SCREENING NEW STRAINS OF SUGARCANE BY AUGMENTED BLOCK DESIGN AND RANDOMIZED COMPLETE BLOCK DESIGN

by

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Abstract

Of the three pillars in which the Kenya vision 2030 is anchored, agriculture is a key sector. Over the past few years the challenges to sugar production i.e. the choice of the variety to plant, soil nutrients variation and market competition amongst others have greatly affected sugar production. This project has effectively and efficiently employed the technique of experimental design to ascertain family selection by comparing augmented block designs and Randomized complete block designs.The augmented block design is widely used in breeding programs, particularly in screening and selection of large number of germ-plasm lines with non- replicated test treatments and replicated control treatments to estimate the experimental errors. The study establishes a relationship between augmented block designs in screening and completely randomized block design in screening new strains of Sugarcane. The data used in this study were generated from IASRI resource server. In the two designs analyzed, we consider 5 test treatments and 2 control treatments for augment design and the same number of treatments for Randomized Complete Block Design. In the event of screening new sugarcane varieties, attempts were made to find the effectiveness of augmented block designs (ABD) and completely randomized block designs (R.C.B.D) in test families vs. control checks where the results reveal that Augmented Block Design is 11.86 times more efficient than a RCBD in standard error ε_{ij}=N(0,1)and drops through to 1.81for error term ε_{ij}=N(0,25). In the conclusion of this study in chapter five, we have shown that Augmented Block Design is better suited when the plots are limited and Randomized Complete Block Design is better suited when treatments are many.

Chapter 1

Introduction

1.1 Background of the Study

Statistics is a science of extracting information from a complex and noisy data with uncertainty, applied statistical methods helps in analyzing data to serve specific purpose in application. This study has effectively analyzed new sugarcane varieties using Augmented Block Design and Randomized Complete Block Design in test families verses check controls by the strength of their effectiveness. Any research investigation involves design of experiments to help make meaningful comparisons[16]. In plant variety selection programmes where comparisons is between newly introduced strains and the commercial controls, the vital designs used are augmented block designs, completely randomized block designs, reinforced balanced incomplete designs, Latin squares and Gaeco Latin squares. In this study we have used augmented block designs and randomized complete block design to screen new sugarcane strains by concentrating on their effectiveness and efficiencies in tests verses control experiments as applied to plant breeding of the new cane varieties. Farmers have several alternatives of varieties for field trials. The tested entries are related to their pedigrees of yield for performance since families selection approach is preferred due to its objectivity and useful traits of low hereditary as opposed mass selection. In this study, analysis of different designs used in screening the newly introduced varieties of sugarcane thus suitable for family selection with replications have their relative efficiencies

discussed into details with particular emphasis laid to an augmented block designs and randomized complete block design.

1.2 Statement of the Problem

In recent years a number of designs of experiments have been developed, many of these designs have programmes involving use of family selection like picking of large numbers of individuals from best performing families than from worst performing strains. Due to the fact that large numbers of seedlings are involved, vast tracks of land are required to evaluate seedlings even though soil nutrients homogeneity is to be a factor. We assumed these factors to be constant in this study. During seedling stage of plant breeding, a large population of genotypes of which only a few would eventually be released for commercial cultivation are considered and thus subjected to test against the controls. Construction of experimental design for such scenarios is possible by use of augmented block designs and completely randomized block designs in screening sugar cane varieties to reveal their efficiencies in test treatment vs. control experiment. This study analyzes different designs seeking to give a statistical approach to farmers "choice of varieties by screening the newly introduced varieties of sugarcane to eliminate poor selection of varieties through augmented block design and randomized complete block design" .

1.3 Purpose of the Study

The specific objectives of this study are:

1. To examine efficiency of Randomized Complete Block Design in test family vs. control experiment.
2. To measure the efficiency of augmented block designs.

3. To compare the efficiencies of Augmented Block Design and Randomized Complete Block Design in screening of new strains of sugarcane.

1.4 Research Hypothesis

Let μ_i be the treatment mean of the i^{th} treatment

μ_{Ai} be the mean for the i^{th} treatment in augmented block design

μ_{Ci} be the mean for i^{th} treatment with replications in $RCBD$.

The hypothesis for this study is

H_o:$\mu_{A_i} = \mu_{C_i}$ against

H_a: $\mu_{A_i} \neq \mu_{C_i}$

1.5 Significance of the Study

The study has analyzed two designs that are useful to farmers in making sound decision and interpretation of the newly introduced cane varieties thus propel them to select varieties in test families with high frequencies of superior clones. Since experimental design plays an important role on establishing an interface between statistical results and statistical applications in several fields like Agriculture, industry and Biology, this study provides a unique opportunity to facilitate farmers input and rapid screening on farm cropping system research. The study also provides vital information for field experiment researchers and breeders for further investigation of experimental and statistical problems related with the application and uses of an augmented block design and randomized complete block design in plant breeding. This study provides designs that can be extended to all other sugar industries. The research is useful to the management of any sugar industry in selection of varieties to be used by their farmers so as to maximize their yield output

and remain a strong force in the globally competitive sugar industry. This study generally aimed at enhancing the agricultural sector by building capacity of the cane farmers to enable them effectively and efficiently screen new sugarcane varieties thus choose high yield families of which the basis of economic pillar of Kenyas vision 2030 is anchored of which the results indicate that both augmented block designs and randomized complete block designs are effective in their own way and at times may be used interchangeably.

1.6 Definition of terms

1.6.1 Design

In this study, we take the view common among statisticians that a design is an allocation Θ of a set v treatments to a set of Ω plots. The design may be thought of as a function [5] f from Ω to Θ: plot w receives λ treatments if $f(w) = \lambda$ is portioned into blocks then f is called a block design. A block is proper if all its blocks have the same size k. if $k = v$ then we have a complete block design if $k < v$ its an incomplete block design

1.6.2 Balanced incomplete block design

B.I.B is an arrangement of v treatment in b blocks such that any block has k treatments, any λ treatment occurs in r blocks and any pair of treatments occurring in blocks. The five parameters are not independent but satisfy these two relations

$$vr = bk \text{ and } \lambda(v-1) = r(k-1).$$

A Balanced Incomplete Block Design is then written as (v, k, and) with

$b = \frac{v(v-1)\lambda}{k(k-1)}$ and

$r = \frac{\lambda(v-1)}{k-1}$

With respect to this study, we define a design in general as an allocation of a set Θ of v treatments to a set Ω of b blocks thus the design may be thought of as a function of f from Ω on to Θ. Plot w receives a treatment λ if $f(w) = \lambda$ and Ω is partitioned into blocks, then f is called a block design with the size k for blocks.
If $k = v$ we have a balanced incomplete block design.

1.6.3 Randomization

This is a method of dealing with nuisance factor by balancing the nuisance factor across the experiment .It's done using random device or pseudo-random device to choose which factor combination is allocated to each experimental unit. Like blocking, randomization is another technique of dealing with nuisance factors only that for randomization the factors are unknown and uncontrollable. Majumda [17] in his handbook of statistics stated that randomization balances out the impact of nuisance factors across the experiment.

1.7 Replication

This is a convenient way of increasing the size of the experiment and precision it implies making more than one measurement at the same combination factor level. It is necessary to let all sources of random variables operate independently on every occasion so that replication can count as proper [15]. According Rao [20] in his book stated that replication can be exploited to produce a pure error estimate of σ which is employed in this study.

