Evaluation of Relative Efficiency of Alpha Lattice Design and Cluster Analysis of Twenty Spring Triticale Field Experiments

R.N.F. Abdelkawy\(^1,2\), A.Z. Turbayev\(^1\), A.A. Soloviev\(^3,4\)  
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**ABSTRACT**

Twenty genotypes triticale were evaluated in an alpha lattice design and RCBD for eight characters to a comparison of the relative efficiency (RE) of alpha-lattice design and RCBD. Two experiments were analyzed according to alpha lattice design and RCBD design. Average estimated (RE) was 12.97, 5.93, 21.79, 35.50, 21.53, 23.96 and 26.69% for number of plants/m\(^2\), tillering fertility, plant height (cm), spike length (cm), number of spikelets/spike, 1000-grain weight (g) and grain yield (g/m\(^2\)), respectively, the high precision is obtained significantly to estimate treatment effects indicating that using an alpha lattice design in place of RCBD. Mean comparisons for both RCBD and alpha lattice design were performed and two designs confirmed to Dublet, Ulyana, 131/1656 and C259 genotypes were the highest yield (g/m\(^2\)). Cluster analysis showed that genotypes were isolated into three principle groups and one of these contains one variety (Dublet). This variety was characterized by a high yield over two years. The results showed that alpha lattice more efficient and it can be used it instead of traditional RCBD design in the agricultural field trials.

**Key words:** Alpha lattice design, Cluster analysis, Efficiency, RCBD, Triticale yield trials.

**INTRODUCTION**

Triticale (\(\times\) Triticosecale Wittmack ex A. Camus) - cereal grain species, artificially created by man as a result of interspecific hybridization of wheat and rye. Triticale is becoming a popular crop due to its resistance to stress factors, high nutritional value and good baking characteristics of wheat gluten. Triticale generally does well in conditions of abiotic stress compared to wheat (Aydogan et al., 2010 and Abdelaal et al., 2019). Triticale has a high potential of yield and grain quality, which allows using this crop for different food purposes-baking, confectionery, pasta industry, etc. (Grabovets et al., 2013; Chernyshova et al., 2015 and Zhu 2018).

Randomized complete block design is one of the common widely used designs in field experiments in the world. Fisher (1926) emphasized the importance of randomized arrangements in the estimation of experimental error and described the randomized complete block designs. However, in some cases, efficiency of the RCBD is low. The problem with complete block is that the size of block increases due to the increase in the number of treatments, the homogeneity of experimental plots within a large block is difficult to sustain and thus local control of experimental variability becomes inefficient (Stroup et al., 1994). Due to the limitation on the number of genotypes that may be evaluated, there have been a number of suggested lattice type designs, the most popular being the alpha design (Giesbrecht and Gumpertz, 2004; Hinkelman and Kempthorne, 2006). Alpha lattice design, introduced by Patterson and Williams (1976), is routinely used for field trials in different countries: United Kingdom (Patterson and Silvey, 1980); Syria (Yau 1997); Germany (Piepho et al., 2006); Pakistan (Kashif et al., 2011, Masood et al., 2018); Denmark (Kristensen 2012); Chile (Xing et al., 2014); Egypt (Abd El-Shafi 2014, Ghareeb et al., 2015) and India (Duppala et al., 2018).

The accuracy of this design depended on the control of heterogeneity within blocks. But unfortunately the use of RCBD is inefficient and unsuitable when the number of genotypes is as large as sixteen in a single block (Costa e Silva et al., 2001 and Yang et al., 2004) because of their failure to adequately minimize the effect of soil heterogeneity (Lentner and Bishop, 1993). Also, when the number of factors and their levels increases, the treatment combinations number increases rapidly and it is impossible to participate all these treatment combinations in a single homogeneous block (Idrees and Khan; 2009). Many researchers used alpha lattice design in field trials (Yau 1997 on barley and wheat; Campbell and Bauer, 2007 on cotton; Masood et al., 2008 on wheat and potato; Kashif et al., 2011).
on rice; Abd El-Mohsen and Abo-Hegazy 2013 on wheat; Abd El-Shafi, 2014 on wheat; Xing et al., 2014 on white clover; Ghareeb et al., 2015 on faba bean; Duppala et al., 2018 on mustard and Bonney et al., 2018 on cowpea). They concluded that alpha lattice design is more efficient than RCBD and has potential to replace RCBD in regional and international trials.

