ADDIS ABABA UNIVERSITY

SCHOOL OF GRADUATE STUDIES

COLLEGE OF NATURAL SCIENCES

DEPARTMENT OF STATISTICS

CONSTRUCTION AND ANALYSIS OF AUGMENTED AND MODIFIED AUGMENTED DESIGNS

A THESIS SUBMITTED TO THE DEPARTMENT OF STATISTICS AS PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE IN APPLIED STATISTICS.

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DECEMBER, 2011

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Acknowledgments

First, and foremost, I would like to honor the Almighty God for giving me the strength continue through the long time process and also giving me an opportunity to pursue my graduate study at the Department of Statistics, Addis Ababa University.

My grateful appreciation goes to my thesis advisor Dr.Girma Taye, his constructive advise, substantial amount of constructive criticisms and suggestions for the successful realization of the study.

My appreciations and thanks to the staff members of the departments of statistics, Addis Ababa University and for all their cooperation.

Finally, I convey my thankful pleasure to my work partner w/ro Birtukan for her continuous encouragement in my studies and moral supports and also I would like to express my appreciation to those who have contributed on this work.

Abstract

The augmented block design is widely used in breeding programs, particularly in screening and selection of a large number of germplasm lines with non-replicated test treatments and replicated control treatments to estimate the experimental error. The study establishes a relationship between augmented design via RIB design and designs for test treatment(s) versus control treatment(s) and 2^v balanced main effect plans (saturated and unsaturated) obtained through BIB designs. The data used in this study were obtained from an experiment of wheat which was conducted by using augmented RIB design and a modified augmented BIB design from scientific journal. In these design, we consider eight test treatments and four control treatment for augmented design and thirteen test treatment and three control treatment for the modified augmented BIB design. The construction and the analysis of modified augmented BIB design can be considered by using the fixed and mixed model analysis, and in addition, a method is proposed for finding A- and MV- Optimal designs such situations and some sufficient conditions are given under which a design obtained using the proposed method will be A-and MV-optimal. Some examples are also given to show how the results obtained can be applied. The results were obtained using excel and SAS. We have seen in this study that when block is greater than two, the modified augmented BIB design is more efficient than augmented RIB designs.

Key words: Augmented Design, Modified Augmented Block Design, Fixed Effect Model and Random Effect Model.

Acronyms

ABD	Augmented block designs
ANOVA	Analysis of variance
ARCD	Augmented Row-column design
BBDVR	Balanced block designs with variable replications
BBPBD	Balanced Bipartite block designs
BBPUB	Balanced Bipartite block with unequal block sizes.
BIBD	Balanced incomplete block design
BLD	Balanced lattice designs
BLUE	best linear unbiased estimator
BTDT	Balanced two disjoint sets of treatments
BTIB	Block treatment incomplete block designs
CBRTED	Control balanced residual treatment effects design
EBLUPS	Empirical best linear unbiased predictions
EBTIBD	Extended balanced treatment incomplete block designs
IBD	Incomplete block designs
IIGBD	Inter and Intra group balanced designs
MABIBD	Modified Augmented balanced incomplete block designs
MV	Minimum variance
RBIBD(R-type BIBD).	Reinforced balanced incomplete block designs
RCBD	Randomized complete block design
SAS	Statistical Analysis System
SBIBD (S-type BIBD)	Supplemented balanced incomplete block designs
SPAD	Statistical packages for augmented designs.
SRD	Standard Reinforced Designs

CHAPTER ONE

INTRODUCTION

1.1. Background of the Study

Designs are usually characterised by the nature of grouping of experimental units and the procedure of random allocation of treatments to experimental units. Block designs are useful in experiments requiring eliminations of heterogeneity in one or two direction. As experiments become larger with more entries and replications, costs will go up. Federer (1956) developed a series of augmented designs to minimize such costs. Augmented designs provide well come flexibility to large experiments and these designs are useful in agricultural experiments.

The augmented designs were proposed by Federer (1956),the designs are a modification of straight forward designs, by adding test treatments that appear only once in the experiment to the set of replicated control treatments. Among the augmented designs, the augmented block design is perhaps the most used, and inferences have been made by means of an intra and inter block analysis.

The available quantity of seed is often not sufficient for replicated trials. Moreover, the number of new germplasm to be tested is very high (usually about 1000-2000 and sometimes up to 3000 accessions), and it is very difficult to maintain the within block homogeneity. These experimental situations may also occur in the fields of entomology, pathology, chemistry, physiology, agronomy and perhaps others for screening experiments on new material and preliminary testing of experiments on promising material.

For in many cases such design is used with treatments being selection units sampled from a population. Besides, recovery of information on treatments among blocks (inter-block approach) can potentially improve the estimates, and this is achieved by regarding block effects as random. Genetic variances can be underestimated if the intra-block analysis is used in the augmented block design (Bearzoti, 1994). Therefore, the theory of mixed models (Henderson, 1984) could be used to take into account the randomness of the effects of test treatments and/or blocks (Robinson, 1991). The effects of control could be considered fixed in plant breeding, for they are generally standard released varieties.

In plant selection programmes, breeders usually start with a large number of test lines, which come either crossing or through introduction from foreign sources. The number of lines can range even up to hundreds. To conduct a field experiment for such a large population is extremely difficult for a number of reasons, among them that environmental heterogeneity in the field can not be easily taken in to account. To complicate the matter further, material available for each test line is often limited, some times being sufficient for only one replication. Thus designs for variety trials involving large numbers of test lines, for example, lattice square and quasi-factorial designs, all of which require replications, can not be used; similarly, designs such as chain blocks (Youden and Connor, 1953; Mandel,1954), which require that a substantial number of test lines have at least two replication cannot be applied.

In plant breeding programs, there are cases where controls include new treatments generated through breeding. The test treatments are supposed to be compared against certain controls. Any of the experimental design can be used depending on the number of treatment and stage of breeding programs. In the early stage of selection process, there could be insufficient seed of the new treatments' to under take replicated experiments or the number of genotypes could be very large to manage in terms of resources. In such cases some plant breeder use single row plots to

evaluate the newly developed test treatments and at a certain regular intervals control varieties are planted. The performance of the new treatments is then compared with the performance of the nearest controls subjectively. The standard statistical analysis is not possible as the new genotypes are not replicated but an objective comparison can be made. The disadvantages of subjective judgment are that the controls are systematically placed and no provision is made to adjust a given measurement for environmental variation from one part of the experiment to another. A better method, when there are many test treatments at the early stage of the breeding programs is to use an experimental design called augmented design that was developed by Federer (1956) and well illustrated by Federer and Raghavarao (1975). This design is of particular interest in an extensive plant breeding programs.

To circumvent the difficulties arising from non replicated experiments, Federer (1956) proposed a class of design called 'augmented design'. The basic idea is to include control lines for which enough material is available and repeat them several times in a standard design. Each repetition of the control lines is embedded in a block (or incomplete block, or cell, depending on the design used) and test lines are assigned to plots that are not allocated to controls. Estimations of block effects and plot error are done only with respect to control lines. The estimated block effects are used to adjust the observed values of the test lines and the error is used to test the significance of line differences.

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 control 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 controls.

1.1.1 Categories of Experimental Situations

There are two categories of experimental situations as described below.

Augmented designs, the material for the tests is scarce and the experimenter cannot afford to replicate the treatments. However, enough material is available for the replications of controls. In second category of experiments, more than one replications of test treatment is possible. Therefore, the designing problem for the two categories of experimental situations has to be different. In the sequel we describe the two categories of experiments and give their historical development.

1.1.1.1. Test Treatments with single replication.

This Category of designs is essentially augmented designs. In genetic resources environment, which is a field in the forefront of biological research, an essential activity is to test or evaluate the test treatments with the existing control treatments. A problem in these evaluation studies is that the quantity of the genetic material collected from the exploration trips is very limited or can not be made available since a part of this is to be deposited in Gene Bank. These types of situations came to be known to Federer (1955) in screening new strains of sugarcane and soil fumigants used in pineapples.

For single control treatment the A-and MV-optimal designs with minimum number of observations for making all possible paired comparisons are A-and MV-optimal for making test treatments versus control treatment comparisons as well. Optimum number of replications of the control treatments in the blocks of a modified augmented balanced incomplete block design has been obtained for maximizing the efficiency per observation of the BLUE of the test treatment versus control treatment contrasts.

1.1.1.2. Test treatments with many replications.

This Category of experiments is in fact a follow up of the first category of experiments. In first category of experiments, the material on tests is scarce and it is not possible to replicate the tests, though the controls are replicated and it is the replications of the controls alone that provide us the experimental error. These types of experiments are generally the screenings of experiments where in the purpose of the experiment is to identify the promising test treatments. Once these are identified, then a further experimentation is carried out with the tests identified as promising. In these experiments, it is possible to replicate the tests also besides replicating the controls. For these experiments, attempts have been made by various research workers to investigate the optimality and construction aspects of designs used for making tests versus control comparisons.

Efficient designs for making test treatments versus control treatments comparisons have been obtained following two approaches. In the first approach, efficient designs for estimation of treatment contrasts of interest have been obtained by minimizing some function of the variance covariance matrix of the BLUE of contrasts of interest. In the second approach, efficient designs have been obtained by minimization of the probability connected with the joint confidence statement concerning many to one comparison between the means of control and test treatments.

A- and MV-optimal proper and non-proper block designs have been obtained and catalogued for the present experimental setting under the usual fixed effects and mixed effects model. It has been shown that a proper block design that is optimal under a fixed effects model is also efficient under a mixed effects model. Optimal proper block designs have also been obtained when the errors are correlated. A-optimality for the present experimental setting has also been studied under the model where the intra-block variances are assumed to be proportional to non-negative real power of block

sizes. Some designs have also been obtained by adding one block of the test treatments in the minimally connected designs. These designs have been shown to be highly efficient.

Major research on 2^v main effect plans has been done by Placket and Burman (1946). They established the relationship of these plans with balanced incomplete block designs (BIBD). Using the conditions of proportional frequencies of Placket (1946) and Addelmann and Kempthorne (1961a), Sharma (1997) obtained 2^v main effect plans (saturated and unsaturated) through BIB design.

In this study we established a relationship between 2^v main effect plans and modified augmented balanced incomplete block design. These designs are found to be similar with R-type balanced treatment incomplete block design (BTIBD) and extended balanced treatment incomplete block designs (EBTIBD) introduced in Mazumdar (1986). The (BTIBD) is balanced with respect to test treatment-control treatment comparison where as the case of (BIBD), all the treatment comparisons are equally important. These designs are found to be more similar with reinforced balanced incomplete block designs considered by Das (1958) and Constantine (1983).

1.2. Statement of the Problem

A common problem which arises in many industrial, agricultural and biological experiments would be that of comparing a set of test treatments with that of one or more control treatments. Plant breeders encounter a similar problem with variety screening experiments in which a large number of varieties must be evaluated; the supply of seed may be limited. In those situations, the uses of augmented experimental designs have proven effective for obtaining the replication needed for valid statistical analysis. Under the following two conditions, randomized incomplete block designs or any other such replicated block designs becomes inefficient.

i) When seeds of test genotypes are small in quantity and replications of the test treatments are not possible.

ii) When large numbers of germplasm collections are to be evaluated.

Such a huge collection can not be accommodated in randomized block design as soil heterogeneity becomes unmanageable. Therefore, in the absence of error term in the ANOVA, with out replication, test of significance can no be applied. Both these problems can be surmounted by employing augmented design.

At present in augmented design, the experimental error is estimated from the control treatments which are randomized in the whole experimental material and replications of test treatments are not possible. As block size increases, this may not be providing precise estimate of experimental error. Since the error estimate of augmented design is only an approximation, to overcome this limitation in this study, an alternative method is proposed known as the modified augmented block design.

This modified augmented block design will enable to augment the size heterogeneity in the experimental material and provide more precise experimental error and efficient over the augmented block design. Although, the comparisons among varieties are not all equally precise and the estimates of the experimental error may be biased. To evaluate all the treatment differences, with the same degree of precision, the modified augmented designs should be BIB designs to compare every treatment with every other treatment an equal number of times in the incomplete block designs and also used to address the block effects and to estimate an accurate error mean squares.

Generally, the purpose of using a modified augmented BIB design is to estimate accurate error mean squares of the experiments. This design is most efficient design for making test versus control treatment comparisons according to varies efficiency criteria. When blocks and replications are increases then the error mean square becomes decline.

Therefore, replication is the most effective means of overcoming the effects of field variability and directly reduces the contribution of plot residuals to estimates the means.

1.3. Objectives of the Study

1. 3. 1. General Objective

To construct the augmented design via randomized incomplete block Design and modified augmented design through balanced incomplete block designs and also investigate the optimality of the MABIB design.

1.3.2. Specific objective

- To make comparisons between modified augmented BIB design with augmented RIB design.
- To estimate the variance of elementary contrasts between any two test, between any two controls and between any tests vs. control treatments in both designs.
- To obtained a precise estimation of experimental error.
- To compare the tests with control treatments in both designs.
- To investigate the optimality and construction aspects of designs.

1.4. Significance of the Study

Experimental Design plays an important role on establishing an interface between theoretical results and statistical applications in several fields, like Agriculture, Industry, Biology, etc.

- The study will provide a unique opportunity to facilitate farmer input and rapid technology screening in to on-farm cropping system research.

- The study will contribute a new method and provide information's for field experimenters, researchers and breeders for further investigations of experimental and statistical problems related with the applications and uses of an augmented block designs and modified augmented block designs in plant breeding and poultry research.

- The study will help for screening large number of experimental lines and preliminary testing of experiments on promising materials in the fields of entomology, pathology, chemistry, physiology, agronomy and others. Particularly, genotypes, insecticides, herbicides, drugs etc.

- In the Modified ABIB design, comparing treatments with one or more controls is an integral part of many areas of scientific experimentation. In plant breeding, in biochemical studied, for example new types of hybrid varieties, new types of genotypes, strains, pesticides, soil fumigants, drug etc. are the test treatments while a standard treatments and /or a placebo is the control treatments.

1.5. Limitations of the Study

The study has the following limitations.

- Since an augmented block designs or modified augmented block designs are incomplete block design, the missing data for un-replicated treatment means loss of more information on that treatment.
- An augmented block design or modified augmented block design need many repeated control treatments. Hence, results can strongly depend on control treatments. But, the proportions of control treatments to test treatments are not clearly defined. Therefore, further study need to know the optimum number of control to test treatments so as to maximizes the efficiency per observation.
- Augmented block design is more appropriate only when there is smaller blocks and large number of test treatments where as the modified augmented block design is applicable only when there is large number of blocks.
- In the augmented block design, control treatments are often systematically placed in each experimental plot, so estimation of experimental error may not be valid.

