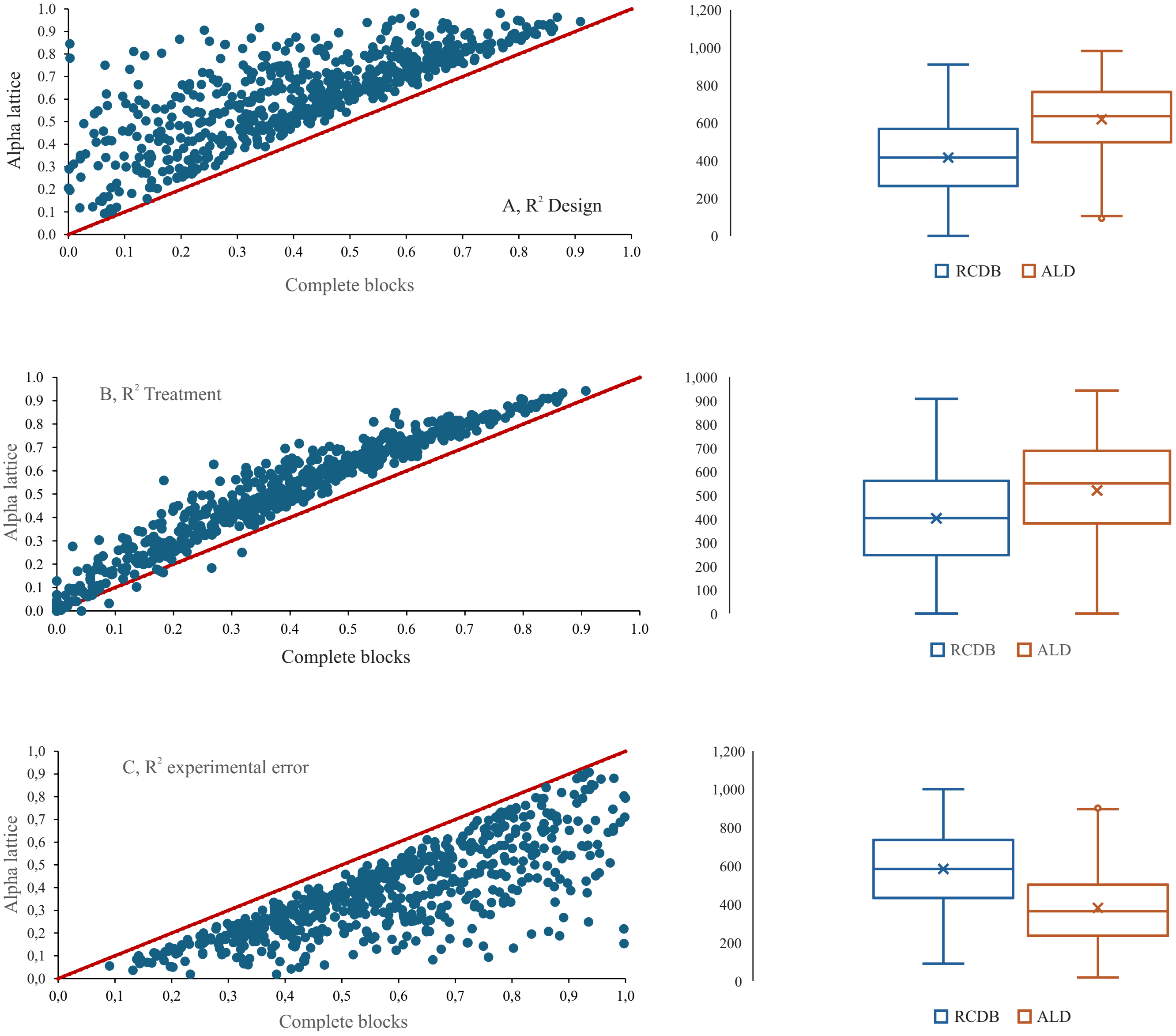

Figure 2. Distribution of intervals and Tukey boxes for the statistics: A, the coefficient of determination of the design (R^2 design); B, the coefficient of determination of the treatment (R^2 treatment); and C, the coefficient of determination of the experimental error (R^2 experimental error), analyzed under the alpha lattice design (ALD) and randomized complete blocks design (RCBD) for the grain yield variable from 627 maize (*Zea mays*) genotype trials.

results to those of the present study. Therefore, the present work extends the possibility of exploring the efficiency of the harmonic mean through other statistics of the model, as well as through the statistics normally used to estimate experimental precision.