1.7.1 Latin squares

We wish to explain the concept of mutually orthogonal Latin squares which will be used in the construction of B.I.B designs A Latin square of order s is an arrangement of s symbols in an s x s array such that each symbol occurs once in each row and once in each

column of the array i.e. for a 4×4 Latin square in symbols $ABCD$ would be

$ABCD\ ABCD\ ABCD$
$BADC\ CDAB\ DCBA$
$CDAB\ DCBA\ BADC$
$DCBA\ BADC\ CDAB$

These 4×4 Latin squares are mutually orthogonal since they are pair wise orthogonal. A complete set of $S - l$ mutually orthogonal Latin squares exists for any $S = p^n$ where p is a prime number[6]. This study uses Latin square method of constructing an augmented block design with given parameters.

1.7.2 Unreduced B.I.B design

According to Mike Jacroux [21] these designs are obtained by taking all combinations of the v treatments k at a time with parameters given by

$$(v, k, b) =^{v} C_k \tag{1.1}$$

$$v =^{v-1} C_{kr} \tag{1.2}$$

and

$$\lambda =^{v-2} C_{K-2} \tag{1.3}$$

1.7.3 Reinforced incomplete block design

According to Das [2], if a number of control treatment p is added in every block of existing incomplete block design with the resulting design having $p + v$ treatment distributed in b

blocks each of size $k+p$, such that newly introduced p treatments are replicated b times and the original v treatments r times, this design is now called reinforced incomplete block design.

1.7.4 Augmented block design

An augmented experimental design is any standard experimental design in standard treatments to which additional (new) treatments have been added. The additional treatments requires enlargement of the complete blocks and incomplete block row column designs. Augmented designs that eliminates heterogeneity in one directions are called augmented block designs [8].

1.7.5 Randomized complete block design

This is the simplest type of layout where in this study treatments are allotted to the experimental unit at random. This design essentially removes variability between blocks from the experimental errors. This was shown by Rajender and Gupta [23] in their abstract of augmented design and randomised complete block design with a two way elimination of heterogeneity.

1.8 Overview of the Chapters

This project consist of five chapters,chapter one gives the background information of the study with respect to statistical methods applied in solving specific problems in screening of new varieties. Chapter two considers related literature on the area of design of experiment.Chapter three describes the methodology used in the study and chapter four gives the analysis with different error terms to compare the efficiency of the two designs.Chapter five gives a conclusion about the research findings which reveal that ABD is 11.86 times

Chapter 2

Literature Review

The problem of comparing a set of more than one control to a set of tests of treatment in block design set up has received very little attention. Federer in 1956 [12] introduced designs to fill the needs arising in screening new strains of sugarcane in Hawaii Sugarcane planter association. Das in 1958 [5] introduced series of incomplete block designs including any number of control treatment say p in every block of an existing incomplete design. The resulting design will have v+p treatments distributed in b blocks, thus reinforced incomplete block designs. Since Federer [12] published his article Augmented (Hoo nuiaku) design in 1956 a lot of research have been published most of which are development of the founders work. Federer [12] illustrated arithmetically and algebraically an augmented randomized complete block design and augmented balance lattice design, where he considered analysis with and without recovery of inter- block information and provided discussions on unequally sized incomplete block design. The results indicated that this design is more efficient than the earlier indicated one. Federer and Raghavarao fed1961b in 1975 gave a precise introduction to some augmented row column designs and to the constructions and analysis of augmented lattice, square design on which Pinney (1991) made use of by implementing augmented designs on farm trials or prototype evaluation trials, He advocated use of augmented designs that minimizes plot number and allows farmers to flexibly decide what treatments are to be tested on their farms, he further concluded that number of plots per farm depend on the region, population density

and farming system employed by the farmers. Federer [4][11] gave analysis of randomization procedure and constructions of the design by adding new treatments to the blocks of Randomized Complete Block Designs and balanced lattice designs. The outcome showed that a randomized complete block design had a simple and rapid procedure as compared to lattice design.Federer [12] gave procedure and designs useful for screening material inspection and allocation. The procedure has since been used by many researchers to develop more designs used in screening of strains. Gupta [14] obtained augmented design using Randomized Complete block design and block designs for one way heterogeneity. The class of augmented experimental designs [4][11][12] was introduced to replace systematically spaced check arrangements in plant breeding research investigations after the named researcher's proved the efficiency of the latter. Federer [12] and Gupta [1] have produced a statistical procedure for analyzing such experiment at a site that takes account of the random nature of new treatments and of the blocking variables. Fisher [6] established that its important and desirable to determine the relative performance of new test treatment with respect to the controls in screening experiments. Majumdar[17] suggested augmenting an incomplete block design in test treatment with one or more replication. Gupta and Das [13] developed systematic approach for designing comparative experiments and made suggestion of supplementation and reinforcement following a study by Das [5] on comparative experiments. Box [10] compared balance incomplete block design with augmented Balanced Incomplete Block Design suggested by Parsad and Gupta [18] for constructing control test treatment contrast. The result indicated that augmented Balanced Incomplete Block Designs were more efficient than a Balanced Incomplete Block Design in test treatments against control treatments experimental contrast set-up.

Parsad and Gupta [19] developed the theory of incomplete block designs for comparing several treatments with a control; their development resulted into a balanced treatment incomplete block design (BTIB) design whose efficiency compares to that of augmented balanced incomplete block designs. They studied their construction and gave an elaborate procedures involved. Searle et.al (1992) estimated the effects under the random effect

assumptions (Best linear unbiased prediction) to be conceptually different from estimation under a fixed effect assumption Blue were he concluded that both Blup and Best linear unbiased estimator assume known variance components. Jacroux [21] considered the problem of optimality in comparing v tests treatments with u controls using block designs this followed a Majumdar[17] research on sufficient conditions derived for balanced treatments of unequal blocks. Parsad [18] introduced an application of the augmented randomized complete block design to poultry research where Avian health researcher had the desire to minimize animal usage, cost prohibit large, all-inclusive experiments they showed that plant breeders experiences a problem with variety screening experiments in which large number of varieties must be evaluated with limited seed supply, this research was published in poultry scientist in may 1996 in college of veterinary medicine. Rao [20] gave an elaborate research on effect of maxillary sinus where Augmentation on the survival endosseous implants where grafting of maxillary sinus was used in the survival invention. Das and Gupta [2] described an on construction of A-efficient balanced test treatment in an incomplete design. Federer (2007) introduced a new class of augmented experimental design as split block designs and split plot designs to help evaluate missing values in a data. Giri and Das Da1979 published the use of germ plasma accessions test treatments verses checks in the journal of horticulture sciences where randomized block designs was employed to evaluate a set of germ plasma accessions alongside local checks.

Fishman [7] evaluated family and done performance using various patterns of environmental variations to examine effectiveness of randomised incomplete designs. Majumdar in 1986 [17] derived some sufficient conditions for determining A-optimal designs in classes D (s,t,b,k) where s = t and k is substantially larger than v, Rajender and Gupta [23] studied optimality of designs comparing s controls to t tests treatment within classes of binary designs. Rajender and Gupta [23] obtained partial results on A-optimality for designs in which the controls appears equally often within blocks. Jacroux [21] have derived sufficient conditions used in establishing A- and MV optimality of augmented block design. The recent paper providing more overviews of known results for comparing test treatments to

checks/controls are Majumdar[17] and Gupta and Parsad [14] compared the effectiveness of augmented block designs and a Balanced Incomplete Block Design in testing of families against set of controls. In this study, we are interested in using analysis of variance to determine the effectiveness of Randomized Complete Block Design and Augmented Block Design in screening new sugarcane varieties by using a given test treatments against set controls.