CHAPTER TWO

LITERATURE REVIEW

Since Federer published his Article "Augmented (or Hoonuiaku) designs" in 1956, a lot of additional research results have been published. Federer (1961) extensively illustrated arithmetically and algebraically an augmented randomized complete block design and an augmented balanced lattice design. For both designs he considered analyses with and without recovery of inter-block information and provided some discussion on unequally sized incomplete blocks. He pointed out that sufficient replications of controls need to be included to have sufficient degrees of freedom nineteen for estimating experimental error variance and effects of blocking used to control field heterogeneity (Federer and Raghavarao, 1975). He also gave a precise introduction to some augmented row-column designs (Federer et al., 1975) and to the construction and analysis of augmented lattice square designs (Federer, 2002).Generally, he conclude that the appropriate design for an augmented design is the randomized incomplete block design.

Augmented designs use replicated controls to assess the performance of non-replicated genotypes in incomplete block designs (Federer, 1998). When the number of genotypes per replicate is large, there is likely to be great soil heterogeneity even within the block.

Pinney (1991) has made use of augmented designs for on-farm trials or prototype evaluation trials. He advocated the use of augmented design that minimises plot number and enables the researcher's and farmer's questions to be answered. It allows the farmer some flexibility to decide what treatments are tested on his/her farms. The technology developed at research station forms the set of core treatments and the

farmer defined treatments are called the augmented treatments. He has described a hypothetical alley cropping example to illustrate the applications of augmented designs to participatory on-farm agro-forestry research by taking two core treatments and five augmented treatments. He also conclude that the number of plots per farm depend upon the region, population density and farming system. The more the number of plots available per farm, the more is the scope for within- farm replications or for more the treatment augmentation.

Augmented designs are available for 0-way, 1-way, 2-way, etc. heterogeneity settings. Augmented designs eliminating heterogeneity in one direction are called augmented block designs and augmented designs eliminating heterogeneity in two directions are called augmented row-column designs. Federer (1956, 1961) gave the analysis, randomizations procedure and constructions of these designs by adding the new treatments to the blocks of RCB design and balanced lattice designs.

Federer (1963) gave procedures and designs useful for screening material inspection and allocation. Federer and Raghavarao (1975) who obtained augmented designs using RCB design and linked block designs for one way heterogeneity setting gave a general theory of augmented designs. They also gave a method of construction of augmented row-column designs using a Youden square design and also provided formulae for standard errors of estimable treatment contrasts.

Federer, Nair and Raghavarao (1997) gave systematic methods of constructions of augmented row-column design (ARCD). An analytic procedure of these designs has also been given. The estimable contrasts in such designs may be(i) among new variety (test treatment) yields, (ii) among check variety (control treatment) yields, (iii) between check and new variety yields, and (iv) among all check and new varieties simultaneously. The analysis of variance of the data generated from an augmented block design with v = u+w treatment comprising of w tests and u controls arranged in b

blocks having k_1 plots in block 1, k_2 plots in block 2, and so on, and k_b plots in block b, such that $k_1 + k_2 + \ldots + k_b$ = v, the total number of plots in the design. The control treatments are replicated in each block and the repeated control treatment in b block is used to estimate error mean square.

The class of augmented experiment designs (Federer, 1956, 1961, 1991; Federer *et al*., 1997; Federer and Raghavarao, 1975) was introduced to replace the systematically spaced check arrangements for screening new genotypes in plant breeding research investigations. Usually material for the new treatments is limited, and it is necessary to include a new treatment only once. If the material is not limited but the number of new treatments is large, it may be desirable to include new treatments only once. Federer (1998) and Federer *et al.* (1997, 1998) have provided a statistical procedure for analyzing such experiments at a site. The analysis takes account of the random nature of the new treatments and of the blocking variables. This result in a more efficient analysis than if this information is ignored.

In problems such as screening experiments or in the beginning of a long-term experimental investigation, it is desirable to determine the relative performance of new test treatments with respect to the control or standard treatment (Hedayat *et al.* 1988). An experiment to compare certain test treatments with a control treatment was first considered by Hoblyn, *et al.* (1954). Cox (1958) suggested augmenting an incomplete block design in test treatments with one or more replications of the control in each block to obtain a good design. Pearce (1960) developed a systematic approach for designing such type of comparative experiments and Pearce (1983) made two suggestions for such experiments; one is supplementation and the other is reinforcement (following Das, 1958).

Pesek (1974) compared a balanced incomplete block design (*BIBD*) with a Modified augmented *BIBD* suggested by Cox (1958) for estimating control-test

treatment contrasts and noticed that the latter design was more efficient. He suggested a design in which control appears an equal number of times in each block and the tests form a BIB design in remaining experimental units.

Bechhofer and Tamhane (1981) developed the theory of incomplete block designs for comparing several treatments with a control. They did not consider the $A-$ or $MV-$ optimality of a design but obtained optimal simultaneous confidence intervals. Their developments led to the concept of Balanced Treatment Incomplete Block (*BTIB*) designs; Notz and Tamhane (1983) studied their construction.

Constantine (1983) showed that a *BIBD* in test treatments augmented by a replication of control in each block is $A-$ optimal in the class of designs with exactly one replication of the control in each block. Jacroux 1984) showed that Constantine's (1983) conclusion remains valid even when the *BIBD*s are replicated by some divisible designs.

Majumdar and Notz (1983) gave a method of obtaining $A-$ and $MV-$ optimal designs among all designs for block designs. Hedayat and Majumdar (1984) gave an algorithm and a catalogue of $A-$ and $MV-$ optimal designs. Ture (1982, 1985) also studied $A-$ optimal designs and suggested their construction. He constructed A-optimal designs when the control treatment replication size, r_0, is a multiple of b for v and k. Hedayat and Majumdar (1985) gave families of $A-$ and $MV-$ optimal designs.

Notz (1985) proposed optimal row columns designs for comparing test treatments with a control. Majumdar (1986) and Hedayat, Jacroux and Majumdar (1988) considered the problem of finding optimal designs for comparing the test treatments with two or more controls. Jacroux (1987a, 1987b, 1988) gave new methods for obtaining $MV-$ optimal design, and also gave catalogues for such designs. Jacroux (1986) also studied

optimal two-column designs for comparing treatments with a control by utilizing techniques of Hall (1935) and Agrawal (1966).

Hedayat and Majumdar (1988) studied designs simultaneously optimal under both block designs and row column designs. Jacroux (1989) generalized the Hedayat and Majumdar's (1984) algorithm for finding $A-$ optimal designs. Cheng *et al.* (1988) introduced new families of $A-$ and $MV-$ optimal block designs. Stufken (1986, 1987, 1988) also studied $A-$ and $MV-$ optimal block designs. Mandal *et al.* (2000) considered distance optimality criterion introduced by Sinha (1970) for comparing a test treatment with control treatments. The matter of comparing test treatments with two or more controls has been discussed in detail by Majumdar (1986) and Hedayat *et al.* (1988) and Majumdar (1996). Jacroux (2000, 2001, 2002) also constructed $A-$ optimal designs for comparing a set of test treatments to a set of standard (control) treatments.

The problem of comparing two disjoint sets of treatments for more than one replication of tests has been studied with different names in the literature. Nair and Rao (1942) termed the existence of such designs as inter and intra group balanced designs (IIGBD). Rao (1947) gave the analysis of such designs. Corsten (1962) investigated combinatorial aspects of these designs and termed them as balanced block designs with two different numbers of replicates. Adhikary (1965) also studied these designs with the name of balanced block designs with variable replications (BBDVR). Kageyama and Sinha (1988) and Sinha and Kageyama (1990) gave systematic methods of construction of these designs along with their catalogues. They called such designs as balanced bipartite block (BBPB) designs. The tests for simultaneous comparisons of multiple comparisons with more than one control have been developed by Hoover (1991); Kwong (2001) and Solorzano and Spurrier (2001).

These designs are found to be more similar with reinforced balanced incomplete block designs (RBIBD) considered by Das (1958) and Constantine (1983) and extended

balanced treatment incomplete block designs (EBTIBD) introduced in Mazumdar (1986). Optimality of these designs were investigated using the conditions given in Constantine (1983), Stufken (1987), Gupta and Prasad (2001) and Jacorux (2002). A survey of the literature reveals that generally these experiments are conducted using an augmented randomized complete block design.

Augmented designs are very flexible and have been applied in different areas, mostly in field experiment, but also in other fields such as poultry research (Boyle and Montgomery, 1996).

Estimation of effects under the random effects assumption (BLUP) is conceptually different from estimation under a fixed effects assumption (BLUE). The transition from BLUE to BLUP is a trivial matter, in so far as implementation with a mixed model package is concerned. Both BLUP and BLUE assume known variance component (Searle et al., 1992). The genetic covariance can also be incorporated into a mixed model, BLUP based on such a model is typically more efficient than BLUE (Searle et al., 1992).

A BTIB design is said to be A-optimal in the class of designs that is binary in test treatments as well as control treatment for comparing tests with one control if $\lambda_0 / \lambda = 1+ (w + 1)^{1/2}$, Where λ_0 is the number of blocks in which a control treatment and test treatments concur and λ is the number of blocks in which any two test treatments concur. Parsad, Gupta and Singh (1996) have shown that this condition is never satisfied by an R-type BTIB design and hence, is useful only to check whether a given *S*-type BTIB design is A-optimal or not.

Jacroux (1984) showed that in the restricted class of block designs with a single replication of control treatment in each block, a design obtained by adding control treatment once to each of block of a most balanced group divisible design is A-optimal.

All such designs in which a standard treatment is reinforced in each block of the design were termed as Standard reinforced (SR-) designs.

A general classes of incomplete block designs that are appropriate for use in the comparison of test treatment-control problem have been discussed. These designs are referred as BTIB designs. BTIB designs are balanced with respect to test treatments-control treatment comparisons. The concept of BTIB designs is extended to compare a set of test treatment to a set of control treatments. The designs for comparing two disjoint sets of treatment are called as Balanced Two Disjoint Sets of Treatments (BTDT).

The most appropriate criteria for searching most efficient (Optimal) designs for making test versus control(s) treatment comparisons are A-Optimal and MV-Optimality criteria. On farm, farmer participatory trials need not suffer from restriction on number of treatments. Effective blocking is principal criterion for achieving good coverage and enhanced impact. The basic trial design will depend on the nature of the block structure and sizes. While design concepts are not at variant from classical and commonly known ones, effective analysis of modified augmented balanced incomplete block design requires the use of MIXED modeling procedure. The procedure enables recovery of both inter and intra block variation.

CHAPTER THREE

METHOD OF CONSTRUCTION

3.1. Family of designs

In randomized complete block design each treatment is replicated in each block. The design is suitable for single-factor trials as well as multi-factor trials. The RCB design has many advantages. It offers flexibility in the number of treatments and number of replications. Control treatment may be introduced more than once. The statistical analysis of RCB design is simple and rapid. The principal disadvantage of this layout is when the trial should include a large number of treatments. This leads to large complete blocks which may be heterogeneous. Also selection in breeding deals with large number of entries which is difficult to include in a block.

In Latin square design treatments are allocated in two directions. The experimental area is divided into rows and columns and each treatment must appear once in a row and once in a column. Therefore treatments are randomized into row and column replicates. The number of replications is equal to the number of treatments. It is suitable for single or multi-factor trials involving a small number of treatments (often less than ten). This design is not satisfying the condition when there is large numbers of germplasm lines to be evaluated.

In randomized incomplete block designs a portion of treatments may be included in a small block resulting in incomplete block layout. The whole replicate is divided into small incomplete blocks. The optimum size of each block depends upon the nature of experimental area and material. Most often control treatments are included in each incomplete block. RICB offers a good flexibility for scientists in designing trials that are

more suitable for their situation. This design is used when analyzing variability among local germplasm entries. Augmented design belongs to this category of designs.

Lattices are special cases of incomplete block designs. A great number of treatments can be included in the same trial with a smaller number of replicates but with the same degree of precision as RCB design. The number of treatments is always a perfect square and blocks are not identical. The number of treatments in each incomplete block is equal to the square root of the total number of treatments. Any particular two treatments should not appear more than once in any one of the blocks. Alpha and lattice designs are replicated designs. It costs no more to conduct an incomplete block than a complete block trial. These designs used to reduce the effect of within complete block variation. But, augmented designs are suitable for un-replicated treatments. They use many extra control plots, however, and are unlikely to be better than designs where block effects are estimated from the lines in the trial rather than from the repeated controls.

3.2. Augmented design

They are suitable for trials including a large number of populations and when the amount of seed is limited and is only enough for one replicate. Controls are repeated systematically in the experiment to control the environmental heterogeneity. Examples of experiments using augmented design: screening plant entries for resistance to diseases, where controls consist of resistant and susceptible genotypes replicated in systematic pattern. The replicated controls measure the variation across the trial and the variables (traits) of the unreplicated entries are assessed against that of adjacent controls.

Augmented designs have several advantages over randomized complete block design. such as: (i) more than one control treatment is include; (ii) standard error of

differences between new treatments are available;(iii) using the survivors 'of previous screening stage as the control is a device for testing the survivors at the same time that a new set of genotypes is being screened, and (iv) Fewer cycles of selection are needed than for the standard method.

The main advantage of augmented design is:

i) Save time and money with smaller blocks, ii) The designs have critical comparisons; iii) Flexible with large number of treatments; iv) Preliminary screening and selection of treatments for future experiment and v) Demonstrations and testing extremes of treatment combinations.

In augmented completely randomized design the whole experimental area is divided in to N plots where N is the number of test genotypes (v) and number of controls (c) which are standard variables or hybrids of known performance) repeated b times (N=v+bc and total number of entries=v+c). When number of seeds is a limitation, the augmented completely randomized design is most suited.

Augmented randomized complete block design is slightly modified version of the augmented completely randomized design, which instead of repeating all the controls b times throughout the field, the whole field is divided distinctly in to b blocks. Then, randomization is done such that all the controls and apart of test genotypes fall only once in each block. Thus, the total number of plots (N) remains the same as in the augmented completely randomized design, but the number of treatments in each block is variable. The advantages of such stratification (block formation) of area is to reduce the error mean square by allocating the block effect which is confounded with error in augmented completely randomized design. Actually, what randomized block design does by replicating the whole entries (e), the augmented randomized complete block design accomplishes the same by replicating only the controls, thus saving space. In an augmented randomized complete block design, the test treatments are replicated once

in the design and control treatments appear exactly once in each block. Augmented randomized complete block design serves as the best design for the initial screening of large collections generally unmanageable by any other design.