The analysis of the precision statistics (H^2, CV, and LSD/range) for both designs confirms previous findings, while the stratified view underscores the ALD's consistent pattern of superiority in diverse replicate and blocking scenarios (Table 7). Even though groups A and C did not show significant improvement in precision under the ALD, groups B and D, representing trials with variation within replicates, exhibited marked gains in efficiency metrics. Specifically, group B showed an improved CV of 13.5–10.9%, a better LSD/range ratio of 0.41–0.35, and a higher H^2 of 0.70–0.78. Moreover, the HMEF for the experimental error and model fit was above 2.0 in group B, indicating more than 100% improvement in error estimation when using the ALD over the RCBD. This reaffirms that the ALD provides substantial gains in experimental precision and statistical power, especially in trials with a high intra-replicate variability.

Considering the obtained results, in order to enhance the precision and efficacy of crop improvement programs, particularly in multi-environment trials, the ALD should often substitute the RCBD when evaluating numerous genotypes. This is because the ALD assists in experimental error minimization and precision improvement, as evidenced by studies across different crops (Jones et al., 2015; Borges et al., 2019; Alivelu et al., 2020; Sedeck et al., 2021). Abd El-Shafi

Table 5. Statistics calculated in the alpha lattice design (ALD) and randomized complete block design (RCBD) as a function of the number of genotypes per trial for data from 627 maize (*Zea mays*) genotype trials(1).

Genotype/ trial	No. of trials	H^2			CV (%)			LSD/R		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
≤ 12	206	0.74	0.78	0.95	12.4	11	1.14	0.44	0.43	1.06
≤ 24	302	0.73	0.78	0.93	12.2	10.6	1.15	0.38	0.34	1.12
> 24	119	0.65	0.71	0.90	14.5	11.9	1.19	0.40	0.34	1.17
	%	RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
≤ 12	33									
≤ 24	48	0.41	0.52	0.75	0.58	0.39	1.76	0.42	0.61	0.66
> 24	19	0.38	0.49	0.74	0.62	0.39	1.94	0.38	0.61	0.62

(1) H^2, heritability; CV, coefficient of variation; LSD/range, least significant difference/range ratio; and HMEF, harmonic mean efficiency factor.

Table 6. Statistics calculated in the alpha lattice design (ALD) and randomized complete block design (RCBD) as a function of the number of genotypes per block in the ALD for data from 627 maize (*Zea mays*) genotype trials(1).

Genotypes per block	N° of trials	H^2			CV (%)			LSD/range		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
2	86	0.68	0.73	0.93	11.6	10	1.18	0.49	0.5	1.03
3	253	0.77	0.81	0.95	12.2	10.7	1.16	0.38	0.35	1.11
4	171	0.69	0.75	0.91	13.3	11.2	1.16	0.41	0.36	1.14
> 4	117	0.69	0.73	0.92	13.7	11.9	1.13	0.38	0.35	1.12
	%	R^2 GEN			R^2 EE			R^2 design		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
2	14	0.33	0.51	0.6	0.65	0.33	2.96	0.35	0.67	0.49
3	40	0.44	0.56	0.77	0.54	0.34	1.87	0.46	0.66	0.67
4	27	0.38	0.49	0.74	0.61	0.42	1.57	0.39	0.58	0.65
> 4	19	0.41	0.49	0.79	0.59	0.45	1.39	0.41	0.55	0.72

(1) H^2, heritability; CV, coefficient of variation; LSD/range, least significant difference/range ratio; HMEF, harmonic mean efficiency factor; R^2 GEN, coefficient of determination of the genotype; R^2 EE, coefficient of the determination of experimental error; and R^2 design, coefficient of determination of the design.

(2014), for instance, found a higher relative efficiency for various yield traits in bread wheat when using the ALD. The same design was adopted by Haseeba (2024) to evaluate numerous wheat genotypes. Similarly, Duppala et al. (2018) demonstrated the advantages of the ALD in mustard [*Brassica juncea* (L.) Czern.] trials, including relative efficiency values above unity for quantitative characters, resulting in the design's broader use under field conditions with many treatments. In oat (*Avena sativa* L.) trials, Sanadya et al. (2022) showed that the ALD had a relative efficiency greater than 1.0 even when considering potential variability from genotype-by-environment interactions. Likewise, Abdelkawy et al. (2020) noted that the ALD consistently offered a higher precision and significantly greater relative efficiency in estimating treatment effects across various yield and agronomic traits of triticale (× *Triticosecale* Wittm. ex A.Camus). These results support prior findings that the ALD offers improved control over experimental error and environmental variability compared with the RDBD. In addition, several studies (Masood et al., 2008; Ghareeb et al., 2015; Masood et al., 2018) have reported similar reductions in CV and mean square errors when using the ALD, confirming its suitability for genotype trials with heterogeneous field conditions. Akinwale et al. (2021), for example, highlighted this adaptability when using the ALD across multiple environments, further endorsing it as a reliable design for multi-location genotype trials.

