JIMMA UNIVERSITY

COLLEGE OF NATURAL SCIENCES

SCHOOL OF GRADUATE STUDIES

DEPARTMENT OF STATISTICS

COMPARING EFFICIENCY OF RANDOMIZED COMPLETE BLOCK AND ALPHA LATTICE DESIGNS IN AGRICULTURAL FIELD EXPERIMENT. (CASE STUDY AT BAKO AGRICULTURE RESEARCH CENTER, WEST SHOA ZONE, ETHIOPIA)

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A thesis submitted to the School of Graduate Studies of Jimma University in partial fulfillment of the requirement for the Degree of Masters of Science in Biostatistics.

Declaration

I, the undersigned, declare that this evaluation thesis is my original work, has not been presented for a degree in this or any other University and that all sources of materials used for the thesis have been fully acknowledged.

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Abstract

The choices of experimental design as well as of statistical analysis are of huge importance in field experiments. The efficiency of alpha lattice design and randomized complete block design (RCBD) were compared in maize trials conducted in 2010 at Bako Agricultural Research Centre (BARC), in Ethiopia on 45 treatments to assess the efficiency of each in minimizing experimental error, coefficient of variation and error mean square for yield variable. Bread wheat variety trials also conducted on 16 treatments to asses the performance of RCBD compared to CRD. Alpha designs are used for field trials because they provide better control on experimental variability among the experimental units under field conditions. The coefficient of variations (CV) compared to be 12.6 % for alpha lattice design and 14.6 % for RCBD respectively. The error mean squares calculated for these trials are 1.0418 for alpha lattice design and 1.4081 for randomized complete block design (RCBD) respectively. The relative efficiency of trials shows that alpha lattice design is more efficient than RCBD. The value of relative efficiency 1.35 indicates that the use of alpha lattice design instead of randomized complete block design (RCBD) increased experimental precision by 35 percent. The gain is considerable in terms of efficiency attained by using alpha lattice design which favors wider use of these designs under field conditions. Based on the results we conclude that alpha lattice designs are more efficient than RCBD. In order to increase the precision of agricultural field experiments researchers are advised to use RCBD for small number of treatments, and alpha lattice designs for large number of treatments.

Key Words: RCBD, Alpha Lattice Design, Precision, Relative Efficiency, Mean Square Error and Coefficient of Variation

Table of contents

List of tables

List of figures

Acronyms

ANOVA = Analysis of Variance

BARC= Bako Agricultural Research Centre

BIBD = Balanced Incomplete Block Design

CRD = Completely Randomized Design

CV = Coefficient of Variation

DMRT =Duncan's Multiple Range Test

ERE = Estimate of Relative Efficiency

EU= Experimental Unit

LSD = Least Significance Difference

LSD^{T} = Tukey's Least Square Difference

MSe = Mean Square error

MSb = Mean Square block

MSt = Mean Square treatment

QQ = Quartile Quartile

RCBD = Randomized Complete Block Design

SSb = Sum of Squares of block

SSc = Sum of Squares of total

SSe = Sum of Squares of error

SSt = Sum of Squares of treatment

RE = Relative Efficiency

DF= Degrees of Freedom

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CHAPTER ONE

1. INTRODUCTION

1.1. Background of the study

The choices of experimental design as well as of statistical analysis are of huge importance in field experiments. These are necessary to obtain the best possible precision of the results. The random arrangements, randomized blocks and alpha lattice designs were reviewed and analyzed from the statistical perspective of error analysis. Precision is the ability of an experiment to detect a true treatment effect. It can be improved by increased replication, treatment selection, improved technique to reduce the variability among units treated alike, increasing the size of experimental units (within limits), the use of covariance, and the employment of a more efficient experimental design and method of analysis (Little and Hills, 1978).

An alternative set of designs for single-factor experiments with a large number of treatments is incomplete block designs, of which one is the lattice design. As the name implies, each block in an incomplete block design does not contain all the treatments and reasonably small block size can be maintained even if the number of treatments is large. With smaller blocks, the homogeneity of experimental units in the same block is easier to maintain and a higher degree of precision can generally be expected (Gomez, 1984).

Infact, experimentation plays a momentous role in the field of agriculture. A good experiment is the one which involves good planning, accurate data collection, proper data analysis and precise interpretation of the data. Experimental designs are basically divided into two categories: complete block designs and incomplete block designs. Complete block designs include completely randomized design (CRD), randomized complete block design (RCBD), Latin square design etc. Among these designs, RCBD is one of the most extensively used designs in agriculture. In RCBD blocks size should be homogeneous and each block must contain a complete set of treatments. It also reduces experimental error through proper blocking though blocking becomes ineffective when the block size increases and cannot be used for a large number of treatments. Therefore in such a situation, RCBD becomes less powerful in controlling experimental error due to soil heterogeneity in experimental site.

The RCB and other blocking designs assume spatial variability can be accounted for by blocking the experimental units in a linear fashion. This assumption is not met under field conditions when the RCB contains considerable within-block heterogeneity. Incomplete block design (IBD) and lattice designs account for spatial trends in the same fashion as the RCB, but also account for a portion of the spatial variability within blocks by reducing a complete block into smaller incomplete blocks. The alpha lattice is an example of a flexible incomplete block design that has been shown to account for spatial trends more efficiently than the RCB, especially, in trials with a large number of entries (Patterson and Hunter, 1983, and Yau, 1997). However, unaccounted spatial variation may still persist within incomplete blocks (Yang et al. 2004). There are also examples of experimental designs that take spatial variability into account at the design stage by accounting for spatial autocorrelation (van Es and van Es, 1993).

The same fashion, the response from field trials is subject to random variation. The two neighboring plots grown with the same variety and treated in the same way will always yield differently. This also applies to all other recordings made on a continuous scale. The size of the differences will depend on several circumstances such as the variability in the soil, variability in the applied fertilizer, historical events and uncertainty in the recording process. In other name, a recorded difference between two varieties may be due to either a true difference in the response of the two varieties or may be due to random variations. In order to help decide whether the difference is caused by the different varieties or by random variation it is necessary to apply some statistical methods to estimate the actual size of the random variation in the field and compare the measured difference with the size of the random variation. To do that in a good manner it is necessary to use properly designed trials and the correct way of analyzing the recorded data correctly.

The randomized block, Latin square, and other complete block types of experiments are inefficient for large number of treatments, because of their failure to adequately minimize the effect of soil heterogeneity (Masood, *et al.* 2008). Generally, the greater the heterogeneity within blocks, the poorer the precision of variety effect estimates. Incomplete block designs are arranged in relatively small blocks that contain fewer varieties than the total number of varieties to be compared. Consequently, there is a gain in precision due to use of small blocks. As far as

the layout of the experiment is concerned the incomplete block designs are no more difficult than randomized blocks. Some extra planning is involved in drawing up and randomizing the experimental plan. Randomized complete block design (RCBD) is affordable when the block size is less than eight varieties/treatments. It is always useful to use incomplete block design when the number of varieties/treatments increases. Because of large number of treatments, the homogeneity among experimental units/plots within a large block cannot be maintained. As a result, estimate of experimental error is inflated and results are low in precision. The usual approach through local control by blocking is inefficient and a lot of research has recently been carried out which suggest new methods of local control in field experiments (Cullis and Gleeson, 1987; 1991); (Kempton et.al, 1994).

Alpha designs introduced by (Patterson and Williams, 1976) are now routinely used for statutory field trials in the United Kingdom (Patterson and Silvey, 1980) and are also widely used for breeding and varietals trials in Australia and elsewhere. They are more flexible than lattice designs and can accommodate any number of varieties. Additional improvement is possible through modeling field variability using spatial features of the field layout. It has been advocated by (Wu and Dutilleul, 1999) use of incomplete blocking is generally more effective in reducing the unexplained structured variation in comparison with complete blocking.

In conclusion, the process of evaluating competing designs for an experiment depends on understanding the statistical methods that will be used to analyze the data resulting from the experiment. The purpose of the typical experiment is to test research hypotheses and/or estimate unknown parameters. The goal of experimental design is to increase the precision of estimates and the power of hypothesis tests. An examination of the statistical analysis provides a guide to the choice of design. It is most helpful to understand the statistical analysis before an experiment is conducted. In this walk-through the investigator discovers whether the experiment provides estimates of important parameters, the expected precision of parameter estimates, whether the research hypotheses are testable, and the power of the tests under the proposed design. These provide a basis for evaluating competing experimental designs.

1.2. Statement of the problem

To obtain good precision of the results, the choices of experimental design as well as of statistical analyses play a crucial role in field experiments. The common experimental designs and treatment structures being used in Ethiopian agricultural research system are randomized complete block design, lattice design, alpha lattice design, factorial experiments, and split-plot treatment structure (Girma, 2002 and Mandefro, 2005).

In Bako Agricultural Research Center (BARC), randomized complete block design and alpha lattice designs are commonly used for field experiments (Bayisa *et al*., 2008; Legese *et al*., 1998). The aim of this study is to answer the question why these two statistical experimental designs are used and to assess the performance and efficiency of RCBD and alpha lattice design in BARC. The best strategy of increasing production of crops is by increasing productivity per unit area using improved production technology. On the other hand, reliable improved technologies can only be achieved if proper designing and modeling is done. Basic questions of these studies are:

- Is randomized complete block design or alpha lattice design improve the precision of agricultural field experiments through design and analysis?
- How to assess efficiency factor for IBD and randomized block design?
- Are treatment effects the same based on the selected design?

1.3. Significance of the study

Use of statistical methods have been at the heart of effective agricultural research for almost a century ,However, despite the development of powerful new research technologies in agriculture and biology, look set to remain at the heart of crop and field experimentation for the foreseeable future. The result of this study will help to identify the appropriate experimental designs for field experiments and will help to improve the precision of agricultural field experiments through design and analysis. Therefore, the outcome of the research will help agricultural researchers to conduct research with efficient use of limited research recourses and to determine optimum estimation methods for specific field crop trials. Moreover, the result helps researchers as a guideline for indicating possible sources of variation that might occur in research activities. In general, the application of this research result will be expected to be beneficial for different

bodies working in the area of agriculture and the result will be used as a basis for future study using IBD model in agricultural area.