An augmented experimental design is constructed by selecting an experiment design for the control treatments. The experiment design could be a randomized complete block, an incomplete block, a row-column design, or some other design. If the selected design for control treatments is an incomplete block designs, then the *rb* blocks are enlarged to accommodate n/rb test treatments per incomplete block. The principles followed in this design are:

- All controls treatment appears in each block.
- Test treatments appear only once in the whole experiment (un-replicated test).
- Block size (k) is determined by number of block (b), control treatment(c) and test treatments (v).
- Number of block (b) is determined by test treatment (v) and control treatment(c).
- Control treatment used to estimate block effects and provides error term
- Effective, but much of the field is taken up with controls.

The control treatments used as a baseline to compare test treatments and allow a certain degree of extrapolation to the performance of test treatment.

3.2.1. Construction and Randomization of Augmented Designs

The first step is to divide the experimental area in to blocks and then assigning plots within the blocks in order to have a single row representing a treatment. Two or more controls are assigned to each block at random and the remaining rows are assigned to the test genotypes. The design is more efficient if blocks of the same size are used. The design helps to estimate experimental error and provides a means to adjust the yield of the new genotypes for variations from block to block.

The number of controls and blocks is determined by the statistical acceptable error degree of freedoms, which are at least twelve (Snedecor and Cochran, 1980).This restriction determines the minimum number of blocks and controls to be used. The maximum number of controls depends on the number of new genotypes and experimental area.

The augmented design follows the standard randomization procedure for the known design in control treatments. Test treatments are randomly allocated to the remaining experimental units. The different treatment entries are assigned to a block at random with the provision that no treatment appears more than one in a block. In general, the randomization procedure for an augmented block design is:-

i) Follows the randomization procedure for the known design in control treatment.

ii) Test treatments are randomly allotted to the remaining experimental units;

iii) If a new treatment appears more than once, assign the different entries of the treatment to a block at random with the provision that no treatment appears more than once in a block until that treatment appears once in each of the blocks. The c controls and n/r test genotypes are randomly allotted to the experimental units (plots) in each block.

For illustration purpose, let us consider four replicated controls and eight non replicated test treatments. A breeder wants to evaluate the performance of eight new hybrids in comparison with four traditional hybrids control treatments. Thus, there are eight test treatments (v) denoted by V1, V2,…, V8 and four control treatments(C) denoted by C1,...,C4. The availability of new hybrid seedling varied between twelve and twenty. Seedlings are just sufficient to have only a single replication for the test treatments.

The layouts of the experiments are as follows:

The experimental area is divided in to three blocks; each block can accommodate seven, six and seven treatments. A randomized incomplete block design is chosen for the control treatments .Each block we can accommodate three test treatments, giving the possibility to include nine test treatments in this trial. As we have only eight test treatments, it is decided to accommodate three test treatments each in the first and third blocks and only two test treatments in the second block.

For random allocation of these treatments in the experiment, we have to follow the field plan and the randomization process by considering the given completely randomized design;

Entry1										
Entry2										

To construct an augmented completely randomized designs and augmented randomized complete block design, we have to precede the following steps.

i) Allocate the four control treatments (C1-C4) to the experimental units randomly. In this process, the following arrangement is incomplete randomized designs.

Entry1	C_2	C_4		C_1		C_3			C_3	C_2
Entry2		C_1	C_4		C_3	C_1		C_2		C_4

ii) Eight test treatments are allotted randomly to the remaining experimental units of the two entries. These way four control treatments and eight test treatments randomly occupy twenty experimental units. The final arrangement of an augmented completely randomized design looks like:

Entry1	C_2	C_4	V_8	C_1	V_1	C_3	V_4	V_3	C_3	C_2
Entry2	V_2	C_1	C_4	V_7	C_3	C_1	V_5	C_2	V_6	C_4

Consider first the augmented randomized complete block design. Here there are Ni = n plots (experimental units) in each of the j = 1,…, b blocks, there are two kinds of treatments, treatments repeated b times and occurring once in every block and treatments repeated only once in the experiment .Hence occurring in only a portion of the blocks. For a large number of situations a number vb of treatments will occur once in each of the b blocks and a number v of treatments will occur once in one of the b blocks.

Now divide the whole experimental field in to 3 distinct blocks.

i) Block 1, consisting of seven plots (C_1 to $C_4 + V_1, V_4$ and V_8),

ii) Block2, comprising six plots (C_1 to $C_4 + V_2$ and V_3),

iii) Block 3, encompassing seven plots (C_1 to $C_4 + V_5$, V_6 and V_7).

The numbers of test varieties falling in each block are three, two and three, respectively. Randomize all the entries (controls plus test treatments) in to each block as depicted below. Field layout of augmented RICB design is as follows.

i) Allocate the four control treatments to each block randomly.

Table 3.1. Data layout of Randomized Complete Block design.

Blocks	Experimental units						
	1	2	3	4	5	6	7
1	C2	C4		C1		C3	
2		C3	C2		C1	C4	
3		C3	C1		C2		C4

The seventh experimental unit is for block 1 and block 3 where as the six experimental unit is for block2.

ii) Allocate eight test treatments at random to the remaining experimental units of the three blocks. These way four control treatments and eight test treatments randomly occupy twenty experimental units. The final arrangement is look like:

Table 3.2. Data layout of augmented randomized incomplete block design.

Blocks	Experimental units						
	1	2	3	4	5	6	7
1	C2	C4	V8	C1	V1	C3	V4
2	V3	C3	C2	V2	C1	C4	
3	V7	C3	C1	V5	C2	V6	C4

Usually, no less than 15% of the total numbers of plots are used for repeated controls. The treatment sum of squares is partitioned in to different components of interest viz. (i) among test treatments, (ii) among control treatments and (iii) among test treatments and control treatments.

3.3. Definitions.

In this section we give some definitions and preliminary results, which are useful in identification of our design and also determining their optimality.

Definition 3.1. *A* 2^v main effect plans (MEP) or resolution III designs are commonly used in exploratory studies when a large number of factors need to be considered or screened. The idea is to try to detect factors that exhibit "large" main effects and discard factors with no noticeable effects from further study. The crucial assumption here is that all interactions are negligible, including 2-factor interactions.

Definition 3.2. A design d^* belonging to a certain class of competing designs **D** is said to be an MV-optimal design if d^* has the least value of the maximum variance of BLUE of elementary contrasts between test treatments and control treatments as compared to any other design $d \in \mathbf{D}$. It may be mentioned here that for the present problem the A-optimal designs are also MV-optimal.

Definition 3.3. A design is said to be A-optimal in such situations if it minimizes the sum of the variances of the least-squares estimates for the elementary treatments contrast between the test treatments and control treatments.

Definition 3.4. A design is said to be MV-optimal in such situations if it minimizes the maximum variances of the same least-squares estimates for the elementary treatments contrast between the test treatments and control treatments.

Both the A-and MV-Optimality criteria depend only on design parameters. These criteria are computationally more feasible.

Definition 3.5. Reinforced BIB design, all test treatments have different number of replications. Under a mixed effects model, a reinforced BIB design is A-Optimal for making test treatments-control comparisons, over all block designs which contain the control once in each block.

Definition 3.6. An incomplete block design is said to be a balanced incomplete block (BIB) design if it satisfies the following conditions. **i)** The experimental material is divided into b blocks of k units each, different treatments being applied to the units in the same block. ii) There are v treatments each of which occurs in r blocks. iii) Any two treatments occur together in exactly λ blocks.

The quantities $v, b, r, k,$ and λ are called the parameters of the BIB design. We note here that for a given set of parameters there may or may not exist a BIB design. Properties of the BIB designs, the following relations hold among the parameters, and even these are only necessary conditions for the existence of a BIB design:

$$rv = kb \quad , \quad \lambda (v - 1) = r (k - 1) \quad , \quad r > \lambda \quad \text{and} \quad b \geq v,$$

Definition 3.7. A treatment control design with v test treatments and one control treatment in b blocks of size k < v + 1 is called a balanced treatment incomplete block design, denoted by BTIBD (v, b, k; λ0, λ1), if

(1) Each test treatment occurs together with the control λ0 times in a block and

(2) Any two test treatments occur together λ1 times in a block.

Incomplete block designs for estimation of treatment-control differences are studied. A class of designs for this purpose, called balanced treatment incomplete block designs, has recently been proposed and studied by several authors. Here, a relatively small subclass of these designs is shown to contain the asymptotically optimal design under the criterion of minimizing the length of simultaneous confidence intervals for test treatment-control treatment differences. These results can be used to easily construct good large designs.

In non-orthogonal setup, under block designs, block treatment incomplete block designs (BTIB) are recommended for single control situation. To be more clear, consider an experimental situation where v_1 test treatments, denoted 1,…., v_1 belonging to a set T of cardinality v_1, are to be compared with each of the u(≥1) control treatment denoted by v_1+1,……, v_1+u belonging to a set S of cardinality u, such that $T \cap S = \phi$.

In this section, we give some preliminary results which are useful for obtaining our main results. To begin with, we consider the problem of finding A- and MV-optimal designs for comparing s controls to t test treatments without block effects. This problem was also considered in Jacroux (1990), but here we derive some specialized results.

3.3.1. Optimality Criteria

The experimental situations addressed here demand that all test treatments are tested against every control treatment. It, therefore, seems logical that in the choice of an appropriate design we put more emphasis on the allocation of control treatment(s) to the plots within a block. Intuitively it appears desirable to have more replications of the control treatments as compared to the test treatments. The statistical problem, therefore, is to obtain a suitable arrangement of treatments in the plots within blocks such that test treatments versus control treatments comparisons are estimated with as high a precision as possible. The most appropriate criteria for searching most efficient design for making test treatments versus control treatment(s) comparisons are A- and MV-optimality criteria. We will mention here only those results, which we will use in proving A-optimality and MV-optimality of our proposed designs.

Result 1. Constantine (1983) showed that in the class of block design having exactly one replication of the control in each block, design obtained by adding treatment once to each block of a BIB design is A-optimal. These designs are known as reinforced BIB designs.

Result 2. A BTIB design obtained by adding a control treatment number of times to each of the blocks of a BIB design with parameters v, b, r, k-t, λ in test treatments is A-optimal whenever $(k-t-1)^2 \leq v t^2 \leq (k-t)^2$ (Stufken, 1987).

Lemma3.1.Consider comparing s controls to t test treatments under a 1-way classification model. Further suppose that a design d^* under this model has the s controls replicated r_1 times and the t test treatments replicated r_2 times. Then d^* is
(a) A-optimal among all other designs in Jacroux (1990) if:

$$tr_2(r_2 - 1)/r_1(r_1 + 1) \leq s \leq tr_2(r_2 + 1)/r_1(r_1 - 1);$$

(b) MV-optimal among all other designs in Jacroux (1990) if:

$$(tr_2(r_2 - 1) - tr_1)/r^2{}_1 \le s \le (tr_2(r_2 + 1) + tr_1)/r^2{}_1;$$

Now we give some lemmas and theorem given in Jacroux (2000) and are stated with out proof.

Lemma 3.2. Suppose $A = \begin{bmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{bmatrix}$ is a nxm positive definite matrix and let

$\mathbf{A}^{-1} = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix}$ where A_{11} and B_{11} have the same dimensions. Then for any vector $X, X`A^{-1}{}_{11}X \le X`B_{11}X$.

Lemma 3.3. Consider the 2x2 matrix A = $\begin{bmatrix} p & -x \\ -x & y \end{bmatrix}$ whose entries fulfil a condition that p>y ≥x ≥0. And y>0 if x = 0.

Also define

$$h(p, x, y) = (1,-1)\,\mathbf{A}^{-1}\begin{bmatrix}1\\1\end{bmatrix} = (p+y-2x)/(py-x^2)$$

For reinforced balanced incomplete block design Jacroux (2001) defined following for each $d \in D(b, k, t, u, n_0)$

$$T_{d11} = \sum_{i=1}^{v_1} n_{di1}, \quad T_{d21} = \sum_{i=v_1+1}^{v} n_{di1}, \quad T_{d1} = \sum_{m=1}^{b} T_{d1m}, \quad T_{d2} = \sum_{m=1}^{m} n_{d2m},$$

$$S_{d1} = \sum_{m-1}^{b} T^2{}_{d1m}, \qquad S_{d2} = \sum_{m=1}^{b} T^2{}_{d2m}$$

$$p(d) = \left(\sum_{i=v_1+1}^{v} r_{di}\,k - \sum_{i=v_1+1}^{v}\sum n^2{}_{di1}\right)/uk$$

$$u(d) = -(S_{d2} - \sum_{i=v_1+1}^{v} n_{dil}) / u(u-1)k$$

$$x(d) = -(\sum_{i=v_1+1}^{v} r_{di}\, k - S_{d2}) / utk$$

$$y(d) = (bk - \sum_{i=v_1+1}^{v} r_{di} - \sum_{i=1}^{v_1} \sum_{i=1}^{b} n^{2}{}_{di1}) / uk$$

$$z(d) = -(S_{d1} - bk + \sum_{i=v_1+1}^{v} r_{di}) / t(t-1)k$$

Jacroux (2000) gave a sufficient condition in the form of theorems for reinforced incomplete block designs to be MV-optimal in classes (b, k, u, t, n_0).

Theorem 3.1. Supposed $d^* \in D$ (b, k, t, u, n_0) is a reinforced block design which satisfies the following conditions:

i. $\left| Td_{*21} - Td^{*}{}_{21} \right| \leq 1$ for $1 \neq 1'$

ii. $f(T_{d*2}, S_{d2}) \leq h(p(d), x(d^*) - 2/utk, y(d^*))$

Where h (p, x, y) is defined in Lemma 2:2 and

$$f(T_{d*2}, S_{d^*2}) = \frac{u-1}{u[p(d) - q(d)]} + \frac{(t-1)}{t[y(d) - z(d)]} - \frac{1}{utx(d)}$$

Then d^* is MV-Optimal in D (b, k, t, u, n_0).

3.3.2. Orthogonality Condition

A method that yields a large number of orthogonal main effect plans (OMEPs) for many different situations was developed by Addelman and Kempthorne (1961). These designs are based on OMEPs for symmetrical factorials with subsequent collapsing and replacement of levels for certain factors. For now we mention only that as a

consequence of this procedure the levels of one factor occur together with proportional frequencies and that is sufficient to guarantee orthogonal estimates of main effects.

