UNIVERSITY FOR DEVELOPMENT STUDIES

YIELD EVALUATION OF FIFTEEN RICE (*Oryza Sativa. L)* GENOTYPES UNDER RAINFED AND IRRIGATED CONDITIONS IN NORTHERN GHANA.

The Savelugu and Navrongo Hubs, a case study.

ADOGOBA DESMOND SUNDAY

Thesis Submitted to the Department of Statistics, Faculty of Mathematical Sciences, University for Development Studies in Partial Fulfillment of the Requirements for the Award of Master of Science Degree in Biometry

2015

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BY

ADOGOBA DESMOND SUNDAY (BSc. Mathematical Science, Statistics option)

(UDS/MBM/0016/13)

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July, 2015

DECLARATION

I hereby declare that this thesis is the result of my original work and that no part of it has been presented for another degree in this university or elsewhere. Related works by others which served as a source of knowledge has been duly referenced.

Adogoba Desmond Sunday	....	21/11/2015
(Candidate)	Signature	Date

I hereby declare that the preparation and presentation of the thesis was supervised in accordance with the guidelines on supervision of thesis laid down by the University for Development Studies

Dr. Albert Luguterah	....	21/11/2015
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ABSTRACT

This study was undertaken to examine the nature and quantify the magnitude of Genotype by Environment interaction effects on rice (*Oryza Sativa* L.) grain yield and to determine the most stable and winning genotype (s) in terms of yield stability and performance in two rice producing hubs. The study was conducted at four locations within two rice producing hubs in Northern Ghana on fifteen (15) rice genotypes including a checking genotype GR18 red. A randomized complete block design with three replications was employed. A multi environment trial analysis depicted differential performance of rice genotypes at the different test environments. The yield stability and adaptability measure using the AMMI Stability value (ASV), Yield Stability Index (YSI), Rank sum (RS) and GGE biplots showed the genotypes *Perfume (short), GH1837*, *Good and new (JP)* and IR72(Ph) to be high yielding and stable in terms of yield performance across all four environments respectively. Panicle length possessed both positive association and high positive direct effects, indicating selection of this agronomic trait could bring about improvements in yield and yield components. The study revealed that the mean technical efficiency of rice farmers across the two hubs is 55.2% (7.8% - 95.1%). It was observed from the study that yield was significantly predicted by water PH, proportion of nitrogen, organic matter, clay and silt in the soil and the relative humidity in the atmosphere. The genotypes *GH1837, Perfume (short)* and IR72(Ph) were found to the high yielding and stable in both rainfed and irrigated conditions across all four mega environments.

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DEDICATION

I dedicate this work to my lovely wife and daughter, Atogboba Matilda and Adogoba Nesta Yinenongma.

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LIST OF ACRONYMS

AMMI	Additive Main effects and Multiplication Interaction
ANOVA	Analysis of variance
ASV	AMMI Stability Value
BLUEs	Best Linear Unbiased Estimators
BLUPs	Best Linear Unbiased Predictors
CSIR-SARI	Council for Scientific and Industrial Research – Savanna Agricultural Research Institute
CSIR-PGRI	Council for Scientific and Industrial Research – Plant Genetics and Resource Institute
CV	Coefficient of Variation
DALs	Disomic Addition Lines
DEA	Data Envelopment Analysis
FAOSTAT	Food and Agriculture Organization of the United Nation Statistics Division
FBO	Farmer Based Organization
GBN	Ghana Business News
GCV	Genotypic Coefficient of Variation

GEI	Genotype by Environment Interaction
GGE	Genotype main effects and Genotype by Environment interaction
GH¢	Ghana cedis
GLM	Generalized Linear Models
GNA	Ghana News Agency
GxE	Genotype by Environment
ha	Hectare
IRRI	International Rice Research Institute
IPCA1	Interactive Principal Component Analysis 1
IPCA2	Interactive Principal Component Analysis 2
MANOVA	Multivariate analysis of variance
MET	Multi Environment Trial
MEYT	Multi Environment Yield Trial
MiDA	Millennium Development Agency
MLE	Maximum Likelihood Estimator
MoFA	Ministry of Food and Agriculture

NDVI	Normalized Difference Vegetation Index
PCA	Principal Component Analysis
PCA1	Principal Component Analysis 1
PCA2	Principal Component Analysis 2
PCV	Phenotypic Coefficient of Variation
QTL	Quantitative Trait Locus
REML	Reduced Maximum Likelihood
RS	Rank Sum
SED	Standard Error of Difference
SREG	Site Regression
SVD	Singular Value Decomposition
t/ha	Tonnes per Hectare
TE	Technical Efficiency
UDS	University for Development Studies
US	United States
VxE	Variety by Environment
YSI	Yield Stability Index

CHAPTER ONE

INTRODUCTION

1.1 Background

Rice (*Oryza Sativa* L) is one of the most important staple foods for more than half of the world's population (IRRI, 2006). It has a great influence on the livelihoods and economies of several billion people. It was reported in 2010 that approximately 154 million hectares were harvested worldwide (FAOSTAT, 2012).

The greatest levels of productivity of rice is found for irrigated rice, which is the most intensified production system, where more than one crop is grown per year and yields are high, ranging from 12.5 tonnes per hectare per year compared with 2.5 tonnes per hectare per year for rainfed rice.

The average yield of rice in Ghana is estimated to be 2.5 tonnes per hectare (MOFA, 2011), while the achievable yield based on on-farm trials is 6 to 8 tonnes per hectare. Studies carried out by Ragasa *et al.* (2013) reveals that low adoption of inputs and improved technologies is often cited as the major reason for this gap in rice production.

In order to overcome the problem of low productivity, a major strategy is to replace the existing low yielding rice varieties with newer high yielding varieties, taking into consideration the preference of taste and market requirements.

The cultivation of improved rice varieties is mainly through rainfed lowland production. Traditional low yielding varieties are still being grown, but are slowly being replaced. Despite their low yielding tendencies, they are well adapted to their local growing environments and have accepted grain quality.

Most crop improvement of upland rice in West Africa has focused more on the introduction of high yielding, input-responsive lowland varieties of Asian rice (*Oryza Sativa*). However, these improved varieties according to Craufurd *et al.* (2000) do not perform well under the low-input conditions typical of upland farms, having poor tolerance to weeds, drought and indigenous disease and pests. African rice (*Oryza glaberrima*), which are well adapted to low input and shifting cultivation system, are consequently still preferred by many farmers and are grown on between 25 and 40% of the upland area.

The current system of rice production rely more on ample water supply and thus are more vulnerable to drought stress. This according to Bouman *et al.* (2005) forms the most important limiting factor for rice production and is increasingly becoming a severe problem.

The growth of agriculture depends largely on yield increasing technological change (Datt and Ravallion, 1996; Hossain, 1989). The adaptation of new agricultural technology such as high yielding varieties according to a World Bank report 2008, could lead to an increase in agricultural productivity in Africa and simulate the transition of low productivity subsistence agriculture to high productivity agro-industrial economy.

1.2 Problem Statement

According to a report by the Millennium Development Authority (MiDA, 2010), between 2010 and 2015, rice demand is expected to grow at a compound annual growth of 11.8 percent. It is also widely acknowledged that in recent times, the Government of Ghana import over 50% of local rice production to cater for the increasing demand levels.

The estimated national rice consumption according to a report by MoFA (2007), stands at 561,400 metric tons per year, whilst rice produced locally is 107,900 metric tons per year leaving a gap of 453,500 metric tons per year, which has to be imported (Public Agenda. 2nd March, 2009). With a population growth rate of 2.5% and an annual rice demand growth rate of 8.9%, a supply of 1.6 million tons of rice will be needed annually in Ghana by 2015. The situation is therefore alarming as the dependency on imports will increase.

As reported by the Ghana News Agency-Joy online (October 30, 2012), it is estimated that Ghana spends more than $450 million annually on rice importation to augment local demand and is expected to import 600,000 metric tons of rice between October 2014 and September 2015 to augment the country's rice needs (GBN, January 14, 2015).

1.3 Research Questions

In order to achieve the objectives of the study, the following research questions are asked;

i. Which rice genotype (s) is best suited to these two hubs?

ii. What characters of rice traits has a direct and indirect effect on yield of rice across the two hubs?

iii. What is the technical efficiency of rice farmers in these two hubs?

iv. What are the contributions of climatic and edaphic variables to the yield of rice across the two hubs?

1.4 Objectives of the Study

1.4.1 General Objective

The main objective of the study is to develop the best predictive model to predict yield of rice in Northern Ghana

1.4.2 Specific Objectives

i. Compare the yield potential of fifteen rice genotypes under rainfed and irrigated conditions.

ii. Determine the optimum environments across the two hubs that are best suited for these rice genotypes.

iii. Determine the Technical Efficiency of rice farmers across the two hubs.

1.5 Justification of the Study

Rice production in Africa has tended to be low-yielding, geographically dispersed, and uncompetitive against low-cost Asian imports, even when protected by high freight costs and substantial trade barriers (Jenny *et al.,* 2011).

Identification of the underlying causes of yield losses in farmers' field can be attributed to some factors that affect crop growth and yield. These factors include stresses that are biotic in nature and others that are mainly abiotic in nature. Factors that relate mainly to management, soil properties as well as their interactions are crucial in managing yield gap.

In bridging the gap in rice production by introducing farmers to improve and high yielding varieties, there will be a whole lot of direct and indirect benefits to producers, consumers, and the country at large. This will result in an increase in farmers yield, thus an increase in their income. Identification of the high yielding and stable improved rice genotypes will be a step taken to solve food insecurity problems, alleviate poverty and improve socio-economic conditions of small holder farmers.

Bridging the yield gap that is accounted for by farmers using traditional rice varieties of low yielding qualities will also ensure more food is available to meet the high domestic demand and possibly for export.

CHAPTER TWO

LITERATURE REVIEW

2.1 Multi-Environment Trial (MET) in crop production

Multi-environment trials (METs) is defined by Coe (2012) as simply trials or experiments carried out in multiple environments or contexts. In agriculture and related environmental and rural development research, Multi-environment trials are standard research tools. Multi-environment trials are experiments: they are planned and managed research studies designed to measure the effect of changing something. When thinking of the environments (E) in a Multi-environment trials, we often first think of the biophysical agricultural environment as dominated by the weather and soil.

Multi-environment trials are used to investigate, for example, the relative performance of crop varieties on different soils, or to look for traits such as drought tolerance in new crop lines. But the same concepts are needed to look at how different germplasm or practices that are adapted to varying social and economic environments (Coe, 2012).

Anputhas *et al.* (2011) used this method to test and identify the consistently performing varieties in wider environments and location specific high performing varieties.

Multi-location trials provide useful information on genotypic adaptation and stability (Crossa, 1990). The GxE interaction estimates help breeders to decide the breeding strategy, to breed for specific or general adaptation, which depends on stability in yield performance under a limited or wide range of environmental conditions (Romagosa and Fox, 1993).

The multi-location testing, however, usually results in genotype-by-environment interactions that often complicate the interpretation of results obtained and reduce efficiency in selecting the best genotypes (Annicchiarico and Perenzin, 1994). This interaction is the result of changes in cultivar's relative performance across environments, due to differential responses of the genotypes to various edaphic, climatic and biotic factors (Dixon and Nukenine, 1997).

Muungani *et al.* (2007) used this method to evaluate and identify high performing ten maize cultivars using a mother-baby trial approach at fourteen sites in twenty eight environments across Zimbabwe.

Romualdo *et al.* (2014) also used this approach to test and evaluate Upland Rice Varieties In Sultan Kudarat Province across four locations for six (6) consecutive wet and dry cropping seasons, to determine the agronomic and yield characteristics and its reaction to pests and diseases.

Genotype by environment interaction (GEI) is the differential response of genotypes evaluated under different environmental conditions. It is a complex phenomenon as it involves environmental (agro-ecological, climatic and agronomic) conditions and all physiological and genetic factors that determine the plant growth and development (Kaya *et al.*, 2006).

Kang (2004) also defines genotype by environment interaction (GxE interaction) as the differential responses of different genotypes across a range of environments. However, only the repeatable GxE interactions according to Baker (1988), causes the ranking of genotypes to change across the macro-environments, which are essential and meaningful for breeding strategy.

Studies conducted by Atnaf *et al.* (2013) suggests that the genotype by environment (GxE) interaction effect is, most often, a common phenomenon in a multi-environment yield trial and presents limitations on variety selection and recommendation for target environments, and hence, must be either exploited by selecting superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Ceccarelli, 1989).

Farshadfar (2008) in study on a multi-environment trial to determine stable bread wheat genotypes under irrigated and rainfed conditions in Iran over four years, obtained highly significant differences between the components of environment, genotype and their interaction.

Studies conducted by Oliveira *et al.* (2013), also revealed highly significant differences for environment, genotype and their interactive components for a multi-environment trial on the yield of twelve cultivars of passion in eight agronomic production areas in State of Bahia, Brazil.

Genotype by environment interaction data obtained from multi-environment trials (METs) across a wide range of environments can be investigated by Pattern Analysis to identify genotypes with similar responses across environments, and to identify those environments that discriminate among genotypes in a similar manner (Cooper and Delacy, 1994; Alagarswamy and Chandra, 1998; Delacy *et al,*. 2000).

Determining the relative proportion of repeatable and non-repeatable GxE interaction effects is an important issue in analysis and interpretation of Multi-environment trials. This partitioning was first shown by Robertson (1959). Muir *et al.* (1992) gave methods for partitioning the GxE interaction into the sources due to heterogeneous variances and lack of correlation.

Highly significant differences were obtained in a study conducted by Farshadfar and Sutka (2006) for components of the environment, genotypes and the interaction between them in a multi-environment trial using twelve rice genotypes, evaluated under irrigated and rainfed conditions.

Yang and Baker (1991) used multivariate analysis of variance (MANOVA) and proposed two tests for the significance of the different sources of GxE interaction. These approximate tests are based on unwarranted assumptions about the sampling distributions of estimated variance and covariance components, resulting in a number of undesirable properties such as non-positive definite estimates of genetic variance covariance matrices. Therefore, Yang (2002) applied a restricted maximum likelihood (REML) approach to estimate genetic parameters and test significance of different sources of GxE interaction.

Reduced Maximum Likelihood (REML) according to Patterson and Thompson (1971), has been used for decades to estimate variance parameters based on mixed model theory (Henderson, 1984). Mixed model analysis for METs data contain frequentist approaches in which the variance parameters are estimated using REML and fixed and random effects are estimated using best linear unbiased estimates (BLUEs) and best linear unbiased predictors (BLUPs), respectively (Smith *et al.*, 2005). The development of statistical packages such as ASREML according to Gilmour (1999), allows REML estimation of a range of mixed models and also enables them to fit more informative and complex models for accommodating different forms of GxE interactions.

Cullis *et al.* (1998) allowed for heterogeneity between trials by fitting a separate variety by environment interaction (VxE) variance for each trial. Smith *et al.* (2001) extended this approach for the analysis of Multi-environment trials data which included multiplicative models for the variety effects in each environment. The model provides an approach that accommodates heterogeneity of VxE variance, correlation among VxE interactions, and appropriate error variance structures for individual trial. In fact, the residual variation can be further partitioned into components due to micro-environment variation and genotype by microenvironment interaction (Nyquist, 1991). The variation within trial has been examined by some authors using spatial analysis in single sites (Casanoves *et al.*, 2005; Cullis *et al.*, 1998; Smith *et al.*, 2001). Some evidence in forestry indicates that gradients and large patch sizes were found within trees (Costa *et al.*, 2001; Fu *et al.*, 1999), and also showed that using a combined spatial model enables to improved analysis of experiment data (Dutkowski *et al.*, 2002, 2006; Hamann *et al.*, 2002; Costa *et al.*, 2001; Magnussen *et al.*, 1990).

2.2 AMMI analysis of Genotype by Environment (GxE) Interactions

AMMI is a unified approach that fits the additive main effects of genotypes and environments by the usual analysis of variance and then describes the non-additive parts by principal component analysis (Anandan *et al.*, 2009).

The presence of genotype by environment (GxE) interaction plays a crucial role in determining the performance of genetic materials, tested at different locations and in different years (Das *et al.*, 2011).

Studies carried out by Molla *et al.* (2013) suggest that the phenotypic performance of a genotype is not always the same in different locations, as it is influenced by abiotic and biotic environmental factors. Some genotypes may perform well in one environment, but fail in several others. Yield and quality traits are influenced by genotype (G), environmental factors (E) and the interaction between genotype and environment (GxE).

Studies conducted by Das *et al.* (2011) showed differential response of the yield of the fifteen rice genotypes to environmental changes, using an integrated analysis for genotypic adaptation in rice using thirty six (36) rice genotypes.

Studies by Hernandez and Crossa (2000) shows that the AMMI model analysis combines the ANOVA (with additive parameters) and the PCA (with multiplicative parameters) into a single analysis. The AMMI model analysis is useful in making cultivar recommendations, specifically by mega environment analysis, in which the best performing cultivar for each sub-region of the crop's growing region is identified (Zobel *et al.,* 1988; Gauch and Zobel, 1997). Gauch and Zobel (1997) confirmed the usefulness of AMMI analysis in supporting breeding program decisions, such as in the selection of environments or test site locations.

Although results from the AMMI model analysis are based only on yielding data (not environmental data), Ebdon and Gauch (2002) reported that AMMI environmental (interaction) statistics were correlated with environmental factors, such as precipitation, mean daily maximum and minimum temperatures, altitude, latitude, nitrogen, fertilization, irrigation and nutrient soil content.

The results of AMMI analysis are useful in supporting breeding program decisions such as specific and broad adaptation and selection of environment (Gauch and Zobel, 1997).