Chapter 3

Research Methodology

3.1 Introduction

Having formulated the problem of screening various sugarcane varieties by use of analysis of variance for ABD and RCBD . The assumptions described for the error terms (ε_{ij}) are very necessary for drawing inferences by adopting a known statistical method. This study uses the analysis of variance techniques by which inferences are made using the F-test in evaluation of the effectiveness of the two design. The sequences of these methods were as follows.

3.2 Data Layout

A conceptual frame work for a Randomized complete block design was constructed, similarly, a layout for augmented block design was also constructed. This followed a generation of data in frequency of one hundred from a definite resource server, an IASRI design. The generated layouts for the two designs were as shown below for three replication of controls in every block.

Table 3.1: Blocks Layout with 3 replication of treatment

Block 1	Block 2	Block 3
Treatment2	Treatment2	N39
N39	N39	CO945
Treatment5	Treatment3	CO945
CO945	CO945	N39
CO945	N39	N39
N39	CO945	Treatment4
N39	CO945	CO945
CO945	N39	

Data was then generated using pseudo random numbers. The different methods of generating random numbers are discussed in the study

3.3 Data Simulation

Methods of Monte-Carlo class of computational algorithms and E.M algorithms that rely on repeated random sampling to compute data[7] was used to simulate the generated data. Monte-Carlo methods are often used when simulating physical and mathematical systems whereas E.M algorithms are employed while dealing with incomplete data and order restricted. If the two happens to occur together in an application of risk assessment, the Monte Carlo method will be employed due to it's advantages over deterministic algorithm. Monte-Carlo simulations are broad classes of computation that rely on repeated random sampling to obtain numerical results. Computer simulation is preferred in this study. In comparison of effectiveness of different designs say Augmented Block Design and Randomized Complete Block Design, we simulated data from standard distributions using Monte Carlo simulation framework because of their reliance on repeated computa-

tion and pseudo random numbers. Monte Carlo methods are most suited to calculation by a computer: Monte- Carlo methods tend to be used when it is infeasible or impossible to compute exact results with a deterministic algorithm. The simulation of data followed a generation of Pseudo-Random numbers which was done by a computer then the polar method was used to relate variables u and r and generates a pair of independent random variables from standard normal distribution N (0, 1). In this study, comparison of RCBD and ABD in screening sugarcane varieties has been achieved through analysis of simulated data from the standard normal distribution where different Pseudo -random numbers used were generated.

3.3.1 Generating Pseudo-random Numbers

The most successful computer process for generating Pseudo-random numbers in U(0,1) is the linear congruently generator (LCG) [10]. For us to have used LCG we had to choose three positive integers

a, is the multiplier

c, is the increment

m, is the modulus

m> a ,

m> c

To obtain the required sequence of random numbers $u_1, u_2, ..., u_N$. We first generate a sequence of integers $x_1, x_2, ...x_N$ in the range $0, 1, 2.....m-1$ starting from an initial value x_o known as the seed. The sequence of integers is the n generated using the recursive rule

$$x_n = (ax_{n-1} + c)(modm), n = 1, 2, ...N \tag{3.1}$$

i.e X_n is the remainder when $ax_{n-1} + c$ is divided by m and after that u_n is set to be equal to $\frac{x_n}{m}$

The technique of analysis of variance described below was employed after the results were

obtained, however, comparisons of treatments of analyzed data was used to give more meaningful screens. Finally, general testing of treatments from the analyzed data as set by research hypothesis was done by use of two sample T- test.

3.3.2 Generating normal Random Variables

Box and muller(1958) developed an algorithm for generating pseudo-random numbers in N(0,1). This algorithm is expounded below.

let $x, y \sim N(0,1)$ therefore

$$f(x) = \frac{1}{\sqrt{2\Pi}} e^{\frac{-x^2}{2}} \tag{3.2}$$

and

$$f(y) = \frac{1}{\sqrt{2\Pi}} e^{\frac{-y^2}{2}} \tag{3.3}$$

As the first step we indicate the following relation.

Intergration of $f(y) = e^{\frac{-x^2}{2}} dx = \sqrt{2\Pi}$ from $-\infty$ to ∞

The proof of the above equation can be presented via the replacement of x and y to r and θ such that

$$x = r\cos\theta y = r\sin\theta \tag{3.4}$$

When this is done the integral interval is given as $0 \leq r < R$,the equation form is then represented as

u$\in$(0,1) and the variable R of $U(R) = u$ is described as $U(R) = u \Rightarrow R = \sqrt{2log(1-u)}$

In setting $u_1 = 1 - u \in (0,1)$ and

$u_2 \in (0,1)$ the values of x and y are given as

$$x = \sqrt{(2log(u_1)\cos 2\Pi u_2} \tag{3.5}$$

and

$$y = \sqrt{(2log(u_1)\sin 2\Pi u_2} \tag{3.6}$$

Thus in the scheme of Box Muller method we can generate gaussian random variables distributed in N(0,1) using uniform distribution on (0,1)

Using the above equation x and y are also held as:

$$x^2 + y^2 = r^2 \tag{3.7}$$

3.3.3 Polar Method

The disadvantage of the box Muller method is the necessity to compute cos(.) andsin(.) which is time consuming for a computer. The polar method counters this by replacing the values in the basic Box Muller method form with rations.It introduces a value $s = u_1^2 + u_2^2$ and identifies the value of s with that of u_1 and $\frac{\theta}{2\Pi}$ with that of u_2 in the basic form. The values

$$eqn8\cos\theta = \cos 2\Pi u_2 \tag{3.8}$$

and

$$\sin\theta = \sin 2\Pi u_2 \tag{3.9}$$

In the basic form,this can be replaced with

$$eqn10\cos\theta = \frac{u}{R} = \frac{u}{\sqrt{s}} \tag{3.10}$$

and

$$\sin\theta = \frac{v}{R} = \frac{v}{\sqrt{s}} \tag{3.11}$$

respectively, where

$$R^2 = u^2 + v^2 \tag{3.12}$$

3.3.4 Polar Algorithm

We use the polar algorithm to generate normal random variates using polar method as follows;

(a) Generate random numbers u_1 and u_2

(b) Set $v_1 = 2u_1 - 1, v_2 = 2u_2 - 1$ and $s = v_1^2 + v_2^2$.
Note that v_1 and v_2 are U(-1,1)

(c) If $s > 1$ go to step 1,Otherwise,return:

$$z_1 = \sqrt{\frac{-2lns}{s}} v_1 z_2 = \sqrt{\frac{-2lns}{s}} v_2 \tag{3.13}$$

Polar algorithm generates a pair of independent random variates from the standard normal distribution,N(0,1) To generate a random variable $x \sim N(\mu, \sigma^2)$, with the mean μ and the variance σ^2 we use the scaling property of the normal distribution. so we generate to random variables from the results above as follows:

$$x_1 = \mu + \sigma z_1 x_2 = \mu + \sigma z_2 \tag{3.14}$$

3.4 Design Model and analysis of variance(ANOVA)

3.4.1 Introduction

A statistical model is basically an assumption relating effects of different levels of factors involved in an experiment alongside one or more terms representing the error effects.

To provide more insight understanding of the design, this study proposes a two factor experiment in screening various sugarcane varieties; we therefore use the analogy of any agricultural experiment and refer to two-way classification as treatments and blocks as proposed by Das and Gupta in 1992 under model of communication in statistics[2]. In this study, we consider v treatments and b blocks and one experimental value which are the yields of sugarcane per acre corresponding to each treatment (plots) and blocks (variety) for i^{th} treatment and j^{th} block denoted by X_{ij} as in the analysis of variance.