Let us consider the case of two factors, *A* and *B* say, where *A* has *a* levels and *B* has *b* levels. Suppose that in a given Fisher factorial design (FFD) the *i*th level of *A* occurs together with the *j*th level of *B* for N_{ij} times.

Let $\sum_j N_{ij} = N_{i.}$, $\sum_i N_{ij} = N_{.j}$, $\sum_i N_{i.} = \sum_j N.j = N$,

Where N is the total number of runs in the Fisher factorial designs.

If the level combinations occur with proportional frequencies, we have $N_{ij} = N_{i.}N_{.j} / N$ for every *i* and *j* (*i* = 0, 1, . . ., *a* − 1; *j* = 0 1, . . ., *b* − 1).

Then we state the following theorem.

Theorem 3.2. A sufficient condition for a main effect plan for two factors *A* and *B* with *a* and *b* levels, respectively, to be an Orthogonal Main Effect Plan is that each level combination for the two factors occurs with proportional frequency.

Proof:

Consider the model $Y = 1`\mu + A`X_{11} + BX_{12} + E$ and rewrite it as

$$E(Y) = (1, X_{11}, X_{12}) \begin{bmatrix} \mu \\ A \\ B \end{bmatrix} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

Where $A` = \{A_0, A_1, A_2, \ldots A_{a-1}\}$ and $B` = \{B_0, B_1, B_2, \ldots B_{b-1}\}$ represent the main effect components for the two factors A and B, respectively. We then write the normal equations of (1) as

$$\begin{bmatrix} 1`1 & 1`X_{11} & 1`X_{12} \\ X_{11}`1 & X_{11}`X_{11} & X_{11}`X_{12} \\ X_{12}`1 & X_{12}`X_{11} & X_{12}`X_{12} \end{bmatrix} \begin{bmatrix} \mu \\ A \\ B \end{bmatrix} = \begin{bmatrix} 1`y \\ X_{11}`y \\ X_{12}`y \end{bmatrix} \quad (2)$$

Denote the coefficient matrix in (2) by K. Then we have.

$$K = \begin{bmatrix} N & N_{O.} & N_{1.} & \cdots & N_{a-1,.} & N_{.0} & N_{.1} & \cdots & N_{.,b-1} \\ N_{0.} & N_{0.} & 0 & \cdots & 0 & N_{00} & N_{01} & \cdots & N_{0,b-1} \\ N_{1.} & 0 & N_{1.} & \cdots & 0 & N_{10} & N_{11} & \cdots & N_{11,b-1} \\ \vdots & & & & & & & & \\ N_{a-1,.} & 0 & 0 & \cdots & N_{a-1,.} & N_{a-1,0} & N_{a-1,1} & \cdots & N_{a-1,b-1} \\ N_{.0} & N_{00} & N_{10} & \cdots & N_{a-1,0} & N_{.0} & 0 & \cdots & 0 \\ N_{.1} & N_{01} & N_{11} & \cdots & N_{a-1,1} & 0 & N_{.1} & \cdots & 0 \\ \vdots & & & & & & & & \\ N_{.,b-1} & N_{0,b-1} & N_{1,b-1} & \cdots & N_{a-1,b-1} & 0 & 0 & \cdots & N_{.,b-1} \end{bmatrix}$$

To obtain a solution to (2) we need to find a generalized inverse for K.

If $N_{ij=}N_{i.}N_{.j}/N$ for every *i* and *j* (*i* = 0, 1, . . ., *a* − 1; *j* = 0 1, . . .,*b* − 1), then such a g inverse is given by

$$K^{-} = \begin{bmatrix} \frac{1}{N} & 0 & \cdots & 0 & 0 & \cdots & \cdots & \cdots & 0 \\ -\frac{1}{N} & \frac{1}{N_{0.}} & & & & & & & 0 \\ -\frac{1}{N} & & \frac{1}{N_{1.}} & & & & & & \\ \vdots & & & & & & & & \\ -\frac{1}{N} & & & & \frac{1}{N_{a-1,.}} & & & & \\ -\frac{1}{N} & & & & & \frac{1}{N_{.0}} & & & \\ -\frac{1}{N} & & & & & & \frac{1}{N_{.1}} & & \\ \vdots & & & & & & & & \\ -\frac{1}{N} & & & & & & & & \frac{1}{N_{.,b-1}} \end{bmatrix}$$

This follows easily by verifying that $K\bar{K}K = K$ using the proportionality condition. $\bar{K}$ can be obtained by imposing the conditions $\sum_i N_{i.}\hat{A}_i = 0 = \sum_j N_{.j}\hat{B}_j$.

Consider now the contrast $\sum_i C_i A_i$ and $\sum_j d_j b_j$ (with $\sum_i C_i$ =0, $\sum_j d_j$ =0) belonging to the main effect A and B, respectively. It follows then immediately that

$$\text{cov}\left(\sum_i C_i \hat{A}_i, \sum_j d_j \hat{B}_j\right) = (0, C, 0)\,\bar{K}\begin{bmatrix} 0 \\ 0 \\ d \end{bmatrix} = 0$$

Where C`= $(c_0, c_1, c_2, \ldots, c_{a-1})$, d`= $(d_0, d_1, d_2, \ldots, d_{b-1})$ that is, estimates of contrast for the two main effects are uncorrelated. Hence we have an orthogonal main effect plan.

In this section, we are going to construct modified augmented designs through balanced incomplete block designs using the Condition of Proportional Frequencies which was shown by Plackett (1946) and also proved independently by Addelman (1960) that a necessary and sufficient condition that estimates of the main effects of any two factors be uncorrelated is that the levels of one factor occur with each of the levels of other factor with proportional frequencies. Consider two factors, A and B, occurring at r and t levels, respectively.

N is the number of run in the plan;

n_i. is the number of times the i level of factor A occurs in the plan;

$n.j$ is the number of times the j level of factor B occurs in the plan,

n_{ij} is the number of times the i level of factor A occurs with in the j level of factor B,

Hence $\sum_{j=1}^{b} n_{ij} = n_{i.}$, $\sum_{i=1}^{a} n_{ij} = n_{.j}$, and $\sum_{i \neq j} n_{ij} = N$

A necessary and sufficient condition that the estimates of the components of two factors A and B be orthogonal to each other and also to the mean in a factorial arrangement, is that

$$n_{ij} = \frac{n_{i.} \times n_{.j}}{N} \text{.....(3.1)}$$

3.4. Methods of Constructions of Modified ABIB design

Let us consider a balanced incomplete block designs (BIBD) with parameters (v, b, r, k, λ). The incidence matrix $N^{\bullet}$ = (n_{ij}) is a b x v matrix, where (n_{ij}) = 1, if j^{th} test variety occurs in i^{th} block and -1 otherwise (i = 1,2,…,b, j = 1,2,…,v). Clearly the number of $1^{`s}$ in each row (column) of $N^{\bullet}$ will be k (or r). Also λ equals the number of times the row (1, 1) occurs in any two columned sub matrix of N. Consider such an incidence matrix $N^{\bullet}$ of a BIB design as b runs of 2^{v} factorials. Then it can be seen that for any two column i and j, we have

$$i) \quad n_{11} = \lambda, \quad n_{1,-1} = n_{-1,1} = r - \lambda \quad and \quad n_{-1,-1} = b - 2r + \lambda$$

Using (i), we can write a frequency table for any two factors, say A and B corresponding to their column.

Table 3.3. Frequency table of any two factors.

Levels of factor B		**Levels of factor A**	
		-1	1
	-1	b – 2r + λ	r- λ
	1	r- λ	λ

Following (3.1), we get following conditions of orthogonal estimation of any two factors in 2^{v} factorials.

$$r^2 = \lambda(b + p_0 + p_1) + p_1(b + p_0 - 2r) \text{..... .....} (3.2)$$

Where $N^{\bullet}$, p_o and p_1 are denote the positive integers, numbers of rows of $-1^{`s}$ and $1^{`s}$, respectively.

Hence an incidence matrix $N^{\bullet}$ of a BIB design can be augmented by p_o rows of $-1^{`s}$ and $p_1$ rows of $1^{`s}$ if it obeys the relation given in (3.2). Hence we get 2^v main effect plan in b+ p_o + p_1 runs.

Now, considering -1 in p_o rows as $0^{`s}$ which is a control treatment and treat the runs of a 2^v main effect plan as treatments and factors as blocks, we get designs for comparing test treatment vs. control treatment(s) where test treatments are the original treatments of the BIB design and control treatment(s) are the number of added rows of -1 and +1 to $N^{\bullet}$ .Thus, we get augmented BIB design with v+ p_o + p_1 treatments, v blocks, $r^{\bullet}$ = (r, v), λ , λ_o = r.

Incidentally these designs are similar to balanced treatment incomplete block design and reinforced balanced incomplete block design introduced by Bechhofer and Tamhane (1981) and Das (1958).

Example 3.1. For illustration purpose we take a BIB design with parameters v = b = 7, r = k = 3, λ = 1. The incidence matrix of this design is given below and follows the condition given in (3.1). Thus we can add one rows of -1`s in the incidence matrix and thus we obtain 2^7 main effect plan in 8 runs given below.

Table 3.4. Incidence Matrix

Variety /Run	Block/factors						
	1	1	- 1	1	-1	-1	-1
	-1	1	1	-1	1	-1	-1
	-1	-1	1	1	-1	1	1
	-1	-1	-1	1	1	-1	-1
	1	-1	-1	-1	1	1	1
	-1	1	-1	-1	-1	1	1
	1	-1	1	-1	-1	-1	-1
	-1	-1	-1	-1	-1	-1	-1

Consider runs as treatments and factors as blocks and then transpose the incidence matrix, we obtain the following modified augmented balanced incomplete block design with parameters $v^{\bullet}$ =v+u = 8, $b^{\bullet}$ = 7, treatment replication ($r^{\bullet}$) = (3, 7), block size ($k^{\bullet}$) = 4, $\lambda^{\bullet}$ = (1, 3).

Table 3.5. Data layout of Modified augmented balanced incomplete block design

B1	1	5	7	8
B2	1	2	6	8
B3	2	3	7	8
B4	1	3	4	8
B5	2	4	5	8
B6	3	5	6	8
B7	4	6	7	8

Properties of the Modified Augmented BIB designs and the following relations hold among the parameters:

$$i) \quad b(k+u) = (v,u)\begin{Bmatrix} r \\ r^{\bullet} \end{Bmatrix}$$

$ii)\ v^{\bullet} > b,\ r^{\bullet} > \lambda^{\bullet}$

Where b is the number of blocks, k is block size; u is number of control treatment; v is number of test treatment (number of treatments in BIB design), r is the number of replications of the test treatment /number of replication in BIB design; r_0 is the number of replications of control treatment; λ is any two test treatments occur together in a blocks and $\lambda^{\bullet}$ is any two treatment of modified augmented BIB design occurring together in a blocks.

The above modified augmented balanced incomplete block design follows the conditions of optimality given by Stufken (1987). Thus we establish relation between balanced main effect plan and design for comparing treatment and control. Now we have the following theorem.

Theorem 3.3. In a 2^{v} factorial experiment, the main effects are orthogonally estimated by the incidence matrix $N^{\bullet}$, where 0`s is replaced by -1`s in the incidence matrix of a BIB design with parameters (v, b. r, k, λ) by adding p_1 rows of 1`s or $p_o$ rows of -1`s or, $p_o + p_1$ rows of -1`s and 1`s respectively, only when

(a) $p_o = \frac{r^2 - b\lambda}{b - 2r + \lambda}$, (b) $p_1 = \frac{r^2 - b\lambda}{\lambda}$ and (c) $r^2 = \lambda$ (b+ $p_o + p_1$) + p_1 (b+ p_o-2r).

Proof

Following the conditions of Placket (1946) and Addelman (1960) (conditions of proportional frequencies), we consider the frequency table given in section 3.2, in which the two factors A and B will be estimated orthogonally.

If $\frac{b - 2r + \lambda}{r - \lambda} = \frac{r - \lambda}{\lambda}$ let $\frac{b - 2r + \lambda}{r - \lambda} \neq \frac{r - \lambda}{\lambda}$

So, to make this ratio equal, we have to consider three conditions:

1. we have to add p_o rows of -1`s in the incidence matrix of $N^{\bullet}$

2. or we have to add p_1 rows of 1`s in the incidence matrix of $N^{\bullet}$

3. or add p_o rows of -1`s and $p_1$ rows of 1`s in the incidence matrix of $N^{\bullet}$.

Then, we have the following conditions, respectively.

$$(b - 2r + \lambda)(\lambda + p_o) = (r - \lambda)^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

$$(b - 2r + \lambda + p_1)\lambda = (r - \lambda)^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (2)$$

$$(b - 2r + \lambda + p_1)(\lambda + p_o) = (r - \lambda)^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3)$$

Solving (1), (2) and (3), we obtained the following conditions for orthogonal estimations of two factors A and B, respectively.

$$p_o = \frac{r^2 - b\lambda}{b - 2r + \lambda} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4)$$

$$p_1 = \frac{r^2 - b\lambda}{\lambda} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (5)$$

$$r^2 = \lambda (b + p_o + p_1) + p_1 (b + p_o - 2r) \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (6)$$

(Proved)

With the above conditions, we identified two classes of symmetrical balanced incomplete block designs (SBIBD) for establishing the relationship between main effects plans and augmented balanced incomplete block designs.

(a) D: ($v = b = 4t+3$, $r = k = 2t+1$, $\lambda = t$), where t = 1, 2... or its complementary designs.

D^c = ($v = b = 4t+3$, $r = k = 2(t+1)$, $\lambda = t+1$), where t = 0, 1, 2...

(b) D^*: ($v = b = 9t-2$, $r = k = 3t$, $\lambda = t$), where t = 0,1,2,…..,

A list of Modified Augmented BIB designs obtained by transposing the incidence matrix N of main effects plans is given along with their optimality status.