**MATERIALS AND METHODS**

A field experiment was conducted at the Department of Genetics, Biotechnology, Breeding and Seed Sciences and on the Field Research Station, Russian State Agrarian University - Moscow Timiryazev Agricultural Academy (RSAU – MTA), during seasons 2017 and 2018 to evaluate the yielding ability of 20 genotypes of triticale. The details of the pedigree for the tested genotypes are presented in Table 1.

### Experimental design

The experiment was conducted according to alpha lattice design with three replications. Each replicate contained 20 genotypes, distributed over 4 blocks, with 5 experimental units per block (Table 2). This arrangement across incomplete blocks has been found to minimize variation within the block. The randomization of 20 genotypes was done with GenStatv.14 software (Payne et al., 2011). Each plot consisted of seven rows, with 5 m length and 1 m apart and 15 cm between rows. Grains of all genotypes were grown at density of 2500 plants per plot.

All agricultural practices of tritcalle were applied. At harvest ten guarded plants were taken at random from each experimental plot for each genotype. The following data were recorded: number of plants / m², tillering general, tillering

### Table 1: Name and origin of the twenty tested triticale genotypes.

| Code | Genotypes      | Origin    | Code | Genotypes      | Origin    |
|------|----------------|-----------|------|----------------|-----------|
| G1   | Grebeshok      | Russia    | G11  | C259           | RSAU – MTA |
| G2   | Ukro           | Ukraine-Russia | G12  | C238           | RSAU – MTA |
| G3   | Ulyana         | Belarus   | G13  | Sandro         | Switzerland |
| G4   | Khlodar Kharkovsky | Ukraine | G14  | Legalo         | Poland    |
| G5   | Yarilo         | Krasnodar-Russia | G15  | 6-35-5        | RSAU – MTA |
| G6   | Pamyat Merezhko | Russia-Belarus | G18  | L8605         | RSAU – MTA |
| G7   | 131/714        | RSAU-MTAA | G17  | 131/1656      | RSAU – MTA |
| G8   | Lana           | Belarus   | G18  | P2-13-5-2     | RSAU – MTA |
| G9   | Dublet         | Poland    | G19  | PL-13-5-13    | RSAU – MTA |
| G10  | 131/7          | RSAU-MTAA | G20  | P2-16-20      | RSAU – MTA |

### Table 2: Field layout of alpha lattice design with 20 genotypes in 3 complete replications. Each replicate contained 4 blocks (B) and each block contained 5 genotypes (G).

| Block | Genotype | Block | Genotype | Block | Genotype |
|-------|----------|-------|----------|-------|----------|
| 1     | G15      | 1     | G13      | 1     | G7       |
| 1     | G2       | 1     | G19      | 1     | G10      |
| 1     | G5       | 1     | G7       | 1     | G20      |
| 1     | G13      | 1     | G12      | 1     | G2       |
| 1     | G6       | 1     | G16      | 1     | G14      |
| 2     | G17      | 2     | G10      | 2     | G6       |
| 2     | G1       | 2     | G3       | 2     | G4       |
| 2     | G9       | 2     | G17      | 2     | G19      |
| 2     | G3       | 2     | G4       | 2     | G11      |
| 2     | G10      | 2     | G5       | 2     | G12      |
| 3     | G16      | 3     | G18      | 3     | G17      |
| 3     | G20      | 3     | G2       | 3     | G15      |
| 3     | G7       | 3     | G11      | 3     | G5       |
| 3     | G11      | 3     | G14      | 3     | G18      |
| 3     | G18      | 3     | G1       | 3     | G13      |
| 4     | G19      | 4     | G9       | 4     | G3       |
| 4     | G8       | 4     | G6       | 4     | G9       |
| 4     | G14      | 4     | G15      | 4     | G8       |
| 4     | G12      | 4     | G8       | 4     | G1       |
| 4     | G4       | 4     | G20      | 4     | G16      |
fertility, plant height (cm), spike length (cm), number of spikelets / spike, 1000-grain weight (g) and grain yield (g / m²), were recorded from the central harvested area (5 m²).