3.4.1.1 Analysis of Variance

The ANOVA is a powerful statistical tool for test of significance. Since t-distribution is not adequate, ANOVA which is based on f- distribution is employed with a basic purpose to test homogeneity of several means. ANOVA is mainly used to dealing with analysis of agronomical data where variation is inherent and may be caused by either chance causes or assignable cause.

3.4.2 Assumption for ANOVA

For reliability of F-test in ANOVA

(i) The observations are independent

(ii) Parent populations from which observations are taken are normal.

(iii) Various treatment and environment effects are the effects

3.4.3 Two Way Classification

The values of response in this classification are affected by two factors. In this study, we have the yield of sugarcane varying for different treatments coded from one up to five

and two others are used as controls i.e. rations as well as the differences in variety. Let us now suppose that n breeds of sugarcane are divided into h different plots with each plot containing k varieties, if we consider the effect of k treatments i.e. rations given at random to cane variation in each plot on the yield of sugarcane.

Let X_{ij}=(yield of sugarcane from plot with j^{th} variety on ration i)

i=1,2 ,3...k,

j=1,2,3...h

We let the yield of sugarcane to be expressed as variable value in $k \times h$ two way table as below.

Table 3.2: ANOVA Table for General model

Treatment (Rations)	Varieties of Sugarcane 1 2....j....h	Raw Total	Raw Means
1	X_{11} X_{12}....X_{1j}....X_{1h}	R_1	$\bar{X}_{1.}$
2	X_{21} X_{22}....X_{2j}....X_{2h}	R_2	$\bar{X}_{2.}$
.	. . ..	.	.
.	. . ..	.	.
.	. . ..	.	.
i	X_{i1} X_{i2}....X_{ij}....X_{ih}	R_i	$\bar{X}_{i}$
.	.....	.	.
.	.....	.	.
K	X_{k1} X_{k2}....X_{kj}....X_{kh}	R_k	$\bar{X}_{k.}$
column total	C_1 C_2.....C_j....C_h	$G = \sum_{i=1}^{k} \sum_{j=1}^{h} X_{ij}$	
column means	$\bar{X}_{.1}$ $\bar{X}_{.2}$.....$X_{.j}$....$X_{.h}$		$\bar{X}_{..}$

from the above table: R_i=$\sum_{j=1}^{h} X_{ij}$ as the sum of observations in the i^{th} row. $i = 1, 2...k$

C_j=$\sum_{i=1}^{k} X_{ij}$ as the sum of observations in the j^{th} column . $j = 1, 2..h$

$\bar{X}_i$=$\frac{1}{h}\sum_{i=1}^{h} X_{ij} = \frac{R_i}{h}$ mean yield of the i^{th} treatment

$\bar{X}_j$=$\frac{1}{k}\sum_{j=1}^{k} X_{ij} = \frac{C_i}{k}$ mean yield of the i^{th} sugarcane

$\bar{X}_{..}$=overall mean =$\frac{1}{hk}\sum_{i=1}^{k}\sum_{j=1}^{h} X_{ij} = \frac{G}{hk}$

=$\frac{1}{h}\sum_{i=1}^{k} \bar{X}_{i.}$

=$\frac{1}{k}\sum_{j=1}^{h} \bar{X}_{.j}$

3.4.4 Mathematical model and underlying assumptions

Since we had only one observation per cell the mathematical model for the means is

$$X_{ij} = \mu_{ij} + \varepsilon_{ij}; i = 1, 2....k; j = 1, 2....h \tag{3.15}$$

Where X_{ij} is the yield from sugarcane of th variety and the random variables having normal distribution with means μ_{ij} and common but unknown variance σ^2 i.e. N (μ_{ij},σ^2) The various effects are assumed additive and becomes

;

(a) The general mean effect $\mu = \sum_{i=1}^{k}\sum_{j=1}^{h} \frac{\mu_{ij}}{n}$
where $n = hk$

(b) The effect α_i due to the i^{th} plot is given by $\alpha_i = \mu_i - \mu$ assume
$\sum_{i=1}^{k} \alpha_i = 0$

(c) The effect β_j due to j^{th} cane variety is given by $\beta_j = \mu_j - \mu$, assume
$\sum_{j=1}^{h} \beta_j = 0$

(d) Interaction effect $(\alpha\beta)_{ij}$ when the i^{th} plot and j^{th} variety of cane occurs simultaneously is given by:

$$(\alpha\beta)_{ij} = \mu_{ij} - \mu_i - \mu_j + \mu \tag{3.16}$$

taking into account one observation per cell the assumptions that

$$\sum_{j=1}^{h} \beta_j = 0, \sum_{i=1}^{k} \alpha_i = 0 \tag{3.17}$$

and

$$\sum_{i=1}^{k}\sum_{j=1}^{h} \varepsilon_{ij} = 0 \tag{3.18}$$

Therefore the mathematical model for the effects used in this study is

$X_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}$

3.4.5 Statistical analysis of the model

The least square estimates of the model are given as:

$$\hat{\mu} = \frac{1}{n}\sum_{i=1}^{k}\sum_{j=1}^{h} X_{ij} = \bar{X}_{..} \tag{3.19}$$

Where $n = hk$,

$$\hat{\alpha}_i = \bar{X}_{i.} - \bar{X}_{..}, \tag{3.20}$$

$$\hat{\beta}_j = \bar{X}_{.j} - \bar{X}_{..}, \tag{3.21}$$

Substituting these in the model we have

$$X_{ij} = \bar{X}_{..} + (\bar{X}_{i.} - \bar{X}_{..}) + (\bar{X}_{.j} - \bar{X}_{..}) + \varepsilon_{ij} \tag{3.22}$$

$$X_{ij} - \bar{X}_{..} = (\bar{X}_{i.} - \bar{X}_{..}) + (\bar{X}_{.j} - \bar{X}_{..}) + (\bar{X}_{ij} - \bar{X}_{i.} + \bar{X}_{.j} - \bar{X}_{..}) \tag{3.23}$$

The mean sum of squares;

MSS due to treatment=$\frac{s_t^2}{k-1}$

MSS due to variation=$\frac{S_v^2}{h-1}$

MSS due to error term=$\frac{s_e^2}{(h-1)(k-1)}$

The least statistic under the null hypothesis

$H_o : \mu_{1.} = \mu_{2.} = ... = \mu_{k.}$

or otherwise

F_t=$\frac{S_t^2}{S_e^2}$ d.f (k-1) and (h-1)(k-1)

F_v=$\frac{S_v^2}{S_e^2}$ d.f (h-1) and (h-1)(k-1)

The ANOVA table then becomes

Table 3.3: ANOVA Table for ABD

Source of variation	SS	df	MSS	F-Ratio
Treatment	$V_R = h\sum(\bar{X}_{i.} - \bar{X}_{..})^2$	$k-1$	$\hat{S}_t^2 = \frac{S_t^2}{k-1}$	$F_t = \frac{S_t^2}{S_e^2}$
Variation	$V_C = k\sum(\bar{X}_{.j} - \bar{X}_{..})^2$	h-1	$\hat{S}_v^2 = \frac{S_v^2}{h-1}$	$F_v = \frac{S_v^2}{S_e^2}$
Residual(error)	$V_E = V - V_R - V_C$	(h-1)(k-1)	$\hat{S}_e^2 = \frac{S_e^2}{(h-1)(k-1)}$	
Total	$V = \sum\sum(X_{ij} - \bar{X}_{..})^2$	hk-1		

We therefore use the rejection region method to test significance of the observed values of test statistics F_t and F_v.