1.4. Objectives

1.4.1. General Objective

- To assess the efficiency of randomized complete block design and alpha lattice designs in agricultural field experiments, using wheat and maize yield data from Bako Agricultural Research Center.

1.4.2. Specific Objectives

- To compare the performance of randomized complete block design and alpha lattice designs in Bako Agricultural Research Center.
- To assess efficiency factor for IBD as compared to randomized block design.
- To test the hypothesis about treatment effect based on the selected design.

CHAPTER TWO

2. LITERATURE REVIEW

Field designs are based on concepts of replication, control of variation among plots and randomization, where replication allows valid estimation of error variance, control of plot variation reduces error variance and randomization allows unbiased estimates of means and variances (Hinkelman and Kempthorne, 2006; Mead, 1990). Assuming the scope of inference and plot size/shape issues have been considered, the main focus of experimental design will be how to arrange entries in the field to minimize the impact of error variance.

The major reason for grouping plots into uniform blocks is to reduce plot-to-plot variation and to improve the precision of the experiment. Failure to adequately block a field experiment can result in unacceptably large error variance and/or biased estimates of genotype effects (Mead, 1997). In fact, effective control of error variance usually requires relatively small blocks. Trials with a large number of entries set out in a complete block experiment where there is considerable variability among plots within a block will likely result in very poor, possibly unusable, information on genotypes. To control field variation, especially with a large number of entries, it is essential to make use of incomplete block designs.

Parsad and Gupta (2000) showed that the simplest and most commonly used block design when the treatments are at several levels of a single factor by the agricultural researcher is a randomized complete block design (RCBD).

Plant breeding trials are typically developed to give an unbiased evaluation of all test entries, and ideally to ensure equal variances of all paired differences. When incomplete block designs are used, achieving the equal variance criteria results in balanced incomplete block designs (BIBD). BIBDs require that all pairs of entries appear together in a block equally often (Mead, 1990; Giesbrecht and Gumpertz, 2004; Hinkelman and Kempthorne, 2006). Actually, balance is often possible in smaller trials, however in trial with a large number of entries, balance is normally not achievable, meaning that some differences between pairs of entries will be estimated more precisely than others. Yet in most plant breeding trials, this disparity in precision across treatment pairs is small and not a major problem, as long as the incomplete blocking is effective

(Mead, 1990). Another important concept in field trial design is resolvability. A field trial is resolvable if it is laid-out in complete replicate blocks, each replicate being split into a number of incomplete blocks. Resolvable designs are useful since the entries in the same incomplete block in one replicate are spread across incomplete blocks in another replicate. In addition, resolvable designs are often easier to manage since all entries are together in complete replicates.

One category of resolvable incomplete block designs is the lattice designs originally proposed by (Yates, 1936). In truth, these designs require that the number of entries is a square of the block size and achieve balance if enough replicates are possible. If not, simple, triple, quadruple lattices are partially balanced designs with two, three or four replicates respectively and have been used extensively in plant breeding trials. However, due to the restriction on the number of genotypes that may be evaluated, there have been a number of proposed lattice type of designs, the most popular being the alpha designs developed by (Patterson and Williams, 1976); (Giesbrecht and Gumpertz, 2004). In fact, Alpha designs are resolvable incomplete block designs where the number of entries is a multiple of block size. Although these designs cannot achieve balance, they are used extensively in plant breeding primarily because they are quite flexible regarding the number of entries to be evaluated and the appropriate size of incomplete block and they allow for good error control. In addition, these designs can be simply adapted to situation where the number of entries is not an exact multiple of block size by omitting treatments from an alpha design with a larger number of treatments.

Although it is well documented that incomplete block designs can greatly improve the efficiency of plant breeding field trials, recent work has suggested that allowing for block differences in two directions can further improve precision (Wright, 2002; Kempton et. al, 1994). Row-column designs ideally are constructed so entries are orthogonal to both rows and columns, such as with a Latin square design. If orthogonality is not possible in both directions, then hopefully it is achieved in one direction and balance (as in BIB) is obtained in the other direction. If orthogonality is not possible, then one attempts to achieve balance in both directions if possible. A lattice square is a special case of a randomized complete design where balance is not achieved in either direction, but that each pair of treatments appears together in at least one row or column (Hinkelman and Kempthorne, 2006). One approach useful in plant breeding is to start with an

alpha design arranged with rows as incomplete blocks and then rearrange the order of the entries in each row to balance as best as possible the entries across the columns. In this case, the alpha design is said to be Latinized (Williams, 1986).

In the early stages of a plant breeding program, expected genetic gains may be increased by screening a large number of genotypes in contrast to having more precise comparisons of a fewer number of genotypes (Bos, 1983; Gauch and Zobel, 1996). This consideration will likely make it necessary to evaluate many entries where there may not be sufficient seed to replicate each. Federer proposed augmented designs where a set of check entries are replicated an equal number of times in a specified field design and an additional set of new or test entries are included in the experiment only once (Federer, 2002; 2005). Any type of block design can be used for the check treatments with the test entries being added or 'augmented' to the blocks and the standard error for a difference between test entries or checks may simply computed. This approach provides a very efficient means of screening test entries and has a considerable amount of flexibility. For row-column designs, the experiment is 'Latinized' so that entries do not occur more than once in a row or column. (Federer, 2002) proposed using this approach with augmented lattice squares while (Williams and John, 2003) used a Latinized α-α designs (α designs for both the rows and columns) to extend the idea of the augmented lattice squares using CycDesigN (Whitaker et. al, 2001).

Similar to augmented designs are unreplicated designs where field variation may be controlled using several different approaches. Traditional unreplicated designs control local variation using a single replicated check variety distributed often systematically across the field. The approach is flexible and simple to use in that genotypes need not be randomized, visual evaluation is possible and the test genotypes are adjusted using the mean yield of the neighboring checks. The problems with the approach are that results can strongly depend on which check is chosen, how the genotypes are adjusted and the frequency and location of the check plots. The frequency of check plots that maximizes genetic gain depends on the heritability and how effective the presence of more checks control field variation (Kempton and Gleeson, 1997). A number of methods are available for adjusting genotypes yields using check plots with most using

environmental indices or covariates over the field (Kempton, 1984; Besag and Kempton, 1986; Cullis et al, 1989; Hooks et. al., 2007).

Multi-environment testing is a crucial step in the development of superior genotypes adapted to a wide range of environmental conditions. The design of efficient multi-environment testing programs to maximize information subject to available resources and practical limitations has been considered by a number of workers. Minimizing the variance of differences between genotypes, and using multi-environment variance components for a number of different crops, Talbot found that using 2 years at 12 sites with 2 replicates was reasonable for most crops, with more years increasing precision more than more locations (Talbot, 1984). When maximizing genetic improvement, similar results were found for corn single crosses (Sprague and Federer, 1951). Generally, the results are based on the assumption of good field designs at each site and will hold with any type of design and with different designs at each site (Federer et. al, 2001).

Patterson et. al, (1978) introduced a new class of cyclically generated lattice designs called alpha designs, which greatly extended the class of lattice block designs then currently available for variety trials. (Patterson & Hunter, 1983) later published a substantial examination of alpha lattice design efficiency based on an analysis of 240 cereal variety trials in the UK. They concluded that the designs improved cereal trial efficiency under UK conditions by about 42% relative to randomized block designs. Row-and-column designs can be particularly useful for trials with small plots and the efficiency of two dimensional alpha lattice type designs was investigated for small plot barley trials by Robinson et.al,1988) using 129 spring barley trials. Gains in efficiency similar to those reported by (Patterson & Hunter, 1983) were obtained and the two-dimension alpha designs were reported to be equally as useful as the one dimensional designs.

Gomez (1984) also described that pair comparison is the simplest and most commonly used comparison (planned and unplanned pair) in agricultural research. The two most commonly used test procedures for pair comparisons in agricultural research are the least significant difference (LSD) test which is suited for a planned pair comparison, and Duncan's multiple range test (DMRT) which is applicable to an unplanned pair comparison. The procedure for applying the DMRT is similar to that for the LSD test; DMRT involves the computation of numerical

boundaries that allow for the classification of the difference between any two treatments mean as significant or non-significant. However, unlike the LSD test in which only a single value is required for any pair comparison at a prescribed level of significance, the DMRT requires computation of a series of values, each corresponding to a specific set of pair comparisons.

CHAPTER THREE

3. MATERIALS AND METHODS

3.1. Study area

The study area is found in western shoa zone of Oromia (western part of Ethiopia) which is located 250 km away from Addis Ababa and established at 1952 E.C. with approximate latitude: 0906^0 N, longitude: 3709^0 E, altitude (m): 1650, temperature: 20.7^0 C**,** rain fall: 1225mm**,** agro-ecology: mid-land**,** major soil type: nito soil**,** land holding (ha): 2.75**.** At Bako national maize research project objectives of the research projects are: 1) to develop improved high yielding and disease resistance maize varieties. 2) to develop technologies for controlling major maize pest problems, and to improve maize production technologies.

3.2. Data

The yield data come from preliminary bread wheat pre regional variety trial around Gedo using RCBD and maize yield trials are conducted by using alpha lattice design layout at Bako Agricultural Research centre, West Shoa Zone, Ethiopia, 2010. The experiment on maize yield crop was laid out with 3 replications, 45 entries, 9 blocks consisting of five entries in each block, where as the experiment on bread wheat crop was laid out with 3 replications, 16 blocks. Computer software named R software used for statistical analysis of alpha lattice design as well as randomized complete block deign.