Statistical Methods

A statistical analysis of two seasons was carried out, according to the technique of analysis of variance (ANOVA) for the alpha lattice design developed by Patterson and Williams (1976) (Table 3).

Data of seasons was statistically analyzed according to the technique of analysis of variance (ANOVA) for the alpha lattice design developed by Patterson and Williams (1976). The linear model of observations in alpha design is as follows:

\[ y_{ijk} = \mu + t_i + r_j + b_{jk} + e_{ijk} \]

Where \( y_{ijk} \) denotes the value of the observed trait for \( i^{th} \) treatment received in the \( k^{th} \) block within \( j^{th} \) replicate (superblock), \( t_i \) is the fixed effect of the \( i^{th} \) treatment \( (i = 1, 2, \ldots, t) \); \( r_j \) is the effect of the \( j^{th} \) replicate (superblock) \( (j = 1, 2, \ldots, r) \); \( b_{jk} \) is the effect of the \( k^{th} \) incomplete block within the \( j^{th} \) replicate \((k = 1, 2, \ldots, s)\) and \( e_{ijk} \) is an experimental error associated with the observation of the \( i^{th} \) treatment in the \( k^{th} \) incomplete block within the \( j^{th} \) complete replicate.

The relative efficiency of alpha lattice design compared with a conventional RCBD was done by using the mean square error from each analysis according to the following equation:

Relative efficiency =

\[
\frac{\text{Error mean squares in RCBD}}{\text{Error mean squares in alpha lattice design}} \times 100
\]

If the relative efficiency (R.E.) is less than 100 % it indicates that a RCBD is a more efficient design, while value nearly equal to 100 % suggests that the two designs yield similar results. Value greater than 100% suggests that alpha lattice design is more efficient than RCBD (Masood et al., 2008). Mean comparisons were performed under both design (RCBD and alpha lattice). All the statistical analyses were carried out through the computer GenStat v.14 software.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance (ANOVA) of RCBD and Alpha Lattice design for both studied seasons is presented in Tables (4 and 5). Results in 2017 - 2018 seasons revealed that the mean squares of the twenty genotypes had significantly differences (\( p \leq 0.05 \)) for all the studied traits, except number of plants, tillering general, tillering fertility and spike length. These results showed that considerable amount of genetic variation is present in these materials. These results are in agreement with those obtained by Abd El-Mohsen and Abo-Hegazy (2013); Abd El-Shafi (2014); Ghareeb et al. (2015) and Duppala et al. (2018).

Efficiency of RCBD and alpha lattice design

Data of triticale experiment during 2017 and 2018 seasons are shown in Table 6. The results detected that error mean squares (error) values of alpha lattice design were lower than error mean squares of RCBD for all the studied traits in two seasons, except tillering general and tillering fertility in 2017 only. Then, the effectiveness of the alpha lattice analysis was reducing the experimental error. These results were in agreement with those obtained by Masood et al., (2008); Idrees and Khan (2009); Abd El-Mohsen and Abo-Hegazy (2013); Abd El-Shafi (2014); Xing et al. (2014); Ghareeb et al. (2015); Duppala et al. (2018) and Masood et al. (2018).

### Table 3: Form of analysis of variance for alpha lattice design.

| Source of variation                  | Degrees of freedom | Sum of Squares | Sum of Squares | Mean squares |
|--------------------------------------|--------------------|----------------|----------------|--------------|
| Replications                         | r-1                | SS_r          | MS_r          |              |
| Blocks (within replications, ignoring treatments) | rs-r               | SS_b          | MS_b          |              |
| Treatments (adjusted for blocks)     | t-1                | SS_t          | MS_t          | F_0          |
| Error                                | rt-rs-t+1          | SS_e          | MS_e          |              |
| Total                                | tr-1               | SS_T          | -             |              |