3.5 Randomized Complete Block Design

This is the simplest type of layout in which treatment are allotted to the experimental unit at random. The design in this study has considered one observation per treatment in each block, the order in which treatments run in each block is done randomly. The model we assumed in this study for RCBD is of the form;

$$X_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij} \tag{3.24}$$

with estimates

$$labeleqn25\hat{\mu} = \bar{X}_{..}\hat{\alpha}_i = \bar{X}_{i.} - \bar{X}_{..}\hat{\beta}_j = \bar{X}_{.j} - \bar{X}_{..} \tag{3.25}$$

These estimates of

μ, $alpha_i$, and β_j help in minimizing error.

Since the study considers treatments and block effects as deviations from the overall mean so that $\sum_{i=1}^{k} \alpha_i = 0$ and $\sum_{j=1}^{h} \beta_j = 0$

The means for the model then appears as below Table 3.4

Table 3.4: The means for the model

	Blocks					
Treatment	1	2	3	....	b	Means
1	μ_{11}	μ_{12}	μ_{13}	...	μ_{1b}	$\bar{X}_{1.}$
2	μ_{21}	μ_{22}	μ_{23}	...	μ_{2b}	$\bar{X}_{2.}$
.	.	.	.	.	.	.
.	.	.	.	.	.	.
.	.	.	.	.	.	.
t	μ_{t1}	μ_{t2}	μ_{t3}	...	μ_{tb}	$\bar{X}_{t.}$
Mean	$\bar{X}_{.1}$	$\bar{X}_{.2}$	$\bar{X}_{.3}$	...	$\bar{X}_{.b}$	$\bar{X}_{..}$

Treatment effects are relative such that the null hypothesis

H_o^T: No treatment effects: $t_1 = t_2 = ...t_b = 0$

or otherwise

H_o^B: No blocks effects: $b_1 = b_2 = ...b_b = 0$

or otherwise

(usually not of interest but assessed to determine if blocking was successful in reducing the variability in the experimental units)

Table 3.5: The ANOVA Table for RCBD

Source of variation	SS	df	MSS	F-Ration
Treatment	SST	v-1	$S_1=\frac{SST}{v-1}$	$\frac{S_1}{S_3}$
Due to blocks	SSB	(b-1)	$S_2=\frac{SSB}{b-1}$	$\frac{S_2}{S_3}$
Due to Error	SSE	(v-1)(b-1)	$S_2=\frac{SSE}{(v-1)(b-1)}=S_3$	
Total	TSS	(bv-1)		

3.6 Augmented Block Design (A.B.D)

ABD is any experimental design in standard treatment to which additional (new) treatment have been added. Augmented block design were introduced by Federer in 1956[11] as an alternative to the systematically arranged checks and new treatments. ABDs provides several advantages in screening new treatments such as Genotypes, Insecticides and Drugs. We consider an experimental design where w tests treatment are to be compared with u control treatment using n experimental units arranged in r blocks such that j^{th} block is of size k_j >u, for augmented block design each of the control treatment is replicated b times and occurs once in every block, while test treatment occurs only once in one block. The analysis of variance generated from ABD with $v = u + w$ treatments comprising of w tests and u controls arranged in b blocks having k_1 plots in block 1, k_2 plots in block 2,....up to k_b plots in block b such that $k_1 + k_2 + ... + k_b = n$ will appear as in the table 3.6.

Table 3.6: The ANOVA Table for Augmented Block Design with $v = u + w$

Source of variation	SS	df	MSS	F-Ratio
Blocks eliminating treatment	b-1	ASSB	$MSSB = S_1$	$\frac{S_1}{S_4}$
Treatment eliminating blocks	v-1	ASST		
Among tests	w-1	SST	$MSST = S_2$	$\frac{S_2}{S_4}$
Among control	u-1	SSC	$MSSC = S_3$	$\frac{S_3}{S_4}$
Error	n-v-b+1	SSE	$MSE = S_4$	
Total	n-1	TSS		

Chapter 4

DATA ANALYSIS, PRESENTATION AND DISCUSSION

4.1 Augmented Block Design

In an augmented block design,the blocks are enlarged to accommodate the new treatments. Augmented block design were introduced by Federer[11] as an alternative to the systematically arranged check and new treatments. ABD's have several advantages over the systematic arrangements. They are very useful for screening new treatments such as genotype, insecticides, herbicides, drugs etc. We consider an experimental situation where w test treatments are to be compared with u control treatments using n experimental units arranged in r blocks such that j^{th} block is of size k_j >u. For an augmented randomized complete block design, each of the control treatments is replicated b times and occurs once in one of the blocks. Therefore, it can easily be seen that in the j^{th} block there are $k_j - u = n_j$ test treatments. The randomization procedure is given as follows;

1. Randomly allot u controls to u of the k_j blocks experimental units in each block

2. Randomly allot the w test treatments to the remaining experimental units

3. If a new treatment appears more than once, assign the different entries of the treatment at random with the provision that no treatment appears more than once in a complete block until that treatment occurs once in each of complete blocks.

An Augmented Block Design (ABD) with Parameters;$v = 7, w = 5, u = 2$ and $b = 3$ was generated using IASRI design resource server. The two control treatments were laid in a block design with three replications. In each block,the treatments were augmented with inclusion of two test treatments randomly allotted to block 1 and 2 and one test treatment in block 3. This was done in conformity to the optimum replication number r of each of the two check varieties in every block design that is given by;

$$r = \frac{\sqrt{(u+b-1)}\sqrt{w}}{ub}, for w > u+b-1 \tag{4.1}$$

and when there u=1, the formula reduces to

$$r = \frac{\sqrt{w}}{b} \tag{4.2}$$

where u=controls

b=the number of blocks

w= number of test varieties

Table 4.1: The Output Generated by IASRI Design Resources Server with three control Replications

Block 1	Block 2	Block 3
Treatment 2	Treatment 1	N39
N39	N39	CO945
Treatment 5	Treatment 3	CO945
CO945	CO945	N39
CO945	N39	N39
N39	CO945	Treatment4
N39	CO945	CO945
CO945	N39	

Table 4.2: Augmented Block Design in different plots without replications

Plot 1 CO945	Plot 8 Treatment 4	Plot 9 N39
Plot 2 treatment2	Plot 7 CO945	Plot 10 CO945
Plot 3 treatment3	Plot 6 treatment5	Plot 11 treatment1
Plot 4 N39	Plot 5 N39	

4.2 Randomized Complete Block Design Layout

A randomized complete block design with parameters $v = 5, b = 3$ and $k = 4$ was generated using IASRI design resource server. The generated design was reinforced by adding two control varieties (i.e. N39 and CO945) in each of the five blocks. Two blocks with all the 7 treatments were also added to the design for ease of analysis. The treatments were randomized in each block creating a completely randomized block design as shown in the table 4.3 below;

Table 4.3: Randomized Complete Block Designs

Blocks				
1	2	3	4	5
plot 1 treatment 5	plot 12 CO945	plot 13 treatment 4	plot 24 treatment 1	plot 25 N39
plot 2 treatment 2	plot 11 treatment 4	plot 14 N39	plot 23 treatment 3	plot 26 treatment 2
plot 3 treatment 3	plot 10 treatment 2	plot 15 CO945	plot 22 treatment 4	plot 27 treatment 4
plot 4 CO945	plot 9 N39	plot 16 treatment 3	plot 21 N39	plot 28 treatment 1
plot 5 treatment 1	plot 8 treatment 5	plot 17 treatment 1	plot 20 treatment 5	plot 29 CO945
plot 6 N39	plot 7 treatment 3	plot 18 treatment 2	plot 19 CO945	plot 30 treatment 5

Table 4.4: Frequencies table of different treatments in the blocks of RCBD

Block	Treatment1	Treatment2	Treatment3	Treatment4	Treatment5	N39	CO945	Block Size
1	1	1	1	0	1	1	1	6
2	0	1	1	1	1	1	1	6
3	1	1	1	1	0	1	1	6
4	1	0	1	1	1	1	1	6
5	1	1	0	1	1	1	1	6
Replication	4	4	4	4	4	5	5	

4.3 Data Simulation

Data was simulated using Monte Carlo simulation as described in Chapter 3. Each of the treatment had unique properties as shown in Table 4.4 and figures 4.1 to figure 4.7. Treatment 1 had the largest dispersion due to large variance while CO945 had the least dispersion due to small variance.This confirms the Fishman G.S [7] Monte carlo concepts about properties of treatments" treatments have unique properties when simulated".