3.2. Methodology

3.3**. Randomized Complete Block Design (RCBD)**

The experimental field is divided into blocks according to the number of replicates. Each Block is divided into a number of plots according to the number of treatments. The treatments are then assigned randomly to the plots. Each treatment occurs one time per block. A benefit of block designs over completely randomized designs is, that differences between blocks (e.g. due to soil quality) do not influence the estimates of treatment differences and can be separated from the experimental error when performing analysis of variance. One drawback of the CBD is that only soil differences in one direction can be modeled. Possible extensions of the block design for two directions are the Latin square, allowing for row and column effects.

A CBD is a good choice when there are no technical aspects that restrict the randomization. Simple block designs are mostly used for one-factorial trials but two or more factors are also possible. The layout of blocks on the field has to be chosen in such a way, that soil differences between blocks are maximized and within blocks are minimized. Homogeneity of conditions within blocks requires that the treatment number and therefore the dimension of the blocks have an upper limit. Depending on plot size and soil conditions block designs are recommended for trials up to 20 treatments. In block designs the assumption is usually made that there are no interactions between treatments and blocks. The primary purpose of blocking is to reduce experimental error by eliminating the contribution of known sources of variation among experimental units. This is done by grouping the experimental units into blocks such that variability within block is minimized and variability among blocks is maximized. At all stages during the experiment, the techniques applied within a block should be as uniform as possible, thus keeping experimental error within blocks as small as possible. Differences between blocks are permitted to be large, but are not of major concern in the analysis since the comparisons of treatments and the computation of experimental error is done within blocks. Blocking will be effective only if the error variance among units within blocks is smaller than the error variance over all units. After the experimental units have been blocked, treatments are then randomly assigned to the units within the blocks. The randomization process for a RCBD is applied separately and independently to each of the blocks. A separate randomization is used in each block and every treatment appears in every block precisely once. In complete block design, each block consists of one complete replication of the set of treatment. As planning and conducting an experiment with the RCBD requires extra effort relative to the CRD, a natural question of interest is how well the blocking has worked or how much has been saved by using an RCBD rather than a CRD with the same number of experimental units. The answer helps to justify the effectiveness of blocking in the experiment being conducted and is also useful for future studies using the same or similar experimental units. It is well recognized that the gain from using an RCBD instead of a CRD is a reduction in error variance, while the loss is a decrease in error degrees of freedom. Blocking stratifies experimental units into homogenous groups, and in field trials, plots are normally blocked according to their proximity to each other. Blocking will increase treatment precision only if plots are blocked according to one or more varying external factors. If an experimental area is homogenous, blocking may actually decrease the precision of

estimating treatment effects. This results from a larger means square error term in the ANOVA since error degrees of freedom are reduced without a comparable reduction in error sum of squares. In this situation, a completely randomized design (CRD) would more precisely estimate treatment effects than a RCBD (Karcher *et al*, 2003). Randomized complete-block designs (RCBDs) group one complete replicate in each block. They are useful when the number of lines in the trial is not large, so that there is less soil and drainage variability within than among blocks. The variability among blocks is thus removed from the plot residuals. For complete-block designs, the plot residual term e_{ij} in the model is divided into a complete-block effect r (also called a replicate effect, since the replicates are synonymous with blocks in the RCBD) and a within-replicate plot residual e. Thus RCBDs remove effects of blocks from the plot residual, reducing the confounding of genotype with plot residual effects. In this study, the efficiency of designs are compared in two different research trials conducted at Bako Agricultural Research Centers to assess the efficiency of each in minimizing experimental error, coefficient of variation (CV) and error mean square for yield. The coefficient of variation (CV) affects the degree of precision with which the treatments are compared and is a good index of the reliability of the experiment. It is an expression of the overall experimental error as percentage of the overall mean; thus, the higher the CV value, the lower is the reliability of the experiment.

3.4. Analysis Procedures

3.4.1. Evaluation of data

3.4.1.1. Check for model assumptions

Every statistical analysis of trial data needs some assumptions to be fulfilled, otherwise the conclusions may be false. Among these assumptions the most common (for analysis of variance) are:

- normality of distribution,
- additivity of treatment and block effects,
- homogeneity of variances,

Normality: All the tests used in analyses of variance and analyses of regression are based on normality assumption. Normality means that the distribution of observations is “bell shaped” for

all treatments under comparison. Mead et al. (1983) say "in most situations it is impossible to decide by examining the data whether the assumption of normality is reasonable and one has to rely on common sense in arguing whether the assumption is biologically likely". So this assumption is rather difficult to be verified unless the sample size is very large. There are some tests for checking this assumption but all of them are rather weak (in the sense that they very rarely reject the null hypothesis) when sample sizes are small and even moderately large. So they can be applied only for large sample sizes (sample size tending to infinity). As in routine experimentation the number of replicates is small (usually smaller than 6) and the sample size for a particular treatment is of the same order, the use of such a test is not possible. Graphical presentation of data can provide a visual inspection for lack of normality. Luckily the tests used in the analysis of variance (as well as regression), namely the F-test and t-test, are resistant against moderate deviations from normality. A method that is often used to check normality is the Shapiro-Wilk test, which is recommended for sample sizes not larger than 50 (Shapiro and Wilk, 1965).

Additivity: In the analysis of variance of block trials (CBD or IBD) it is assumed that there is no interference between blocks and treatments. In practice this means, that differences between any two treatments are the same in all blocks in which they appear together and that possible fluctuations are caused solely by experimental error. This assumption is usually fulfilled if the differences between blocks are not very large. A simple test for non-additivity in a CBD design was proposed by Tukey (1949), known as "one degree of freedom for nonadditivity". In this approach the sum of squares for error is subdivided into two parts. One is attributed to non-additivity, the other to the residual. Then, using the usual Fisher F-test with one degree of freedom for the numerator, the hypothesis that there is lack of additivity is tested. In the case of multiplicative effects, a logarithmic transformation can improve the situation.

Homogeneity: The typical assumption in an analysis of variance is that the treatments do not influence the variance of experimental error, in other words that the variance is the same for all treatments. This assumption is likely to be fulfilled when levels of expression are similar for all treatments. When levels of expression (mean values) differ considerably between treatments,

normality and additivity as well as homogeneity of variances can be violated. This assumption can be verified using Bartlett's or the Cochran test. In both tests, the estimates of variances are calculated for all treatments and next the hypothesis of equal variances is tested against the alternative that some of them (at least one) are different. If the variances (standard deviations) are related to the level of expression (mean values) of the characteristic that is analyzed, a logarithmic (or square root) transformation can improve the situation.

3.4.1.2. Method of Diagnostic Testing

Having fitted a statistical model to the data, diagnostic tests are needed to assess the fit of the model. The simplest check for normality involves plotting the empirical quantiles of the residuals against the expected quantiles. This is known as the normal QQ-plot. Thus, QQ-plots are useful for diagnosing violations of the normality assumption. In this method, observed value and expected value are plotted on a graph. If the scatter plots deepest from a straight line, then the data are not normally distributed. One common test for checking the normality is Shapiro-Wilk test. This test works well even for a small sample size, so generally we just need to use this. The null hypothesis of Shapiro-Wilk test is that the samples are taken from a normal distribution. So, if the p value is less than 0.05, we reject the hypothesis, and thinks that the samples are not taken from a normal distribution. Kolmogorov-Smirnov test is appropriate for only large data. The p-values that is larger than 0.05 indicate that values are normally distributed at the 5% level of significance. If the test is significant, the assumption of normality is violated. In this case, transforming the data will frequently correct the problem. When the normality assumption fails, and transformations don't seem to help, Friedman's test is a nonparametric alternative for the RCBD.

3.4.1.3. Analysis of Variance (ANOVA)

ANOVA is a technique for analyzing experimental data in which one or more response variables are measured under various conditions identified by one or more classification variables. The analysis of variance has proved useful in the statistical analysis of experiments in the estimation of components of variation, in the estimation of the variance of estimates of treatment comparisons, and in making tests of significance.

The assumptions required for ANOVA are:

1) Normally distributed data (i.e., experimental errors are normally distributed).

2) Independence of errors. Analysis of variance (ANOVA) is the main tool used for statistical interpretation of agricultural trial data. The analysis of variance is based on linear model of observation. For experiments performed in a randomized complete block design (RCBD), the linear model is of the form

$y_{ij} = \mu + t_i + b_j + e_{ij}$ ………………………………………………(1)

Where *y*ij denotes the value of observed trait for the i^{th} treatment (i=1, 2… t), received in the jth block (j=1,2,…, r) with a total number of observations n = rt; t_i is the fixed effect of the i^{th} treatment, b_j is the effect of the j^{th} block and e_{ij} is an experimental error associated with observation of the i^{th} treatment in the j^{th} block. Different assumptions can be made on the block effects b_j. If the assumption is that b_j is fixed, meaning that the only random term in (1) is e_{ij}, the model is called fixed. In that case all conclusions are confined to treatments and blocks used in the analyzed experiment. More common is to consider bj as the random component of model (1). In this case the model is called mixed. In the mixed model the blocks are treated as a random sample of an infinite set of all possible blocks and conclusions are not confined to the blocks actually used in experiments. The conclusions are "valid" in the population of blocks from which the blocks can be considered as a random sample. As we will see, the blocking factor is included in the study only as a way of explaining some of the variation in responses (*Y*) of the experimental units. As such, we are not interested in testing hypotheses about the blocking factor.

Analysis of variance of trial data is based on a division of the sum of squares of total variability (SSc) into a component attributed to blocks (*SSb)* a component attributed to treatments (SSt) and to the error (SSe) according to the equality

$$SS_c = SS_b + SS_t + SS_e \quad \text{……………………………………… (2)}$$

Usually the main aim of the analysis of variance is to test the hypothesis, that there are no differences between treatments under comparison, namely the hypothesis

$H_0: \tau_1 = \tau_2 = ... = \tau_t$ against H1: "H_0 is not true" ………………. (3).