### Table 4: Mean squares (RCBD) of the studied traits in triticale genotypes for 2017 and 2018 seasons.

| S.O.V | df | Year | NP | TG | TF | PH | SL | NS | GW | GY |
|-------|----|------|----|----|----|----|----|----|----|----|
| Replication | 2  | 2017 | 3706 | 0.20 | 0.14 | 4.50 | 0.25 | 3.01 | 9.15 | 219 |
|          |    | 2018 | 249  | 0.01 | 0.02 | 7.37 | 0.11 | 0.10 | 0.10 | 1807 |
| Genotypes | 19 | 2017 | 1701 | 0.14 | 0.09 | 215.16** | 0.88 | 8.14* | 32.62** | 10426** |
|          |    | 2018 | 1376 | 0.10 | 0.03 | 101.83** | 0.74 | 6.61* | 23.88** | 8934** |
| Error   | 38 | 2017 | 5041 | 0.09 | 0.07 | 15.01 | 0.95 | 4.28 | 3.43 | 3452 |
|          |    | 2018 | 3635 | 0.10 | 0.02 | 22.40 | 0.73 | 3.02 | 1.34 | 3296 |

** and * = Significant at 1 and 5% probability level, respectively.

NP: number of plants/m², TG: tillering general, TF: tillering fertility, PH: plant height, SL: spike length (cm), NS: number of spikelets / spike, GW: 1000-grain weight (g) and GY: grain yield (g/m²).
In general, the results indicated that the relative efficiencies (R.E. %) were greater than 100% showing that alpha lattice design was more efficient than RCB design for all the studied traits in two seasons except the tillering fertility (65.18%) only 2017 season. The value of relative efficiency indicates the advantage of the Alpha Lattice design alternatively of RCBD design increased in improving the accuracy of the experiment for most yield attributes analysis. Meanwhile, the average of relative efficiency indicated that the use of alpha lattice design instead of RCBD design increased experimental precision by 12.97, 5.93, 21.53, 26.69% for number of plants/m², tillering fertility, plant height (cm), spike length (cm), number of spikelets/spike, 1000-grain weight (g) and grain yield (g/m²).

Mean comparisons of RCBD and alpha lattice designs

The genotypes mean performance of traits were estimated in two seasons 2017 and 2018 (Table 7). The results showed that the mean of genotypes according to their traits was different under the RCBD compared with alpha lattice design. These differences between means of genotypes may be attributed to the effect of environmental factors and their interactions with genotypes, beside the high value of experimental error mean square due to the high number of experimental plot (20 plots) included in each replicate. These results are in accordance with Abd El-Mohsen and Abo-Hegazy (2013); Abd El-Shafi (2014); Ghareeb et al., (2015).

For plant height, among genotypes, 131/714 was the shortest genotype under RCBD (83.80 cm), whereas alpha lattice was P2-13-5-2 (85.5 cm), meanwhile, Khlebodar Kharkovsky was the highest genotype in both designs with mean (107.76 cm) and alpha lattice (108.1cm) (Table 7).

The average of relative efficiency indicated that the use of alpha lattice design increased experimental precision by 12.97, 5.93, 21.79, 35.50, 21.53, 23.96 and 26.69% for number of plants/m², tillering fertility, plant height (cm), spike length (cm), number of spikelets/spike, 1000-grain weight (g) and grain yield (g/m²), respectively.

Table 7: Mean squares (alpha lattice design) of the studied traits in triticale genotypes for 2017 and 2018 seasons.

| S.O.V       | df | Year | NP | TG | TF | PH | SL | NS | GW | GY  |
|-------------|----|------|----|----|----|----|----|----|----|-----|
| Replication | 2  | 2017 | 2581 | 0.21 | 0.20 | 0.45 | 0.19 | 2.74 | 0.76 | 5692 |
|             | 2  | 2018 | 118  | 0.22* | 0.02 | 3.64 | 0.14 | 0.17 | 0.10 | 295  |
| Blocks      | 9  | 2017 | 6207 | 0.20 | 0.14 | 98.41** | 0.28 | 2.68 | 7.11* | 9151** |
|             | 9  | 2018 | 3065 | 0.06 | 0.05** | 44.85** | 0.77 | 4.42 | 5.54** | 10352** |
| Genotypes   | 19 | 2017 | 3204 | 0.09 | 0.04 | 197.26** | 0.73 | 7.90* | 30.01** | 12398** |
|             | 19 | 2018 | 3290 | 0.09 | 0.04** | 67.36** | 0.65 | 6.23** | 24.69** | 9755** |
| Error       | 29 | 2017 | 4511 | 0.12 | 0.11 | 11.93 | 0.63 | 3.54 | 2.48 | 2629 |
|             | 29 | 2018 | 3183 | 0.06 | 0.02 | 20.27 | 0.60 | 2.48 | 1.22 | 2700 |