Table 4.5: Properties of the simulated data by Monte Carlo Method

	Treatment1	Treatment2	Treatment3	Treatment4	Treatment5	N39	CO945
N Valid	100	100	100	100	100	100	100
Mean	81.1595	59.8622	49.6476	100.1882	29.8397	61.9054	59.9619
Std. Dev	9.87291	4.37486	3.92000	4.15725	2.08491	2.10284	1.43678
Variance	97.474	19.139	15.366	17.283	4.347	4.422	2.064

Figure 4.1: treatment1 properties

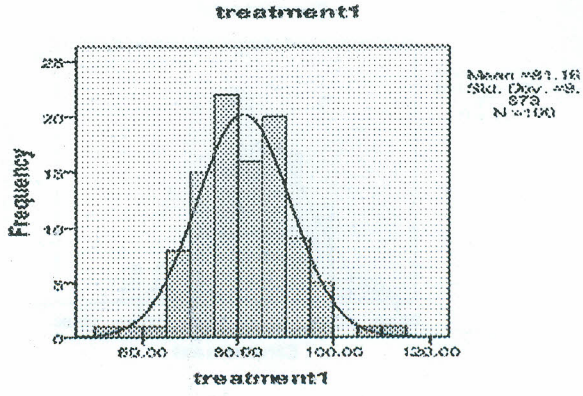


Figure 4.2: treatment2 properties

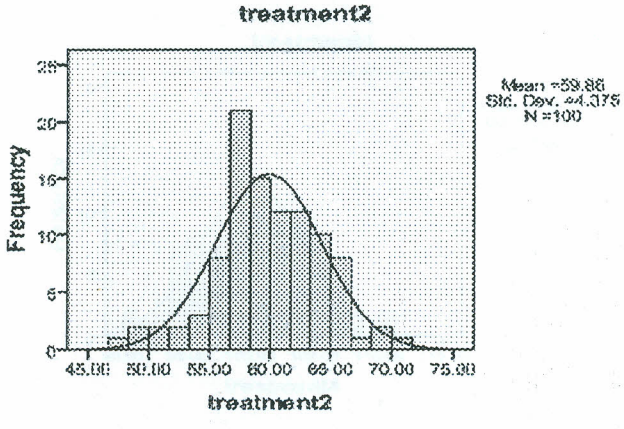


Figure 4.3: treatment 3 properties

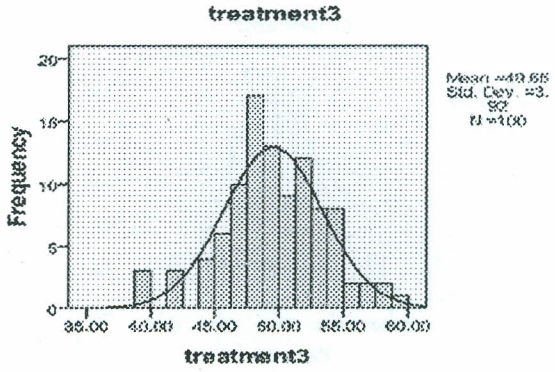


Figure 4.4: treatment4 properties

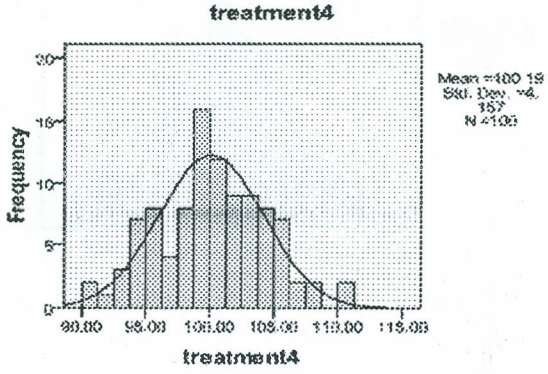


Figure 4.5: treatment5 properties

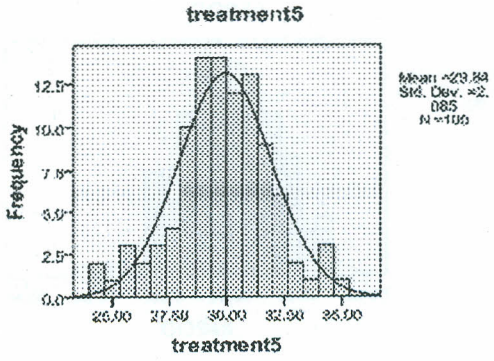


Figure 4.6: N39 properties

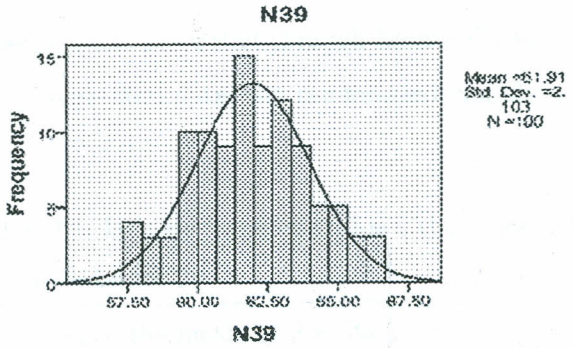
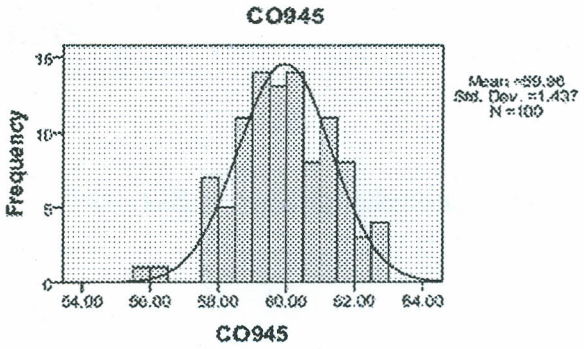


Figure 4.7: CO945 properties



The data generated was inserted in the design and adjusted for block effects. For ease of computation, block effects were assumed to be uniformly distributed in the range [-5, 5]. The block effects were again generated through Monte Carlo simulation as described in Chapter 3. From the generated data, the randomized complete Block design had the following block effects;

Table 4.6: The blocks were assumed to have the following properties

Block	Radom No	Block Effect
1	3	Enhance the mean by 3 units
2	-3	Depress the mean by 3 units
3	1	Enhance the mean by 1 unit

From the experiment above, it was observed that the results of the ABDs are dependent on the error term. Therefore,to explore different scenarios, we added three different random error terms to the simulated data, viz;