Bose *et al.* (2014), obtained significant components of the environment, genotypes and genotype by environment interaction for the AMMI analysis of variance for selecting rice genotypes for yield and stability under direct seeded conditions using seeds of twelve (12) popular rice genotypes in the Central Rice Research Institute experimental farm, Cuttack, India. The presence of genotype by environment (GxE) interaction plays a crucial role in determining the performance of genetic materials, tested at different locations and in different years, influencing the selection process (Becker and Leon, 1988; Purchase *et al.*, 2000).

Anandan *et al.* (2009), used AMMI analysis to study the Yield Performances in Rice Genotypes under Coastal Saline Environments by using 46 rice genotypes in three locations. The results they obtained showed highly significant genotypic and GxE interaction. The GxE interaction influenced the relative ranking of the genotypes across saline stress environment condition.

In a study to determine fourteen stable genotypes of bread wheat using AMMI stability analysis, Farshadfar *et al.* (2011), obtained highly significant differences for the components the environments, genotypes and the interaction between genotypes and environments for the AMMI analysis of variance.

Genotype by environment interaction has been studied by various researchers (Singh *et al.*, 1987; Jain and Pandya, 1988; Zubair and Ghafoor, 2001). Specific-adapted cultivars may raise crop yields by exploiting Genotype by Environment interaction effects (Annicchiarico, 2002) and site specific cultivar recommendation can be defined if the best yielding material differs depending on site. Therefore, recommending more than one cultivar per region or a sub-region will be preferred so as to limit the risk of disasters arising from unforeseen biotic or abiotic stress of one cultivar recommended for a wide range of environments (Annicchiarico, 2002).

Several methods have been proposed to analyze genotype by environment interaction and phenotypic stability. These methods can be divided into two major groups: univariate and multivariate stability statistics (Lin *et al.*, 1986). A combined analysis of variance can quantify the interactions and describe the main effects. However, it is uninformative for explaining genotype × environment interaction. Among multivariate methods, the additive main effect and multiplicative interaction analysis (AMMI) has been extensively applied in the statistical analysis of multi-environment cultivar trials (Kempton, 1984; Crossa, 1990; Gauch and Zobel, 1997).

2.3 AMMI Yield Stability and Adaptability Analysis

Abeysiriwardena *et al.* (1991) and Annicchiarico (2002), defines yield stability of a cultivar as a similarity (consistency) degree of its yield response function across environments to mean of all studied cultivar yield response function.

Studies conducted by Syed *et al.* (2007) suggest that, in the presence of significant GxE interactions, stability parameters are estimated to determine the superiority of individual genotypes across the range of environments.

Many publications described the importance of GxE interactions and concluded that mean yields are not a satisfactory basis and emphasis should therefore be given on the evaluation of genotypes which could perform better irrespective of environmental fluctuations (Golmirzaie *et al.*, 1990; Kinyua, 1992; Lin *et al.*, 1986; Qari *et al.*, 1990; Sial *et al.*, 2000; Yan and Hunt, 2001; Viana and Cruz, 2002; Kaya *et al.*, 2002).

According to Sedghi-Azar *et al.* (2008) there are a number of statistical methods for consideration of genotype by environment interaction and its relationship with stability. From all of these methods, regression of mean of each genotype on environmental index is one of the most applicable methods (Tesemma *et al.*, 1998). This method has been suggested by Finaly and Wilkinson (1963), modified by Eberhart and Russell (1966).

Farshadfar (2008) identified stable wheat genotypes with high grain yield by employing AMMI stability value stability measure using twenty genotypes in a field experiment conducted under irrigated and rainfed conditions over four years.

Farshadfar et *al.* (2012) also employed the use of ASV method in their study to evaluate grain yield stability of wheat-barley disomic addition lines, and located the QTLs controlling static and dynamic phenotypic stability in barley, using 7 disomic addition lines (DALs) of barley across five environments.

Gómez-Becerra *et al.* (2006) also determined the stability and adaptability patterns of a set of 40 promising spring wheat genotypes from Kazakhstan and Siberia across twenty two environments using the ASV technique.

The method of Yield Stability Index (YSI) was used by Bose *et al.* (2014) in their study to select stable and high yielding genotypes for twelve (12) popular rice genotypes

Farshadfar *et al.* (2011) also selected stable bread wheat genotypes with high grain yield through a single parameter, field experiments conducted with fourteen (14) genotypes over three years, under irrigated and rainfed conditions using the method of YSI.

Tariku *et al.* (2013) carried out a study on grain yield stability analysis of rice (*Oryza sativa L.*) genotypes evaluated in north western Ethiopia using sixteen genotypes at three locations in eight environments to identify stable and high yielding genotypes for possible release.

Mahapatra and Das (1998) and Chandrasari *et al.*, (2002) used CV to predict adaptability in rice. Among the multivariate approaches AMMI model is widely used (Asenjo et *al.*, 2003; Mahalingam *et al.*, 2006 and Das *et al.*, 2008). In AMMI, the response patterns of the genotypes to environmental change can be extrapolated to a much wider range of environments. AMMI stability value (ASV) statistic was developed by Purchase (1997) to quantify and rank the genotypes on the basis of their yield stability.

The method of Rank Sum (RS) measure of yield stability was also used by Farshadfar *et al.* (2011) to select high yielding and stable wheat bread genotype.

The Additive Main and Multiplicative Interaction (AMMI) stability value (ASV) is based on AMMI model's PCA 1 and PCA 2 scores for each genotype. It is in effect the distance from the co-ordinate point to the origin in a two dimensional scatter gram of PCA 1 score against PCA 2 score. Many methods are available for the analysis of GxE interaction and adaptability (Lin *et al.*, 1986; Hohls, 1995). But the prediction of adaptability of the genotypes may vary depending on the biometrical methods followed, implying a genotype found to be stable in one biometrical method may not be stable in others. Therefore, the integration of several biometrical approaches may give a better result than the use of a single method in predicting the adaptability and stability in yield performance.

Plant breeders generally agree on the importance of high yield stability, but disagree with the different methods used for stability analysis (Becker and Leon, 1988). Therefore, several biometrical methods including univariate and multivariate ones have been developed to assess stability (Akcura et *al.*, 2005). Among the univariate approaches, the linear regression model of Eberhart and Russell (1966) is most widely adopted by the breeders (Bose et *al.*, 2004; Francis et *al.*, 2005; Nanita Devi *et al.*, 2006; Das *et al.*, 2008) as it is mathematically simple.

The yield stability is influenced by several factors, such as environmental factors, agricultural managements and pest pressures (Hu and Buyanovsky, 2003; Berzsenyi and Dang, 2008).

Genotype by environment interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments, to help plant breeders in selecting varieties. Instability is the result of cultivars response in different environments which usually indicates a high interaction between genetic and environmental factors (Jusuf *et al.*, 2008; Lone *et al.*, 2009). Grain yield depends on genotype, environment and management practices and their interaction with each other (Messina *et al.*, 2009). Under the same management conditions, variation in grain yield is principally explained by the effects of genotype and environment (Dingkuhn *et al.*, 2006). Interaction between these two explanatory variables gives insight for identifying genotype suitable for specific environments. The environmental effect is typically a large contributor to total variation (Blanche *et al.*, 2009).

Lestari *et al.* (2010) reported that there was significant different stability and adaptability of 35 aromatic new plant type rice lines across different environments. Similarly, Sreedhar *et al.* (2011), evaluate 60 hybrid rice cultivars for yield and its component stability across three different agroclimatic zones, and also found that stability in single plant yield was due to plasticity and stability in yield components. In the study of Mosavi (2013) in some rice promising genotypes, it showed that highly significant yield differences among rice genotypes, environment and genotype by environment interaction. Some rice genotypes were adjudged stable when different yield stability parameters were considered.

2.4 GGE Biplot measure of yield stability

The Genotype main effect and Genotype by Environment (GGE) biplot according to Yan *et al.* (2000) is shown to be effective in identify the genotype by environment (GxE) interaction pattern of the data. It also clearly shows which genotype won in which environments, and thus facilitates Multi-Environment identification.

Samonte *et al.* (2005) reported that the ANOVA is an additive model which describes the main effects effectively and determines if the Genotype by Environment interaction is a significant source of variation, but it does not provide insight into the genotypes or environments that give rise to the interaction. In a related studies, Yan *et al.* (2000) proposed a method, namely GGE-biplot, which allowed visual examination of the Genotype by Environment interaction pattern of Multi-Environment Yield Trial (MEYT) data.

Kaya et al. (2006) proposed that the GGE-biplot is based on two concepts. First, although the measured yield is the combined effect of genotype (G), environment (E), and genotype by environment interaction (GxE), only genotype (G) and genotype by environment interaction (GxE) are relevant to, and must be considered simultaneously, in genotype evaluation, as such giving rise to the term GGE. Secondly, the biplot technique which was developed by Gabriel (1971), is employed to approximate and display the GGE of a MEYT, hence the term GGE biplot. This GGE-biplot is constructed by the first two principal components, which is the PC1 and PC2, which is also referred to as the primary and secondary effects, respectively which is derived from subjecting environment centered yield data, which is the yield variation due to GGE, to singular value decomposition. This

site regression (SREG) analysis according

to Yan et al. (2007) are useful in mega environment analysis, test environments, and genotypes evaluation.

Bhan *et al.* (2005) used the method of GGE biplot to select high yielding and stable six varieties or strains of Lemongrass (*Cymbopogon spp.*) for oil yield across four years. In their study, they obtained higher proportion of variation (80%) for the Principal component 1(PCA1).

Muugani *et al.* (2007) also applied the method GGE biplots analysis on a multi-environment, mother-baby trial using ten pre-released maize hybrids and open pollinated varieties tested at fourteen sites across Zimbabwe. Gauch and Zobel (1996, 1997) defined a mega environment as a portion of a crop species' growing region with a homogenous environment in which some genotypes perform similarly. They used the maize Multi-environment Trial (MET) dataset for identification of maize mega environments.

A number of statistical methods to analyze and visualize the nature and magnitude of genotype by environment interaction have been proposed, however, studies conducted by Amira *et al.* (2013) and Yan *et al.* (2007) suggest that the GGE best fits for mega environment analysis which shows 'Which-genotype won-where' pattern of genotype evaluation and test environment evaluation which provides discriminating power versus representativeness of the test environment.

The GGE has been recognized and implemented as useful method for analyzing and visualizing the pattern of genotype by environment interaction. This according to Atnaf *et al.* (2013) have been used in multi environment cultivar evaluation of different crops including wheat, maize, soybean, and oilseeds. This GGE biplot according to Yan *et al.* (2000) graphically displays the genotype main effect plus genotype by environment interaction of a multi-environment trial in a way that facilitates visual evaluation of cultivars and mega environment identification. Badu-Apraku *et al.*(2008) and Badu-Apraku and Lum (2010) used the GGE biplot analysis to decompose the genotype by environment interaction in West and Central Africa and to obtain information on the early maturing maize cultivars that were suitable for Striga-infested and Striga-free environments and to investigate stability of cultivars in the various environments.

The method of selecting stable and high yielding genotypes using GGE biplot has again been used by Badu-Apraku *et al.* (2011) for targeting early maturing maize cultivars to mega environments in West Africa.

2.5 Correlation and Path coefficient analysis

Grain yield is a complex character and is controlled by many factors. Selection for desirable types should not only be restricted to grain yield alone but other components related to grain yield should also be considered (Mugemangango and Vinod, 2011).

Mugemangango and Vinod (2011) defined Path coefficient analysis as a statistical technique of partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated.

In most studies involving path coefficient analysis, researchers have considered the predictor characters as first-order variables in order to analyze their effects over a dependent variable such as yield.

Studies conducted by Meenakshi *et al.* (1999), Nayak *et al.* (2001), Madhavilatha (2002), on agronomic trait characters on grain yield showed that panicle length had a positive significant association with grain yield.

According to Hasan *et al.* (2011), genetic variability, correlation and path coefficients are pre-requisites for improvement of any crop including rice in any trait by selection of superior genotypes. Yield component directly or indirectly increasing grain yield if the components are highly heritable and genetically independent or positively correlated with grain yield.

Babu *et al.* (2012), in a study on the association of agronomic trait characters on grain yield obtained a significant positive correlation between days to 50% flowering with plant height, panicle length and number of filled grains per panicle for a path and correlation analysis using twenty one popular rice hybrids in India. They also obtained a significant positive correlation between days to 50% flowering with days to maturity, plant height at maturity, panicle length and grain length.

In a study carried out by Oad *et al.* (2002) using thirty varieties and advanced lines of rice to study the rice ratoon grain yield, ratoon rating, quantitative parameters, and their correlation and path coefficients, grain yield showed positive correlation with plant height, ratoon rating, 1000 grain weight, number of panicles, panicle length, seed length, and tillers at harvest. Path analysis indicated that ratoon crop parameters had low positive direct effects.

Dewey and Lu (1959), found that Simple correlation analysis that relates seed yield to a single variable may not provide a complete understanding about the importance of each component in determining seed yield.

Joshi (2005) in a related study also obtained a negative and significant correlation between thousand grain weight and plant. It was also observed from the study that there was a significant negative correlation for thousand grain weight with plant height at maturity, panicle length and grain length.

Mugemangango and Vinod (2011), carried out path coefficient analysis of rice cultivars to determine the nature of relation between grain yield and yield components by partitioning the correlation coefficients between grain yield and its components into direct and indirect effects under three experimental trials.

Akbar *et al.* (1995) carried out path coefficient analysis to study genetic variability and inter-relationships between agronomic traits in 24 bread wheat genotypes which revealed higher direct effect of number of grains per spike, followed by number of spikes and 1000-grain weight on grain yield.

Uddin *et al.* (1997) observed that grain yield per plant was positively and significantly correlated with spikelets per spike and 1000-grain weight; whereas, in path coefficient analysis high direct effect was observed for spikelets per spike and tillers per plant.

Scheiner *et al.* (2000) expanded current methods for calculating selection coefficients using path analysis and demonstrated how to analyze nonlinear selection. They demonstrated their method with an analysis of selection in an experimental population of Arabidopsis thaliana consisting of 289 individuals. They showed that path analysis has great promise for improving our understanding of natural selection but must be used with caution since coefficient estimates depend on the assumed causal structure.

Jedynski (2001), explained the correlation and path coefficient for grain yield and its components in wheat. He also obtained heritability estimates which were very high for plant height, high for 1000-grain weight, intermediate for number of grains per spike and very low for grain yield per plant.

Kashif and Khaliq (2004), performed path coefficient studies in a 5×5 diallel cross of wheat. They investigated that plant height, flag leaf area, spike length and grains per spike had positive direct effects on grain yield. While fertile tillers per plant, spikelets per spike and 1000-grain weight exhibited negative direct effects on grain yield. The traits having positive direct effects on grain yield are considered to be suitable selection criteria for evolving high yielding genotypes.

Royo *et al.* (2004) investigated the genotypic and environmental effects on the pattern of leaf and green area

Coşge *et al.* (2009) used correlation and path analysis to determine relationships between seed yield and some yield components of 20 sweet fennel (Foeniculum vulgare Mill. var dulce) lines. They suggested that single plant yield, number of umbellets and plant height are good phenotypic selection criteria to improve seed yield and essential oil percentage of sweet fennel.

Dalkani *et al.* (2011) performed the correlation and sequential path analysis in Ajowan. They Carried out an investigation on 10 populations of Ajowan to investigate the association among yield components and their direct and indirect effects on the seed yield of Ajowan. Positive and significant correlations were detected between single plant yield and most of the studied traits while the correlation between single plant yield and ripening period length was negative and significant ($r = -0.41$). It was concluded on the basis of sequential path analysis that the plant height and number of umbels can be used as selection criteria for improving seed yield in Ajowan breeding programs.

Study was also carried out by Hasan *et al.* (2011) using twenty four hybrid rice varieties of diverse origin for genetic variability, using correlation and path analysis under medium high land of Gazipur. In the study, the PCV values were greater than GCV, revealing little influence of environment in character expression.

2.6 Technical efficiency and inefficiency Analysis

The productivity of rice farmers can be raised either by adoption of improved production technologies or improvement in efficiency or both (Idiong, 2007).

Tijani (2006) defined Technical efficiency as the ability to produce a given level of output with a minimum quantity of inputs under a given technology. Allocative efficiency refers to the ability to choose optimal input levels for given factor prices.

Technical Efficiency is also defined by Donkoh *et al.* (2013) as the ability to achieve a higher level of output, given similar levels of inputs. It is the relationship between what an organization (producer, production unit, or any decision–making unit) produces and what it could feasibly produce, under the assumption of full utilization of the resources available (Garcia del Hoyo *et al.*, 2004).

Enwerem and Ohajianya (2013), in a related work defined Technical or production efficiency as the ability of making use of implement or mechanical skills to bring about measure of a farm success in producing maximum output for a given set of inputs.

A study by Solís *et al.*, (2007) examined the connection between adoption of soil conservation practices and the technical efficiency of farmers participating in specific projects in Honduras and El Salvador by comparing high and low adopter farm households. In particular, they address the issue of whether unobserved effects lead farmers to self-select into one of the groups by implementing a switching regression model.

Numerous studies (Obwona, 2000; Son *et al.*, 1993) have attempted to determine technical efficiencies of farmers in developing countries because determining the efficiency status of farmers is important for policy purposes.

Studies conduct by Ahmadu and Alufohai (2012) and Enweren and Ohajianya (2013) on the technical efficiency of rice farmers revealed that males dominated in rice production.

Ugwuanyi *et al.* (2008) concluded in their studies that a high literacy rate recorded by farmers might increase their ability to use resources more efficiently.

Enwerem and Ohajianya, (2013), carried out a study to analyze the technical efficiency and the sources of inefficiency in large scale and small scale rice production in Imo State, Nigeria during the 2009 cropping season, using a stochastic frontier production function which incorporates a model for inefficiency effects.