** and * = Significant at 1 and 5% probability level, respectively.
NP: number of plants / m², TG: tillering general, TF: tillering fertility, PH: plant height, SL: spike length (cm), NS: number of spikelets / spike, GW: 1000-grain weight (g) and GY: grain yield (g / m²).
values of under RCBD and alpha lattice (19.67), (21.5), respectively; however, P2-16-20 the lowest mean value under RCBD with mean (15.05) while under alpha lattice was P2-13-5-2 (16.0). All genotypes at the level of Ukro standard in both designs except P2-13-5-2 and P2-16-20. As for Weight of 1000 grains, genotypes C 259, 131/714 and C 238 at the level of Ukro standard in both designs. The genotype C259 showed the highest mean values of under RCBD and alpha lattice (52.88), (53.3), respectively; meanwhile, P2-13-5-2 the lowest mean value under RCBD and alpha lattice was (43.93), (44.5), respectively (Table 7).

In the case of grain yield/m², indicates that among genotypes, the highest mean value for grain yield / m² were scored by Dublet, Ulyana, 131/1656 and C259 under RCBD and alpha lattice when compared with Ukro standard; however, the lowest mean value were scored by 6-35-5 (372.8 grams) under RCBD, while PL-13-5-13 recorded the lowest mean value under alpha lattice (387 grams) (Table 7). All genotypes at the level of Ukro standard in both designs except 6-35-5 and P2-16-20.

Cluster analysis for twenty genotypes spring triticale

A dendogram was created with the use of these data for alpha lattice design (Fig 1). Cluster analysis showed that the twenty spring triticale genotypes were divided into three main groups; the first main group included variety Dublet. This variety isolated from Poland and shows a stable manifestation over two years of higher yields, the number of spikelets and grain weight. The second main group contains most of selection genotypes of RSAU – MTA and is probably caused by selection of forms, includes 2R/2D or other substitution (Divashuk et al., 2010). This group was divided into two subgroups the first subgroup IIA included the two line triticale genotypes 6-35-5 and PL-13-5-13. The second subgroup IIIB included two subgroups, the first sub subgroup IIIB1 included C 259, the second sub subgroup IIIB2 included Yarilo, P2-16-20 and 131/714.

The third main group III was divided into two subgroups, the first Subgroup IIIA included Khlebodar, the second Subgroup IIIB included three Sub group. The first Sub subgroup IIIB1 included C 259, the second Sub subgroup IIIB2 and C 238, the second sub subgroup IIIB3 was divided into two groups, group1 included Sandro, C 238, Legalo and Pamyaty Merezhko, group2 included Ukro, Lana and Grebeshok. In general cluster analysis divided into main groups and subgroups similar results were found by Misra and Swain (2010); Dogan and Vural, (2013) and Arain et al., (2018).

CONCLUSION

The results obtained from this study could be useful for plant breeders, statisticians and agronomists in order to increase the precision of field trials. According to the results obtained, it may be concluded that alpha lattice design provided smaller
coefficients of variation and error mean squares as compared to RCBD presented more efficiency in comparing different genotypes. Preferably use alpha lattice design on triticale field trials and other crops when the number of genotypes in the experiments is large and this allows the adjustment of treatment means for block effects. At present, the expansion of the experiment is required to include more research stations on a larger scale of these designs for crops and some other crops as well. For plant breeding and selection trials, alpha lattice design should be used like form a resolvable incomplete block design and this design also provides effective control within replicate variability. Both designs confirmed to Dublet, Ulyana, 131/1656 and C259 genotypes were the highest yield/m². Cluster analysis showed that the twenty spring triticale genotypes were divided into three principle groups; one of these groups included only one variety (Dublet). The results indicated a greater efficiency for alpha design in reducing the mean error squares and the coefficient of variation.

Authors’ contributions
In this work Soloviev Aleksandr with the co-authors set the task and formulation of the study; Abdelkawy Ramy and Turbayev Zhoksyngalievich conducted a field experiment (two seasons) and collecting data and results; Soloviev Aleksandr assisted in the results discussion and corrected the appropriation in text; Abdelkawy Ramy analyzed the data and prepared the manuscript.

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