This hypothesis is always tested by application of a Fisher F-test of the form

Now if H_0 is true, then $\frac{SS_t}{\sigma^2} \sim \chi^2_{t-1}$ and since $\frac{SS_e}{\sigma^2} \sim \chi^2_{tr-t-r+1}$

and ss_t and ss_e are independent, the ratio of these two Chi-Square statistics (divided by their respective degrees of freedom) yields

$$\frac{SS_t/\left[(t-1)\sigma^2\right]}{SS_e/\left[(rt-r-t+1)\sigma^2\right]} = \frac{SS_t/(t-1)}{SS_e/(rt-r-t+1)} = \frac{MS_t}{MS_e} \sim F_{t-1,rt-r-t+1}$$

$F_0 = MSt/ MSe$ ……..… (4)

where ms_t and ms_e are the mean squares for treatment and error respectively. Usually the results of ANOVA are presented in an analysis of variance table as in table 3.1.

Table 3.1. Analysis of variance for a randomized complete block design (CBD)

Source of Variation	Degree of Freedom (df)	Sum of Square(SS)	Mean Square (MS) *	F value
Block	r-1	SSb	MSb	MSt/ MSe
Treatment	t-1	SSt	MSt	
Error	(t-1)(r-1)	SSe	MSe	
Total	tr-1	Total SS		

*The MS for each source of variation is obtained by dividing each SS by it corresponding df.

If $F_0 > F_{t-1,rt-r-t+1}$, where $F_{t-1,rt-r-t+1}$ is the critical value of the F distribution for (t-1) and (r-1)(t-1) degrees of freedom at a significance level, the hypothesis (3) is rejected, meaning that not all treatments are the same (some treatments differ from the others). If hypothesis (3) is rejected, the researcher is usually interested to identify which pairs of treatment are different. To answer this question usually the least significant difference (LSD) is calculated. If the researcher is interested in one particular comparison (that was chosen before establishing the experiment), the best way is to calculate the Fisher LSD, using formula

$$LSD = t * \sqrt{\frac{MS_e}{n}} \quad \text{……} \quad (5)$$

The number of degrees of freedom for t is always that of MSe. The LSD is used only when the F-test indicates a significant difference exists. If the absolute value of the difference between treatment-means calculated is bigger than LSD, these two treatments are declared significantly different at a significance level. If many comparisons between treatments are planned, it is

recommended to use a method that minimizes the risk of erroneously declaring pairs significant. Turkey's least significance difference LSD^T which is applicable to such pair comparison.

$$LSD^T = q^{\alpha}_{t,r} * \sqrt{\frac{2MS_e}{n}} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots.. \ldots\ldots\ldots\ldots\ldots (6)$$

Where $q^{\alpha}_{t,\ r}$ is the critical value from studentised range distribution read at a significance level for t treatments involved in comparisons and r degrees of freedom (degrees of freedom for error in the ANOVA table). The rules of using LSD^T are the same as for LSD, but now all treatment comparisons can be made and still ensure that the risk of erroneous declaring any of these significant will be less than α.

3.5. Incomplete block design (IBD)

These design were introduced by Yates in order to eliminate heterogeneity to a greater extent than is possible randomized blocks and Latin squares when the number of treatments is large. The precision of the estimates of a treatment effect depends on the number of replications of the treatment – the larger the number of replications, the more is the precision. Similar is the case for the precision of estimate of the difference between to treatment effects. If a pair of treatment occurs together a large number of times in the design, the difference between these two treatment effects can be estimated with more precision. To ensure equal or nearly equal precision of comparisons of different pairs of treatment effects, the treatments are allocated to the experimental units in different blocks of equal sizes such that treatment occurs at most once in a block and it has an equal number of replications and each pair of treatments has the same or nearly the same number of replications. In trials with high treatment numbers, e.g. variety trials, complete blocks are too large to give a good control of the experimental error due to soil heterogeneity. In these cases designs with incomplete blocks are useful. Every block only contains a fraction of the total number of treatments and is therefore incomplete. Several incomplete blocks form one complete replication. One type of such designs is the lattice design. The blocks of an incomplete block design can be arranged in any way that is useful for controlling soil heterogeneity. With an IBD the arithmetic mean of a treatment is not the best estimator for the expected mean value. Treatment means have to be adjusted according to the linear model used for data analysis.

3.5.1. Alpha lattice design.

More flexibility is reached with the new class of alpha designs or generalized lattices (Patterson & Williams 1976, Patterson et al. 1978). The following requirements have to be met: (1) The number of plots per block (k) has to be smaller or equal to the square root of the number of treatments (v). (2) The number of replicates has to be smaller or equal to the ratio v/k. (3) The number of treatments has to be a multiple of k. Where the number of treatments does not meet these conditions, a design for the next possible number is developed and the redundant treatments are discarded. When the number of genotypes per replicate is large, there is likely to be great soil heterogeneity even within the block. This variability may be partly controlled by grouping plots within large replicates or complete blocks into much smaller incomplete blocks. The most commonly-used incomplete-block experimental designs are alpha-lattices for replicated trials. In brief, the partitioning of complete blocks into smaller, more homogeneous incomplete blocks permits more of the residual variation among plots to be removed from estimates of genotype means. Alpha-lattice designs are replicated designs that divide the replicate into incomplete blocks that contain a fraction of the total number of entries. Genotypes are distributed among the blocks so that all pairs occur in the same incomplete-block in nearly equal frequency. The design permits removal of incomplete-block effects from the plot residuals and maximizes the use of comparisons between genotypes in the same incomplete-block. How effective are alpha-lattice designs in increasing the precision of genotype means estimated from rain fed maize variety trials? There are several ways to address this question. One way is to compare a related statistic like the LSD for trials laid out as alpha-lattices, and analyzed both as alpha-lattices and RCBDs. A slightly more complicated situation appears in the case of incomplete block design (which includes the alpha designs). Because blocks and treatments are not orthogonal to each other (Which is in CBD), the division of the total sum of squares into parts attributed to blocks and a treatment is not unique. Usually the ANOVA table instead of single sum of squares for blocks (as in CBD), will mention two sums, the first attributed to complete replicates (superblocks), the second attributed to blocks (within superblocks) ignoring treatments.

The linear model of observations in alpha design is of the form

$$y_{ijk} = \mu + t_i + r_j + b_{jk} + e_{ijk} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad (7)$$

Where y_{ijk} denotes the value of the observed trait for i^{th} treatment received in the k^{th} block with in j^{th} replicate (superblock), t_i is the fixed effect of the i^{th} treatment (i = 1, 2… t); rj is the effect of the j^{th} replicate (superblock) (j = 1,2,…,r); b_{jk} is the effect of the k^{th} incomplete block within the j^{th} replicate (k = 1,2,…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 jth complete replicate. There are n = rt observations in total. The whole experiment consists of rb incomplete blocks forming r complete replicates. The whole discussion concerning randomness of blocks in randomized complete block design also applies to incomplete blocks and complete replicates in alpha design. In accordance with the linear model of observations (7), the analysis of variance is usually presented in the form given in table 3. 2.

Table 3.2. Analysis of variance for alpha lattice design

Source of variation	Degree of Freedom (DF)	Sum of Square(SS)	Mean Square (MS) *
Replicates	r-1	SS_r	MS_r
Block(with in replicates, ignoring treatments)	rb-r	SS_b	MS_b
Treatment (adjusted for block)	t-1	SS_t	MS_t
Error	rt-rb-t + 1	SS_e	MS_e
Total	rt-1	Total SS	

*The MS for each source of variation is obtained by dividing each SS by it corresponding df.

The term "ignoring treatments" means that the sum of squares for blocks is not free of treatment effects. Instead of the sum of squares for treatments (as for CBD), the sum of squares for treatments adjusted for block effects appear. It means that this sum of squares is free from block effects. The hypothesis tested is the same as in CBD (see (3)) and it is verified in exactly the same manner using a Fisher F-test. The value of F_0=MSt / MSe is now compared with the critical $F\alpha_{,\ t-1,\ rt-rs-t+1}$ value with t-1 and rt-rs-t+1 degrees of freedom. Treatment means are now not just simple averages over replicates as in CBD but are "adjusted". This adjustment is different for a fixed model of observation (in so-called intra-block analyses) and for a mixed model (in analyses with recovery of inter-block information). Additional difficulties arise when LSD is applied for treatment comparisons. Due to the lack of orthogonality, the variances of treatment comparisons (treatment contrasts) will often be different for different pairs of treatments. So in an extreme case for every pair of treatments specific LSD (Fisher or Turkey) should be applied. However for

moderate variations it may be acceptable to average the variance of treatment-comparisons and then use the average LSD value. But in this situation comparisons must be made with special caution. Usually the design is chosen so that the difference between the largest and the smallest variance of treatment comparisons is as small as possible. This means that balanced designs are preferable.

3.6. Relative Efficiency

The success of blocking is best measured by the relative efficiency of the RCBD as compared with that of the CRD. In general, the relative efficiency is a positive number that can be interpreted as the ratio by which the sample size of the CRD would have to be in order to achieve the same efficiency as that of the RCBD. The quality of an incomplete block design is judged by the harmonic mean of efficiency factor, which is the ratio of the average variance with which a complete block design would estimate treatment differences and the average variance with which the incomplete block design would estimate these differences, if the error mean square were the same in both cases. The value of harmonic mean efficiency factor is always greater than zero and less than 1. The difference simply measures the confounding between treatments caused by using incomplete block design. However, when laying out the trial in the field, we should try to achieve maximum homogeneity possible within each incomplete block depending on soil conditions, fertility gradients, moisture, slope, e.t.c.