A: $\varepsilon_{ij} = N(0,1)$

B: $\varepsilon_{ij} = N(0,5)$

c: $\varepsilon_{ij} = N(0,25)$

Data was analyzed for each level of the error term

```
ONEWAY simulatedyield, blockeffect, yieldwithblkeffect, plotyield, BY errorterm
/STATISTICS EFFECTS
/MISSING ANALYSIS.
.
ONEWAY simulatedyield, blockeffect, yieldwithblkeffect, plotyield BY errorterm
/STATISTICS EFFECTS
/MISSING ANALYSIS.
ONEWAY simulatedyield blockeffect yieldwithblkeffect plotyield BY errorterm
/STATISTICS EFFECTS
/MISSING ANALYSIS.
```

4.4 Results

4.4.1 Scenario One: ε_{ij}= N(0, 1)

Table 4.7: ANOVA Table for Augmented Block Design when N (0, 1)

Source of variation	Type III SS	df	MSS	F-Ratio	Sig.
Blocks	33.84	2	16.92	46.96	0.0209
Treatments	2889.52	6	481.59	1336.44	0.0007
Among Tests	2681.47	4	670.37	1860.32	0.0005
Among Controls	3.11	1	3.11	8.63	0.9900
Tests vs Controls	52.75	1	52.75	156.37	0.0068
Error	0.7207	2	0.3604		
Corrected Total	2924.09	10			

From Table 4.7 above, it can be seen that difference among the test treatments is significant (p- value 0.0005) but difference among controls is not. This was expected and we can conclude that ABD is able to bring out the difference in treatments.

Table 4.8: The Least square mean yield for ABD Yield when ε_{ij} = N (0, 1)

Treatments	Least Mean Yield	Standard Error	Pr> $\|t\|$
Treatments1	80.32	0.69316	>0.0001
Treatments2	62.77	0.69316	0.0001
Treatments3	51.82	0.69316	0.0002
Treatments4	99.77	0.69316	>0.0001
Treatments5	30.37	0.69316	0.0005
N39	61.25	0.34658	>0.0001
CO945	59.81	0.34658	>0.0001

The same treatments and data scheme when applied to a randomized complete block design with three replicates gives the following results;

Table 4.9: ANOVA Table for Randomized complete Block Design when ε_{ij} =N (0, 1)

Source of variation	SS	df	MSS	F-Ratio	Sig.
Treatments	9086.94	6	1514.49	1019.63	<0.0001
Blocks	163.71	2	81.85	55.11	<0.0001
Error	17.82	12	1.49		
Total	9268.47	20			

Table 4.10: Least square Mean Yield for RCBD Yield when ε_{ij} = N (0, 1)

Treatments	Least Mean Yield	Standard Error	Pr> $\|t\|$
Treatments1	81.59	0.70364	>0.0001
Treatments2	60.3	0.70364	>0.0001
Treatments3	49.7	0.70364	>0.0001
Treatments4	100.59	0.70364	>0.0001
Treatments5	30.2	0.70364	>0.0001
N39	61.52	0.70364	>0.0001
CO945	59.94	0.70364	>0.0001

For RCBD the p-values for treatments and the blocks are highly significant (p<.0001, Table 4.10)

4.4.2 Scenario two $\varepsilon = N(0, 5)$

When the error term is distributed as N(0,5)

Table 4.11: ANOVA Table for Augmented Block Design when ε_{ij} =N (0, 5)

Source of variation	Type III SS	df	MSS	F-Ratio	Sig.
Blocks	33.23	2	16.61	6.59	0.1318
Treatments	2883.43	6	151	190.62	0.0052
among tests	2679.53	4	669.88	265.72	0.0038
among controls	8.28	1	8.28	3.29	0.2116
Test vs Control	8.83	1	8.83	3.50	.2021
Error	5.04	2	2.52		
Corrected Total	2921.70	10			

Table 4.12: The Least square mean Yield for Augmented Block Design Yield when ε_{ij} = N (0, 5)

Treatments	Least Mean Yield	Standard Error	Pr> $\|t\|$
Treatments1	80.71	1.83341	0.0005
Treatments2	59.56	1.83341	0.0009
Treatments3	49.74	1.83341	0.0014
Treatments4	97.63	1.83341	0.0004
Treatments5	28.96	1.83341	0.0040
N39	62.66	0.91671	0.0002
CO945	60.31	0.91671	0.0002

When the variance of the error term increases to 5, the p-values increase considerably for both among the test treatments and test vs. Control treatments (Table 4.11). The structure of Duncan's multiple range tests remains unchanged though the treatment means are different from Scenario One especially among test families. The control treatments are stable. This can be attributed to lack of replication in the test treatments and thus errors are not averaged out. The same treatments and data scheme above was used in a RCBD with Three replicates on and the following results were observed;

Table 4.13: ANOVA Table for Randomized complete Block Design when ε_{ij} =N (0, 5)

Source of variation	Type III SS	df	MSS	F-Ratio	Sig.
Treatments	8793.05	6	1465.51	334.94	<0.0001
Blocks	174.12	2	87.06	19.90	<0.0002
Error	52.50	12	4.37		
Total	9019.67	20			

In the RCBD the difference between treatments remains highly significant, but as shown in the table 4.14 below the standard error increases to 1.21

Table 4.14: The Least square mean Yield for RCBD Yield when ε_{ij} = N (0, 5)

Treatments	Least Mean Yield	Standard Error	Pr> $\|t\|$
Treatments1	80.45	1.20767	>0.0001
Treatments2	62.60	1.20767	>0.0001
Treatments3	50.72	1.20767	>0.0001
Treatments4	100.66	1.20767	>0.0001
Treatments5	30.56	1.20767	>0.0001
N39	61.68	1.20767	>0.0001
CO945	60.17	1.20767	>0.0001

It can be noted that the results are very similar to scenario One RCBD results. This is because even though the errors have different variances when averaged, they give nearly the same figures in the region of zero.

4.4.3 Scenario Three: ε_{ij} = N (0, 25)

When the error term is distributed as N (0, 25)

Table 4.15: ANOVA Table for Augmented Block Design when ε_{ij} =N (0, 25)

Source of variation	Type III SS	df	MSS	F-value	Pr> $\|F\|$
Blocks	56.61	2	28.30	0.89	0.5285
Treatments	3315.80	6	552.63	17.42	0.0553
among tests	3113.29	4	778.32	24.53	0.0396
among controls	37.35	1	37.35	1.18	0.3913
test vs controls	14.71	1	14.71	0.46	0.5662
Error	63.45	2	31.73		
Total	3435.87	10			

In the scenario above, the augmented block design is unable to bring out the difference among the test vs. control treatments. The significance of the difference among the test treatments drop significantly to 0.0396

Table 4.16: The Least square mean yield for Augmented Block Design yield ε_{ij} = N (0, 25)

Treatments	Least Mean Yield	Standard Error	Pr> $\|t\|$
Treatments1	80.45	6.50407	0.0065
Treatments2	62.46	6.50407	0.0107
Treatments3	51.46	6.50407	0.0156
Treatments4	100.81	6.50407	0.0041
Treatments5	25.63	6.50407	0.0588
N39	64.29	3.25203	0.0025
CO945	59.30	3.25203	0.0030

On using the same treatments and data scheme as used in Scenario Three of the Augmented Block design and applied to the randomized Complete Block design with three blocks, the following results are obtained:

Table 4.17: ANOVA Table for Randomized complete Block Design when ε_{ij} =N (0, 25)

Source of variation	SS	df	MSS	F-Statistics	Sig.
Treatments	7986.96	6	1331.16	59.93	0.0008
Blocks	600.30	2	300.15	13.51	<0.0001
Error	266.55	12	22.21		
Total	8853.80	20			

Table 4.18: The Least square mean Yield for RCBD Yield when ε_{ij} = N (0, 25)

Treatments	Least Mean Yield	Standard Error	Pr> |t|
Treatments1	83.22	2.72104	>0.0001
Treatments2	62.02	2.72104	>0.0001
Treatments3	52.14	2.72104	>0.0001
Treatments4	100.42	2.72104	>0.0001
Treatments5	35.39	2.72104	>0.0001
N39	64.14	2.72104	>0.0001
CO945	59.99	2.72104	>0.0001

For the RCBD, Table 4.18 shows that the p-value for significance in treatments increases with increase in variance of the error term. The Least Square means results show that the RCBD is still robust in bringing out the difference among the treatments.