Farrell (1957), distinguishes between technical and allocative efficiency (or price efficiency) in production through the use of a "frontier" function.

According to Tijani (2006), Efficiency is also an important factor in productivity growth. In an economy where resources are scarce and opportunities for new technologies are lacking, inefficiency studies will be able to show that it is possible to raise productivity by improving efficiency without increasing the resource base or developing new technology. Estimates of the extent of inefficiency also help in deciding whether to improve efficiency or to develop new technologies to raise agricultural productivity.

Kalirajan and Flinn (1983), applied the methodology proposed by Jondrow *et al.* (1982) to data for 79 rice farmers in the Bicol region of the Philippines. They estimated the parameters of their model using the maximum likelihood method. The Cobb-Douglas model was found to be an inadequate representation of the farm-level data, and so a translog stochastic frontier production function was estimated to explain variations in rice output in terms of several inputs. The estimated technical efficiencies ranged from 0.38 to 0.91. Kalirajan and Flinn (1983), then regressed the predictive technical efficiencies on several farm-level variables and farm-specific characteristics to determine which factors are associated with estimated technical efficiency scores. Several variables including the practice of transplanting rice seedlings, the incidence of fertilization, years of farming and number of extension contacts, were found to have significant relationships.

Lingard *et al.* (1983) measured farm-specific technical efficiencies of rice farmers in Central Luzon of the Philippines using the "Loop Survey" data from the International Rice Research Institute (IRRI). They estimated a production function for 32 farmers from panel data for 1970, 1974 and 1979 using covariance analysis. Measures of technical efficiency were calculated from the farm-specific dummy variables. The results showed that the least farm achieved only 29 percent of the maximum possible output for the given input levels.

Dawson and Lingard (1989), extended the analysis of Lingard *et al.* (1983) and estimated farm-specific technical efficiencies from stochastic frontier production function using data for 1970, 1974, 1979 and 1982. For each year, a stochastic frontier production function was estimated applying the composed error model of Aigner *et al.* (1977) and Meeusen and van den Broeck (1977). Dawson and Lingard calculated technical efficiencies for each farm in each year by using methodology of Jondrow *et al.* (1982) and assuming a Cobb-Douglas functional form.

The results showed a fairly uniform distribution of estimated efficiencies across a range that was greater than that reported by Lingard *et al.* (1983). The mean technical efficiency for the four years ranged between 0.60 and 0.70.

Shapiro (1983) concluded that government can enhance productivity among efficient farmers by emphasizing new investment or technologies, rather than extension and education efforts which are aimed at less efficient farmers.

Awunyo-Vitor *et al.* (2013) revealed in their study that the number of extension contact received in a year by farmers influenced their technical inefficiency, but studies by Enweren and Ohajianya (2013) and Tijani (2006) rather showed that number of extension contacts did not influence technical inefficiency.

Shapiro (1983), Tadesse and Krishnamoorthy (1997), Habibullah and Ismail (1994), Son *et al.* (1993) and Obwona (2000) found evidence of technical inefficiency among farmers in developing countries. Their recommendation was that government efforts would have to be directed to education, extension, social change and support. An emphasis according to Tijani (2006), on these activities would improve the allocation and the use of available resources so that more farmers would come closer to the efficiency level achieved by their counterparts.

In order to estimate and analyze the technical efficiency of rice farmers, the Stochastic Frontier Analysis is used. The stochastic frontier approach, unlike the other parametric frontier measures from studies conducted by Donkoh *et al.* (2013), makes allowance for stochastic errors due to measurement errors. The stochastic frontier model decomposes the error term into a two sided random error that captures the random effects outside the control of the farmer and the one-sided inefficiency component.

There have been many studies on efficiency in agriculture in developing countries in which majority is stochastic frontier studies. Thiam *et al.* (2001) summarizes 51 observations of Technical Efficiency in developing countries from 32 studies published before 1999. They include 27 stochastic frontier, six deterministic frontier and two Data Envelopment Analysis (DEA) studies. Rice is the most studied crop (in 17 studies). However, the application of DEA method has gradually increased. Recent application of DEA method on the estimation and explanation of agricultural efficiency in developing countries include Dhungana *et al.* (2004) on Nepal rice farms, Krasachat (2003) on Thailand rice farms, Chavas *et al.* (2005) on Gambia farms, Shafiq and Rehman (2000) on Pakistan farms. There are several studies that use both DEA and stochastic methods such as Sharma *et al.* (1999), Wadud (2003) and Wadud and White (2000).

Inefficiency in crop production is one of the major factors hindering the exploitation of full potential of the innovated technologies, particularly in the developing countries (Bravo-Vrata and Evenson, 1994).

Inefficiency, the inability of a farmer to realize optimum output, is influenced by various socioeconomic factors that interfere in the decision-making process of a farmer (Dawson, 1985; Kalirajan and Shand, 1989).

2.6.1 Stochastic Frontiers analysis

Stochastic frontier analysis, independently developed by Aigner *et al.* (1977) and Meeusen and van den Broeck (1977), is a procedure for production function estimation which determines the production frontier, or maximum level of output for each combination of inputs.

One particular characteristic of stochastic frontier models according to Zaeske (2002), is the use of two types of uncorrelated errors rather than just a single random error as in many regression models. One is standard normal random error, while the other is a non-negative technical inefficiency effect, which can be viewed as a negative productivity shock. Crucially for this analysis, the technical inefficiency effects are allowed to depend on characteristics of the producers, allowing for a more in depth analysis of production behavior and the effects of policy and environmental factors.

This parametric method according to Zaeske (2002), is preferable to non-parametric methods such as data envelopment analysis, because it allows for the use of standard hypothesis testing procedures and because it does not restrict producer observations to lie within the frontier estimated. The latter property is particularly desirable because it allows for the presence of measurement errors or other forms of statistical noise in the model, while with nonparametric approaches all deviations from the frontier are assumed to be due to inefficiency.

A stochastic frontier production function according to Battese and Coelli (1995), is defined for panel data on firms, in which the non-negative technical inefficient effects are assumed to be a function of firm-specific variables and time. The inefficiency effects are assumed to be independently distributed as truncations of normal distributions with constant variance, but with means which are a linear function of observable variables.

In terms of the functional form of the Stochastic Frontier Model, the two commonly used according to Donkoh *et al.* (2013) are the Cobb Douglas and the Translog. The main advantage of the latter is that it is flexible, which implies that it does not impose assumptions about constant elasticity of production nor elasticities of substitutions between inputs. However, multicollinearity problems may show up. A case in point is the Cobb-Douglas functional form however is not only simple but it is self-dual, and has been applied widely in agricultural production technologies in many developing countries.

A number of studies according to Donkoh *et al.* (2013) have estimated both the Cobb-Douglas and the translog functional forms and then tested the null hypothesis that the former is an adequate representation of the data, given the specification of the translog functional form. The test is conducted using the generalized likelihood-ratio test.

The stochastic frontier framework according to Nkegbe (2012), accounts for the stochastic nature of agricultural production and also allows for estimating inefficiency effects in a single approach.

Bagi and Haung (1983), estimated a translogarithmic stochastic frontier production function and found technical efficiencies to vary from 0.35 to 0.92 for mixed farms and 0.52 to 0.91 for crop farms. Kalirajan and Flinn (1983) assumed a translogarithmic stochastic frontier production and by maximum likelihood estimation, the parameters were estimated and individual technical efficiencies ranged from 0.38 to 0.91. They went further to regress the predicted technical efficiencies on several farm-level variables and farm-specific characteristics to determine the factors affecting farm level technical efficiencies. In most of the studies, it was found that the Cobb Douglas stochastic frontier does not provide an adequate representation for describing the data, given specification of a translog model.

The analysis of efficiency is generally associated with the possibility of farms producing a certain optimal level of output from a given bundle of resources at least cost. Farrel (1957), distinguished between three types of efficiency;

(i)Technical Efficiency, which is the physical ratio of product/output to the factor input. The greater the ratio, the greater the magnitude of technical efficiency.

(ii) Allocative or Price Efficiency: A farm is allocatively efficient when production occurs at a point where the marginal value product is equal to the marginal factor cost.

(iii) Economic Efficiency: This is the product of technical and allocative efficiencies. It obtains where both technical and allocative efficiencies have been attained.

Dawson *et al.* (1991) used a Cobb-Douglas stochastic frontier production function to estimate the technical inefficiency of rice farmers in Central Luzon of the Philippines.

Rola and Quintana-Alejandrino (1993), used a stochastic frontier production function to estimate the technical efficiencies of rice farmers in different rice environments in selected regions of the Philippines. The study used a Cobb-Douglas production frontier and estimated the model by the maximum likelihood method. Input variables in the production frontier included farm size, fertilizer (nitrogen), insecticide, herbicide and labor. In addition, variables such as education of the household head, tenurial status and water source were used in the production function.

Input-output data and other demographic information were gathered from farmers in the irrigated, rainfed and upland environments of five rice-producing regions in the Philippines. Rola and Quaintana-Alejandro (1993) estimated mean technical efficiencies of 0.72, 0.65 and 0.57 for irrigated, rainfed and upland environments, respectively, indicating high variability in the technical efficiency estimates between the different rice environments. Education, access to capital and tenurial status were factors that affected the levels of technical efficiencies of farmers in the different environments.

Larson and Plessmann (2002), used data collected in the Bicol region in the years 1978, 1983 and 1994 to construct a balanced panel data set comprising 144 observations. They estimated a translog stochastic frontier production function that included the inputs of irrigated area, rainfed area, fertilizer and labour. A model that takes into account the factors associated with technical inefficiency was also estimated. Larson and Plessmann (2002), found that diversification and technology choices affected efficiency outcomes among Bicol rice farmers, although these effects were not dominant. Other factors associated with efficiency were accumulated wealth, education, favorable market conditions and weather.

Idiong (2007) reported that labour, farm size and seed positively and significantly related to swamp rice output, while fertilizer was not significant.

The results of the Cobb-Douglas maximum likelihood estimate given by Backman *et al.* (2009) in their study showed that land, labour and seeds, among other factors significantly influenced rice production, while fertilizer had no significant effect.

Etwire *et al.* (2013) obtained a mean technical efficiency of 53% for soybean farmers in the Sabobo and Cheriponi District of Northern Ghana, whilst studies conducted by Tijani (2006), Donkor *et al.* (2013) and Ahmadu and Alufohai (2012), rather obtained mean technical efficiency score above 80% for rice farmers.

The study by Ewtire *et al.* (2013) also revealed that a greater proportion of farmers produced above an efficiency score of 0.5, whilst related studies by Idiong (2007); Tijani (2006); Donkor *et al.* (2013) and Sekhon *et al.* (2010) rather revealed a lower proportion of farmers producing below the technical efficiency score of 0.5

2.7 Crop modelling using linear models

Pandey *et al.* (2013) develop models for forecasting rice yield at district level on the basis of weather variables. Weekly data on seven weather variables over a span of 21 years period (1989-90 to 2009-10) were used along with the annual rice production data for Faizabad district of Eastern Uttar Pradesh. They employed a Stepwise regression to screen out the important weather variables and multiple regression approach was subsequently employed to estimate model parameters.

A Stepwise regression models for the remotely sensed rice-yield predictions was developed for five typical rice-growing provinces in China. The prediction models for the remotely sensed rice yield according to Huang *et al.* (2013) indicated that the influences of the normalized-difference-vegetation-index (NDVI) on the rice yield were always positive. The association between the predicted and observed rice yields was highly significant according to their study, and independent validation found that the overall relative error was approximately 5.82%, and a majority of the relative errors were less than 5%.

Following previous researches conducted on crop yield response, the crop response model was estimated in a single-equation framework (Gallagher, 1986; Huff and Neill, 1980; Offutt *et al.,* 1987). Various algebraic forms of these yield response regression have been estimated in prior yield response studies. Huff and Neill (1980) used linear specifications for precipitation and temperature and a quadratic trend variable. Thompson (1969) used an additive model with precipitation and temperature specified in linear and quadratic terms. Offutt *et al.* (1987) also used a linear specification for mean temperature, precipitation, and a trend variable. Heyman and Chatterjee (2014) also constructed partial linear models for Minnesota corn and soybean yields.

Tannura *et al.* (2008) conducted a study to investigate the relationship between weather, technology, corn, and soybean yields in the U.S. Corn Belt. Corn and soybean yields, monthly temperature, and monthly precipitation observations were collected over 1960 through 2006 for Illinois, Indiana, and Iowa. Multiple regression models were developed based on specifications found in studies by Thompson (1962, 1963, 1969, 1970, 1985, 1986 and 1988), where the estimated models explained at least 94% and 89% of the variation in corn and soybean yields for each state. From their study it was observed that rainfall did not significantly affect yield.

Diagnostic tests for heteroskedasticity, autocorrelation, and mis-specification were performed on the models to assess the validity of model estimates. Coefficients of the estimated models were then analyzed to determine the relationship between yields, technology, and weather. Formal parameter stability tests were used to determine whether structural change [illegible]

period. Several tests were used by Tannura *et al.* (2008) to determine if a significant change in trend yield growth in corn occurred during the mid-1990s.

Several studies by Thompson (1962, 1963, 1969, 1970, 1985, 1986 and 1988) were particularly influential. He developed regression models of the relationship between technology, monthly rainfall, monthly temperatures, and U.S. corn and soybean yields. The multiple regression models developed by Thompson used time and monthly weather observations to explain variation in corn and soybean yields. His most significant findings were: (1) corn yields were particularly boosted by abundant rainfall during July and cooler-than-usual temperatures during August, (2) above-average July and August rainfall particularly boosted soybean yields, and (3) favorable weather in the early 1960s coincided with rapidly increasing corn yields, which provided evidence that technology was not solely responsible for observed yield increases.

In addition, only a handful of previous studies investigate the out-of-sample forecasting performance of weather and technology regression models (Teigen 1991a, 1991b; Dixon *et al.,* 1994; Teigen and Thomas 1995), and these studies evaluated very small forecast samples, at most three years. Hence, previous studies provide limited evidence on the forecasting performance of regression models.

In this study, a combination of statistical techniques is employed to predict yield using the concept of yield gap, since it forms the primary objective of the study.

The outcome variable yield is used as the dependent variable in a generalized linear model with climatic data and edaphic data collected from the study location in the two rice producing hubs used as independent variables to come out with a predictive yield model, that will be used to predict yield gap in rice production in these two rice producing hubs in Northern Ghana. Other interest in exploring the relationship between yield and climatic variables as well as between yield and edaphic variables were also explored using Pearson correlation test.

CHAPTER THREE

METHODS AND MATERIALS

3.1 Study Area

Data for the study was collected from the Savelugu Municipality in the Northern Region of Ghana and the Kasena-Nankana Municipality in the Upper East Region of Ghana.

3.2 The Savelugu Municipal

The Savelugu Municipality is located at the northern part of the Northern Region of Ghana. It shares boundaries with West Mamprusi to the North, Karaga to the East, Kumbungu to the West and Tamale Metropolitan Assembly to the South. The Municipality falls approximately between latitude 9°37'North and longitude 0°50'West.

The Municipality has about 149 communities with a total population of 139,283 according to the 2010 population and housing census. The municipality also has a total land area of about 1,790.70 square kilometers. A map of Savelugu Municipality with the study location is shown below.

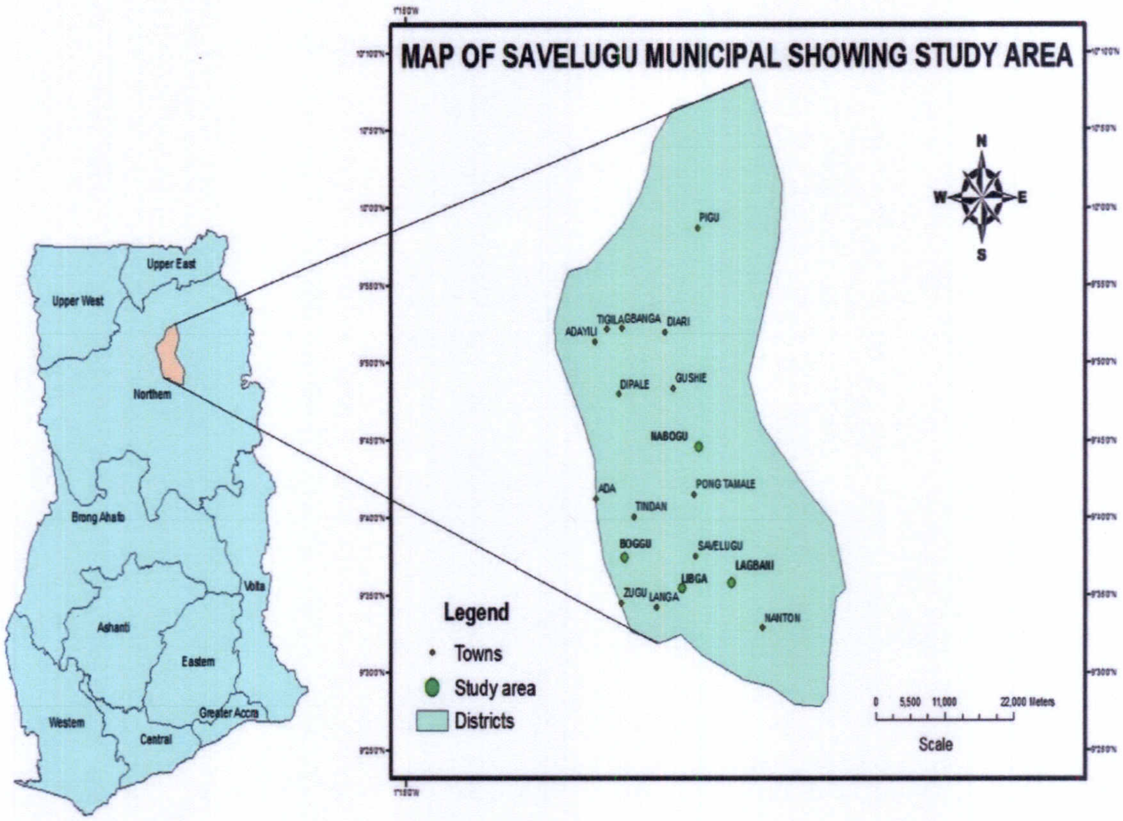


Fig 3.1 Sketch map of Savelugu Municipal showing study location

3.2.1 Soil and Drainage

The main drainage system in the Municipality is made up of White Volta and its tributaries. The Middle and Upper Voltaian sedimentary formation characterize the geology of the Municipality. The middle Voltaian covers the northern part comprises of sandstone, shale and siltstone. The Upper Voltaian covers the southern part of the Municipality and consists of shale and mudstone.