To judge whether the incomplete block arrangements was more effective than the complete block design, we have to wait for the experiment to be completed and compare the corresponding experimental errors. The relative efficiency of a lattice design is defined as the ratio between the average variance of the differences between treatments (ignoring the use of incomplete block and assuming that the replicates were complete blocks), and the average variance of the differences between treatments in the incomplete block design (including recovery of inter-block information). The relative efficiency is analogues to the difference of the harmonic mean of efficiency factor, but the former uses observed estimates of the experimental error. If blocking has succefully removed variation (i.e. if the reduction in the error mean square compensates for the effect of confounding caused by incomplete blocks), then the relative efficiency will be greater than 1.

The most widely used measure of relative efficiency is the relative precision defined as follows:

$$RE = \frac{MSe_{CRD}}{MSe_{RCBD}} X100 \quad \text{..... (8)}$$

If the blocking was not helpful, then the relative efficiency equals 1. The larger the relative efficiency is, the more efficient the blocking was at reducing the error variance.

The relative efficiency (RE.) of an alpha lattice design compared with a RCBD is estimated (Masood *et al.*, 2008) as the mean square error from each analysis will be used to estimate the relative efficiency of an alpha lattice design compared with a RCBD according to the following equation:

$$RE = \frac{MSe_{RCBD}}{MSe_{alphalatticedesign}} X100 \quad \text{..... (9)}$$

An estimated relative efficiency less than 1 indicates that a RCBD is a more efficient design, while value nearly equal to 1 suggests that the two designs yield similar results. Value greater than 1 suggests that alpha lattice design is more efficient design than RCBD. In this study, the efficiency of alpha lattice design and randomized complete block design (RCBD) will be compared in this research trials conducted in Bako Agricultural Research Centre, west shoa zone, Ethiopia to assess the efficiency of each in minimizing experimental error, coefficient of variation and error mean square for yield.

3.7. Analysis of Incomplete Block Design

We shall now derive the intrablock analysis for the general incomplete block design. Suppose we have *t* treatments replicated $r_1, r_2 \ldots r_t$ times, respectively, and b blocks with $k_1, k_2, \ldots, k_b$ units, respectively. We then have

$$\sum_{i=1}^{t} r_i = \sum_{j=1}^{b} k_j = n$$

Where *n* is the total number of observations. Following the derivation of a linear model for observations from a randomized complete block design (RCBD), using the assumption of additivity in the broad sense, an appropriate linear model for observations from an incomplete block design is

$$y_{ijl} = \mu + \tau_i + \beta_j + e_{ijl} \quad \text{………………………………………………………….} \quad (10)$$

(i = 1, 2. . . t; j = 1, 2, . . . ,b; l= 0, 1, . . . , n_{ij}), where τ_i is the effect of the ith treatment, βj the effect of the jth block, and e_{ijl} the error associated with the observation y_{ijl}. As usual, the e_{ijl} contain both experimental and observational (sampling) error,,

$$e_{ijl} = \varepsilon_{ijl} + \eta_{ijl}$$

With ε_{ijl} representing experimental error and η_{ijl} representing observational error. Also, based on previous derivations, we can treat the e_{ijl} as i.i.d. random variables with mean zero and variance $\sigma_e^2 = \sigma_\varepsilon^2 + \sigma_\eta^2$. Note that because n_{ij} , the elements of the incidence matrix *N*, may be zero, not all treatments occur in each block which is, of course, the definition of an incomplete block design.

Model (10) can also be written in matrix notation as

$$y = \mu J + X_\tau \tau + X_\beta \beta + e \quad \text{…………………………………………………...} \quad (11)$$

Where J is a column vector consisting of *n* unity elements, X_β is the observation-block incidence matrix

$$X_\beta = \begin{bmatrix} J_{k1} & & & & & \\ & J_{k2} & & & & \\ & & . & & & \\ & & & . & & \\ & & & & . & \\ & & & & & J_{kb} \end{bmatrix}$$

with J_{kj} denoting a column vector of kj unity elements *(j* = 1, 2, . . . , *b)* and $X\tau = (x_1, x_2, \ldots x_t)$ is the observation-treatment incidence matrix, where ***xi*** is a column vector with *ri* unity elements and (n − ri) zero elements such that $X_i'X_i = r_i$ and $X_i'X_i = 0$ for i≠i' (i,i' = 1, 2, . . . , *t).*

The normal equations (NE) for μ, τi, and βj are then

$$n\hat{\mu} + \sum_{i=1}^{t} r_i\hat{\tau}_i + \sum_{j}^{b} k_j\hat{\beta}_j = G$$

$$r_i\hat{\mu} + r_i\hat{\tau}_i + \sum_{j=1}^{b} n_{ij}\hat{\beta}_j = T_i \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \; \ldots\ldots\ldots\ldots\ldots \; (12)$$

$$k_j\hat{\mu} + \sum_{i=1}^{t} n_{ij}\hat{\tau}_i + k_j\hat{\beta}_j = B_j$$

Where

$$T_i = \sum_{jl} y_{ijl} = i^{th} \text{ treatment total}$$

$$B_j = \sum_{il} y_{ijl} = j^{th} \text{ block total}$$

$$G = \sum_i T_i = \sum_j B_j = \text{overall total}$$

$$\begin{pmatrix} J_n'J_n & J_n'X_\tau & J_n'X_\beta \\ X_\tau'J_n & X_\tau'X_\tau & X_\tau'X_\beta \\ X_\beta'J_n & X_\beta'X_\tau & X_\beta'X_\beta \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{\tau} \\ \hat{\beta} \end{pmatrix} = \begin{pmatrix} J_\beta'y \\ X_\tau'y \\ X_\beta'y \end{pmatrix} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \; (13)$$

which, using the properties of J,X*τ* ,X*β*, can be written as

$$\begin{pmatrix} J_n'J_n & J_\tau'R & J_b'K \\ RJ_t & R & N \\ KJ_b & N' & K \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{\tau} \\ \hat{\beta} \end{pmatrix} = \begin{pmatrix} G \\ T \\ B \end{pmatrix} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (14)$$

where

R' = diag (ri)   t × t

K' = diag (kj) b × b

N' = (n_{ij}) t × b (the incidence matrix)

T' = (T_1, T_2. . . T_t)

B' = (B_1,B_2, . . . ,B_b)

T'= (τ_1, τ_2, . . . , τ_t)

B' = (β_1, β_2, . . . , β_b)

and the J's are column vectors of unity elements with dimensions indicated by the subscripts. From the third set of equations in (14) we obtain

$$\hat{\mu} J_b + \hat{\beta} = k^{-1}(B - N'\hat{\tau}) \quad \text{……………………………………..………. (15)}$$

Substituting (15) into the second set of (14), which can also be expressed as $NJ_b\hat{\mu} + N\hat{\beta} + R\hat{\tau} = T$ (since $NJ_b = RJ_t$), leads to the *reduced normal* equations (RNE) for ***τ***

$$(R - Nk^{-1}N)\hat{\tau} = T - Nk^{-1}B \quad \text{……………………………………………………. (16)}$$

Standard notation for (1.7) is

$$C\hat{\tau} = Q \quad \text{……………………………………………………..…..…(17)}$$

Where

$$C = R - Nk^{-1}N' \quad \text{……………………………………….………..…….(18)}$$

$$Q = T - Nk^{-1}B \quad \text{……………………………………..………..(19)}$$

the (*i*, *i*) element of *C* being we note that the matrix *C* of (18) is determined entirely by the specific design, that is, by the incidence matrix *N*. It is, therefore, referred to as the *C* matrix (sometimes also as the information matrix) of that design. The *C* matrix is symmetric, and the elements in any row or any column of *C* add to zero, that is, $CJ = 0$ which implies that r(C) = rank(C) ≤ t − 1. Therefore, *C* does not have an inverse and hence (17) cannot be solved uniquely. Instead we write a solution to (17) as

$$\hat{\tau} = c^{-}Q \quad \text{……………………………………………………………(20)}$$

Where c^{-} is a generalized inverse for *C***.** If we write C = (c_1, c_2. . . c_t), where ***ci*** is the *i*th column of *C*, then the set of linear functions $c_i'\tau$ where, i = 1, 2, . . . , t which span the totality of estimable functions of the treatment effects, has dimensionality r(C).

Let $c'\tau$ be an estimable function and $c'\hat{\tau}$ its estimator, with $\hat{\tau}$ from (20). Then

$$E\left(c'\hat{\tau}\right)=E\left(c'c^{-}Q\right)$$

$$= c'c^{-}E(Q)$$

$$= c'c^{-}c\tau$$

For $c'\tau$ to be an unbiased estimator for $c'\hat{\tau}$ for any τ ,we then must have

$$c'c^{-}c=c' \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(21)$$

Since $CJ=0$,it follows from (21) that $C'J=0$.Hence, only treatment contrasts are estimable .If r(C) = t1, then all treatment contrasts are estimable. In particular, all differences $\tau_i-\tau_{i'}$ (i≠i') are estimable, there being t-1 linearly independent estimable functions of this type**.**

Then the design is called a connected design. In what follows we shall assume that the design is connected; that is, r(C) = t − 1. This means that *C* has t − 1 nonzero (positive) eigen-values and one zero eigenvalue.

From $$c\begin{pmatrix}1\\1\\.\\.\\.\\1\end{pmatrix}=0=0\begin{pmatrix}1\\1\\.\\.\\.\\1\end{pmatrix}$$

It follows then that $(1,1,\ldots,1)'$ is an eigenvector corresponding to the zero eigenvalue. If we denote the nonzero eigenvalues of *C* by $d_1, d_2, \ldots d_{t-1}$ and the corresponding eigenvectors by $e_1, e_2, \ldots, e_{t-1}$ with $e_i'e_i=1$ (i = 1, 2, . . . , t − 1*)* and $e_i'e_{i'}=0$ (i ≠ i), then we can write *C* in its spectral decomposition as

$$c=\sum_{i=1}^{t-1}d_ie_ie_i' \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(22)$$

or with $d_t=0$ and $e_t=\frac{1}{\sqrt{t}}(1,1,\ldots.,1)$ alternatively as

$$c = \sum_{i=1}^{t} d_i e_i e_i' \quad \text{.....(23)}$$

We note that $e_i' e_t = 1$ and $e_i' e_t = 0$ for $i = 1, 2. . . t - 1$.