Table 3.6. Incidence matrix of main effect plan

S.No.	V	B	R	K	λ	p_o	p_1	control	Optimality
1	18	16	6	8	2	2	-	2	MV-optimal (J)
2	27	25	9	11	3	2	-	2	MV-optimal (J)
3	75	71	15	19	3	4	-	4	MV-optimal (J)
4	8	7	3	4	1	-	1	1	A-optimal (S)
5	12	11	5	6	2	-	1	1	A-optimal (S)
6	16	15	7	8	3	-	1	1	MV-optimal (J)
7	20	19	4	5	1	-	1	1	MV-optimal (J)
8	24	23	11	12	5	-	1	1	MV-optimal (J)
9	28	27	13	13	6	-	1	1	MV-optimal (J)
10	32	31	15	16	7	-	1	1	MV-optimal (J)
11	36	35	17	18	8	-	1	1	MV-optimal (J)
12	16	13	4	7	1	3	-	3	MV-optimal (J)
13	25	21	5	9	1	4	-	4	MV-optimal (J)
14	36	31	6	11	1	5	-	5	MV-optimal (J)
15	64	57	8	15	1	7	-	7	MV-optimal (J)
16	38	37	9	10	2	-	1	1	MV-optimal (J)
17	81	73	9	17	1	8	-	8	MV-optimal (J)
18	48	45	12	15	3	3	-	3	MV-optimal (J)
19	143	133	12	22	1	10	-	10	MV-optimal (J)
20	46	40	13	19	4	3	3	6	MV-optimal (J)
21	36	35	17	18	8	-	1	1	MV-optimal (J)

CHAPTER FOUR

METHODS OF ANALYSIS

4.1. Analysis of Augmented Designs

The most commonly-used incomplete-block experimental designs are augmented designs. Models for these designs are more complex than for randomized complete block designs and randomized complete designs, and will not be presented separately here.

The experimental test genotypes are usually considered as random effects and the controls treatments are fixed effects. The experimental error is estimated considering the controls placed in randomized complete block design. After conducting the analysis of the controls, the error mean square from this analysis is used to compute the standard errors for different comparisons; the different between the mean of the controls in a given block and the mean of the controls over the entire experiment. The statistical model for the augmented design is the same as that of the randomized complete block design. The analysis can be evaluated according to the following model.

$$Y_{ij} = \mu + \tau_i + \rho_j + e_{ij} \quad ; \quad \text{i=1, 2,…, v, v+c and j=1, 2,…, b.} \qquad (4.1).$$

Where Y_{ij} is the observation of treatment i in j^{th} block; μ is the general mean; τ_i is the effect of treatment i (test treatment and control treatment); ρ_j is the effects of j^{th} block and e_{ij} is the residual variation or error.

The first step in the analysis is to conduct ANOVA on the data measured for controls. Then; a table is constructed to organize the different entities (controls, blocks,

sum for the controls and blocks, mean for the controls and blocks and adjustment).We compute the least square means using SAS software and the adjusted means using GENSTAT.

Let X_{ij} be the yields of the i^{th} control in j^{th} block. Block effects (b_j) $= \frac{1}{c}(T_{Vj} - \bar{c} - T_{Vbj})$ where T_{Vbj} is total test treatments in the j^{th} blocks. Then, the adjusted means of test varieties $(v`_i) = v_i - b_j$ .The control effects $(c_i) = \bar{c}_i - m$ .The mean effects (m) $= \frac{1}{n}(GT - (b-1)\bar{c} - \sum_{j}^{b} n_j b_j)$ .The variable of interest in the test treatments is adjusted for the effects of the block in which it was given as shown:

Table 4.1. Two way tables of totals for controls and blocks.

Controls variety	Blocks 1 2 3 … b	Sum(C_i)	Mean controls
1 2 3 . C	x_{11} x_{12} x_{13} … x_{1b} x_{21} x_{22} x_{23} … x_{2b} x_{31} x_{32} x_{33} … x_{3b} . . . . x_{C1} x_{C2} x_{C3} ... x_{Cb}	C_1 C_2 C_3 . Cc	Mean1 Mean2 Mean3 . Mean c
Sum(B_j)	B1 B2 B3… Bb	Grand total	
Mean (block)	mean1mean2 mean3....mean b		Grand mean
Adjustment	a1 a2 a3 …… ab		

Where C_i is the sum of the i^{th} controls.

B_j is the sum of the controls in the j^{th} blocks.

Mean of a controls = total number of that control/number of blocks.

Mean of a block = total number of that block/number of control and

Grand mean = Grand total/bc.

Table 4.2. Adjusted Yields of test treatments

Test treatments	Observed Yield	Adjusted Yield
1	Y_{1j}	$\hat{Y}_{1j}$
2	Y_{2j}	$\hat{Y}_{2j}$
3	Y_{3j}	$\hat{Y}_{3j}$
.	.	.
V	Y_{vj}	$\hat{Y}_{vj}$

Where Y_{ij} is yield of i^{th} genotype grown in j^{th} block.

Since all test treatments did not occur together in a block, a direct comparison of them is not possible. The adjusted yield of test treatment is:

$$\hat{Y}_{ij} = Y_{ij} - v_i$$

Total SS = $\sum X_{ij}^{\ 2}$ -C.F, SSR= $\sum \frac{R_j^{\ 2}}{c}$ -C.F, SSC= $\sum \frac{C_j^{\ 2}}{b}$ -C.F,

SSE = Total SS- SSR- SSC and Mean square error (MSE) = $\frac{SSE}{(c-1)(b-1)}$

Table 4.3. Analysis for the controls in augmented designs

Sources of Variations	Degrees of Freedom	Sum of Squares	Mean Squares
Blocks	b-1	SSB	MSB
Controls	c-1	SSC	MSC
Errors	(c-1)(b-1)	SSE	MSE

Standard Errors.

It should be noted that the precision of residual mean square depends on the number of controls plots you included per block. Particularly, controls below 3 are not acceptable in trials with augmented designs.

Due to non-balance created as a result of occurrence of new entries in a block, different standard errors are used in comparing different terms. Consequently there are four types of standard error /comparisons of difference to compare the means in augmented design. These standard errors of differences are computed as follows.

To compare two controls means standard error of difference.

$$SE(d) = \sqrt{\frac{2MSE}{b}}$$

For comparing between two test treatments in the same block;

$$SE(d) = \sqrt{2MSE}$$

For comparing between two test treatments in different blocks;

$$SE(d) = \sqrt{\frac{2(c+1)MSE}{c}} \quad \text{and}$$

For comparing between test treatments and controls:

$$SE(d) = \sqrt{\frac{2(c-1)(b-1)MSE}{c}}$$

For comparing between a test treatments and a control mean

$$SE(d) = \sqrt{MSE(1+\frac{1}{b})}$$

These standard errors of differences can be used to compare the difference of two means. The most common method is to compute the least significant difference (LSD).The LSD is a useful measure of precision and is therefore often reported along with test treatment means.

4.2. Analysis of Modified Augmented BIB Design

Suppose that we have a BIB design with parameters b, v, r, k and λ .Suppose further that we have m additional control treatments and that we want to compare these control treatments with those given in the BIB design. If we add these m control treatments to each block of the BIB design, then we obtain a new design which also has b blocks but each block has k+m plots. In essence this design is a BIB design combined with a randomized complete block design. We call this new design modified augmented BIB design.

In this study we assume a mixed model and try to obtain the linear unbiased and minimum variance estimators (LUMVE) of the treatment effects. The corresponding results in the fixed model case will be obtained from those of model by setting the variance components zero.

Furthermore, incomplete blocks should be considered as a random effect so that the recovery of inter-block information is possible so as to get adjusted and unadjusted means for the new genotypes. Depending on the values of the variance components for block and test treatments, different models are fitted. When a random effect has zero variance components, then it is considered as a fixed effect. The intra-block treatment means and variances and the inter-block treatment means and variances are presented in matrix form.

Following Das (1958) and Wai-Yuan Tan (1965) suppose we have a BIB designs with parameters (v = b = 4t +3, r = k = 2t +1, λ = t), where t = 1, 2…v or its complementary design and (v = b = 9t-2, r = k = 3t, λ = t), where t = 1, 2…v.

A modified augmented designs with parameters $v^{\bullet}$ = v+ p_0 + p_1, b = v, r = (r, v), λ , λ_0 = v can be obtained through above designs by using theorem 3.3.The data obtained by augmented designs can be analyzed using the following model.

The Statistical model can be written as

$$Y_{ij} = \mu + t_i + b_j + e_{ij} \ldots\ldots\ldots\ldots\ldots\ldots (4.2)$$

i=1, 2,…, v, v+1…, v+ p_0 + p_1, j=1, 2,…, b

where μ is the over all mean, Y_{ij} is the observed value of the i^{th} treatment in the j^{th} block; t_i ,i=1, 2,…, v,v+1,….v+ p_0 + p_1, is the i^{th} treatment effect (i=1, 2,…, v for the BIB portion and the other portions of treatments which is labeled by i =v+1…,v+ p_0 + p_1 are called augmented treatments); b_j , j=1,2,…,b is the effect of the j^{th} block ; e_{ij} is the error attached to Y_{ij} .

Assumptions:

i) Block effects and random errors are independent.

Inter- block, $\beta_j \sim N(0, I_b \sigma^2{}_b)$

Intra-block, $\varepsilon_{ij} \sim N(0, \sigma_e{}^2)$

ii) The test treatments can replicate in the experimental unit.

iii) The control treatments are replicated in each block.

iv) $E(y_{ij}) = \mu 1_N + \chi_t$

v) $\text{var}(Y_{ij}) = \sigma_b{}^2 + \sigma_e{}^2$

vi) ε_{ij} is identically and independently distributed with mean zero and variance σ^2. $\varepsilon_{ij} \sim N(0, \sigma_e{}^2)$

In matrix notation we may write (4.2) as:

$$Y = \mathbf{1}_N \mu + Xt + Zb + e \ldots\ldots\ldots \ldots(4.3)$$

Where Y is the N×1 (N= (k+ p_0 + p_1) b) column vector of observations, 1_N is the N×1 column vector of which each component is unity; $t_{v+p0+p1}$ and $b_{b\times1}$ are the column vector of t_i`s and $b_i$`s, respectively. Let the component of Y be arranged first by order of the block subscripts and then by that of the treatment subscripts, with the $p_0 + p_1$ modified augmented treatments in each block placed at the tail part of each sub vector of Y which corresponds to the subscript of that block.

Now from on words we denote m = $p_0 + p_1$.

$$Z = \begin{pmatrix} 1_{k+m} & & 0 \\ & \ddots & \\ 0 & & 1_{k+m} \end{pmatrix} = \mathbf{1}_{k+m} \otimes \mathbf{1}_b$$

Where $\otimes$ denotes kroncker product.

$$X = \begin{pmatrix} x_1 \\ x_2 \\ \vdots \\ x_b \end{pmatrix}$$

With

$$X_{\underset{(k+m)x(v+m)}{j}} = \begin{bmatrix} \delta[(k+m)(j-1)+1],1 \ldots \delta[(k+m)(j-1)+1],v, & 0 \ldots\ldots 0 \\ \vdots & \vdots \\ \delta[(k+m)(j-1)+k],1 \ldots \delta[(k+m)(j-1)+k],v, & 0 \ldots\ldots 0 \\ 0 \quad \ldots \quad 0 & 1 \ldots\ldots\ldots 0 \\ \vdots & \vdots \\ 0 \quad \ldots\ldots \quad 0 & 0 \ldots\ldots\ldots 1 \end{bmatrix}$$

Where

$$\sigma_{st} = \begin{cases} 1, & \text{if the } s^{th} \text{ observation associated with the } t^{th} \text{ treatment.} \\ 0, & \text{otherwise} \end{cases}$$

s=1, 2,…, N, t=1, 2,…,v+m

In this model, we shall assume that the t_i`s are constants and b ~N $(0, I_b\sigma_b^{\,2})$, and further that the $b_i$`s are distributed independently of the e_{ij}`s with this convention (4.2) then becomes the linear mixed model. Before we proceed with our analysis, it should be remarked that Y_{ij} i=1, 2,…,v+m, j=1, 2,…, b may or may not exist. Depending on whether or not the i^{th} treatment appears in the j^{th} block. To allow for the effect of incomplete block, we introduce.

$$n_{ij} = \begin{cases} 1, & \text{if the } i^{th} \text{ treatment occurs in the } j^{th} \text{ block} \\ 0, & \text{otherwise} \end{cases}$$

i=1, 2,…, v+m, j=1, 2,…, b

The matrix $N = (n_{ij})_{(v+m\times b)}$ is usually called the incidence matrix. The following relation ship can easily shown to hold:

$$X_{(k+m)b\times(v+m)}\mathbf{1}_{(v+m)} = \mathbf{1}_N \quad , \quad \mathbf{1}`_N X = (r\mathbf{1}`_v, b\mathbf{1}`_m)$$

$$X`X = \begin{pmatrix} r\mathrm{I}_v & 0 \\ 0 & b\mathrm{I}_m \end{pmatrix} \quad , \quad X`Z = N, \; N\mathbf{1}_b = \begin{pmatrix} r\mathbf{1}_v \\ b\mathbf{1}_m \end{pmatrix}$$

$$\mathbf{1}`_{v+m} N = (k+m)\mathbf{1}_b$$

and $$NN`= \begin{pmatrix} (r-\lambda)I_V + \lambda 1_V 1`_V & r\mathbf{1}_v 1'_m \\ r1_m 1`_v & b1_m 1`_m \end{pmatrix}$$

4.2.1. Analysis under Mixed Model

We now try to obtain the estimates under the mixed effect model

t_i`s ,i = 1,2,…v+m

$$E(Y) = \mu\mathbf{1}_N + X_t, \; N = b(k+m)$$

$$V(Y) = (\sigma^2\mathrm{I}_{k+m}\mathrm{I}`_{k+m}) \otimes \mathrm{I}_b + \sigma^2\mathrm{I}_{b(k+m)}.$$

Define Now

$$T_i = \sum_{j=1}^{b} n_{ij}Y_{ij} \qquad B_j = \sum_{i=1}^{v+m} n_{ij}Y_{ij}$$

$$Q_i = T_i - \frac{1}{k+m}\sum_{j=_1 1}^{b} n_{ij}B_{ij} \text{ and } \mathrm{G} = \sum_{j=1}^{b} B_j \qquad \text{……4.4}$$

$$Q`_i = T_i - Q_i - \frac{r_i}{N}\mathrm{G}$$

i=1, 2,…, v+m, j=1, 2,…, b

Then it can be easily shown the least unbiased minimum variance estimator $\hat{t}$ of t satisfies

$C\hat{t}$ = P …… (4.5)

Where P is a (v+m)×1 column vector whose i^{th} component p_i , i=1,2,…, v+m is.