3.2.2 Climate and Vegetation

The area receives an annual rainfall averaging 600mm, considered enough for a single farming season. The annual rainfall pattern is erratic at the beginning of each raining season, starting in April.

The main vegetation of the Municipality is Savanna woodland which could sustain large scale livestock farming, as well as the cultivation of staples like rice, groundnuts, yam, cassava, maize, cowpea and sorghum.

3.3 The Kassena-Nankana Municipal

The Kassena-Nankana Municipality lies within the Guinea Savannah woodlands. It covers a land area of 1,685 square kilometers, and falls approximately between latitude 11°10' and 10°3' North and longitude 10°1'. The Municipality shares boundaries to the North with Burkina Faso, to the East with Bolgatanga Municipal, West with the Builsa District and South with West Mamprusi District (in the Northern Region). The Municipality has a total of 97 communities with a total population of 109,944 according to the 2010 population and housing census. A map of Kassena-Nankana Municipality with the study location is shown below.

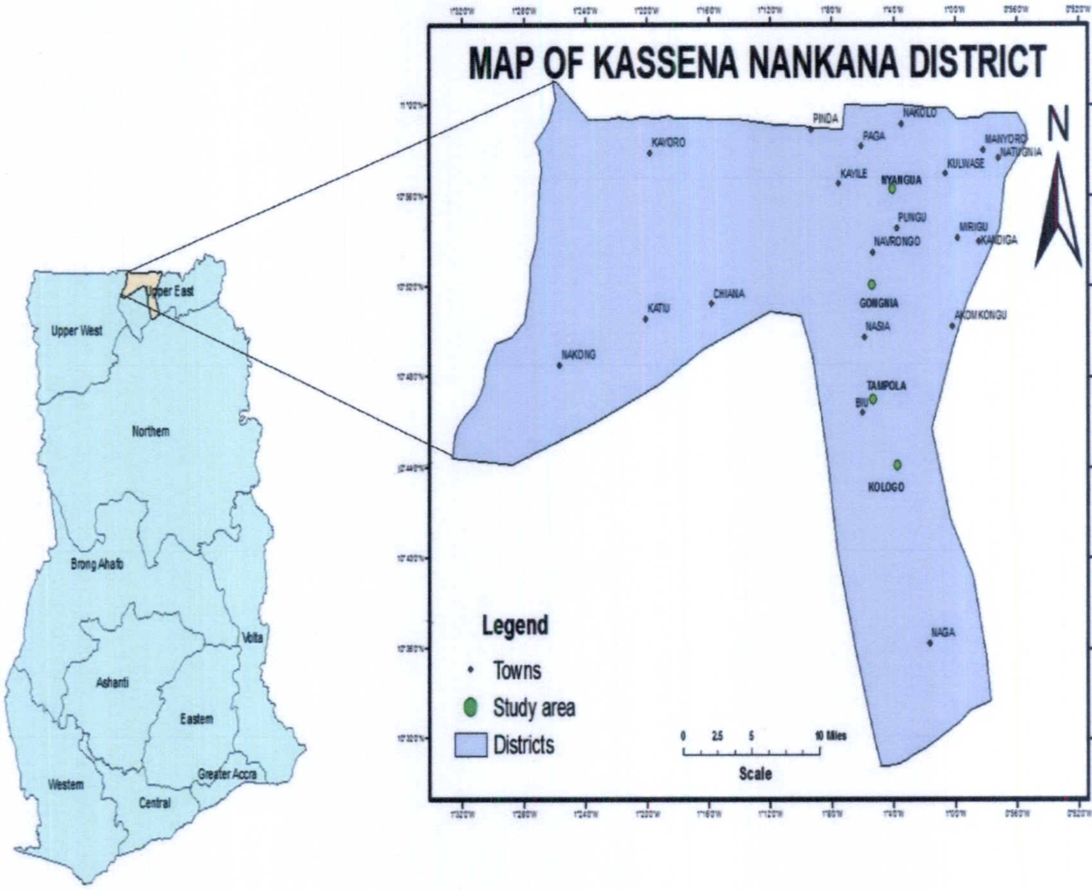


Fig 3.2. Sketch map of Kassena-Nankana Municipal showing study location

3.3.1 Soil and Drainage

Two main types of soil are present within the Municipality, namely the Savannah ochrosols and groundwater laterite. The northern and eastern parts of the Municipality are covered by the Savannah ochrosols, while the rest of the Municipality has groundwater laterite.

The drainage system of the Municipality is constituted mainly around the tributaries of the Sissili River Asibelika, Afumbeli, Bukpegi and Beeyi. A tributary of the

Asibelika River (Tono River) has been dammed to provide irrigation facilities, which is of great economic importance to the entire Municipality.

3.3.2 Climate and Vegetation

The climate conditions of the Municipality are characterized by the dry and wet seasons, the area receives an average annual rainfall of 950mm.

The Municipality is covered mainly by the Sahel and Sudan-Savannah types of vegetation's, comprising open savannah with fire-swept grassland and deciduous trees. Some of the most densely vegetated parts of the District can be found along river basins and forest reserves.

3.4 Sources of Data

Data for the study was obtained from CSIR-SARI, Ghana. Both qualitative and quantitative data were utilized from data collected from a multi-environment trial conducted across four locations within the two rice producing hubs, and a yield gap survey conducted across eight locations also within the two hubs.

The data extracted for the study from the multi-environment trial included; Days to fifty percent flowering, number of productive tillers, days to maturity, plant height (cm) at maturity, panicle length (cm), thousand grain weight (g), grain length (mm), data on yield adjusted at 14(t/ha), climatic data and edaphic data.

Data extracted from the yield gap survey included yield of farmer managed field and research managed fields which were adjusted at 14(t/ha). Socio-economic data on farmers in the two hubs was also utilized.

3.4.1 Estimation of yield adjusted at 14 (t/ha)

All yield used in the analysis was adjusted at 14(t/ha) using the agronomic relation for estimating yields at 14(t/ha).

The adjusted yield at 14(t/ha) was estimated as;

$$Quantity_{adjusted} = \frac{100 - A.M(\%)}{100 - B.\mathrm{M}(\%)} \times M.\mathrm{Q} \quad \text{.. (3.0)}$$

Kenneth and Hellevang (1995).

Where $A.M$ = Actual Moisture (%)

$B.M$ = Base Moisture (%)

$M.Q$ = Measured Quantity (%)

For the adjusted yield of rice at 14(t/ha), the standard base moisture content of 14% was incorporate into equation (3.0) to estimate the adjusted yield of rice at 14% (t/ha) as shown in equation (3.1) below.

$$Yield_{adjusted\,(rice)} = \frac{100 - M.C(\%)}{86} \times G.W_{rice} \quad \text{.. (3.1)}$$

Where $M.C\ (\%)$ = Moisture Content of rice at harvest

$G.W_{rice}$ = Grain Weight of rice at harvest

3.5 Research Design

The research design used for the study was a randomized complete block design, where blocks consisted of rainfed and irrigated fields located in Boggu and Libga respectively for the Savelugu hub and Kologo and Gongnia in Navrongo respectively for the Navrongo hub. Three (3) replications of the rice genotypes were used in all locations, and the blocks were laid 5m by 3m giving a total block size of $15m^2$.

3.6 Randomized Complete Block Design

The model for the randomized complete block design is given as:

$$Y_{kg} = \mu_{..} + \rho_g + \tau_k + \varepsilon_{kg} \quad \text{...} \quad (3.2)$$

(Nsowah-Nuamah, 2009)

Where:

Y_{kg} = the value of the response variable for the k^{th} treatment (K=1, 2,…,*t)* in the g^{th} block (g = 1,2,…,r)

$\mu_{..}$ = constant

ρ_g = block effects subject to the restriction $\sum \rho_g = 0$

τ_k = treatment effects subject to the restriction $\sum \tau_k = 0$

$\varepsilon_{kg} \sim N(0, \sigma^2)$

3.6.1 Assumptions of Randomized Complete Block Design

i. The population follows a normal distribution with means $\mu_1, \mu_2, \ldots, \mu_k$

ii. The variance σ^2 is equal for all bk combination of treatments and blocks.

iii. The samples are independent random samples in b independent blocks from each population.

iv. The error is normally, independently and identically distributed with mean of 0 and constant variance.

3.6.2 Analysis of Variance for the Randomized Complete Block Design

The analysis of randomized complete block design followed the two-way ANOVA model with one observation per cell.

The total variation in the randomized completed block design consists of three sources; blocks, treatment, and random variation as defined below:

$$SS_{Block} = t\sum_{g=1}^{r}(\bar{Y}_{.g} - \bar{Y}_{..})^2 \quad (3.3)$$

$$SS_{TR} = r\sum_{k=1}^{t}(\bar{Y}_{k.} - \bar{Y}_{..})^2 \quad (3.4)$$

$$SS_{E} = \sum_{k=1}^{t}\sum_{g=1}^{r}(Y_{kg} - \bar{Y}_{.g} - \bar{Y}_{k.} + \bar{Y}_{..})^2 \quad (3.5)$$

$$SS_{Total} = \sum_{k=1}^{t}\sum_{g=1}^{r}(\bar{Y}_{kg} - \bar{Y}_{..})^2 \quad (3.6)$$

Where:

$Y_{k.}$ = the total of observation for the k^{th} treatment, that is: $Y_{k.} = \sum_{g=1}^{r} Y_{kg}$

$\bar{Y}_{k.}$ = the sample mean for the k^{th} treatment; that is: $\bar{Y}_{k.} = \frac{\sum_{g=1}^{r} Y_{kg}}{r} = \frac{Y_{k.}}{r}$

$Y_{.g}$ = the total of observations for the g^{th} block; that is: $Y_{.g} = \sum_{k=1}^{t} Y_{kg}$

$\bar{Y}_{.g}$ = the sample mean for the g^{th} block, that is: $\bar{Y}_{.g} = \frac{\sum_{k=1}^{t} Y_{kg}}{t} = \frac{Y_{.g}}{t}$

$Y_{..}$ = the grand total of all observations in the experiment given by:

$$Y_{..} = \sum_{k=1}^{t}\sum_{g=1}^{r} Y_{kg} = \sum_{k=1}^{t} Y_{k.} = \sum_{g=1}^{r} Y_{.g}$$

$\bar{Y}_{..}$ = the overall (grand) mean for all observations and given by: $\bar{Y}_{..} = \frac{\sum_{k=1}^{t}\sum_{g=1}^{r} Y_{kg}}{rt} = \frac{Y_{..}}{rt}$

3.7 Additive Main effects and Multiplicative Interaction (AMMI) analysis

Additive main effects and multiplicative interaction analysis (AMMI) allows for a large set of technical interpretations (Duarte and Vencovsky, 1999) and uses a principal component (autovector) to interpret cultivar performance.

The AMMI method is widely used in stability and adaptability analyses because it:

i. provides an initial diagnosis of the model and is well-suited for data analysis with many environmental influences.

ii. allows greater unfolding of the G×E interaction and summarizes the patterns and relationships between genotypes and environments, and

iii. improves the accuracy of trait estimates (Gauch, 1988; Zobel *et al.*, 1988; Crossa *et al.*, 1990).

The AMMI analysis used for the study is as according to Zobel *et al.* (1988) which combines in a single model additive components for the main effects of genotype (g_i) and environments (e_j), and multiplicative components for the effect of GE interaction (ge_{ij}).

The AMMI model for genotypes and environments is given as:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n \alpha_{in} \gamma_{jn} + \varepsilon_{ij} \quad \text{...} \quad (3.7)$$

Y_{ij} = overall mean yield

μ = is the general mean

g_i = the effects of genotype *i*

e_j = the effects of environment *j*

λ_n = the eigen value of the principal component analysis (PCA) axes, n.

α_{in} = the i^{th} genotype PCA score for n the PCA axes

γ_{jn} = the j^{th} environment PCA score for the n^{th} PCA axes

N = the number of PCA axes retained on the model.

$e_{ij} \sim N(0,\sigma^2)$; i = 1, 2, …,G J = 1,2,…, E

3.7.1 Assumptions of the AMMI model

i. The error is normally and independently distributed

ii. The variance is homogeneous

And the multiplicative interaction term satisfy the constraints

$\lambda_1 > \lambda_2 > \ldots > \lambda_N > 0$

The genotype and environment PCA scores are expressed as a unit vector times the square root of the eigen vector, that is:

$$\lambda_n \alpha_{ij} \gamma_{jn} = (\sqrt{\lambda_n \alpha_{in}})(\sqrt{\lambda_n \gamma_{jn}}) \quad \text{...} (3.8)$$

Where:

$\sqrt{\lambda_n \alpha_{in}}$ = Genotype score

$\sqrt{\lambda_n \gamma_{jn}}$ = Environmental score,

3.8 Genotype main effects and Genotype by Environment (GGE) Biplot

The GGE-biplot methodology, which is composed of 2 concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.,* 2000), was used to visually analyze the multi environment yield trials (MEYTs) data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the sources of variation in genotype by environment interaction analysis of MEYTs data (Yan *et al.,* 2000, 2001). The GGE-biplot shows the first 2 principal components, that is the PC1 and PC2, also referred to as primary and secondary effects, which is derived from subjecting environment-centered yield data, that is yield variation due to GGE to singular value decomposition (Yan *et al.,* 2000).

The GGE Biplot method used in this study is based on the model outlined by Yan *et al.,* (2000):

$$Y_{ij} - \bar{y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad \text{..} (3.9)$$

Where

Y_{ij} = the grain yield mean of the i^{th} cultivar, in the j^{th} environment

$\bar{y}_j$ = the overall mean of the cultivars in the j^{th} environment

$\lambda_1 \xi_{i1} \eta_{j1}$ = the first principal component (IPCA1)

$\lambda_2 \xi_{i2} \eta_{j2}$ = the second principal component (IPCA2)

λ_1 and λ_2 are the autovalues (characteristic roots) associated with IPCA1 and IPCA2, respectively.

ξ_{i1} and ξ_{i2} are scores of the first and second principal components, respectively, for the i^{th} cultivar.

η_{ji} and η_{j2} are the scores of the first and second principal components, respectively, for the j^{th} environment.

ε_{ij} is the error associated with the model.

The values of $\lambda_1, \lambda_2, \xi_{i1}, \xi_{i2}$, η_{ji} and η_{j2} according to Muungani *et al.*, (2007) are obtained all together by subjecting the environment centered data ($Y_{ij} - \bar{y}_j$) to singular value decomposition (SVD).

3.9 Yield Stability and Adoptability Analysis

Yield stability of a cultivar is defined as a similarity (consistency) degree of its yield response function across environments to mean of all studied cultivar yield response function (Abeysiriwardena *et al.*, 1991; Annicchiarico, 2002). When genotype by environment (GE) interactions are present, it is important to analyze them and utilize the results in evaluating wide adaptability of crop cultivars (Kang, 1998).

Adaptability of a crop cultivar is the cultivars wide adaptation or specific adaptation of its relatively high mean productivity (measured usually by yield) and yield stability across environments either in locations or seasons or both (Anputhas *et al.*, 2011).

As a means of assessment, adaptability of a crop variety is defined as a function of both mean productivity and production stability is further defined as a function of yield variation due to changing environment (Abeysiriwardena *et al.*, 1991).

In order to evaluate cultivars for both yield mean and stability, two parameters are defined on the basis of variety environmental yield deviations d_{ijk}. The first parameter is mean deviation across locations for each variety, D_k calculated as:

$$D_k = \frac{d_{\bullet\bullet k}}{nq} \quad \text{.......... (3.10)}$$

(Anputhas *et al.*, 2011)

Where n is number of environment or locations, q is number of blocks, $d_{\bullet\bullet k}$ is sum of yield deviation over blocks and locations for k^{th} variety. The D_k would estimate the average effect of a variety and be either positive, negative or zero. The second parameter is stability measure for each variety, s_k^2 called also cultivar interaction variance. It can be computed as:

$$s_k^2 = \left[\sum_{i=1}^{n} d_{i\bullet k}^2 - \frac{\sum_{i=1}^{n} (d_{i\bullet k})^2}{n} \right] / q(n-1) \quad \text{.......... (3.11)}$$

Where:

s_k^2 = stability measure

$d_{i\bullet k}$ = mean of environmental yield deviation over blocks for k^{th} variety in i^{th} environment, n is number of environments or locations, q is number of blocks.

With above estimates of parameters selection of varieties for recommendation is made as follows:

i. Select for non-significant s_k^2 in a case of recommending cultivars for yield stability only. This would identify most stable varieties in the test, where s_k^2 value close to zero for stability indicates that the variety does not interact with the environment in an unpredictable manner and thus as the environment improves the performance of the variety, it improves it in a predictable manner.

ii. Select simultaneously for higher D_k and less, that is rather non-significant in a case of recommending cultivars for wide adaptation, that is cultivars indicating compromisely both belonging to those highest D_k and least or non-significant s_k^2 for yield, which show high level of wide adaptation.

iii. A variety with the highest $d_{i\bullet k}$ in a particular location is the most adaptable one for that location regardless of its D_k and s_k^2, this cultivar shows the local (wide) adaptation to this particular location, that is according to the rule of "which won where" (Yan and Kang, 2003; Kang, *et al.,* 2006).