We now return to (17) and consider a solution to these equations of the form given by (20). This method is based on the following theorem, which is essentially due to Shah (1959).

We have further

$$\text{var}(c'\hat{\tau}) = c'\tilde{c}^{-1}c\sigma_e^2 \quad \text{..... (24)}$$

It follows from general principles that the two forms of analysis of variance are as given in. We shall henceforth refer the block -after- treatment ANOVA model.

$$y = \mu J + X_\tau \tau + X_\beta \beta + e$$

3.8. Efficiency factor of an incomplete block design

We can compare different error control designs with each other by using the notion of relative efficiency. In this case, we compare two error control designs after we have performed the experiment using a particular error control design. For example, after we have used an RCBD we might ask: How would we have done with a corresponding CRD? In other cases, however, we may want to compare error control designs before we begin an experiment. In particular, we may want to compare an incomplete block design (IBD) with either a CRD or an RCBD, or we may want to compare competing IBDs with each other. For this purpose we shall use a quantity that is referred to as the efficiency factor of the IBD. It compares, apart from the residual variance, σ_e^2, the average variance of simple treatment comparisons for the two competing designs.

Based on (Hinkelmann and Kempthorne, 2005) average variance for treatment comparisons for an IBD is given by

$$av.\text{var}_{i \neq i'}(\hat{\tau}_i - \hat{\tau}_{i'}) \quad \text{.....(25)}$$

for a connected IBD. Suppose now that all the block sizes are equal to *k*. Then we have

$$c = R - \frac{1}{k} NN' \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(26)}$$

and we know that C has one zero root, dt = 0 say, with associated normalized eigenvector $e_t = (\frac{1}{\sqrt{t}})J$. Let the other roots be d_1, d_2. . . d_{t-1} with associated

Orthonormal eigenvectors e_1, e_2, . . . e_{t-1}. Then

$$e_i'c = d_i e_i' \quad \text{(i = 1, 2 . . . t − 1)}$$

and from

$$e_i c_\tau = d_i e_i \tau$$

it follows that

$$e_i' 1 = \frac{1}{d_i} e_i' Q$$

And

$$\operatorname{var}(e_i'\hat{\tau}) = \frac{1}{d_i^{'}} e_1' C e_1 = \frac{1}{d_i^{'}} \sigma_e^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(27)}$$

Using the fact that $e_t = (\frac{1}{\sqrt{t}})J$, that e_1, e_2, . . . , e_{t-1} are mutually perpendicular

and perpendicular to e_1, and that

$$\sum_{i=1}^{t} e_i e_i' = I$$

We have with $z' = (z_1, z_2, ..., z_t)$

$$Z'(I - e_t e_t')Z = \sum_{i=1}^{t-1} (e_i' z)^2 = Z'(\sum_{i=1}^{t-1} e_i e_i')Z \sum_{i=1}^{t} z_i^2 - \frac{1}{t}\left(\sum_{i=1}^{t} z_i \right)^2$$

$$= \sum_{i=1}^{t} \left(z_i - \overline{z} \right)^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(28)}$$

It is also to verify that

$$\frac{1}{t(t-1)} \sum_{i \neq i'} \left(z_i - \overline{z} \right)^2 = \frac{2}{t-1} \sum_{i=1}^{t} \left(z_i - \overline{z} \right)^2 \quad \ldots\ldots\ldots\ldots\ldots \text{(29)}$$

Taking $z_i = \hat{\tau}_i - \tau_i$ substituting into (29) using (28) and then taking expectation and using (27) yields for (25).

$$av.\underset{i\neq 1}{\text{var}}(\hat{\tau}_i - \hat{\tau}_{i'}) = \frac{2}{t-1}\sum_{i=1}^{t-1}\sigma_e^2 \quad \text{..... (30)}$$

Where av.var stands for average variance for connected IBD.

3.8.1. Definition of Efficiency Factor

It is natural in attempting to evaluate the efficiency of an IBD to compare it with a CRD since this is always a possible competing design. For a CRD with r_i replications for treatment i, the average variance of treatment differences is

$$av.\underset{i\neq i'}{\text{var}}(\hat{\tau}_i - \hat{\tau}_{i'}) = \underset{i\neq i'}{av.}\left(\frac{1}{r_i} + \frac{1}{r_i'}\right)\sigma^2_{e(CRD)} = \frac{2}{\sqrt{r_h}}\sigma^2_{e(CRD)}$$

Where $\overline{r}_h$ is the harmonic mean of the ri, that is,

$$\frac{1}{\overline{r}_h} = \frac{1}{t}\sum_i \frac{1}{r_i}$$

We shall digress here for a moment and show that the best CRD is the one with all ri = r, and that is the design with which we shall compare the IBD. For this and later derivations we need the "old" result that the harmonic mean of a set of positive numbers is not greater than the arithmetic mean. Depending on this idea, let the set of numbers be {Xi, i = 1, 2 ,. . . ,m}. Consider the quadratic

$$q(\beta) = \sum_{i=1}^{m}\left(\sqrt{x_i} - \beta\frac{1}{\sqrt{x_i}}\right)^2$$

Clearly q(β) ≥ 0 for all β. The minimizing value of β is obtained by using least squares which gives the NE

$$\sum_i \frac{1}{x_i}\tilde{\beta} = m$$

The minimum sum of squares is

$$\sum_i x_i - \tilde{\beta}m \geq 0$$

Hence

$$\sum_i x_i - \frac{m^2}{\sum_i \frac{1}{x_i}} \geq 0$$

Or

$$\left(\frac{1}{m}\sum_i x_i\right)\left(\frac{1}{m}\sum_i \frac{1}{x_i}\right) \geq 1$$

Or

$$\frac{\bar{x}}{\bar{x}_h} \geq 1$$

with equality if and only if xi = x for all i. This result implies that the best CRD will have $r_i = r$ and r = n/t where *n* is the total numbers of EUs. This can happen, of course, only if n/t is an integer. If n/t is not an integer so that n = pt + q (0 < q < t), then the best CRD will have q treatments replicated p + 1 times. Consider now the case of an IBD with b blocks of size k and ri replications for the i^{th} treatment. Then the total number of EUs is n = bk = ri . Suppose also that *n* = rt, so that an equireplicate CRD is possible. The average variance for such a design is $\frac{2\sigma^2_{e(CRD)}}{r}$, where as the average variance for the IBD is $\frac{2\sigma^2_{e(CRD)}}{c}$ where, as shown in (30), c is the harmonic mean of the positive eigenvalues of $\boldsymbol{R} - (1/k)\,\boldsymbol{NN}$ (Kempthorne, 1956). It is natural to write c = rE, so that with $\sigma^2_{e(CRD)} = \sigma^2_{e(IBD)}$ we have

$$\frac{av.\mathrm{var}(\hat{\tau}_i - \hat{\tau}_{i'})_{CRD}}{av.\mathrm{var}(\hat{\tau}_i - \hat{\tau}_{i'})_{IBD}} = \frac{2/r}{2/rE} = E \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad (31)$$

The quantity E thus defined is called the efficiency factor of the IBD. It is clearly a numerical property of the treatment-block configuration only and hence a characteristic of a given IBD. We add the following remarks:

1. The same definition of E in (31) could have been obtained by using the average variance

for an RCBD with b = r blocks instead of the average variance for an equireplicate CRD assuming that $\sigma^2_{e(RCBD)} = \sigma^2_{e(IBD)}$

2. Although *E* is a useful quantity to compare designs, it does not, of course, give the full story. It compares average variances only under the assumption of equality of residual variances, whereas we typically expect $\sigma^2_{e(IBD)} < \sigma^2_{e(CRD)}$) and $\sigma^2_{e(IBD)} < \sigma^2_{e(RCBD)}$
3. The efficiency factor pertains only to the intrablock analysis and ignores the interblock information.
4. Each IBD will have associated with it an efficiency factor E. In order to compare two competing IBDs with the same n and with efficiency factors E_1 and E_2, respectively, we would typically choose the one with the higher E value.

3.8.2. Upper Bound for the Efficiency Factor

Using again the fact that the harmonic mean of positive numbers is not greater than the arithmetic mean, we have

$$(t-1)c \le \sum_{i=1}^{t-1} d_i = trace\left(R - \frac{1}{k}NN'\right)$$

$$= \sum_{i=1}^{t} r_i - \frac{1}{k}\sum_{ij} n_{ij}^2$$

$$= n - \frac{1}{k}\sum_{ij} n_{ij}^2 \quad \text{..... (32)}$$

The largest value of the right-hand side of (32) is obtained for the smallest value of $\sum_{ij} n_{ij}^2$. Since n_{ij} is one of the numbers 0, 1, 2. . . K, the minimum value of $\sum_{ij} n_{ij}^2$ will be achieved when *n* of the n_{ij} 's are 1 and the remaining are zero. Since the $\sum_{ij} n_{ij}^2 = n_{ij}$ and $\sum_j n_{ij} = r_i$, it follows from (16) that

$$(t-1)c \le \sum_i r_i - \frac{1}{k}\sum_i r_i = \frac{k-1}{k}t\bar{r}$$

Or, since C=rE $E \le \dfrac{(k-1)t/(t-1)k}{\bar{r}/r}$

But since $t\bar{r} = n = tr$, we have finally

$$E \le \frac{(k-1)t}{(t-1)k} \quad \text{..... (33)}$$

Since for an IBD $k < t$, we can write further

$$E \le \frac{(k-1)t}{(t-1)k} < 1 \quad \text{.....(34)}$$

The upper bound given in (34) will be achieved for the incomplete block design. Sharper upper bounds for certain classes of IBDs are given by Jacroux (1984) and Paterson (1983).