4.4.4 Relative Efficiency

To compare the efficiencies of the two designs, Fishers approach was used by calculating the amount of information which the estimated difference between two treatments means supplies about the true difference. Thus the relative efficiency of the ABD and RCBD design is projected as;

$$\frac{(n_1+1)(n_2+3)s_2^2}{(n_2+1)(n_1+3)s_1^2} \tag{4.3}$$

Where

n_1 is the ABD error degree of freedom

n_2 is the RCBD error degree of freedom

s_1 is error mean square for ABD

s_2 is error mean square for RCBD

The required parameters are found in the ANOVA tables presented above. Upon calcu-

lating the relative efficiency for the three different scenarios, we established that ABD has comparatively smaller efficiency as opposed to RCBD (Table 4.19

Table 4.19: Relative Efficiency of ABD against RCBD

SCINERION	DESIGN	ERROR df	ERROR MSS	Efficiency OF ABD vs RCBD
N(0,1)	ABD	2	0.36	11.86
	RCBD	12	1.49	
N(0,5)	ABD	2	2.52	2.08
	RCBD	12	4.37	
N(0,25)	ABD	2	13.73	1.81
	RCBD	12	22.21	

From Table 4.19 above, it is evident that the relative efficiency of ABD against RCBD is dependent on the variance of the error term. ABD designs are relatively efficient than RCBD for standard normal error but this efficiency depreciates rapidly as the variance of the error term increases. As evident, the error variance from 5 to 25 registers efficiency drop of only 0.27 points. We would expect the efficiency of ABD to be the same as the efficiency of RCBD as error term $(\varepsilon_i j)$ tends to infinity. As such it would be recommendable to use augmented block design even when variance of experimental error is unknown as is the case with agricultural experiments.

Table 4.20: Comparison of ABD and RCBD means and paired t-test result

$\varepsilon_{ij} = N(0,1)$		$\varepsilon_{ij} = N(0,5)$		ε_{ij}=N(0,25)	
ABD	RCBD	ABD	RCBD	ABD	RCBD
80.32	81.59	80.71	80.45	80.45	83.22
62.77	60.30	59.56	62.60	62.46	62.02
51.82	49.70	49.74	50.72	51.46	52.14
99.77	100.59	97.63	100.66	100.81	100.42
30.37	30.20	28.96	30.56	25.63	35.39
59.81	59.94	60.31	60.17	59.30	59.99
62.25	61.52	62.66	61.68	64.29	64.14
T-Test:p=0.41		T-Test:p=0.14		T-Test:p=0.23	

From Table 4.16 above, it is palatable that there is a trivial difference between means generated by augmented block design and those generated by randomized complete block design. We can conclude without fear of disapproval that augmented block design and randomized block design are equally effective at some point.

Chapter 5

DISCUSSION AND CONCLUSION

5.1 ABD and RCBD

The two block designs are similar in the sense that in Randomized block design the control treatments are added to the design containing the test treatments whereas in the Augmented block design the test treatments are added to a design containing the control treatments. The outcomes produced by the two methods were insignificantly different as can be seen in the Table 4.17.

Table 5.1: Comparison of treatment means generated by both ABD and RCBD

		Augmented Block Design Scenario		
Treatments	RCBD	ABD N(0,1)	ABD N(0,5)	ABD N(0,25)
Treatments1	86.22	80.32	80.71	80.45
Treatments2	57.34	62.77	59.56	62.46
Treatments3	49.32	51.82	49.74	51.46
Treatments4	98.03	99.77	97.63	100.81
Treatments5	31.17	30.37	28.96	25.63
N39	59.56	61.25	62.66	64.29
CO945	60.68	59.81	60.31	59.30

The paired t-test generated the following results;

Table 5.2: RCBD - ABD N(0,1)

	Paired Differences							
				95% C.I of the Difference				
	Mean	Std.Deviation	Std.Error Mean	Lower	Upper	t	df	Sig(2-tailed)
RCBD - ABD N(0,1)	-.54143	3.55372	1.34318	-3.82807	2.74521	-.403	6	.701

Table 5.3: RCBD ABD N(0,5

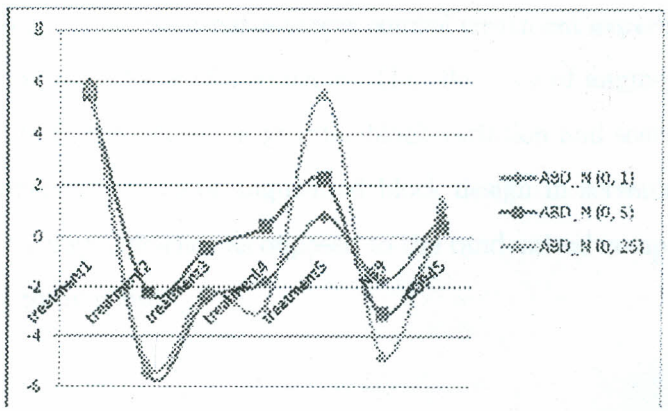
	Paired Differences							
				95% C.I of the Difference				
	Mean	Std.Deviation	Std.Error Mean	Lower	Upper	t	df	Sig(2-tailed)
RCBD - ABD N(0,5)	.39286	2.86285	1.08206	-2.25484	3.04055	.363	6	.729

Table 5.4: RCBD ABD N(0,25

	Paired Differences							
				95% C.I of the Difference				
	Mean	Std.Deviation	Std.Error Mean	Lower	Upper	t	df	Sig(2-tailed)
RCBD - ABD N(0,25)	-.29714	4.58560	1.73319	-4.53811	3.94383	-.171	6	.870

From the results above the two blocks designs can be interchangeably used.

Figure 5.1: Deviation of various ABD from RCBD



From figure 5.1above, it is clear that deviations were equally likely to occur in both

positive and negative. RCBD design produced higher figures for treatment1 though it is still within the treatment standard deviation.

5.2 Conclusion and Reccommendation

In agricultural experiments, setting a block will always have some degree of intra block variation. The major factors affecting the variation are the number of plots per block. The more the number of plots or experimental units in a block, the higher the degree of intra blocks variations and vice-versa. A randomized complete block design is discouraged by this study when evaluating large number of treatments instead augmented block designs are encouraged due to the capability of having few plots per block. The study has revealed that in any randomized complete block designs the number of plots in every block is dictated by the number of treatments being evaluated. In conclusion, the study has revealed that augmented block designs are more efficient than randomized complete block design for a finite error variance. In most cases under agricultural experiments, error variances are assumes to be finite as it has been shown in the study.

Finally, we say that augmented block designs are more efficient than randomized complete block design in test treatments versus control treatment experiments hence more valuable in screening new stains of sugarcane. The efficiency of augmented block design when it is tailored to fit strongly in large inter block variation and scarce test treatment. This study recommends the use of augmented block design in screening new strains of sugarcane due to it's high efficiency as opposed to the randomized complete block designs which only appear to be simple.

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