3.9.1 AMMI Stability Value (ASV)

The ASV is the distance from zero in a two dimensional scattergram of the Interaction Principal Component Analysis axis 1 (IPCA1) scores against the Interaction Principal Component Analysis axis 2 (IPCA2) scores. Since the IPCA1 score contributes more to GE sum of square, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total Genotype by Environment sum of squares. The distance from zero is then determined using the theorem of Pythagoras (Purchase *et al.,* 2000).

The AMMI stability value was calculated as:

$$ASV = \sqrt{\left[\frac{IPCA1_{sumofsqaure}}{IPCA2_{sumofsquare}}(IPCA1_{score})\right]^2 + (IPCA2_{score})^2} \quad \text{.......................} \quad (3.12)$$

(Purchase *et al.* 2000)

Where $\frac{IPCA1_{sumofsquare}}{IPCA2_{sumofsquare}}$ .... (3.13)

is the weight derived from dividing the sum of IPCA1 squares by the sum of IPCA2 squares. The larger the absolute value of IPCA, the greater the adaptability of a specific variety for a certain environment. Conversely, lower ASV values indicate greater stability in different environments.

3.9.2 Yield Stability Index (YSI)

Stability should however not be the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammadi *et al.,* 2007; Mohammadi and Amri, 2008), hence there is a need for approaches that incorporate both mean yield and stability in a single index. In this regard, as ASV takes into account both IPCA1 and IPCA2 that justify most of the variation in the Genotype by Environment interaction, therefore the rank of ASV and yield mean in such a way that the lowest ASV takes the rank one, while the highest yield mean takes the rank one and then the ranks are summed in a single simultaneous selection index of yield and yield stability named as: yield stability index (YSI). The least YSI is considered as the most stable with high grain yield.

The yield stability index (YSI) is calculated as:

$$YSI = RASV + RY \qquad (3.14)$$

(Bose *et al.*, 2014)

Where $RASV$ is the rank of the AMMI stability value and RY is the rank of the mean grain yield of genotypes (RY) across environments.

3.9.3 Rank Sum

The *RS* incorporates both yield and yield stability in a single non-parametric index. Low values of both parameters show desirable genotypes with high mean yield and stability (Farshadfar *et al.,* 2011).

The Rank Sum is calculated as:

RS = Rank mean *(R)* + Standard deviation of rank *(SDR)* .... (3.15)

(Bose *et al.*, 2014)

Where *RS* = Rank Sum

The standard deviation of rank (*SDR*) was measured as:

$$S_i = \sqrt{\frac{\sum_{j-1}^{m}(R_{ij} - \bar{R}_i)^2}{l-1}} \quad \text{...} \quad (3.16)$$

Where:

R_{ij} = the rank of X_{ij} in the j^{th} environment, $\bar{R}_i$ is the mean rank across all environments for the i^{th} genotype, and

$SDR = (S_i^2)^{0.5}$ .... (3.17)

3.10 Pearson coefficient of correlation

To estimate the relationship between yield and agronomic trait characters, Karl Pearson's coefficient of correlation known as correlation coefficient r_{xy} was used. This was based on the variance and covariance of the variables and ranged between -1 and +1. It is given by:

$$r_{xy} = V\frac{Cov(x,y)}{\sqrt{V(x)\mathrm{V(y)}}} \quad \text{.......} \quad (3.18)$$

Variances and covariance are calculated by the following formulae:

$$V(x) = \frac{1}{n}\left[\sum x^2 - \frac{\left(\sum x\right)^2}{n}\right] \quad \text{.......} \quad (3.19)$$

$$V(y) = \frac{1}{n}\left[\sum y^2 - \frac{\left(\sum y\right)^2}{n}\right] \quad \text{.......} \quad (3.20)$$

$$Cov(x,y) = \frac{1}{n}\left[\sum xy - \frac{\left(\sum x\right)\left(\sum y\right)}{n}\right] \quad \text{.......} \quad (3.21)$$

To test the significance of correlation coefficient, the calculated t-value was compared with tabulated t-value at (n-2) degree of freedom (Mugemangango and Vinod, 2011):

$$t_{cal} = \frac{r}{\sqrt{1-r^2}} \times \sqrt{n-2} \quad \text{.......} \quad (3.22)$$

3.11 Path Coefficient Analysis

The technique of path analysis used in this study is an extension of a standardized

arranged in an orderly manner and examined through a series of regression equations. This unlike the conventional multiple regression and correlation analysis, it was possible to isolate the direct effects and the indirect effects of each independent variable on the dependent variable.

The correlation coefficients were partitioned into direct and indirect effects, yield was taken as dependent variable (effect) which was assumed to be influenced by the other characters like fifty percent flowering, number of productive tillers, days to maturity, plant height at maturity (cm), panicle length (cm), thousand grain weight (g), grain length (mm) called independent variables.

In order to describe the cause-effect system of the relationship between yield and the selected explanatory variables, the following simple linear model proposed by Iwunor (1999) was used.

$$X_0 = P_{01}X_1 + ... + P_7X_7 \qquad (3.23)$$

Where,

X_0 = grain yield (t/ha), X_1 = Days to fifty percent flowering, X_2 = Number of effective tillers,
X_3 = Days to maturity, X_4 = Plant height at maturity (cm), X_5 = 1000 grain weight,
X_6 = grain length (mm), X_7 = Panicle length (cm), e = residual effects

and P_{0i} is the path coefficient denoting the direct effects of X_i on X_0.

The analysis of path model is done by solving the simultaneous system of linear equations:

$$r_{0i} = \sum_{j=1}^{7} P_{oi} r_{ij}\ ,\ i = 1, 2, \ldots, 7 \ldots\ldots (3.24)$$

Where r_{0i} is the correlation coefficient between X_i and X_0 and r_{ij} is the correlation coefficient between X_i and X_j. The solution of the system of equation in (3.24) gives the path coefficient.

The total effect of X_i on X_0 can be decomposed into:

Total effect = Direct effect and Indirect effect .... (3.25)

The effect of residual factor (z) which measures the contribution of remaining traits not included in the path coefficient analysis is estimated as follows:

$$P_{zy} = \sqrt{1 - R^2} \ldots\ldots (3.26)$$

Where R^2 is the coefficient of multiple determinations defined by:

$$R^2 = \sum_i P_{iY}^2 + 2\sum_{i<j} P_{iY} P_{jY} r_{ij} \ldots\ldots (3.27)$$

Also fundamental to the path analysis is the path diagram. The path diagram is a diagrammatic representation of the pattern of linkages between the explanatory variables fifty percent flowering, number of productive tillers, days to maturity, plant height at maturity (cm), panicle length (cm), thousand grain weight (g), grain length (mm) as well as the path through which these linkages influence the dependent variable yield. This diagram is based on the conceptual framework of the nature of the interrelationships among the variables.

3.12 Technical Efficiency and Inefficiency Analysis

3.12.1 Stochastic frontier model

The stochastic frontier model is used to parametrically estimate production frontiers and technical efficiency levels in crop production. The stochastic frontier framework accounts for the stochastic nature of agricultural production and also allows for estimating inefficiency effects in a single approach. Within the stochastic frontier framework, proposed by Aigner *et al.* (1977) and Meeusen and van den Broeck (1977), the econometric technology of the crop producers can be represented by:

$$y_i = f(x_i;\beta).\exp\{v_i - u_i\} \quad (3.28)$$

With $\varepsilon_i = v_i - u_i$ and $i = 1,2,3,\ldots N$

Where

y_i = the crop output of the i^{th} farm

x_i = vector of inputs

β = vector of unknown parameters to be estimated

ε_i = error term

v_i = the symmetric (random) error term accounting for measurement errors and other factors not under the control of operators

u_i = the asymmetric error term denoting technical inefficiency.

It is assumed that the two-sided random errors v_i are independently and identically distributed with zero mean and variance, σ_v^2 and the u_i and v_i are distributed independently of each other and of the explanatory variables. Further assumptions made regarding the distribution of the u_i, to enable the determination of the density function for ε_i for use in a maximum likelihood estimation procedure, are considered subsequently. Within the framework of equation (1) technical efficiency is given by:

$$TE_i = \frac{f(x_i;\beta).\exp\{v_i - u_i\}}{f(x_i;\beta).\exp\{v_i\}} = \exp\{-u\} \quad \text{(3.29)}$$

With $0 \leq TE_i \leq 1$

The marginal density function for the error term $\varepsilon_i = v_i - u_i$ is given by:

$$f(\varepsilon_i) = \left(2/\sigma\right).\phi\left(\varepsilon_i/\sigma\right).\Phi\left(-\varepsilon_i\lambda/\sigma\right) \quad \text{(3.30)}$$

(Greene, 2008; Kumbhakar and Lovell, 2000)

For $-\infty < \varepsilon_i < \infty$

Where:

$$\sigma = \sigma_u^2 + \sigma_v^2 \quad \text{.......... (3.31)}$$

and

$$\lambda = \sigma_u / \sigma_v \quad \text{.......... (3.32)}$$

are the parameterized variance parameters, and

$\phi\left(\varepsilon_i\lambda / \sigma\right)$ and $\Phi\left(-\varepsilon_i\lambda / \sigma\right)$ are the standard normal density and cumulative distribution functions, respectively. The log-likelihood function is then formed from the equation above from which estimates for β, σ and λ are obtained using maximum likelihood estimation procedure. Using the conditional mean function, $E(u_i \mid \varepsilon_i)$, the inefficiency component, from which individual technical efficiency is predicted, can be separated from the estimate of ε_i as described by Jondrow *et al.* (1982):

$$E(u_i \mid \varepsilon_i) = \frac{\sigma\lambda}{1+\lambda^2}\left[\frac{\phi\left(\varepsilon_i\lambda / \sigma\right)}{1-\Phi\left(-\varepsilon_i\lambda / \sigma\right)} - \frac{\varepsilon_i\lambda}{\sigma}\right] \quad \text{.......... (3.33)}$$

Other assumptions regarding the distribution of the u_i include:

i. Stevenson's (1980) generalization of the half normal model which yields the truncated normal distribution

ii. The exponential distribution proposed by Aigner *et al.* (1977) and Meeusen and van den Broeck (1977), and

iii. The gamma distribution, a generalization of the normal-exponential model (introduced by Greene (1980a, 1980b) and Stevenson (1980), and later extended by Greene (1990)).

Using the stated distributions for the one-sided non-negative error term; assume the translog functional form given by:

$$\ln Y_i = \beta_0 + \sum_{k=1}^{4} \beta_k \ln x_{ik} + \frac{1}{2}\sum_{k=1}^{4}\sum_{j=1}^{4} \beta_{jk} \ln x_{ik} \ln x_{ij} + v_i - u_i \quad \text{.........................} (3.34)$$

Where:

Y = value of crop output

X = is a set of four input categories (Farm size, Seed, Inorganic fertilizer, Labour).

β = parameters to be estimated

v = the symmetric disturbance term accounting for random shocks and other statistical noise, and

u = the one-sided non-negative random term depicting inefficiency in production.

The subscripts $i, j,$ refers to the i-th farmer (i = 1, 2,…,82), and the j –th input (j = 1,2,…,4).

The inefficiency component of the stochastic frontier is further specified as:

$$u_i = \delta_0 + \sum_{l=1}^{4} \delta_l Z_{il} + \epsilon_i \quad \text{...} (3.35)$$

Where:

δ_i = a set of parameters to be estimated, where $i = 0, l$

Z_{il} = a set of variables explaining inefficiency – which are; age, educational level, household size, number of extension contact per year, rice farming experience and a membership of farmer based organization are the farm/farmer characteristics that have direct influence on the farmers' efficiency and

ϵ_i = the error term in the inefficiency component.

The empirical model estimated is as specified according to Awunyo-Vitor *et al.* (2013) as:

$$\begin{aligned} \ln yield &= \beta_0 + \beta_1 \ln Fmsize + \beta_2 Seed + \beta_3 Fert + \beta_4 lab + \\ &\delta_1 Age + \delta_2 Edu + \delta_3 Hhs + \delta_4 Extcon + \delta_5 Far\exp + \delta_6 FBO + u \end{aligned} \quad \text{.....................} (3.36)$$

Where:

$yield$ = Output of rice measured in t/ha

$Fmsize$ = land area measured in hectares

$Seed$ = Seed input measured in kilograms

$Fert$ = quantity of inorganic fertilizer measured in bags

lab = measured in man/days

Age = Age (years)

Edu = Education (1=Educated 0=Not educated)

Hhs = Household size of farmers (Numbers)

$Farmexp$ = Farming experience in number of years

$Extcon$ = Extension contact (1=Contact and 0= No contact)

FBO = Farmer Based Organization (1=Member and 0=Non-member)

u = Error term.

In this study, parameters of the stochastic frontier production function ($\beta_0 - \beta_4$ and $\delta_1 - \delta_6$) are estimated using maximum likelihood estimation method.

3.13 Generalized Linear Models

i. A generalized linear model is made up of a linear predictor

$$\eta_i = \beta_0 + \beta_1 x_{1i} + ... + \beta_p x_{pi} \qquad (3.37)$$

And two functions

ii. A link function that describes how the mean, $E(Y_i) = \mu_i$ depends on the linear predictor

$$g(\mu_i) = \eta_i \qquad (3.38)$$

iii. A variance function that describes how the variance, $\mathrm{var}(Y_i)$ depends on the mean

$$\mathrm{var}(Y_i) = \phi V(\mu) \quad (3.39)$$

Where the dispersion parameter ϕ is constant.

The model is partitioned into three components, that is:

i. The Random component, which identifies Y_i response and its probability distribution. Y_i is assumed to follow distribution that belongs to the exponential family.

$$Y_i \mid X_i \sim f(\theta_i, \phi) \quad (3.40)$$

Where ϕ is the dispersion parameter.

ii. Systematic component, where we have explanatory variables in a linear predictor function. Given covariates X_i, the mean of Y_i can be expressed in terms of the following linear combination of predictors.

$$\eta_i = X_i^T \beta \quad (3.41)$$

iii. Link function component, which is an invertible function that links the mean of the response to the systematic component. This link function associates the linear combination of predictors with the transformed mean response.

$$\eta_i = g(\mu_i) \quad (3.42)$$

Where $\mu_i = E(Y_i \mid X_i)$ .... (3.43)

In the random component of Generalized Linear Model, Y_i is assumed to follow a probability distribution that belongs to the exponential family.

The density functions of the exponential family of distributions have this general form:

$$f(y;\theta,\phi) = \exp\left\{\frac{y\theta - b(\theta)}{a(\phi)} + c(y,\phi)\right\} \quad (3.44)$$

Where θ is called the canonical parameter and ϕ the scale (dispersion) parameter.

$a(\phi)$ and $b(\theta)$ are some specific functions that distinguish one member of the exponential family from another. If ϕ is known, this is an exponential family model with only canonical parameter of θ.

3.13.1 Assumptions of the Generalized Linear Model

Four major assumptions underlie the Generalized Linear Model

Linearity, the assumption of linearity implies that the relationship between the dependent variable and the recently freed independent variable is also linear.

Normality of the residuals, the normality assumption implies that the dependent variable is normally distributed within each group.

Equality of residual variances, the assumption of the equality of residual variances holds that all these variances will be the same.

Fixed independent variables measured without error, this assumption is required only when one wishes to have a point estimate of the population parameter.

3.13.2 Maximum Likelihood Estimation for GLMs

Solve score equations, for $j = 1,\ldots, p, S_j(\beta) = \dfrac{\partial \ell}{\partial \beta_j} = 0$ .... (3.45)

The Log-likelihood:

$$\ell = \sum_{i=1}^{m} \left\{ \frac{y_i\theta_i - b(\theta_i)}{a(\phi)} + c(y_i, \phi) \right\} = \sum_i \ell_i \quad \ldots\ldots (3.46)$$

$$S_j(\beta) = \frac{\partial \ell}{\partial \beta_j} = \sum_i \frac{\partial \ell}{\partial \theta_i} \frac{\partial \theta_i}{\partial \mu_i} \frac{\partial \mu_i}{\partial \eta_i} \frac{\partial \eta_i}{\partial \beta_j}$$

$$\frac{\partial \ell_i}{\partial \theta_i} = \frac{1}{a(\phi)}(y_i - b'(\theta_i)) = \frac{1}{a(\phi)}(y_i - \mu_i)$$

$$\frac{\partial \theta_i}{\partial \mu_i} = \left(\frac{\partial \mu_i}{\partial \theta_i} \right)^{-1} = \left(\frac{\partial b'(\theta_i)}{\partial \theta_i} \right)^{-1} = \frac{1}{b''(\theta_i)} = \frac{1}{V(\mu_i)}$$

$$\frac{\partial \mu_i}{\partial \eta_i} = \left(\frac{\partial \eta_i}{\partial \mu_i} \right)^{-1} = \left(\frac{\partial g(\mu_i)}{\partial \mu_i} \right)^{-1} = \frac{1}{g'(\mu_i)}$$

$$\frac{\partial \eta_i}{\partial \beta_j} = X_{ij} \quad \ldots\ldots (3.47)$$

Therefore

$$S_j(\beta)=\sum_{i=1}^{m}\frac{X_{ij}}{g'(\mu_i)}[a(\phi)V(\mu_i)]^{-1}(y_i-\mu_i) \quad (3.48)$$

$$\left(\frac{\partial\mu_i}{\partial\beta_j}\right)=\frac{X_{ij}}{g'(\mu_i)}: \text{Jacobian matrix} \quad (3.49)$$

For fixed ϕ, the score function depends on μ_i and V_i only.