CHAPTER FOUR

4. RESULTS AND DISCUSSION

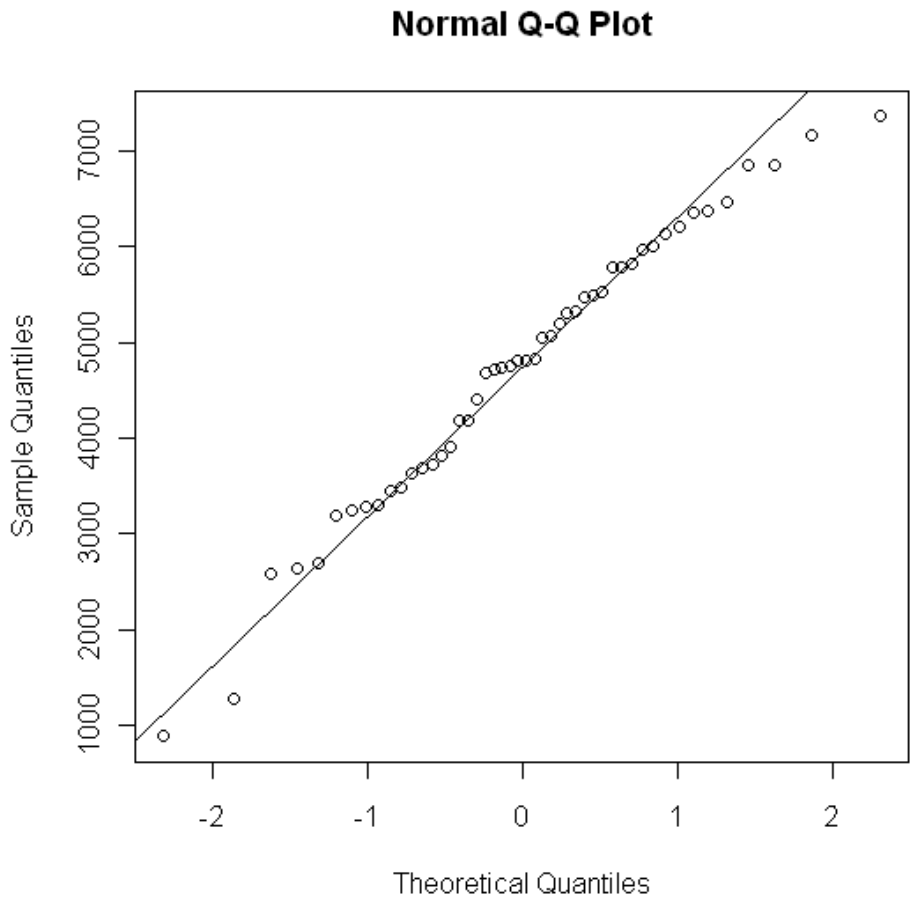
4.1 The common assumption for all data sets

4.1.1. Testing for Normality assumption

The QQ-plots of residuals in (figure 4.1) and (figure 4.2) and the formal test (Shapiro Wilks test) shows that the data conforms to the hypothetical normality assumptions. The fact that the plot is scattered around the straight line and does not show considerable pattern indicates that the distribution of the error term and the response variable is normal (linearity of the error term is fulfilled).

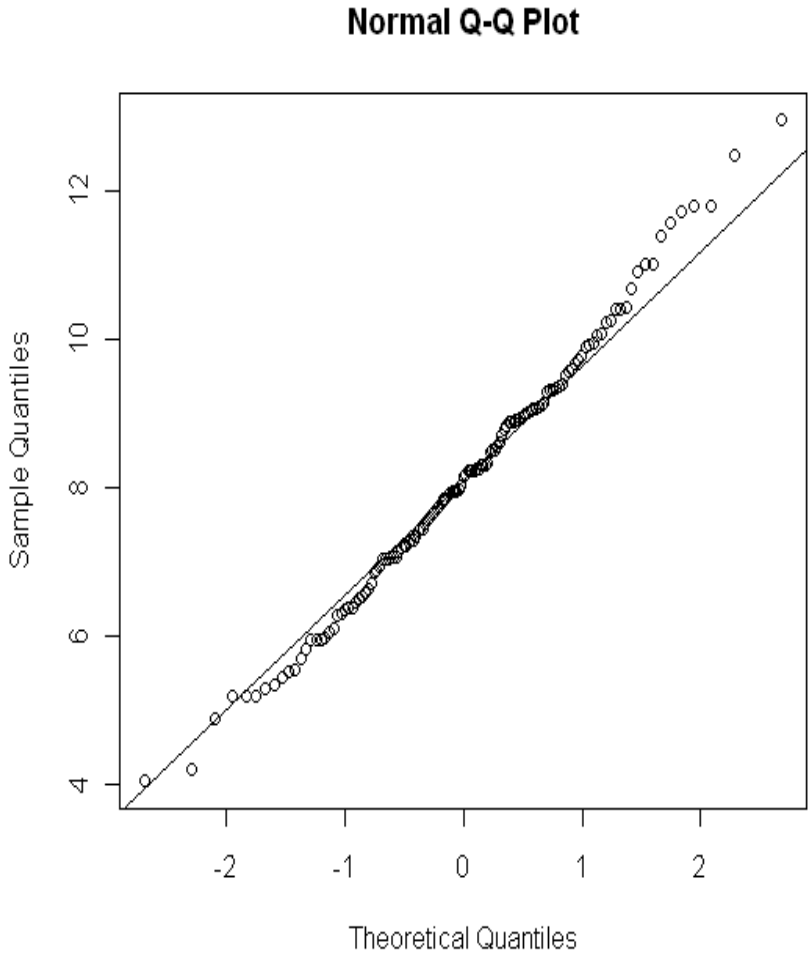
Diagnosis for the assumption of normality for bread wheat data.

Figure 4.1



Diagnosis for the assumption of normality for maize data.

Figure 4.2



One common test for checking the normality is Shapiro-Wilk test. This test works well even for a small sample size, so generally we just need to use this. The null hypothesis of Shapiro-Wilk test is that the samples are taken from a normal distribution. So, if the p value is less than 0.05, we reject the hypothesis, and thinks that the samples are not taken from a normal distribution. From (table 4.1) below for bread wheat data set and maize data set p-value = 0.4631 and p-value = 0.8039 respectively. In both cases, the p values are statistically insignificant and we can still assume the normality. From the results of model checking, normality assumption is satisfied and the original data is appropriate and can be used in statistical analysis and inference without transformation of the response variable.

Table 4.1: Tests for normality of alpha lattice design and RCBD.

Type of Design	Shapiro-Wilk Test	
	W-statistic	p-value
Alpha lattice	0.9936	0.8039
RCBD	0.9771	0.4631

4.1.2. Constant Variance Assumption

Once again there are graphical and formal tests for checking the constant variance assumption. The hypothesis of interest is H_0: $\sigma_1^2 = \sigma_2^2 = \ldots = \sigma_t^2$ versus H_A: $\sigma_i^2 \neq \sigma_j^2$ for at least one pair i≠j:

One procedure for testing the above hypothesis is Bartlett's test. Bartlett's test is too sensitive deviations from normality. So, it should not be used if the normality assumption is not satisfied. The two types of designs statistically not significant this implies that the homogeneity assumption satisfied (table 4.2).

Table 4.2: Bartlett test of homogeneity of variances for alpha lattice design and RCBD.

Type of Design	Bartlett test	
	Bartlett's K-squared	p-value
Alpha lattice	25.4445	0.4939
RCBD	0.2982	0.8615

4.1.3. Additivity test

The initial assumption we made when considering the model

$$y_{ij} = \mu + t_i + b_j + e_{ij}$$

is that the model is additive. A formal test of nonadditivity is Tukey's one degree of freedom test for nonadditivity. To perform this test, one starts out by fitting the interactive model. It has a *p* value of 0.5077 for RCBD for wheat data set and 0.3178 for alpha lattice design for maize data set. Thus we have no evidence to declare nonadditivity.

Table 4.3 : Tukey's one DF test for additivity for alpha lattice design and RCBD.

Type of Design	Tukey's one df test	
	F	p-value
Alpha lattice	4.7628	0.3178
RCBD	0.4498	0.5077

4.2. Analysis of Randomized Complete Block Design

As can be seen in (table 4.4), the bread wheat variety is significant ($p < 0.05$) while block effects is not significant ($p > 0.05$) in bread wheat pre regional variety trial. The relative efficiency for the rest of the bread wheat pre regional variety trial is nearest to one the RCBD is almost as efficient as the CRD. Thus, for this bread wheat pre regional variety trial, blocking seems to be insignificant and unnecessary.

Table 4.4: ANOVA of RCBD for bread wheat wariety in 2010 of data set

Source of variation	Df	Sum Sq	Mean Sq	F value	Pr(>F)	RE
block.unadj	2	2459773	1229886	1.1823	0.3204528	1.01
trt.adj	15	67202516	4480168	4.3068	0.0003285	
Residuals	30	31207400	1040247			

From (table 4.5) below, the relative efficiency was 101.1% for bread wheat data set implying that the use of RCBD almost similar to CRD. The significance of blocking within replication (group) in RCBD for bread wheat data set indicates that blocking was ineffective ($p > 0.05$) in reducing experimental error .The coefficient of variation (CV) in both RCBD and CRD was similar and the relative efficiency for bread wheat was nearest to one. The RCBD was almost as efficient as the CRD. Thus, for bread wheat blocking seems to be insignificant and unnecessary.

Table 4.5: Efficiency of RCB design as compared to CRD in 2010 season for bread wheat variety trial.

Design	CV	MSE	P value for block
RCBD	12.6 %	1040247	0.3204528
CRD	21.7%	1052099	
Relative Efficiency	1.011		

4.3. Analysis of Alpha lattice Design

The interesting feature of the design is the blocks within replication sum of squares are highly significant and therefore, formation of blocks within replications has been fruitful. Thus the formation of incomplete blocks with in replications has been very effective and the error mean square is quite small. The treatment effects are also highly significant (table 4.6).