When comparing the performance of different designs in maize trials, it is important to consider the statistical methods used for variety selection. In this line, Yiğit (2025) found that the Tukey test and the analysis of mean tests maintain a better control over Type I error rates compared with the LSD and Duncan tests in balanced and partially balanced lattice designs. Therefore, the analysis of means offers a more understandable approach, especially when a high number of groups is considered.

The present study further strengthens the argument for adopting the ALD over the RCBD in multi-

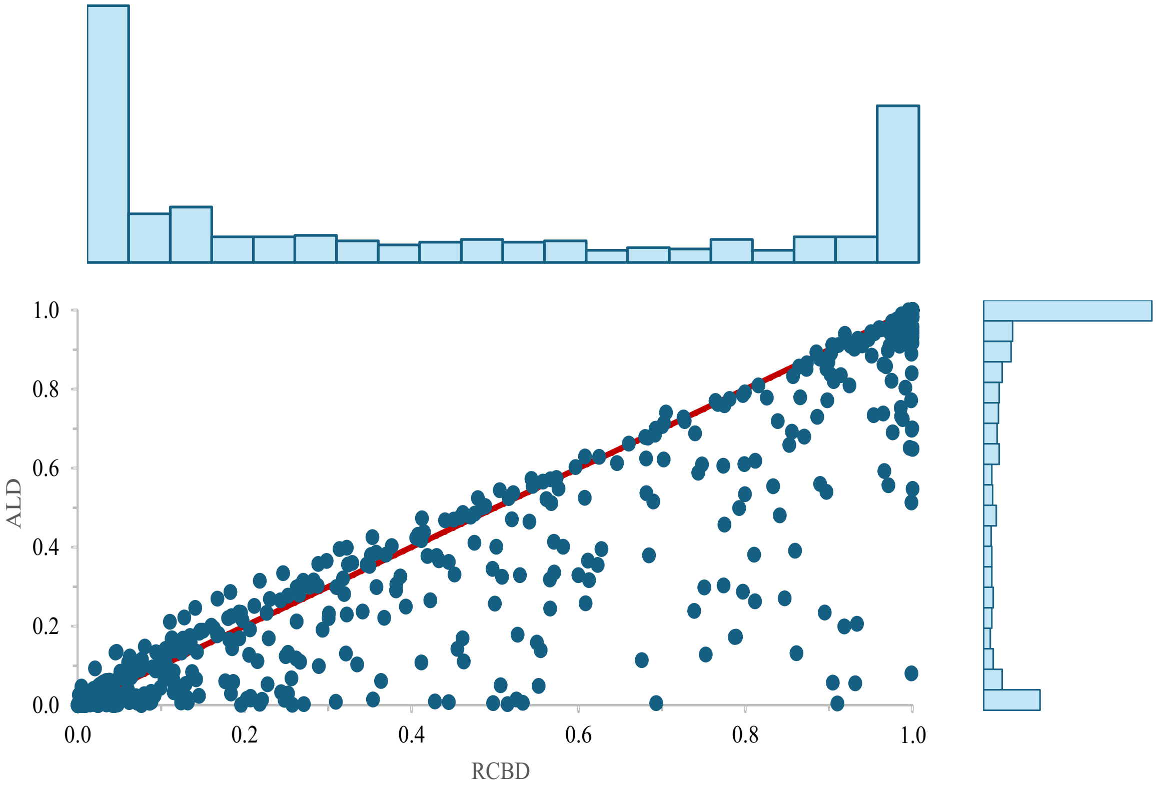

Figure 3. Significance of genotypes by the F-test when performing the alpha lattice design (ALD) and randomized complete blocks design (RCBD) analysis for the grain yield variable from 627 maize (*Zea mays*) genotype trials.

Table 7. Statistics calculated in the alpha lattice design (ALD) and randomized complete block design (RCBD) as a function of the variation between the replicate and of the replicate within the block for data from 627 maize (*Zea mays*) genotype trials(1).