$$P_i = \frac{1}{\sigma^2} Q_i + \frac{1}{\sigma^2 + (k+m)\sigma_t^2} Q`_i = w\,Q_i + w`\,Q`_i \text{ with } w = \frac{1}{\sigma^2}$$

and $w` = \dfrac{1}{\sigma^2 + (k+m)\sigma_t^2}$

The matrix $C_{(v+m)\times(v+m)}$ is given by

$$C = \begin{pmatrix} \dfrac{w(rm+\lambda v)+w`(r-\lambda)}{k+m} I_v + \dfrac{1}{b(k+m)}\left[w`(\lambda b - r^2) - \lambda b w\right] 1_v 1`_v, & \left(-\dfrac{r}{k+m}\right) w 1_v 1`_m \\ \left(-\dfrac{r}{k+m}\right) w 1_m 1`_v & wb\left[I_m + (-\dfrac{1}{k+m}) 1_m 1`_m\right] \end{pmatrix}$$

With rank(C) = v+m-1

By imposing the restriction,

$$r = \sum_{i=1}^{v} t_i + b \sum_{i=v+1}^{v+m_1} t`_i = 0 \text{……..……..…..……} \quad (4.6)$$

We now solve (4.4) to obtain the estimates of $\hat{t}$ and t. on subtracting the row vectors $(-\frac{w}{k+m})(r1`_{\underset{\sim}{v}}, b1`_{\underset{\sim}{m}})$ and $\frac{1}{k+m} \times \frac{r}{b})(r1`_v, b1`_m)$, respectively. From each of the last m rows vectors of C and from each of the first v vectors of C, we obtain

$C^* t = P$

Where

$$C^* = \begin{pmatrix} \dfrac{w(rm+\lambda v)+(r-\lambda)w`}{k+m} I_v + \dfrac{w`-w}{b(k+m)}(\lambda b - r^2) 1_v 1`_v, & 0 \\ 0 & wb I_m \end{pmatrix}$$

Now

$$(C^*)^{-1} = \begin{pmatrix} \dfrac{k+m}{w(rm+\lambda v)+w`(r-\lambda)}\left[\mathrm{I}_v + \dfrac{(w`-w)(r^2-\lambda b)}{wbr(m+k)}1_v 1`_v\right], & 0 \\ 0 & \dfrac{1}{wb}\mathrm{I}_m \end{pmatrix}$$

So, for 1≤i≤v,

$$\hat{t}_i = \frac{k+m}{w(rm+\lambda v)+(r-\lambda)w`}\left[C_i + \frac{(w`-w)(r^2-\lambda b)}{wbr(m+k)}\sum_{i=1}^{v} C_i\right]$$

$$= \frac{k+m}{(rm+\lambda v)+(r-\lambda)\dfrac{w`}{w}}\left[(Q_i + \frac{w`}{w}Q_i`) + \frac{(\lambda b - r^2)}{br(k+m)}(1-\frac{w`}{w})\sum_{i=1}^{v}(Q_i + \frac{w`}{w}Q`_i)\right] \ldots\ldots (4.7)$$

and for v+1≤i≤v+m,

$$\hat{t}_i = \frac{1}{wb}C_i = \frac{1}{wb}wQ_i = (\ \overline{T}_{i.} - \overline{T}_{..}),$$

Where $\overline{T}_{i.} = \frac{1}{r}\sum_{j=1} n_{ij} y_{ij}$, $\overline{T}_{..} = \frac{1}{v+m}\sum_{i=1}^{v+m_1} T_i$

The variance and covariance of $\hat{t}$ is given by

$$\begin{pmatrix} \dfrac{k+m}{w(rm+\lambda v)+w`(r-\lambda)}\{\mathrm{I}_v + T_0 1_V 1`_V\}, & -\dfrac{1}{wb(k+m)}1_v 1`_m \\ -\dfrac{k+m}{wb(k+m)}1_m 1`_v, & \dfrac{1}{wb}\left[\mathrm{I}_m + (-\dfrac{1}{k+m})1_m 1`_m\right] \end{pmatrix}$$

$$\sigma^2 = \begin{pmatrix} \dfrac{k+m}{(rm+\lambda v)+\dfrac{w`}{w}(r-\lambda)}\{\mathrm{I}_v + T_1 1_V 1`_V\}, & -\dfrac{1}{b(k+m)}1_v 1`_m \\ -\dfrac{1}{b(k+m)}1_m 1`_v, & \dfrac{1}{b}\left[\mathrm{I}_m + (-\dfrac{1}{k+m})1_m 1`_m\right] \end{pmatrix}$$

Where $T_0 = \dfrac{w`m(r^2-\lambda b) - w\left[r^2(k+2m)-\lambda bm\right]}{wbr(m+k)^2}$ and

$$T_1 = \frac{\lambda bm - r^2(k+2m) - \frac{w`}{w}m(r^2 - \lambda b)}{br(m+k)^2}$$

The variances of elementary contrast between any two test treatments is:

1≤i≤v

$$\text{var}\,(\hat{t}_i - \hat{t}`_i) = \frac{2(k+m)}{\{rm + \lambda v\} + \frac{w`}{w}(r-\lambda)}\sigma^2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(4.8)$$

The variances of elementary contrast between any two contrl treatments is:

v+1≤i≤v+m

$$\text{var}\,(\hat{t}_i - \hat{t}`_i) = \frac{2}{b}\sigma^2$$

The variances of elementary contrast between any test versus control treatments is:

1≤i ≤v , v+ 1≤i`≤v+m, or v+1≤i≤v+m , 1≤i` ≤v

$$\text{Var}\,(\hat{t}_i - \hat{t}`_i) = \frac{(k+m)\sigma^2}{\{rm + \lambda v\} + \frac{w`}{w}(r-\lambda)}\left\{\begin{array}{l} 1 + \dfrac{\left[\lambda bm - r^2(k+2m)\right] - \frac{w`}{w}m(\lambda b - r^2)}{br(w+k)^2} \\ + \dfrac{1}{b}\left(1 + \dfrac{1}{k+m}\right)\sigma^2 \end{array}\right\} \ldots\ldots\ldots \quad (4.9)$$

4.2.2. Analysis under Fixed Model

Assuming that both $t_i`s$ and $bj`s$ are fixed effect, the model (4.3) is a fixed model. Since it can be shown by applying the Guass-Markov theorem that least unbiased minimum variance estimators of the $t_i`s$ satisfies.

$$\mathbf{C}t = \mathbf{Q}$$

Where $E(Q) = Ct$, C is an information matrix, Q is the treatment adjusted and t is the treatments.

We can then obtain the desired estimators by setting w` = 0 in (4.6).

$$\hat{t} = \begin{pmatrix} \frac{k+m}{(rm+\lambda v)}\left[I_v + \frac{(\lambda b - r^2)}{br(m+k)} 1_v 1`_v\right] & 0 \\ 0 & \frac{1}{b} I_m \end{pmatrix} \mathbf{Q}$$

The adjusted test treatment means:

$$\hat{t}_i = \frac{(k+m)}{(rm+\lambda v)}\left\{Q_i + \frac{\lambda b - r^2}{br(m+k)}\sum_{i=1}^{v} Q`_i\right\} \text{ for } 1 \le i \le v \qquad (4.10)$$

and $\hat{t}_i = \overline{T}_{i.} - \overline{T}_{..}$ for v+1≤i≤v+m

The variance and the covariance matrix of $\hat{t}_i$ is given by

$$\sigma^2 \begin{pmatrix} \frac{k+m}{rm+\lambda v}\left[I_v + \frac{\lambda bm - r^2(k+2m)}{br(m+k)} 1_v 1`_v\right], & -\frac{1}{b(m+k)} 1_v 1`_m \\ -\frac{1}{b(m+k)} 1_m 1`_v, & \frac{1}{b}\left[I_m + (-\frac{1}{k+m}) 1_m 1`_m\right] \end{pmatrix}$$

Moreover ,

The variances of elementary contrast between any two test treatments is:

$$\text{Var}(\hat{t}_i - \hat{t}`_i) = \frac{2(k+m)}{(rm+\lambda v)}\sigma^2, \text{ for } 1 \le i \le v \qquad (4.11)$$

The variances of elementary contrast between any two contrl treatments is:

$$\text{var}(\hat{t}_i - \hat{t}`_i) = \frac{2}{b}\sigma^2, \quad \text{for } v+1 \le i, i` \le v+m$$

The variances of elementary contrast between any test versus control treatments is:

$$\text{var}(\hat{t}_i - \hat{t}`_i) = \left\{\frac{k+m}{rm+\lambda v}\left[1 + \frac{\lambda bm - r^2(k+2m)}{br(m+k)^2}\right] + \frac{1}{b}(1 + \frac{1}{m+k})\right\}\sigma^2$$

$$= \left[\frac{k+m}{rm+\lambda v}(1 - \frac{1}{v}) + \frac{1}{bk}(1+k)\right]\sigma^2 \qquad (4.12)$$

for 1≤i≤v, v+1≤i`≤ v+m or v+1≤i ≤v+m,1≤i`≤v.

The treatment (adjusted) sum of square for modified augmented BIB design is given by

$\frac{1}{r(1-\mu^*)}\sum_i Q_i^2 - \frac{\mu*}{(1-\mu*)rv}Q_.^2 + \sum_j Q^2{}_j / bm, where\ \mu* = \frac{r-\lambda}{rk^*}$ where Q_i is the adjusted total of the i^{th} treatment. Q_j denotes the adjusted total of j^{th} control treatment and

$$Q_. = \sum_i Q_i$$

The error sum of square for augmented BIB design can be calculated as:

Total sum of square -Treatmet (adjusted) sum of square-blocks(unadjusted)sum of square.

$$\sum_{i=1}^{b(k+m)} (Y_{i.} - \overline{Y_{..}})^2 - \sum_{i=1}^{v+m} \hat{t}_i Q_i - \sum_{j=1}^{b} \frac{b_j^2}{k+m} + \frac{G^2}{b(k+m)},$$

$$= \sum_{i=1}^{b(k+m)} Y_{i.}^2 - \sum_{i=1}^{v+m} \hat{t}_i Q_i - \sum_{j=1}^{b} \frac{b_j^2}{k+m}\ is\ SSE$$

Therefore, the error mean square for modified augmented BIB design will be

$$\hat{\sigma}^2 = MSE = \frac{SSE}{df.E}$$

4.3. Efficiency factors of MABIB design to Augmented RICB design.

The efficiency factors of the intra-block of modified augmented balanced incomplete block design versus augmented randomized complete block design is given by

$$Ef = \frac{MSE_{MABIBD}}{MSE_{ARICBD}}$$

$$= \frac{\sigma_e^2}{(b-1)\sigma^2{}_e} = \frac{1}{b-1} < 1\ if\ b > 2,$$

This implies that when block size is greater than two, the modified augmented balanced incomplete block design is more efficient in comparison to augmented design through randomized complete block design. As block number increase; we can not use the augmented randomized complete block design.

The simple way of comparing relative efficiency factors of the intra-block of balanced incomplete block design versus randomized incomplete block design will be

$$Ef = \frac{MSE_{BIBD}}{MSE_{RICBD}}$$

$$= \frac{2\sigma^2 / \mathrm{r} \quad E}{2\sigma^2 / r}$$

Assuming per observation variances are the same.

$$\sigma_1^2 = \sigma^2,$$

$$E = \frac{\lambda v}{rk},$$

Is loss of precision when using BIB design in case residual variance is not decreased in comparison to RICB design.

$$Ef = E = \frac{\lambda v}{rk}$$

$$Ef = \frac{v}{k}\left[\frac{\lambda}{r}\right] = \frac{v}{k}\left\{\frac{r(k-1)/v-1}{r}\right\}$$

$$= \frac{v}{k}\left\{\frac{k-1}{v-1}\right\} = \left\{\frac{1-\frac{1}{k}}{1-\frac{1}{v}}\right\} < 1 \Rightarrow \quad v > k .$$

From the above relation we can conclude that balanced incomplete block designs are more efficient than randomized complete block designs.

4.4. Analysis Of Variance and Pair-wise Comparisons of treatments.

4.4.1. Hypothesis Testing

4.4.1.1. Under Fixed Effects Model

Testing the general hypothesis

$H_0: Ct = 0$ vs $H_1: Ct \neq 0$.

Where $t = (t_1, t_2 = ... t_{v+m})$,rank(t) = m+k,then the appropriate F-statistic

$$F_{v-1,b(k+m)-b-v+1} = \frac{MST_1}{MSE} = \frac{\frac{SST_1}{SSE}}{\frac{(v-1)}{b(k+m)-b-v+1}}$$ in table (4.5)

Testing the individual effect/ Testing the least square means of the treatments.

$H_0: t_1 = t_2 = ... = t_{v+m} = 0$ vs $H_1: t_1 \neq t_2 \neq .... \neq t_{v+m} \neq 0$

4.4.1.2. Under Mixed Effects Model

In the general case of mixed model, no exact methods of testing the hypothesis $H_0: t_1 = t_2 = ... = t_{v+m} = 0$ vs $H_1: t_1 \neq t_2 \neq .... \neq t_{v+m} \neq 0$, and for the comparison of any two treatments are available.

Testing the differences of least square means.

i. $H_0: t_1 - t_2 = 0$ vs $H_1: t_1 - t_2 \neq 0$ at $\alpha = 0.05$ level of significance

$H_0: t_1 - t_3 = 0$ vs $H_1: t_1 - t_2 \neq 0$,

.....

$H_0: t_1 - t_{v+m} = 0$ vs $H_1: t_1 - t_{v+m} \neq 0$,

ii. $H_0: t_2 - t_3 = 0$, vs. $H_1: t_2 - t_{v+m} \neq 0$,

$H_0: t_2 - t_4 = 0$ vs $H1: t_2 - t_4 \neq 0$,

……..…….

iii. H_0: $t_{v+m-1} - t_{v+m} = 0$ vs. H_1: $t_{v+m-1} - t_{v+m} \neq 0$

Testings of the random component/Testings of the variance component.

$H_{0:}\sigma_b^2 = 0$ vs $H_{1:}$ $\sigma_b^2 \neq 0$ (under the null hypothesis, there is no variations among the Blocks variability)

$H_{0:}\sigma_t^2 = 0$ vs $H_{1:}$ $\sigma_t^2 \neq 0$ (under the null hypothesis, there is no variations among the test treatment variability),

The variance component measures the performances of the test treatments. Under mixed model the estimates of the t_i `s are usually obtained from the $t_i$ `s given in (4.6) by replacing w and w` by their unbiased estimates. This process, however, introduces further random errors in the $t_i$ `s and therefore its efficiency may be very low, especially if the sample size is small. The estimates of the treatments were obtained for both in fixed effect model and mixed effect model in the construction Modified augmented BIB design frame work.

Now, we will describe the analysis of variance for augmented RIB designs and we will also describes the analysis of variance for fixed effect model and mixed effect model analyses of F-test of the hypothesis and the t-test hypothesis for modified augmented BIB design.