Table 4.6: Analysis of variance for alpha lattice design

Source of variation	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Replicates	2	25.175	12.5873	12.0828	0.00
Block(with in replicates, ignoring treatments)	24	57.238	2.3849	2.3849	0.00
Treatment (adjusted for block)	44	258.614	5.8776	5.8776	0 .00
Error	64	66.673	1.0418	1.0418	

The relative efficiency was 135.16% for maize data set (table 4.7) implying that the use of alpha lattice design increased experimental precision by 35.16% compared to RCBD. The coefficient of variation (CV) and mean square error (MSE) of alpha lattice design (12.6 and 1.0418) were comparatively low as compared to RCBD (14.6 and 1.4081).

Table 4.7: Efficiency of Alpha lattice design as compared to RCBD in 2010 Season.

Design	CV	MSE	P value for blocks
Alpha lattice design	12.6 %	1.0418	0.004509
RCBD	14.6 %	1.4081	0.0002922
Relative Efficiency		1.351603	

From the (table 4.8) below, the degrees of freedom of the error in RCBD are (t-1) (r-1), in the alpha design, there is an effect of error that is the block in each repetition, its degrees of freedom for the error is r(s-1). Then, a way to approximate the efficiency factor is relating these degrees of freedom. $E = df(RCBD) / (df(RCBD) + r(s-1))$

$E = (45-1)(3-1) / ((45-1)(3-1) + 3(9-1)) = 0.7857$

If blocks are complete, it is not necessary to indicate the blocks within each repetition and then the efficiency factor would be equal to 1. When more treatments are on every block, the

efficiency factor tends to 1. The efficiency is calculated only with the estimate of error. An alpha design in the efficiency only uses the parameters of the dimension of the design and not the source of error. In complete block the efficiency factor is 100% and alpha designs are less than 100%. There could be an approximation of the efficiency upon using the variance of the error. It is assumed that each repetition of the alpha design is a block regarding the alpha design used.

Table 4.8: Efficiency factor alpha lattice design as compared to RCBD in 2010 Season.

design	Efficiency factor
RCBD	1
Alpha Lattice	0.7857

Means with the same letter are not significantly different. As we observed from the following (table 4.9) below, treatments 6, 4,11,2,16,7,12,1 and 5 were the same, not significantly different. Mostly for bread wheat variety trial, treatments 6 and 4 are important to use since, their means were higher than the others.

Table 4.9: Comparison of treatments of bread wheat variety trial.

Groups	**Treatments**	**means**
a	6	6066.567
a	4	5897.867
a	11	5861.333
a	2	5837.733
a	16	5814.533
a	7	5452.8
a	12	5213.6
a	1	5005.167
a	5	4758.067
ab	3	4607.3
ab	9	4532.533
ab	15	4219.6

ab	14	4013
ab	8	3529.233
ab	10	3091.3
b	13	1602.6

To sum up the results of the analysis of the presented maize data set, it should be noted that among all used varieties, the most promising is variety 33. Its estimated mean yield 11.71 tone per hectare (t/ha) is the highest among all tested varieties (table 4.10). This means that it is particularly necessarily to use it for environments with high yielding conditions and also better than the other varieties.

Table 4.10: Comparison of treatments maize data set

Groups	Treatments	means
a	33	11.71333
ab	38	11.13
abc	30	10.33
abcd	41	10.11667
abcde	14	9.996667
bcdef	31	9.66
bcdef	37	9.636667
bcdefg	45	9.523333
bcdefgh	42	9.413333
cdefghi	5	9.126667
cdefghij	18	8.966667
cdefghij	32	8.85
cdefghij	21	8.75

cdefghij	8	8.746667
cdefghij	39	8.566667
cdefghij	4	8.41
defghij	13	8.396667
defghij	24	8.306667
defghij	6	8.243333
efghijk	9	8.12
efghijk	10	8.076667
fghijkl	43	8.003333
fghijkl	2	8
fghijklm	11	7.94
fghijklm	1	7.826667
fghijklm	20	7.826667
fghijklm	26	7.74
ghijklm	12	7.653333
ghijklm	15	7.653333
ghijklm	27	7.616667
hijklm	36	7.573333
hijklm	3	7.496667
ijklm	19	7.483333
ijklm	44	7.4
ijklm	35	7.31
ijklmn	28	7.243333
jklmn	23	7.13

jklmn	40	7.093333
jklmn	17	7.056667
klmno	16	6.26
klmno	25	6.196667
lmno	29	6.08
mno	34	6.053333
no	22	5.323333
o	7	5.056667

4.4. Discussion

Alpha-design is a class of resolvable design for almost any practical number of entries (Patterson & Williams 1976; Patterson *et al*. 1978; Paterson *et al*. 1988). Alpha-lattice has been shown to be more efficient than RCBD in field trials conducted in the UK (Patterson & Hunter 1983) and Poland (Pilarczyk 1991), and appears to have the potential to replace RCBD in many regional and international trials. This study also is in line with the idea. Hence, an alpha design cannot be less efficient than a RCBD. This study was conducted to compare the relative efficiency of two statistical experimental designs based on mean square errors. For this purpose, maize datasets were analyzed with alpha lattice design and randomized complete block design (RCBD). The results of the maize dataset show that 35.16% precision increased with alpha Lattice design over RCBD. Coefficient of variation of alpha lattice design is 12.6 % while that of RCBD is 14.6 %, which proves the efficiency of alpha lattice design.

Masood et.al (2006 & 2008) compared efficiency of alpha lattice design. The results indicated that alpha lattice design improved the efficiency 8-9 and 14 percent as compared to RCBD in these studies. YAU, (1997) reported the use of alpha lattice design in international yield trials of different crops and found average efficiency 18 % higher than the RCBD. The value of relative efficiency greater than one for maize data set show that alpha lattice design was clearly more efficient than RCBD (table 4.7). Relative efficiency indicates that the use of alpha lattice design instead of RCBD increased experimental precision by 35 percent in maize data set. Therefore,

results from the alpha lattice design analysis indicate that the coefficient of variation (CV) and the mean square error (MSE) of maize variety trial was calculated for Bako Agriculture Research Center. The coefficient of variation and error mean squares of the randomized complete block design was greater than that of lattice design. This indicates that, alpha lattice design was more efficient than RCBD (table 4.7). Due to technical or cultural practices, the blocking effect was low (not significant) in certain trials and the technical problem results from wrong block orientation and direction which render blocking ineffective (Girma, 2005). For bread wheat variety trial data set used in this study, block effects were insignificant. This can be due to technical issues such as orientation and direction of blocking.

The best alpha lattice designs obtained from the algorithm of (Patterson, 1983) come with in 0.8% of the lower upper bounds of the efficiency factor and 99.9% of the lowest upper bound. In practice this is likely to make the design acceptable. From (table 4.8) the upper bound of the efficiency factor for alpha lattice design was 78.5% which supports the above idea.

From the alpha lattice design, the interesting feature of the design is the blocks within replication sum of squares are highly significant and therefore, formation of blocks within replications has been fruitful. Thus the formation of incomplete blocks with in replications has been very effective and the error mean square is quite small. The treatment effects are also highly significant (table 4.6).

The residual variance of RCBD was less than the residual variance of CRD in 2010 season from the ANOVA of RCBD on bread wheat variety trial (table 4.5). This shows that RCBD is more efficient than the CRD in increasing the precision of the bread wheat variety experiments. The residual variances of alpha lattice design for maize data sets were smaller than the residual variances of RCBD. The variation among block within replication were greater than the variation among block of RCBD. This shows that alpha lattice design was more efficient than RCBD.

CHAPTER FIVE

5. CONCLUSIONS AND RECOMMENDATIONS

5.1. Conclusions

The results of this study focused on identification of the more efficient experimental design for field experiments. We conclude the findings of this study as follow. For regional maize variety trial, alpha lattice design was more efficient than RCBD to increase the precision of the field experiments. Under land heterogeneity and in a situation where a large number of entries are tested, the chance that families of IBD are more appropriate in quite high and researches are encouraged to use one of these designs under such conditions. In conclusion that RCBD and alpha lattice design were the more efficient designs than the CRD for agricultural field experiments. Thus, researches must be caution in using CRD in field experiments.

This study show that alpha lattice design provided smaller standard errors of differences, coefficients of variation and error mean squares as compared to RCBD providing efficiency in comparing different entries. Therefore, this design should be employed while conducting field research trials on different crops in field experiment when number of varieties in the experiments is large. There is also need to extend experimentation to more research stations for wider applicability of these designs for these crops and for some other crops too. For plant breeding and selection trials alpha lattice design should be used in such a way that they form a resolvable incomplete block design so that the results could be analyzed through RCBD for comparison to check the required gains in efficiency.

To control variability in field experiments, it is suggested that an experiment with a RCB design could be replaced with an alpha lattice design when the number of varieties in the experiment is large. The use of alpha lattice design allows the adjustment of treatment means for block effects. This in turn brings benefit from the small incomplete blocks which help varietal comparisons under more homogenous conditions. The alpha lattice design also provides effective control within replicate variability. The results presented here make a case of using alpha lattice design which enhances the chances of detecting varietal differences to a great extent.

5.2. Recommendations

- Since the alpha lattice design have greater efficiency than RCBD to increases the precision of agricultural field experiments, alpha lattice design is better to use than RCBD based on available land resource and size of experiments.
- Since the arbitrary selection of an experimental design can result in dramatically different treatment conclusions, agronomist is advised to use the procedure of design selection that have been used in this study. Thus, first, use the relative efficiency to check performance of the designs; second, use upper bounds of the efficiency factor for IBD which makes the design acceptable.
- For bread wheat variety trial data set used in this study, block effects were insignificant. This can be due to technical issues such as orientation and direction of blocking. So, we recommend that further studies should be done in this area.

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