No knowledge on ϕ is needed for deriving the MLE of β

We write (3.48) in the form

$$S(\beta)=\sum_{i=1}^{m}\left(\frac{\partial\mu_i}{\partial\beta}\right)^T[a(\phi)V(\mu_i)]^{-1}(y_i-\mu_i) \quad (3.50)$$

Hence, the Fisher's Information is:

$$I(\beta)=-E\frac{\partial S(\beta)}{\partial\beta}=\sum_i\left(\frac{\partial\mu_i}{\partial\beta}\right)^T[a(\phi)V(\mu_i)]^{-1}\left(\frac{\partial\mu_i}{\partial\beta}\right) \quad (3.51)$$

The observed counterpart is:

$$-\partial S(\beta)/\partial\beta=I(\beta)-\sum_{i=1}^{m}\frac{\partial A_i}{\partial\beta}(y_i-\mu_i(\beta)) \quad (3.52)$$

Where $A_i=\left(\frac{\partial\mu_i}{\partial\beta}\right)^T[a(\phi)V(\mu_i)]^{-1}$ (3.53)

For canonical links, the observed one equals the expected one, that is:

$$I(\beta,\phi) = E\left\{\frac{\partial^2 S(\beta)}{\partial\beta\partial\phi}\right\} = 0 \quad (3.54)$$

The information matrix is of the form

$$\begin{pmatrix} I(\beta) & 0 \\ 0 & I(\phi) \end{pmatrix}$$

The MLEs β and ϕ are asymptotically independent, $I^{-1}(\beta)$ is the asymptotic variance of β and $I^{-1}(\beta)$ is the asymptotic variance of ϕ . .

3.14. Model Diagnosis

Like ordinary linear models, residuals can be used to assess model fit. For Generalized Linear Models, we require extended definitions of residuals.

Types of Residuals

Pearson residuals (standardized residuals)

$$r_P = \frac{y-\hat{\mu}}{\sqrt{V(\hat{\mu})}} \quad (3.55)$$

Constant variance and mean zero if the variance function is correctly specified.

Useful for detecting variance misspecification (and autocorrelation).

Deviance residuals: contribution of Y_i to the deviance.

$$r_D = sign(y-\mu)\sqrt{d_i} \quad (3.56)$$

Where $\sum_{i=1}^{m} d_i = D \quad (3.57)$

Closer to a normal distribution (less skewed) than Pearson residuals.

Often better for spotting outliers.

3.15 Data validation techniques.

Data for the analysis was subjected to a series of validation tests to ensure that it followed the assumption of linearity, independence, normality, and homoscedasticity of the variance. The variance for the yield from the yield gap was validated using the Jackknife procedure.

3.15.1 Checking for Independence

To check the assumption of independence in the study, a plot of residuals against climatic, edaphic and yield contributing variables and any other variables used in the study was carried out. A pattern that is not random in the plot will suggest lack of independence.

3.15.2 Checking for linearity

A plot of the residual versus the predictor was carried out. A random pattern of the plot suggested that a simple linear model was appropriate, whilst a non-random pattern suggested that a simple linear model was not appropriate and the response or predictor needed to be transformed or a quadratic or higher term needed to be added to the model.

3.15.3 Test of Normality Assumption

The Shapiro Wilk test of normality was used in the study to test the assumption of normality. The null hypothesis H_0 of the data being normally distributed was tested against the alternative hypothesis H_1 of the data not being normally distributed.

The test statistic (*W*) for normality is given as:

$$W = \frac{R^4\hat{\sigma}^2}{C^2S^2} = \frac{b^2}{S^2} = \frac{(a'y)^2}{S^2} = \left(\sum_{i=1}^{n} a_i y_i\right)^2 / \sum_{i=1}^{n}(y_i - \bar{y})^2 \text{ .... } (3.58)$$

Shapiro and Wilk (1965)

Where:

$R^2 = m'V^{-1}m$

$C^2 = m'V^{-1}V^{-1}m$

$a' = (a_1, \ldots, a_n) = \dfrac{m'V^{-1}}{(m'V^{-1}V^{-1}m)^{\frac{1}{2}}}$

$b = R^2\hat{\sigma} / C$

$m' = (m_1, m_2, \ldots, m_n)$ is the vector of expected values of standard normal order statistics.

$V = (v_{ij})$ is the corresponding $n \times n$ covariance matrix.

W is always greater than zero and less or equal to 1, that is ($0 < W \leq 1$). Hence small values of W will lead to the rejection of the null hypothesis of normality.

3.15.4 Jackknife bias, variance, confidence and interval

The jackknife bias, variance and confidence intervals are estimated by using the following equations from $F_{(\hat{\beta}^{(J)})}$ distribution defined by Miller (1974).

The jackknife bias is given by:

$$bi\hat{a}s_J(\hat{\beta}) = (n-1)(\hat{\beta}^{(J)} - \hat{\beta}) \qquad (3.59)$$

And the jackknife variance is estimated as:

$$\operatorname{var}(\hat{\beta}^{(J)}) = \frac{(n-1)}{n} \sum_{i=1}^{n} \left(\hat{\beta}^{(Ji)} - \hat{\beta}^{(J)}\right)\left(\hat{\beta}^{(Ji)} - \hat{\beta}^{(J)}\right)' \qquad (3.60)$$

Where $\hat{\beta}_j^{(Ji)}$ is the estimate produced from the replicate with i^{th} observation set or i^{th} group deleted according to Friedl and Stampfer (2002a).

Jackknife $(1-\alpha)100\%$ confidence interval is estimated according to Efron and Tibshirani (1993), which is given by:

$$\hat{\beta}^{(J)} - t_{n-p,\alpha/2} * S_e(\hat{\beta}^{(J)}) < \beta < \hat{\beta}^{(J)} + t_{n-p,\alpha/2} * S_e(\hat{\beta}^{(J)}) \qquad (3.61)$$

Where $t_{n-p,\alpha/2}$ is the critical value of t with probability $\alpha/2$ for $n-p$ degrees of freedom; and

$S_e(\hat{\beta}^{(J)})$ is the standard error of the $\hat{\beta}^{(J)}$.

3.15.5 Variance Inflation Factor and Tolerance test for Multicollinearity (VIF test)

These two measures are used to identify multicollinearity among predictor variables. Consider the linear model below

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + ... + \beta_j X_j + \varepsilon \quad (3.62)$$

The estimate of the variance of β_j can be expressed as

$$\text{var}(\hat{\beta}_j) = \frac{s^2}{(n-1)\text{var}(X_j)} \cdot \frac{1}{1-R_j^2} \quad (3.63)$$

Where: R_j^2 is the multiple R^2 for the regression X_j on other covariates.

s = Standard deviation

n = sample size

$\text{var}(X_j)$ = estimated variance of X_j

The variance inflation factor is estimated as: $VIF(\hat{\beta}_j) = \frac{1}{1-R_j^2}$ .... (3.64)

The Tolerance is estimated as: $Tolerance(\hat{\beta}_j) = \frac{1}{VIF} = 1 - R^2$ .... (3.65)

The higher the value of *VIF* (> 10) or the lower the value of the tolerance index, the higher the variance of $\hat{\beta}_j$ and the greater the chance of finding β_j insignificant, which means severe multicollinearity is present.

Table 4.1: Summary statistics of Socio-economic characteristics of rice farmers in the two hubs

Variable	Unit	Savelugu hub (Average statistics)	Navrongo hub (Average statistics)	Overall (Average statistics)
Gender:				
Male	%	90.24	60.98	73.17
Female	%	9.76	39.02	26.83
Educational level				
None	%	75.61	48.78	62.20
Primary	%	0.00	14.65	7.32
JHS	%	17.07	17.05	17.07
SHS	%	7.32	12.20	9.76
Tertiary	%	0.00	7.32	3.65
Membership of FBO				
Member	%	70.73	68.29	69.51
Non-member	%	29.27	31.71	30.49
Extension contact	Number	2	3	2
Quantity of inorganic fertilizer	Bags	5	4	4
Quantity of seeds	Kg	142.80	64.88	103.80
Off farm income	GH¢	2,569.17	2,406.83	2,488.00
Total labour	Man/day	230	121	176
Age	Years	38	41	39
Household size	Number	13	8	11
Farming experience	Years	18	17	17
Sample size	Number	41	41	82

CHAPTER FOUR

RESULTS AND DISCUSSIONS

4.1 Socio-Economic characteristics of rice farmers in the two hubs

The result (Table 4.1) indicates that rice farming is dominated by males across the two hubs (73.17%). Majority of the farmers (62.2%) interviewed across the two hubs are not educated, with the proportion of educated farmers (17.07%) having JHS education.

Majority of the farmers interviewed (69.51%) were also members of Farmer Based Organizations (FBO's) in their respective communities, with a greater proportion (70.73%) of membership found in the Savelugu hub compared to the Navrongo hub (68.29%).

4.2 Pearson Correlation Analysis

Grain yield was significantly positively correlated with panicle length (Table 4.2), but with a low magnitude. The correlation between grain yield with number of productive tillers, days to maturity, plant height at maturity and grain length was however a positive non-significant one of lower magnitude.

Days to 50% flowering and thousand grain weight on the other hand had a negative non-significant correlation of low magnitude with grain yield.

A significant positive correlation of very high magnitude was recorded between days to 50% flowering and days to maturity and also between plant height at maturity and panicle length.

Days to 50% flowering was significantly positively correlated with plant height at maturity, panicle length and grain length. Plant height at maturity, grain length and panicle length also had a positive significant association with days to maturity.

The correlation between plant height at maturity and panicle length with grain length was also a significant positive one, as seen in Table 4.2.

Table 4.2 Correlation coefficients (r) among yield and its contributing characters

Characters	Days to 50% flowering	1000 grain weight (g)	No. of Productive tillers	Days to Maturity	Plant height at maturity (cm)	Panicle Length (cm)	Grain length (mm)	Grain Yield (t/ha)
Days to 50% flowering	1	-0.066	0.078	0.997**	0.501**	0.381**	0.499**	-0.029
1000 grain weight (g)		1	0.019	-0.060	-0.392**	-0.407**	-0.269**	-0.039
No. of productive tillers			1	0.082	-0.333**	-0.014	0.087	0.021
Days to maturity				1	0.506**	0.401**	0.503**	0.023
Plant height at maturity (cm)					1	0.805**	0.434**	0.237
Panicle length (cm)						1	0.537**	0.469**
Grain length (mm)							1	0.055
Grain Yield (t/ha)								1

** = Significant (P<0.05)

4.3 Multi-Environment Trial (MET) Analysis

The environment (E) was found to be a major determinant of yield as it posited a significant P-value of 0.0001 across the two hubs (Table 4.3). Yield performance across genotypes (G) and the interaction between the genotypes and the environment (GxE) were also observed to be significant ($P < 0.05$) across the two hubs, for the fifteen (15) rice genotypes evaluated using the Multi-Environment Trial (MET) analysis.

Table 4.3: Combined analysis of variance for grain yield under rainfed and irrigated conditions

Source of variation	Df	Sum of Squares	Mean Square	% of total SS	P > 0.05
Environment (E)	3	47.136	15.712	37.4	<0.0001
Genotype (G)	14	34.366	2.455	27.3	<0.0001
Genotype*Environment(GxE)	42	15.532	0.369	12.3	0.0396
Error	120	29.078	0.242		
Total	179	126.112			
CV %					16.92
R-squared					0.769

It was realized that the genotype *GH1837* was high yielding compared to other genotypes for the combined environments (irrigated and rainfed), whilst the genotypes Sebota41 and Sebota69 were the lowest in terms of yield performance as can be seen in Table 4.4

For combined irrigated environments, the genotype *GH1837* was also found to be the highest yielding genotype, whilst Sebota69 was observed to be the lowest yielding genotype. The genotype *GH1837* was again observed to be the highest yielding for combined rainfed environments, whilst the lowest yielding genotype was *Matigey*.

For the location specific environments, the genotype *GH1837* was again found to have the highest yield performance across three out of the four environments. That is the Gongnia (irrigated) and Kologo (Rainfed) in the Navrongo hub and Libga (irrigated) in the Savelugu hub respectively, whilst the genotypes *Koshihikari*, *Basmati 370-1* and *Local Basmati-2* were found to have the lowest yield across these three environments respectively. For the Boggu environment (Rainfed) in the Savelugu hub, the genotype *Perfume (short)* was the highest yielding whilst the genotype *Matigey* was the least in terms of yield performance.

Table 4.4: Mean grain yield under rainfed and irrigated conditions

Genotype	Combined Environment Yields (t/ha)			Location Specific Yields (t/ha)			
	Combined Environments	Irrigated Env.	Rainfed Env.	Irrigated Gongnia	Irrigated Libga	Rainfed Kologo	Rainfed Boggu
Basmati 370-1	2.71	2.76	2.76	3.45	2.06	2.87	2.47
GH1837	3.77	3.99	3.54	4.68	3.31	4.12	2.97
Good and new (JP)	3.63	3.75	3.51	4.62	2.87	4.02	3.01
GR 18 red	3.44	3.58	3.29	4.33	2.84	3.56	3.03
IR 72 (Ph)	2.95	3.04	2.85	3.64	2.44	3.58	2.12
Kawawa red	2.48	2.55	2.40	2.85	2.25	2.85	1.95
Koshihikari	2.63	2.58	2.67	2.61	2.55	3.24	2.10
Local Basmati – 2	2.84	3.09	2.59	3.90	2.29	2.39	2.79
Local red	2.71	2.76	2.67	3.38	2.14	2.88	2.40
Matigey	2.79	3.41	2.17	4.28	2.55	2.85	1.49
Perfume (short)	3.53	3.60	3.46	4.28	2.93	3.84	3.07
Sebota1	2.66	2.93	2.40	3.68	2.18	3.12	1.68
Sebota33	2.61	2.68	2.54	3.08	2.28	2.64	2.43
Sebota41	2.45	2.58	2.33	2.70	2.46	2.76	1.89
Sebota69	2.45	2.53	2.36	2.85	2.21	2.76	1.97
Mean	2.91	3.06	2.76	3.62	2.49	3.17	2.36
CV	25.70	28.40	22.50	20.60	15.10	8.90	19.60
SED	0.31	0.50	0.36	0.61	0.31	0.23	0.38
Pr>F (5%)	<0.001**	0.04**	<0.001**	0.012**	0.013**	<0.001**	0.001**

** = significant at P<0.05

4.4 Additive Main effects and Multiplicative Interaction (AMMI) Analysis

The study employed the use of AMMI analysis which used ANOVA to test the main effects of genotypes and environments, and Principal Component Analysis to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the genotype by environment (GxE) interaction, with a minimum number of degrees of freedom. This according to Zobel *et al.* (1988), the ANOVA and Principal Component Analysis forms part of the AMMI model, and this model is likely to be more suitable for characterizing the genotype by environment (GxE) interaction.

The AMMI analysis also helped to estimate the adaptability and yield stability of the fifteen rice genotypes and to select genotypes that have both high performance and phenotypic stability in reducing the effects of the interaction of the genotype and the environment and make selection of genotypes more precise and refined.

Table 4.5: AMMI analysis of grain yield in 15 rice genotypes under rainfed and irrigated conditions

Source	Df	SS	MS	% of total SS	% of GxE
Genotypes (G)	14	34.37	2.46**	27.25	
Environments (E)	3	47.14	15.71**	37.38	
GxE	42	15.53	0.37**	12.31	
IPCA 1	16	7.94	0.49**		51.13
IPCA 2	14	5.76	0.41		37.09
Residuals	12	1.84	0.153		
Error	112	27.70	0.25		
Total	179	126.11	0.71		

** = Significant (P<0.05)

The results of the AMMI analysis (Table 4.5) showed that a greater proportion of the variation in the sum of squares was attributed to the environment (37%), whilst the lowest proportion (12%) was attributed to the interaction between the environments and the genotypes. The Interactive Principal Component Analysis 1 (IPCA1) accounted for a greater (51%) proportion of variation for the interaction between the environment and the genotypes, whilst 37% of the variation was accounted for by the Interactive Principal Component Analysis 2 (IPCA2).

4.5 Yield Stability Analysis

The genotype *Perfume (short)* was observed to have smaller ASV values of 0.05, and as such assumed to be more stable, whilst the genotype *Matigey* was the least stable with an ASV value of 1.15 as can be seen in Table 4.6.

The most stable genotypes according to the Yield Stability Index (YSI) is *Perfume (short)*, which had a YSI of 4. Sebota41 was observed to be less stable in terms of yield performance, with a YSI value of 26.

Ranks were also assigned in increasing order to the genotypes and as such the genotype with the lowest rank sum was observed to be the more stable in terms of yield performance and the one with the highest rank sum was observed to be the less stable in terms of yield performance. From Table 4.6, the genotype *GH1837* had a rank sum of 1.30 and was observed to be more stable in terms of yield performance, whilst genotype Sebota69 was the least stable in terms of yield performance with a rank sum of 15.39.