Table 4.4. Analysis of Augmented Randomized incomplete block Designs

Source of variations	Degrees of freedom	Sums of squares	Mean squares
Blocks (eliminating treatments)	b-1	$bSS = \sum_{1}^{b} T_{bj}^{2} /(c + n_j) - C.F$	bMS
Treatments (eliminating blocks)	t-1	$tSS = (MXGT) + (\sum_{1}^{b} b_j T_{bj}) + (\sum_{i}^{c} Tc_i c_i) - (\sum_{1}^{b} T_{bj}^{2} /(c + n_j)$	tMS
Among test treatments	v-1	$vSS = \sum_{1}^{v} V_i - vC.F$	vMS
Among control treatments	c-1	$cSS = \sum \frac{Tc_i^{2}}{b}$ -cC.F	cMS
Test vs. control treatments	1	CvSS = tSS-cSS –vSS	CvMS
Error	n-v-b+1	ESS = TSS- bSS- tSS	EMS = $\frac{ESS}{(c-1)(b-1)}$
Total	n-1	TSS- = $\sum X_{ij}^{2}$ -GC.F $= \sum_{1}^{C}\sum_{1}^{b} C_{ij}^{2} + \sum_{1}^{v} V_i^{2} - GC.F$	

Table 4.5. Analysis of Modified Augmented Balanced Incomplete Block Designs

Sources	Sum of square	Degrees of freedom	Expected values of Mean squares
Treatments adjusted	$\sum_{i=1}^{v+m} t_i C_i = \mathrm{SS}T_1$ $(\sum_{i=1}^{v+m} \hat{t}_i Q_i$ under model 4.2 assumption)	v-1	$\sigma^2 + \frac{\sum_{j=1}^{v+m}\sum_{j=1}^{v+m} c_{ij} t_i t_j}{v-1}$ $(\sigma^2 + \frac{\sum_{j=1}^{v+m}\sum_{j=1}^{v+m} e_{ij} t_i t_j}{v-1}$,under model 4.2 assumption
Blocks unadjusted	$\sum_{j=1}^{b} \frac{b_j^{\,2}}{k+m} - \frac{G^2}{b(k+m)} = SSB_2$	b-1	$\sigma^2 + (k+m)\sigma_b^2$
Treatments unadjusted	$\sum_{i=1}^{v+m} \frac{T_i^2}{r_i} - \frac{G^2}{b(k+m)} = SST_2$	v-1	$(\sum_{i=1}^{v+m}\sum_{j=}^{v+m} e_{ij} t_i t_j$ under model 4.2 assumption) $\sigma^2 + \frac{v-k}{v-1}\sigma_b^2 + \frac{\sum_{i=1}^{v+m} r_i (t_i - t_j)^2}{v-1}$
Blocks adjusted	$SST\text{-}\ SST_2\text{-}SSE = SSB_1$	b-1	$\sigma^2 + \frac{b(k+m)-(v+m)}{b-1}\sigma_b^2$
Error (intra-block)	SSE = SST - SST_1 - SSB_2 =SST- SST_2 - SSB_1	b(k+m)-b-v+1	σ^2
Total	SST = $\sum_{i=1}^{b(k+m)} (Y_i - Y_{..})^2$	b(k+m)-1	$\sigma^2 + \frac{(k+m)(b-1)}{b(k+m)-1}\sigma_b^2 + \frac{\sum_{i=1}^{v+m} r_i (t_i - t)^2}{b(k+m)-1}$

$MS\,B_1 = SSB_1/(b-1)$ $MSE = SSE/df.E$ *so* the estimate of $\frac{w`}{w}$ is given by $\frac{v(r-1)+m(b-1)}{(k+m)(b-1)MSB_1/MSE-(v-k)}$

Table 4.6. The ordinary t-distributions under model 4.2 and under mixed model assumptions.

	Under model 4.2 assumption	Under mixed model assumption with $w`/w$ known
1≤i,i`≤v	$t=\frac{t_i-t`_i}{\left(\frac{2(k+m)}{rm+\lambda v}\hat{\sigma}^2\right)^{1/2}}$	$t=\frac{t_i-t`_i}{\left[2\frac{k+m}{(rm+\lambda v)+\frac{w`}{w}(r-\lambda)}\hat{\sigma}^2\right]^{1/2}}$
v+1≤i,i`≤v+m	$t=\frac{t_i-t`_i}{\left(\frac{2}{b}\hat{\sigma}^2\right)^{1/2}}$	$t=\frac{t_i-t`_i}{\left(\frac{2}{b}\hat{\sigma}^2\right)^{1/2}}$
1≤i≤v,and v+1≤i`≤v+m, 1≤i`≤v and v+1≤i≤v+m	$t=\frac{t_i-t`_i}{\left\{\left[\frac{k+m}{m+\lambda v}(1-\frac{1}{v})+\frac{1}{bk}(1+k)\hat{\sigma}^2\right]\right\}^{1/2}}$	$t=\frac{t_i-t`_i}{\left\{\frac{(k+m)\hat{\sigma}^2}{(rm+\lambda v)+\frac{w`}{w}(r-\lambda)}\left[1+(\lambda bm-r^2k+2m)\frac{w`}{w}m\lambda b\_r^2\right]+\frac{1}{b}(1+\frac{1}{m+k})\hat{\sigma}^2\right\}^{\frac{1}{2}}}$

$\hat{\sigma}^2$ =MSE=$\frac{SSE}{df.E}$

CHAPTER FIVE

ILLUSTRATIVE EXAMPLE

5.1. Introduction

For illustration purpose, the Analysis of variances and comparisons of the adjusted means can be analyzed by using different statistical software. The most commonly used types of statistical software's for comparing control treatments with tests treatments are SPAD, GENSTAT and SAS. We use SAS statistical software's for calculating analysis of variance, estimation of model parameters and also estimates of the contrast.

5.2. Presentation and Interpretation of Augmented RIB Design

For illustration purpose, an experiment was conducted with eight new selections (that were to be tested) denoted by N_t, t=1, 2…8 and four control treatments denoted by u_s, s=1.2…4, of a genotype. There are twenty experimental units that can be arranged in three blocks. There are seven plots (four for control treatments and three for new selections) in the first and third block and six plots (four for control treatments and two for new selections) in the second block.

I.e. $k_1 = k_3 = 7, k_2 = 6$.

Table 5.1. Data layout of the Augmented Randomized Incomplete Block designs.

Blocks	Experimental units						
	1	2	3	4	5	6	7
1	C2(3)	C4(15)	V8(30)	C1(10)	V1(6)	C3(10)	V4(24)
2	V3(4)	C3(9)	C2(5)	V2(40)	C1(8)	C4(14)	
3	V7(8)	C3(8)	C1(6)	V5(11)	C2(6)	V6(18)	C4(18)

A source of this data is Jawahar R.Sharma (1988).The analysis of the data has been carried out and the results of the data are given.

Since all test treatment did not occur together in a block, a direct comparison of them is not possible, but since controls occurred together in a block it is possible to get a reasonable estimate of block effect so that it will be used in adjusting treatment. In the analysis of the above data, it is possible to determine the adjusted mean of new treatment, the analysis of variance and comparisons of means (among test treatment in different blocks, among test treatments in the same blocks and test treatment versus control treatment) using critical difference. The analysis of variance, the least square means and least squares of treatment effect were computed using SAS software.

The generalized form of the analysis of variance for an augmented design with one-way elimination of heterogeneity, the adjusted treatment means, and variances for mean differences are presented.

In this design, the controls and test genotypes as treatments and blocks. That means since we have four control treatments the data can be analyzed based on augmented RICBD with twenty experimental units. A wheat breeder would like to evaluate genotypes in augmented design because the seed for each test genotype is not enough for replicated trials, there is a limited resource for the research or observations (preliminary information is enough to narrow down the number of test genotypes for further test).There are four controls to be used as a reference to evaluate the test genotypes. The twelve treatments (eight test genotypes and four controls) were put in three blocks each containing seven, six and seven treatments respectively. The results of the data are given in the following tables.

Table 5.2. Control totals, mean and control effects

Controls	B1	B2	B3	Control Total	Control mean	Control effect
C1	10	8	6	24	8	-6.8
C2	3	5	6	14	4.7	-10.1
C3	10	9	8	27	9	-5.8
C4	15	14	18	47	15.7	0.9
Total	38	36	38	112	37.4	

Table 5.3. Test genotype total, blocks total and block effects.

Block	Ni	Block total	Test genotypes total	Number of test genotypes	Bi
B1	7	98	60	3	0.17
B2	6	80	44	2	-0.32
B3	7	75	37	3	0.17
Total	20	253	141	8	≈0

Table 5.4. Adjusted test genotype means/Adjusted test treatments.

Types of genotypes	Observed mean /unadjusted mean(vi)	Adjusted (bi)	Adjusted mean(vi`)	genotype Effect
V1	6	0.17	5.83	-8.97
V2	40	-0.32	40.32	25.52
V3	4	-0.32	4.32	-10.48
V4	24	0.17	23.83	9.03
V5	11	0.17	10.83	-3.97
V6	18	0.17	17.83	3.03
V7	8	0.17	7.83	-6.97
V8	30	0.17	29.83	15.03
Total	141			

Table 5.5. Analysis of variance for augmented design

Sources of Variations	Degrees of freedom	Type III Sum of squares	Mean squares	F-Value	Pr>F
Block	2	41.79	0.89	5.53	0.0435
Treatment	11	1632.10	148.37	39.28	< 0.0001
Controls	3	191.10	63.70	19.18	0.0018
Test genotypes	7	1150.61	164.37	43.51	< 0.0001
Controls vs. Test	1	290.38	290.38	76.87	< 0.0001
Error	6	22.67	3.78		
Total	19	1696.55			

R-Square	C V	Root MSE	yield Mean
0.98	15.36	1.94	12.65

Table 5.6. Mean comparison

Treatment	Adjusted mean	Test genotypes different blocks	Test genotypes same blocks	Test genotypes vs. controls
Test genotype		CD=7.52	CD=6.73	CD=6.72
V2	40.32	V2	V1	V2
V8	29.83	V8	V2	V8
V4	23.83	V4	V3	V4
V6	17.83	V6	V4	V6
V5	10.83	V5		V5
V7	7.83	V7	V5	V7
V1	5.83	V1	V6	V1
V3	4.32	V3	V7	V3
			V8	

Standard error of the adjusted mean for test genotypes =1.94

Critical difference at 5 percent level of significance =3.78

Standard error of the difference between any two test treatments mean (adjusted) = 3.07.

Critical difference at 5 percent level of significance =7.52.

Standard error of the difference between a test vs. control treatments = 2.74

Critical difference at 5 percent level of significance =6.72.

2.Controls				
C4	15.7			
C3	9.0			
C1	8.0			
C2	4.7			

Standard error of the least square mean for control treatments=1.12

Critical difference at 5 percent level of significance=2.18

Standard error of the difference between any two control treatments =1.59

Critical difference at 5 percent level of significance =3.89

5.3. Presentation and Interpretation of Modified ABIB Design

For illustration purpose, we consider the data of an experiment of wheat which was conducted by using a modified augmented balanced incomplete block design with parameter

$\nu^{\bullet}$ = v+u = 13+1 = 14, $b^{\bullet}$ = 13, $r^{\bullet}$ = (4, 13), $k^{\bullet}$ = 5, $\lambda^{\bullet}$ = (1, 4).

(Nigam and Gupta, 1979)

In the data, we added two additional control treatments. It should be noted that the precision of residual mean square depends on the number of controls plots we included per block. Include as much controls as possible given the resource and the material. Particularly controls below 3 are not acceptable in trials with augmented designs .Now the data is given in table 4.8 with the parameters.

$\nu^{\bullet\bullet}$ = v+u = 16, $b^{\bullet\bullet}$ = 13, $r^{\bullet\bullet}$ = (4, 13), $k^{\bullet\bullet}$ = 7, $\lambda^{\bullet\bullet}$ = (1, 4).

The above modified augmented balanced incomplete block design follows the conditions of MV-optimality given by Jacroux (2000). The layout of the experiment is given below. Inside and outside the parenthesis are the yields of variety and the numbers of the corresponding variety, respectively are given.

Table 5.7. Data layout of modified augmented Balanced Incomplete Block design.

Block-1	3(25.3)	6(19.9)	9(29.9)	11(24.6)	14(20.5)	15(24.6)	16(19.9)
Block-2	3(23.0)	4(19.8)	8(33.3)	12(22.7)	14(18.6)	15(19.8)	16(25.6)
Block-3	10(19.2)	11(19.3)	12(31.7)	13(26.6)	14(20.7)	15(21.9)	16(21.8)
Block-4	2(27.3)	5(27.0)	8(35.6)	11(17.4)	14(18.7)	15(23.5)	16(20.5)
Block-5	7(23.4)	8(30.5)	9(30.8)	10(32.4)	14(22.0)	15(18.7)	16(17.5)
Block-6	4(30.6)	5(32.4)	6(27.2)	10(32.8)	14(19.3)	15(22.8)	16(16.9)
Block-7	1(34.7)	5(31.1)	9(25.7)	12(30.5)	14(24.1)	15(21.5)	16(20.8)
Block-8	3(34.4)	5(32.4)	7(33.3)	13(36.9)	14(17.5)	15(17.8)	16(26)
Block-9	1(38.2)	2(32.9)	3(37.3)	10(31.3)	14(21.2)	15(25.2)	16(18.8)
Block-10	2(28.7)	4(30.7)	9(26.9)	13(35.3)	14(23.5)	15(19.5)	16(23.9)
Block-11	1(36.6)	4(31.1)	7(31.1)	11(28.4)	14(21.2)	15(18.9)	16(25.2)
Block-12	1(31.80	6(33.7)	8(27.8)	13(41.1)	14(20.7)	15(23.8)	16(22.8)
Block-13	2(30.3)	6(31.5)	7(39.3)	12(26.7)	14(19.8)	15(20.8)	16(27)

The analyses of the above data under the following three models are given in Appendices A, B and C, respectively.

i. Fixed Effect Model (assume that all factors are fixed),
ii. Mixed Effect Model (assume that only blocks are random),
iii. Mixed Effect Model (assume that only test treatments are random),

There are three controls to be used as a reference to evaluate the test treatment. The sixteen treatments (thirteen test treatment and three controls) were put in thirteen blocks each containing seven treatments. The results are given in the following table.