Variation	N° of trials	H^2			CV (%)			LSD/range		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
REP = 0	230	0.72	0.77	0.92	12.8	10.9	1.19	0.41	0.37	1.14
REP > 0	397	0.72	0.76	0.94	12.6	11.0	1.14	0.40	0.37	1.09
BL (REP) = 0	194	0.78	0.78	1.00	10.3	10.3	1.00	0.37	0.39	0.35
BL (REP) > 0	433	0.69	0.76	0.90	13.8	11.3	1.23	0.42	0.36	1.18
A) REP = 0, BL(REP) = 0	63	0.75	0.75	1.00	11.0	11.0	1.00	0.41	0.44	0.95
B) REP = 0, BL(REP) > 0	167	0.70	0.78	0.89	13.5	10.9	1.25	0.41	0.35	1.21
C) REP > 0, BL(REP) = 0	131	0.80	0.80	1.00	10.0	10.0	1.00	0.35	0.37	0.95
D) REP > 0, BL(REP) > 0	266	0.69	0.74	0.91	13.9	11.5	1.21	0.42	0.37	1.16
	%	R^2 GEN			R^2 EE			R^2 design		
		RCBD	ALD	HMEF	RCBD	ALD	HMEF	RCBD	ALD	HMEF
REP = 0	37	0.41	0.54	0.72	0.59	0.38	1.96	0.41	0.62	0.64
REP > 0	63	0.40	0.51	0.76	0.58	0.38	1.79	0.42	0.62	0.66
BL (REP) = 0	31	0.46	0.57	0.78	0.53	0.41	1.36	0.47	0.59	0.78
BL (REP) > 0	69	0.38	0.50	0.73	0.61	0.37	2.07	0.39	0.63	0.60
A) REP = 0, BL(REP) = 0	10	0.43	0.55	0.76	0.57	0.45	1.35	0.43	0.55	0.76
B) REP = 0, BL(REP) > 0	27	0.40	0.53	0.70	0.60	0.35	2.19	0.40	0.65	0.59
C) REP > 0, BL(REP) = 0	21	0.47	0.58	0.78	0.51	0.39	1.36	0.49	0.61	0.78
D) REP > 0, BL(REP) > 0	42	0.37	0.48	0.74	0.61	0.38	2.00	0.39	0.62	0.60

(1)H^2, heritability; CV, coefficient of variation; LSD/range, least significant difference/range ratio; HMEF, harmonic mean efficiency factor; REP, replicate; BL(REP), replicate within the block; R^2 GEN, coefficient of determination of the genotype; R^2 EE, coefficient of determination of the experimental error; and R^2 design, coefficient of determination of the design.

environment genotype evaluations involving moderate to large numbers of treatments, particularly where spatial variability is a concern. An enhanced relative efficiency and improved precision, as indicated by lower CV values, highlight the practical advantage of the ALD. Future research could further explore the specific conditions under which this advantage is most pronounced.

Conclusions

1. The alpha lattice design has a higher relative efficiency than the randomized complete block design in the analysis of maize (*Zea mays*) genotype trials.
2. The statistics coefficient of variation, heritability, range, least significant difference, and standard error are suitable for evaluating the relative efficiency of the alpha lattice design in maize genotype trials.
3. An increased genotype number or replicate length in maize genotype trials correlates with a greater variation within blocks.
4. Experimental design adjustments may be necessary when dealing with a high number of genotypes or longer replicates to account for an increased heterogeneity.
5. Decreasing the number of genotypes within a block improves block uniformity and, consequently, increases experimental precision in the evaluated trials.

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Author contributions

Román Gordon Mendoza: conceptualization (lead), data curation (lead), formal analysis (lead), funding acquisition (lead), investigation (lead), methodology (lead), project administration (lead), resources (lead), software (equal), supervision (equal), validation (equal), visualization (equal), writing - original draft (equal), writing - review & editing (equal); **Ismael Camargo Buitrago**: conceptualization (equal), formal analysis (equal), investigation (equal), resources (equal), supervision (equal), validation (equal), visualization (equal), writing - original draft (supporting), writing - review & editing (supporting); **Jaime Espinosa-Tasón**: conceptualization (supporting), software (equal), visualization (equal), writing - original draft (equal), writing - review & editing (equal).

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No generative artificial intelligence (AI) was used in this study.

Conflict of interest statement

The authors declare no conflicts of interest.

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