Table 4.6: First and second IPCA, mean yield, and various yield-stability statistics under rainfed and irrigated conditions

Genotype	IPCA1	IPCA2	Grain Yield (t/ha)	ASV	YSI	RS
Basmati 370-1	0.01	-0.30	2.71	0.10	11	9.10
GH1837	-0.20	0.18	3.77	0.30	7	1.30
Good and new (JP)	-0.26	0.01	3.63	0.36	9	2.36
GR 18 RED	-0.14	-0.21	3.44	0.24	9	4.24
IR 72 (Ph)	-0.03	0.34	2.95	0.16	8	5.16
Kawawa red	0.29	0.12	2.48	0.41	22	13.41
Koshihikari	0.63	0.31	2.63	0.96	25	11.96
Local Basmati – 2	-0.23	-0.74	2.84	0.87	19	6.87
Local red	0.08	-0.27	2.71	0.18	12	8.18
Matigey	-0.74	0.36	2.79	1.15	22	8.15
Perfume (short)	-0.03	-0.08	3.53	0.05	4	3.05
Sebota1	-0.32	0.33	2.66	0.55	21	10.55
Sebota33	0.26	-0.30	2.61	0.45	22	12.45
Sebota41	0.41	0.18	2.45	0.59	26	14.59
Sebota69	0.28	0.06	2.45	0.39	23	15.39

IPCA1 = Interactive Principal Component Analysis 1, IPCA2 = Interactive Principal Component Analysis 2 ASV = AMMI Stability Value, YSI = Yield Stability Index, RS = Rank Sum

4.6 GGE BIPLOT Analysis of yield stability

The GGE biplots were constructed using the first two principal components (PC1 and PC2) that were derived from subjecting environment centered grain yield means for each location (environment) to singular value decomposition.

According to Yan (2001) and Yan *et al.* (2000; 2005; 2010), in the polygon view of the biplot used in the study, the vertex cultivar in each sector represented the highest yielding cultivar in the location that falls within that particular sector.

The biplot used in the study was divided into four sectors (A, B, C and D) representing the performance of the different genotypes in the different environments. PCA1 was plotted against PCA2. Positive PCA1 scores represented positive performance whilst negative or low PCA2 scores indicated stability. Sector A represented poor and unstable performance as well as negative interaction with the environment. Sector B represented high but unstable performance, sector C represented unresponsive genotypes with consistently poor performance. Sector D represented high stable performance across environments. Statistically stable genotypes and environments are located near to the origin of the biplot.

All four environments across the two hubs were identified as mega-environments. A mega environment according to Gauch and Zobel (1996, 1997) is a portion of a crop species' growing region with a homogenous environment in which some genotypes perform similarly. These environments share similar conditions and as such genotypes that fall within any of these environments could be evaluated in any of the other environments for optimum results.

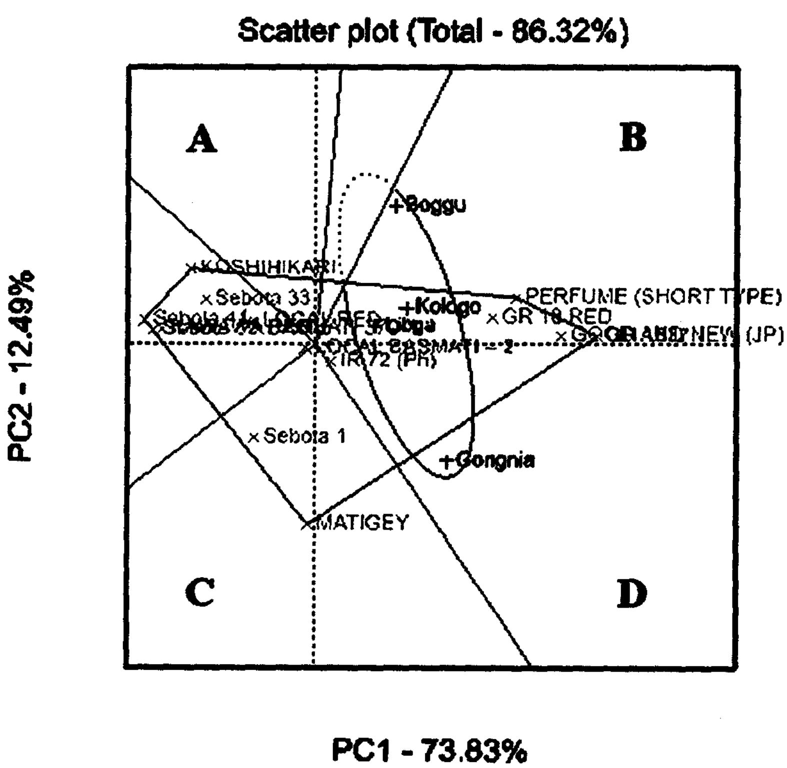


Fig 4.1: GGE biplot showing which genotype won in which environment

From the GGE biplot above (Fig 4.1), the genotype *GH1837* "won" in all four environments. The genotypes IR72(Ph), *Perfume (short)* and GR18 red were also genotypes found in this mega environments. The genotypes *Koshihikari* and Sebota41 were also observed to perform better than the genotypes *Local Red, Basmati 370-1, Kawawa red,* Sebota33, and Sebota69 which were found in the same sector.

The genotype *Matigey* won in the presence of Sebota1 and *Local Basmati*-2 and hence assumed to perform better than the two genotypes.

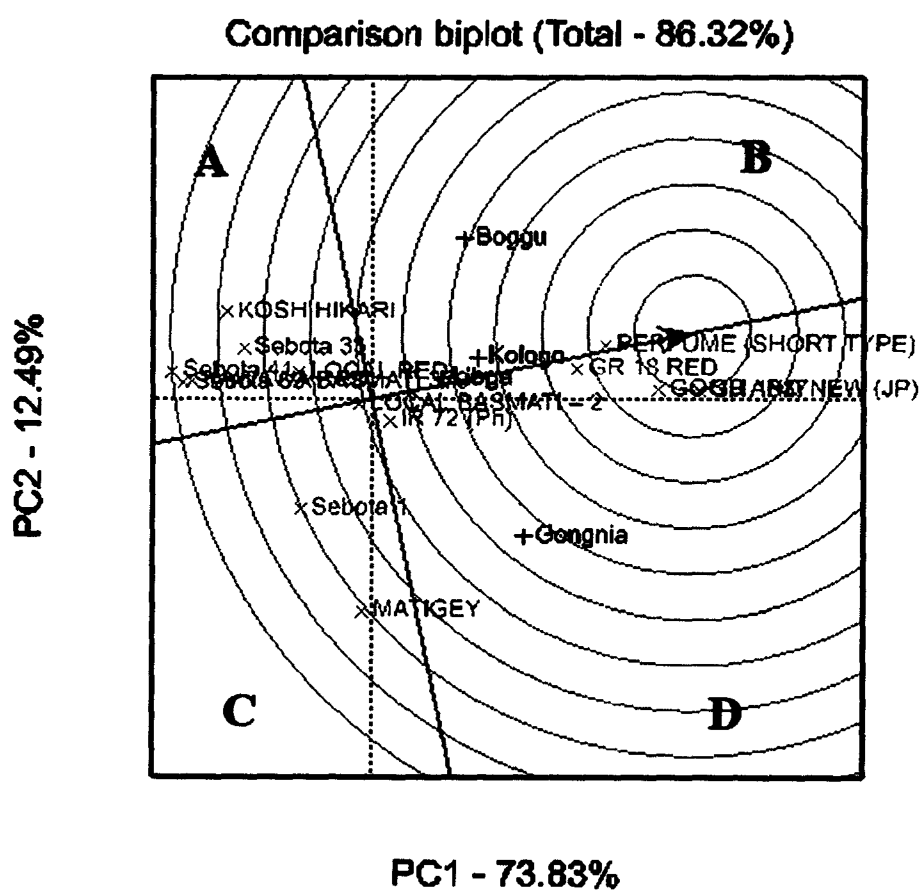


Fig 4.2: GGE biplot ranking of genotypes based on both average grain yield and stability for grain yield across 4 environments

A = low stable, B = high but unstable, C = low and unstable and D = high and stable

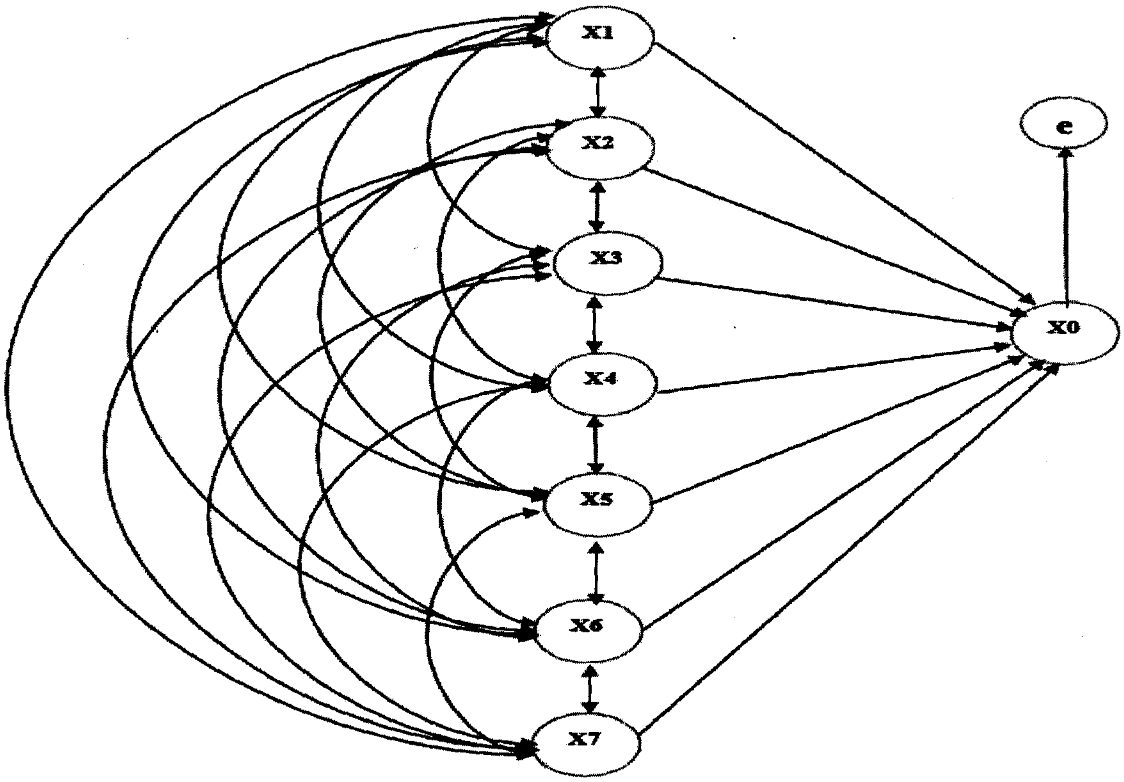
From the comparison GGE biplot above (Fig 4.2), the genotype *GH1837* had the highest yield performance but was unstable in all four environments. Genotypes like *Perfume (short)*, *Good and new* (JP) and GR18 red were also observed to be high yielding but unstable across all four environments. The genotype IR72(Ph) was however observed to be high yielding and stable across all environments.

The genotypes Sebota33, Sebota41, Sebota69, *Local red*, *Koshihikari*, *Kawawa red*, *Local Basmati*-2 and *Basmati* 370-1 were found to be low yielding but stable in terms of yield performance. The genotypes Sebota1 and *Matigey* were however observed to be low yielding and unstable in terms of yield performance across all environments and as such assumed to be unresponsive genotypes.

4.7 Path coefficient analysis

The path coefficient analysis for the various agronomic trait characters across the two rice producing hubs provided an insight into the inter-relationship of the various characters with grain yield of rice in the study. Considering grain yield as artifact of all causal characters, that is Days to 50% flowering, number of productive tillers, days to maturity, plant height at maturity (cm), thousand grain weight (g), grain length (mm) and panicle length (cm), the correlation coefficient of these causal factors in the study were partitioned into direct and indirect effects (Table 4.7). The path diagram (Fig 4.3) is such that all the explanatory variables interlinked and each of them was also directly linked to the dependent variable grain yield. The single headed arrows denotes direct effect on grain yield and the double headed arrows denotes the indirect effects of the agronomic trait characters on yield.

In the case of the explanatory variables $X_1, X_{2,} X_3, X_4, X_5, X_6$ and X_7 and the response variable X_0, the path diagram for the exploratory model is shown below:



X_0 = grain yield (t/ha), X_1 = Days to fifty percent flowering, X_2 = Number of effective tillers, X_3 = Days to maturity, X_4 = Plant height at maturity (cm), X_5 = 1000 grain weight, X_6 = grain length (mm), X_7 = Panicle length (cm), e = residual effects

Fig 4.3: Path diagram of seven agronomic trait characters

Table 4.7: Direct and indirect effects of agronomic trait characters on grain yield

			Indirect effect through						
Characters	Correlation with grain yield	Direct effect	Days to 50% flowering	No. of Productive tillers	Days to Maturity	Plant height at maturity (cm)	1000 grain weight	Grain length (mm)	Panicle Length (cm)
Days to 50% flowering	-0.029	-0.441**	-	-0.019	-0.437**	-0.013	0.053	-0.136	0.201**
No. of Productive tillers	0.021	-0.019	-0.003	-	0.002	0.003	0.003	0.003	-0.019
Days to Maturity	0.023	0.435**	0.434**	-0.011	-	-0.009	0.0612	-0.075	0.183**
Plant height at maturity (cm)	0.237	0.012	-0.019	0.029	0.014	-	0.013	0.044	-0.087
1000 grain weight	-0.039	0.041	-0.007	-0.003	0.009	-0.001	-	-0.022	-0.005
Grain length (mm)	0.055	-0.449**	-0.013	0.002	0.007	0.003	0.015	-	-0.059
Panicle Length(cm)	0.469**	0.374**	-0.105**	0.072**	0.096**	0.032**	-0.019	0.323**	-

** = significant (P < 0.05)

Panicle length exhibited a significant positive direct effect of low magnitude on grain yield followed by a significant negative direct effect by days to 50% flowering, days to maturity, and grain length also of low magnitude on grain yield (Table 4.7). Days to fifty percent flowering, number of productive tillers, days to maturity, plant height at maturity and grain length had a significant indirect effect of lower magnitude though panicle length on grain yield.

4.8 Technical Efficiency and Inefficiency Analysis

4.8.1 Stochastic Frontier production function for rice farmers in the two hubs

The stochastic frontier production function used the Maximum Likelihood Estimation (MLE) technique to estimate the production function for the rice farmers in these two hubs and obtained the farmers' level of efficiency.

From the frontier production function (Table 4.8), farm size, quantity of inorganic fertilizer and total labour correlated negatively with yield of rice across the two hubs. The quantity of seeds and the total labour used were observed to significantly affect yield of rice across the two hubs. The inefficiency model in table 4.8, showed that the number of extension contacts per year significantly affected the yield of rice across the two hubs.

The mean technical efficiency for the rice farmers across the two hubs (Table 4.9) was 55.2% with a higher proportion of the rice farmers (40%) across the two hubs producing below a technical efficiency score of 0.5.

Table 4.8: Maximum likelihood estimate of stochastic production frontier and technical inefficiency model

Variable	Coefficient	Standard error	Z-Ratio	P>|z|
Production frontier				
Farm size (ha)	-0.032	0.194	-0.17	0.868
Seed (kg)	0.275**	0.099	2.78	0.005
Inorganic Fertilizer (bags)	-0.040	0.162	-0.25	0.803
Total labour (man-days)	-0.133**	0.064	-2.08	0.038
Constant	0.675**	0.298	2.26	0.024
Technical inefficiency model				
Age (years)	0.097	1.914	0.05	0.960
Education	-1.090	1.625	-0.67	0.502
Household size	-0.276	0.668	-0.41	0.679
Number of extension contacts	-0.649**	0.361	1.80	0.007
Farming experience (years)	1.474	1.011	1.46	0.145
Membership of FBO	3.362	2.647	1.27	0.204
Constant	-9.214**	4.043	-2.28	0.023
Log-likelihood	-84.002			
Sigma u	0.802	0.104		

**, Significant at 5%

Table 4.9: Technical efficiency score of production

Technical efficiency score	Savelugu hub (N = 41)	Navrongo hub (N = 41)	Overall (N = 82)
0 – 0.49	34	46	40
0.50 – 0.59	5	7	6
0.60 – 0.69	27	10	18
0.70 – 0.79	5	12	10
0.80 – 0.89	17	22	20
0.90 – 1.00	10	2	6
Mean	0.585	0.519	0.552
Min	0.078	0.099	0.078
Max	0.951	0.921	0.951
Standard deviation	0.263	0.287	0.276

4.9 Generalized linear model

The Generalized linear model was used in the study to identify the relationship between the response variable yield gap and covariates of climatic and edaphic variables. The generalized linear model assumed the response variable yield to have a distribution which was normal, where the link function was chosen to constrain the range to permissible values. The yield was modelled with a normal Generalized Linear Model and an identity link function. The backward selection procedure was used.

The model incorporated both edaphic and climatic variables as the covariates and grain yield as the response variable. These variables were subjected to test to make sure they did not violate the assumptions for the Generalized Linear Model. The Shapiro-Wilk normality test was performed on the covariates and the dependent variable to determine if they followed the assumption of normality. The normality test indicated that all the variables used in the model were normally distributed. A graphical analysis performed on the residuals indicated a random pattern which showed that the data did not violate the assumption of linearity and independence.

4.9.1 Variance Inflation Factor and Tolerance test for Multicollinearity (VIF test)

Results of the variance inflation factor test are shown in table 4.11. The test indicates no multicollinearity among the predictor variables.