Table 5.8. Control totals, mean and control effects

Control	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12	B13	Control total	Control mean
C1	20.5	18.6	20.7	18.7	22	19.3	24.1	17.5	21.2	23.5	21.2	20.7	19.8	267.8	20.6
C2	24.6	19.8	21.9	23.5	18.7	22.8	21.5	17.8	25.2	19.5	18.9	23.8	20.8	278.8	21.45
C3	19.9	25.6	21.8	20.5	17.5	16.9	20.8	26	18.8	23.9	25.2	22.8	27	286.7	22.05
Total	65	64	64.4	62.7	58.2	59	66.4	61.3	65.2	66.9	65.3	67.3	67.6	833.3	21.37

Table 5.9. Test treatment total, blocks total and block effects

Test	B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12	B13	Total	Mean
T1							34.7		38.2		36.6	31.8		141.3	35.33
T2				27.3					32.9	28.7			30.3	119.2	29.8
T3	25.3	23						34.4	37.3					120	30
T4		19.8				30.6				30.7	31.1			112.2	28.05
T5				27		32.4	31.1	32.4						122.9	30.73
T6	19.9					27.2						33.7	31.5	112.3	28.08
T7					23.4			33.3			31.1		39.3	127.1	31.78
T8		33.3		35.6	30.5							27.8		127.2	31.8
T9	29.9				30.8		25.7			26.9				113.3	28.33
T10			19.2		32.4	32.8			31.3					115.7	28.93
T11	24.6		19.3	17.4							28.4			89.7	22.43
T12		22.7	31.7				30.5						26.7	111.6	27.9
T13			26.6					36.9		35.3		41.1		139.9	34.98
Total	99.7	98.8	96.8	107.3	117.1	123	122	137	139.7	121.6	127.2	134.4	127.8	1552.4	29.85

Table 5.10. Analysis of variance for modified augmented design

Sources of Variations	Degrees of freedom	Type III Sum of squares	Mean squares	F-Value	Pr>F
Blocks(adjusted for treatment)	12	427.2	35.6	2.28	0.018
Treatments(adjusted for blocks)	15	1978.51	131.9	8.44	<0.0001
Controls	2	13.87	6.93	0.444	0.6435
Test treatment	12	542.66	45.22	2.89	0.0031
Control vs. Test treatment	1	1421.99	1421.99	90.98	<0.0001
Error	63	984.67	15.63		
Total	90	3390.38			

R-Square	C V	Root MSE	yield Mean
0.71	15.1	3.95	26.18

Table 5.11. Mean comparisons

Treatment	Adjusted mean	Among any two test treatments	Among any two control treatments	Among test vs. control treatment
Test treatment		CD=5.8	CD=3.03	CD=4.61
T13	35.05	T13	T13	T13
T1	33.80	T1	T1	T1
T8	32.97	T8	T8	T8
T7	30.87	T7	T7	T7
T5	30.60	T5	T5	T5
T3	30.15	T3	T3	T3
T12	28.79	T12	T12	T12
T2	28.77	T2	T2	T2
T9	28.56	T9	T9	T9

T10	28.48	T10	T10	T10
T4	28.13	T4	T4	T4
T6	27.47	T6	T6	T6
T11	23.48	T11	T11	T11

Standard error of the least square mean for test treatments=2.08

Critical difference at 5 percent level of significance =4.08.

Standard error of the difference between any two test treatments mean (adjusted) = 2.96.

Critical difference at 5 percent level of significance =5.8.

Standard error of the difference between a test vs. control treatments = 2.354.

Critical difference at 5 percent level of significance =4.61.

Control			V8	
C3	22.13			
C2	21.39			
C1	20.60			

Standard error of the least square mean for control treatments=1.097

Critical difference at 5 percent level of significance=2.15

Standard error of the difference between any two control treatments =1.551

Critical difference at 5 percent level of significance =3.03

CHAPTER SIX

CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

We have seen in this study that the modified augmented BIB design can be analyzed based on the fixed and random effects model. The genetic covariance can be incorporated in to a mixed model, the random effects estimates in the model are typically more efficient than the fixed effects estimates.

Test treatments should be considered as fixed and random effects (best to use mixed model procedures for analysis) to see the BLUE and EPLUPS for the realizations of the random and the fixed effects parameters.

Augmented design is more efficient when block size is constant. When block number is greater than two, the modified augmented balanced incomplete block design is more efficient in comparison to augmented design through randomized complete block design.

Balanced incomplete block designs are more efficient than randomized complete block designs. A balanced incomplete block design, whenever existent, is the most efficient design for making test versus control treatment comparisons.

The A-and MV-optimality criteria are computationally more feasible and efficiency of augmented block designs or modified augmented block designs depends on the parameters of the designs.

The literature reports and our results indicate that the varieties are considered to be fixed or random, because these are the breeders' best varieties, they are interested in their performance per standard error, and we would say that they are fixed. They could be considered as random if they were merely intended to

represent the population of available varieties, and the interest was to estimate the variance among them rather than their individual performance.

6.2 Recommendations

- An augmented design or a modified augmented design should be used for selection in early stages of breeding programs where there is no replication. But the researchers or breeders need to take account of many repeated controls (no less than 15% of the total numbers of plots are used for repeated controls).

- When large numbers of germplasm lines/test treatment are to be evaluated with in limited facility of uniform land, it is advisable to use augmented design.

- If the researchers have no sufficient seed to plant more than one replication and when they are interested to comparing new entries to the controls, an augmented design would be a good choice. If resources are limited, it may be preferable to plant a single replication at several locations than several replications at a single location. Use of an augmented design will give for the researchers an estimate of the experimental error at each site (to confirm ANOVA assumptions of homogeneity of variance). The location with entry interaction can serve as the error for testing entries.

- In Ethiopia, there is no more literature on augmented or modified augmented design had been done. Perhaps because, these designs are not familiar for most researchers. Therefore, a recommendation is addressed to breeders and other researchers to consider these types of design.

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Appendices

Appendix A: Fixed Effect Model Estimations of Modified ABIB designs/assuming that all factors are fixed.

Class Level Information

Class	Levels	Values
Block	13	1 2 3 4 5 6 7 8 9 10 11 12 13
Treat	16	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

Number of observations 91

Dependent Variable: yields of wheat

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
Among controls	2	48.184	24.09	1.54	0.2220
Control vs. test treatment	1	99.58	99.58	6.37	0.0141

Appendix B: Mixed Effect Model Estimations of Modified ABIB designs/Assuming that only blocks are random.

Model Information

Data Set	WORK.AUGMENTED2
Dependent Variable	yield
Covariance Structure	Variance Components
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Containment

Class Level Information

Class	Levels	Values
Block	13	1 2 3 4 5 6 7 8 9 10 11 12 13
Treatments	16	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

Dimensions

Covariance Parameters	2
Columns in X	30
Columns in Z	13
Subjects	1
Max Obs. Per Subject	91
Observations Used	91
Observations Not Used	0
Total Observations	91

Iteration History

iteration	Evaluations	-2 Res Log Like	Criterion
0	1	397.1265233	
1	1	812.1170527	0.00000000

Convergence criteria met but final Hessian is not positive definite

Covariance Parameter Estimates

Cov Parm	Estimate
Block	1.142E+15
Residual	15.6296

Fit Statistics

-2 Res Log Likelihood	812.1
AIC (smaller is better)	816.1
AICC (smaller is better)	816.3
BIC (smaller is better)	817.2

Solution for Fixed Effects

Effect	treat	Estimate	Standard Error	DF	t Value	Pr > |t|
Intercept		24.3271	1.8737	0	12.98	.
Treat	1	11.6659	2.3543	63	4.96	<.0001
Treat	2	6.6379	2.3543	63	2.82	0.0064
Treat	3	8.0219	2.3543	63	3.41	0.0011
Treat	4	5.9979	2.3543	63	2.55	0.0133
Treat	5	8.4659	2.3543	63	3.6	0.0006
Treat	6	5.3419	2.3543	63	2.27	0.0267
Treat	7	8.7419	2.3543	63	3.71	0.0004
Treat	8	10.8379	2.3543	63	4.6	<.0001
Treat	9	6.4339	2.3543	63	2.73	0.0081
Treat	10	6.3539	2.3543	63	2.7	0.0089

Treat	11	1.3499	2.3543	63	0.57	0.5684
Treat	12	6.6579	2.3543	63	2.83	0.0063
Treat	13	12.9179	2.3543	63	5.49	<.0001
Treat	14	-1.5308	1.5507	63	-0.99	0.3273
Treat	15	-0.7385	1.5507	63	-0.48	0.6356
Treat	16	0	.	.	.	.

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
Block	12	0	1.46	.
Treat	15	63	8.44	<.0001

Contrasts

Contrast	Num DF	Den DF	F Value	Pr > F
Among controls	2	63	1.54	0.222
Control vs. test treatment	1	63	6.37	0.0141

Appendix C: Mixed Effects Model Estimations of Modified ABIB designs/Assuming that only test treatments are random.

Model Information

Data Set	WORK.AUGMENTED2
Dependent Variable	yield
Covariance Structure	Variance Components
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Containment

Class Level Information

Class	Levels	Values
Block	13	1 2 3 4 5 6 7 8 9 10 11 12 13
Control treatments	4	0 1 2 3
Test Treatments	14	0 1 2 3 4 5 6 7 8 9 10 11 12 13

Dimensions

Covariance Parameters	2
Columns in X	32
Columns in Z	14
Subjects	1
Max Obs. Per Subject	91
Observations Used	90
Observations Not Used	1
Total Observations	91
Covariance Parameters	2

Iteration History

iteration	Evaluations	-2 Res Log Like	Criterion
0	1	390.8858168	
1	1	390.8858168	0.00000000

Convergence criteria met but final Hessian is not positive definite

Covariance Parameter Estimates

Cov Parm	Estimate
Test treatment	0
Residual	15.5814

Fit Statistics

--2 Res Log Likelihood	390.9
AIC (smaller is better)	392.9
AICC (smaller is better)	393
BIC (smaller is better)	393.5

Solution for Fixed Effects

Effect	block	controls	Estimate	Standard error	DF	t Value	Pr > |t|
Intercept			24.3271	1.8708	0	13	.
Block	1		-2.9716	2.3113	62	-1.29	0.2033
Block	2		-5.4655	2.2418	62	-2.44	0.0176
Block	3		-5.3	2.2329	62	-2.37	0.0207
Block	4		-3.616	2.2329	62	-1.62	0.1104
Block	5		-3.584	2.2329	62	-1.61	0.1136
Block	6		-1.74	2.2329	62	-0.78	0.4388
Block	7		-1.792	2.2329	62	-0.8	0.4253
Block	8		-1.3415	2.2418	62	-0.6	0.5518
Block	9		0.3825	2.2418	62	0.17	0.8651
Block	10		-1.644	2.2329	62	-0.74	0.4644
Block	11		-0.468	2.2329	62	-0.21	0.8347
Block	12		-1.012	2.2329	62	-0.45	0.652
Block	13		0	.	.	.	. .
Control		0	12.9723	2.3511	62	5.52	<.0001
Control		14	-1.5308	1.5483	62	-0.99	0.3267
Control		15	-0.7385	1.5483	62	-0.48	0.6351
Control		16	0	.	.	.	.

Appendix D : Incidence Matrix

$N_{16 \times 13} =$

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12	B13
0	0	0	0	0	0	1	0	1	0	1	1	0
0	0	0	1	0	0	0	0	1	1	0	0	1
1	1	0	0	0	0	0	1	1	0	0	0	0
0	1	0	0	0	1	0	0	0	1	1	0	0
0	0	0	1	0	1	1	1	0	0	0	0	0
1	0	0	0	0	1	0	0	0	0	0	1	1
0	0	0	0	1	0	0	1	0	0	1	0	1
0	1	0	1	1	0	0	0	0	0	0	1	0
1	0	1	0	1	0	1	0	0	1	0	0	0
0	0	1	0	1	1	0	0	1	0	0	0	0
1	0	1	1	0	0	0	0	0	0	1	0	0
0	1	1	0	0	0	1	0	0	0	0	0	1
0	0	0	0	0	0	0	1	0	1	0	1	0
---	---	---	---	---	---	---	---	---	---	---	---	---
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0

NB:-1=0

$N_{16 \times 13} =$

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12	B13
3	3	10	2	7	4	1	3	1	2	1	1	2
6	4	11	5	8	5	5	5	2	4	4	6	6
9	8	12	8	9	6	9	7	3	9	7	8	7
11	12	13	11	10	10	12	13	10	13	11	13	12
---	---	---	---	---	---	---	---	---	---	---	---	---
14	14	14	14	14	14	14	14	14	14	14	14	14
15	15	15	15	15	15	15	15	15	15	15	15	15
16	16	16	16	16	16	16	16	16	16	16	16	16

Appendix E: The SAS code for augmented Design Data Analysis

Tests of fixed effect using GLM

DATA augmented/File Name; /*one can enter any other name for data*/

Input var $ block treat yield/list of all the variables;

Cards;

Data set/*one can enter the data of values of the above variables*/

/*to test the significance of treatments (accessions and controls taken together) one can perform the analysis of variance of the data and can perform Contrast analysis by Using PROC GLM. This can be done using the following steps. The following SAS statements can be made use of*/

Proc glm;

Class block treat;

Model yield = block treat/solution;

Lsmeans treat/pdiff;

Contrast 'Among treatments'

Contrast <among test treatments> treat 1-1, treat 11-2, treat 111-3,...,;

Contrast<among controls> treat 00000000000001-1,…,;

Contrast <tests vs. control >11111111111111-13, ….,;

Run;

Mixed effect test where Block is random.

```
DATA augmented;   /*one can enter any other name for data*/
Input block   treat   yield;
Cards;
Data set/*one can enter the data of value of input*/;
Proc mixed data = augmented/File Name ;< options>;
                                Options = method = MLE or REME (the default);
 Class block treat; /* list of the categorical variables */;
 Model yield = block treat/fixed effect variables</options>; Options: alpha = level of
significance/the default = 5 %    S=solutions   residuals;
  Random block /random effects </options>; Options = G= the variance component;
          Run;
```

Mixed effect test where test treatment is random

```
DATA augmented;   /*one can enter any other name for data*/
 Input block control test yield
          Cards;
Data set/*one can enter the data of value of input*/
                                                ;
Proc mixed data = augmented/File Name; </options>;
                                Options = method = MLE or REME (the default);
      Class block control test/* list of the categorical variables */;
      Model yield = block control/fixed effect variables</options>;
        Options: S = solution alpha = level of significance residuals;
Run;
```

DECLARATION

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

Name: Aragaw Eshetie

Signature: _____

Date: _____

This thesis has been submitted for examination with my approval as a University Advisor.

Name: Girma Taye (PhD)

Signature: _____

Date: _____