Table 4.10: Estimates of the general model (Full model)

		Error	Limits		Chi-	
			Lower	Upper	square	
Intercept	7.212	4.038	-0.703	15.127	3.19	0.0074
Water PH	-1.057	0.558	-2.151	0.036	3.59	0.0058
Nitrogen (%)	0.628	0.235	0.168	1.088	7.16	0.0074
Organic (%)	0.147	0.053	0.043	0.251	7.65	0.0057
Phosphorus(mg/kg)	0.003	0.049	-0.093	0.098	0.00	0.9551
Clay (%)	0.123	0.037	0.049	0.196	10.84	0.0010
Silt (%)	-0.039	0.015	-0.069	-0.009	6.43	0.0112
Sand (%)	0.026	0.017	-0.007	0.058	2.34	0.1261
Rainfall (mm)	-0.001	0.005	-0.011	0.009	0.05	0.8318
Min. temp(°C)	-0.064	0.056	-0.175	0.046	1.31	0.2530
Max. temp(°C)	0.002	0.034	-0.065	0.069	0.00	0.9462
Min. Relative Humidity (%)	0.049	0.019	0.012	0.086	6.61	0.0102
Max. Relative Humidity (%)	-0.033	0.012	-0.055	-0.009	7.98	0.0047
Scale	1.108	0.112	0.909	1.349		

The general (full model) in Table 4.10 is a model that contained both significant and non-significant variables, it was further reduced (Table 4.11) to include only significant variables to predict yield across the two hubs. The full model is expressed as:

$$
\begin{aligned}
&Yield = 7.212 - 1.057 * waterPH + 0.628 * nitrogen(\%) + 0.147 * organic(\%) + \\
&0.003 * phosphorus(mg/kg) + 0.123 * clay(\%) - 0.039 * \mathrm{silt}(\%) + 0.026 * sand(\%) \\
&-0.001 * \mathrm{rainfall(mm)} - 0.064 * \mathrm{min.temp} + 0.002 * \mathrm{max.temp} + \\
&0.049 * \mathrm{min.humidity}(\%) - 0.033 * \mathrm{max.humidity}(\%) \ldots\ldots\ldots\ldots (4.1)
\end{aligned}
$$

The significant predictors of yield ($p < 0.05$) was found to be water PH, percentage of nitrogen in the soil, percentage of organic matter in the soil, percentage of clay and silt in the soil, percentage minimum relative humidity and percentage maximum relative humidity (Table 4.11). However, the presence of phosphorus in the soil, the percentage of sand in the soil, the total rainfall recorded for the two hubs, as well as the minimum and maximum temperature in the two hubs did not significantly contribute in predicting the yield of rice across the two hubs ($p > 0.05$), as can be seen in Table 4.11.

Table 4.11: Parameter estimates of the reduced model

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits Lower	Wald 95% Confidence Limits Upper	Wald Chi-square	Pr > Chi-Square	Tolerance	Variance Inflation
Intercept	10.122	3.119	4.007	16.2360	10.53	0.0012		0
Water PH	-1.231	0.519	-2.249	-0.2125	5.61	0.0178	0.82348	1.21436
Nitrogen (%)	0.427	0.176	0.083	0.7709	5.91	0.0150	0.76453	1.30800
Organic (%)	0.113	0.052	0.012	0.2140	4.81	0.0284	0.61669	1.62155
Clay (%)	0.061	0.021	0.021	0.1015	8.93	0.0028	0.64380	1.55328
Silt (%)	-0.040	0.012	-0.064	-0.0165	11.09	0.0009	0.50513	1.97967
Min. Relative Humidity (%)	0.036	0.009	0.018	0.0534	15.33	<0.0001	0.37634	2.65715
Max. Relative Humidity (%)	-0.033	0.008	-0.047	-0.0180	19.16	<0.0001	0.39214	2.55013
Scale	1.167	0.118	0.957	1.4223				

The reduced predictive model (Table 4.12) is an expression for only variables that turned out significant after entry into the general predictive model. The equation 4.1 below is the reduced predictive model for predicting yield in the two rice producing hubs in Northern Ghana and is expressed as:

$$Yield = 10.122 - 1.231 * waterPH + 0.427 * Nitrogen(\%) + 0.113 * organicmatter(\%) + 0.061 * clay(\%) - 0.040 * silt(\%) + 0.036 * \min.\mathrm{Relative}\, humidity(\%) - 0.033 * \max.\mathrm{Relative}\, humidity \qquad (4.2)$$

4.10 Discussion of results

4.10.1 Socio-Economic characteristics of rice farmers in the two hubs

The summary statistics of the socio-economic characteristics of the rice farmers in the two hubs are presented in Table 4.1. The results indicated that rice farming was dominated by males across the two hubs (73.17%) who are relatively young (39 years) with a high average family size of 11.

The average age of farmers in the two hubs (39 years) shows that majority of them are still in their active productive age which agrees with the findings of Ahmadu and Alufohai (2012). The large average household size across the two hubs implied a positive implication on the farmers' production due to the family labour contribution from the household members *ceteris paribus*. The dominance of males in rice production in the two hubs confirms the fact that males are the household heads and therefore are in charge of the core farm production activities while women are mostly into processing and marketing corroborating the findings of Ahmadu and Alufohai (2012) and Enweren and Ohajianya (2013). Majority of the farmers interviewed (62.20%) were not educated, and had an average rice farming experience of 17 years. The proportion of farmers (51.17%) who were educated or had little education in the Navrongo hub out-weighed those in the Savelugu hub (24.39%). The high literacy rate recorded by farmers in the Navrongo hub and their average rice farming experience of 17 years might increase their ability to use resources more efficiently in rice production, which is in unison with the findings of Ugwuanyi *et al.* (2008)

Membership of a Farmer Based Organization (FBO) is relatively higher across the two hubs (69.51%), with majority of the farmers in the Savelugu hub recording a higher membership (70.73%) compared to farmers in the Navrongo hub (68.29%).

The average yield of rice from the yield gap survey for the two hubs was found to be 2.64 t/ha which was validated by the Jackknife technique, with a Jackknife mean of 2.77t/ha and a 95% confidence interval of (1.5654, 3.9819). Since the Jackknife interval enclosed the mean yield, it meant it approximated the true yield with an appreciable level of precision.

4.10.2 Multi-Environment Trials (MET)

The joint Analysis of Variance (ANOVA) for the fifteen rice genotypes grown under rainfed and irrigated conditions showed differences ($P < 0.01$) for environments (E), genotypes (G) and the interaction between the environments and genotypes (GxE) ($P < 0.05$) as seen in Table 4.3. The experimental coefficient of variation for the joint analysis was low (16.9%), indicating good experimental precision. A significant effect of the genotype by environment (GxE) interaction demonstrates the differential performance of genotypes in different environments. The significant genotype by environment interaction also suggested that the grain yield of genotypes varied across irrigated and rainfed conditions. The significant differences for the components of the environment (E), genotype (G) and Interaction (GxE) indicated the effects of environments in the GxE, genetic variability among entries and the possibility of selecting high yielding genotypes. This agrees with results obtained by Oliveira *et al.* (2013) who obtained similar results for a joint ANOVA of yield of passion fruit in a multi-environment trial using twelve cultivars in eight agronomic production areas in the State of Bahia, Brazil. The results also corroborates with the findings of Farshadfar (2008), who obtain similar results in a joint analysis of variance for a multi-environment trial to determine stable bread wheat genotypes for four consecutive years (1998-2001) in rainfed and irrigated conditions in Iran. Farshadfar and Sutka, (2006) also obtained similar results for the combined ANOVA for 12 rice genotypes under irrigated and rainfed conditions which resulted in highly significant differences ($P < 0.01$) between the environment, genotypes and the interaction between the environment and genotypes.

The large proportion of variation attributable to the environment (37%), is an indication that the environment had a larger influence on the yield of the genotypes. However this large proportion of variation due to environment did not reduce the importance of the differences due to the genotypes or the interactions between the genotypes and the environment. A comparison of the genotype sum of squares with the interaction of the genotype and environment sum of squares indicated substantial differences in genotype response in different environments.

The proportion of variation attributed to the genotypic (G) effects was 27%, whilst 12% of variation was attributed to the interaction between the Genotype and the Environment (GxE).

The table of mean yield (Table 4.4) for the combined environments that is rainfed and irrigated conditions indicated that the genotype *GH1837* was the highest yielding genotype across all environments, with a mean grain yield of 3.77 t/ha. The genotypes GR18, *Good and new (JP)*, *Perfume (short)* and IR72(Ph) were also found to have higher grain yields of 3.44 t/ha, 3.63 t/ha, 3.53 t/ha and 2.95 t/ha respectively, which exceeded the overall average yield of 2.91 t/ha. The high yielding ability of these five genotypes is an indication that they might do well under both rainfed and irrigated conditions.

The remaining ten genotypes were found to have low mean grain yield compared to the average overall yield of 2.91 t/ha. This implies they may not be high yielding across all environments, but might be well adapted to some specific environments in terms of yield performance.

An average yield of 3.06 t/ha was observed for irrigated environments where genotype yields varied significantly at the 5% level. The genotypes *GH1837*, *Perfume (short)*, *Good and new (JP)*, *GR18 Red*, *Local Basmati-2*, *Matigey*, and *Perfume (short)* were observed to have grain yield above the average for irrigated environments, with grain yield of 3.99 t/ha, 3.75 t/ha, 3.58 t/ha, 3.09 t/ha, 3.41 t/ha and 3.60 t/ha respectively.

The genotype Sebota69 had the lowest yield of 2.53t/ha. The low yield performance of this genotype in the irrigated environment might be due to the fact that it might not be adapted to irrigated environments, but might perform well in other environments.

This method was employed by Anputhas *et al.* (2011) to test and identify the consistently performing varieties in wider environments and location specific high performing varieties.

An average significant yield of 2.76 t/ha was recorded for the rainfed environment. Five genotypes, namely *GH1837*, *Good and new (JP)*, *Perfume (short)*, GR18 IR72(Ph) and *Perfume (short)* had mean yields 3.54 t/ha, 3.51 t/ha, 3.29 t/ha and 2.85 t/ha and 3.46 respectively, which exceeded the average yield for combined rainfed environments. The rest of the ten genotypes had a yield performance lower than the overall average yield obtained for the combined rainfed locations across the two hubs.

The analysis of yield performance was also viewed on environment specific basis as seen in Table 4.4. For the Gongnia environment (irrigated) in the Navrongo hub, an average overall yield of 3.62 t/ha was obtained. Eight genotypes had higher yield than the overall average yield, whilst the remaining seven genotype's yield performance was lower than the overall average yield. The genotype *GH1837* was the highest yielding, with an average yield of 4.68 t/ha, whilst the genotype *Koshihikari* had the lowest average yield of 2.61 t/ha. The greater number of genotypes performing above the overall average is an indication that the environment is a conducive one that supports a wide range of rice cultivars and does not suppress their genotypic yield performance.

For the Libga environment (irrigated) in the Savelugu hub, the genotypes *GH1837* (3.31 t/ha), *Good and new (JP)* (2.81 t/ha), GR18 (2.84 t/ha), *Koshihikari* (2.55

t/ha), *Matigey* (2.55 t/ha) and *Perfume (short)* (2.93 t/ha) had mean grain yield above the overall average grain yield of 2.49 t/ha. Lower yields were recorded for the other nine genotypes, where their yield performance was lower than the overall mean yield.

For the Kologo environment (rainfed) in the Navrongo hub, six genotypes were observed to have out yielded the overall average yield of 3.17 t/ha. The genotypes *GH1837* recorded the highest yield of 4.12 t/ha, whilst the genotype *Local Basmati-2* recorded the lowest yield of 2.39 t/ha.

The Boggu environment, a rainfed environment in the Savelugu hub, had an overall average yield of 2.36 t/ha. The genotype GR18 red was observed to out yield (3.03 t/ha) the overall average yield. The lowest yield performance was recorded for the genotypes *Matigey* which recorded an average yield of 1.49 t/ha.

Romualdo *et al.* (2014) used this approach to test and evaluate Upland Rice Varieties In Sultan Kudarat Province across four locations for six (6) consecutive wet and dry cropping seasons, to determine the agronomic and yield characteristics and its reaction to pests and diseases.

Muungani *et al.* (2007) also used this method to evaluate and identify high performing ten maize cultivars using a mother-baby trial approach at fourteen sites in twenty eight environments across Zimbabwe

4.10.3 Additive Main effects and Multiplicative Interaction (AMMI) Analysis

In the study, AMMI analysis was employed to estimate the adaptability and yield stability of the fifteen rice genotypes.

The analysis of variance for the AMMMI model was partitioned into genotype (G) main effects, environment (E) main effects, and the interaction between the genotype and the environment (GxE). The GxE interaction was further partitioned by principal component analysis (Table 4.5), that is the Interactive principal component 1 and 2 (IPCA1 and IPCA2).

The AMMI analysis of variance of the yield data showed significant differences ($P < 0.05$) among environments, genotypes and the interaction between the genotypes and environments. The significant interaction indicated a differential response of the yield of the fifteen rice genotypes to environmental changes. Similar results were obtained by Das *et al.* (2011) who performed an integrated analysis for genotypic adaptation in rice using thirty six (36) rice genotypes and Bose *et al.* (2014) who also obtained a significant ($P < 0.05$) components of the environment, genotypes and genotype by environment interaction for the AMMI analysis of variance for selecting rice genotypes for yield and stability under direct seeded conditions using seeds of twelve (12) popular rice genotypes in the Central Rice Research Institute experimental farm, Cuttack, India.

The results of the AMMI analysis of variance also corroborates with the results of the AMMI analysis of variance obtained by Farshadfar *et al.* (2011), who conducted a yield trial to determine fourteen stable genotypes of bread wheat using AMMI stability analysis.

The results of the AMMI analysis indicated that 12% of total variation was accounted for by the interaction between the genotype and environment, 37% by the environment and 27% by the genotypes. A large contribution of environment indicated that environments were diverse, with large differences among environment means causing most of the variation in the grain yield.

4.10.4 AMMI Stability Value (ASV) measure of yield stability

AMMI analysis does not provide a quantitative measure of stability. For this reason, Purchase *et al.* (2000) proposed an ASV measure to quantify and classify genotypes according to their yield stability. This method has been used as a criterion to define more stable genotypes, as such genotypes with low ASV values are assumed to be more stable and high yielding.

The genotypes *Perfume (short)* and *Basmati 370-1* were observed to have smaller ASV values and as such assumed to be more stable. The least stable genotype in terms of yield performance is *Matigey* with an ASV of 1.15 as can be seen in Table 4.6. This implies genotypes *Perfume (short)* and *Basmati 370-1* are assumed to be high yielding and has a stable yield across all environments and can be assumed to be well adapted to all four environments. Farshadfar (2008) employed this method to select stable bread wheat genotypes with high grain yield using twenty genotypes in a field experiment conducted for four consecutive years under irrigated and rainfed conditions. Farshadfar *et al.* (2012) also used the ASV method to evaluate the grain yield stability of wheat-barley disomic addition lines and locate the QTLs controlling static and dynamic phenotypic stability in barley, 7 disomic addition lines (DALs) of barley across five environments.

Gómez-Becerra *et al.* (2006) determined the stability and adaptability patterns of a set of 40 promising spring wheat genotypes from Kazakhstan and Siberia across twenty two environments using the ASV technique.

4.10.5 Yield Stability Index (YSI) measure of yield stability

The most stable genotypes according to the Yield Stability Index were *Perfume (short)* (YSI=4), and *GH1837* (YSI=7), whilst the least stable genotype was Sebota41 (YSI=26). This method incorporated both yield and stability into a single index, reducing the problem of using only yield stability as the sole criterion to select varieties, taking into account that the most stable genotypes do not always have the best yield performance (Oliveira and Godoy, 2006). The result indicates that the genotypes *Perfume (short)* and *GH1837* are assumed to be well adapted to all the four environments in terms of yield stability and performance. This methods been used by Bose *et al.* (2014) to select stable and high yielding genotypes for twelve (12) popular rice genotypes and Farshadfar *et al.* (2011) to select stable bread wheat genotypes with high grain yield through a single parameter, field experiments conducted with fourteen (14) genotypes for three consecutive years (2008-2011) under irrigated and rainfed conditions.

genotype *GH1837* won in the presence of *Perfume (short),* GR18 and IR72(Ph), and hence was assumed to be high yielding.

The genotype *Koshihikari* won in the presence of Sebota41, *Local red, Basmati* 370-1, *Kawawa red,* Sebota33 and Sebota69. This genotype was assumed to be highest yielding among other genotypes that fell in the same sector.

The genotype *Matigey* won in the presence of *Local Basmati*-2. The genotype was hence assumed to be high yielding than the genotype *Local Basmati*-2.

All four environments used in the study were identified as mega-environments. These environments had conditions that were assumed to be similar, and hence any genotype could be evaluated across any of these four environments to achieve optimum yield response.

The evaluation of the fifteen genotypes was again viewed on the basis of comparison using the GGE biplot graphical comparison analysis (Fig 4.2). The biplot was divided into four sectors for comparison of yield stability and yield performance. The sectors were labeled such that the genotypes could be categorized into low yielding but stable genotypes, high yielding but unstable genotypes, low yielding and unstable genotypes and high yielding and stable genotypes.

The genotypes *GH1837*, *Perfume (short),* and GR18 were observed to be high yielding but unstable in terms of yield performance as seen in Fig 4.2. This implied a change in the growing environments of these genotypes would have an effect on their optimum yield output.

For genotypes that were low yielding but stable, seven genotypes were identified, that is Sebota41, *Koshihikari*, *Local red*, *Basmati* 370-1, *Kawawa red*, Sebota33 and Sebota69. This implied these seven genotypes would maintain a low level of yield despite a change in their growing environments. Their yields are unaffected by a change in environment.

This method of selecting stable and high yielding genotypes has been used by Badu-Apraku *et al.* (2011) for targeting early maturing maize cultivars to mega-environments in West Africa.

The genotypes *Matigey*, Sebota1 and *Local Basmati-2* were observed to be unresponsive genotypes. Their yields were low and unstable. This implied, with a change in growing environments, yield output would be expected to be still low, though that environment might have adequate resource to support the growth of the genotypes.

The genotype IR72(Ph) was observed to be high yielding and stable. This implies the environment has little influence on its yield performance and as such a change in environment would have little impact on the optimum yield output of the genotype. This method of selecting stable and high yielding genotypes was also used by Bhan *et al.* (2005) to select high yielding and stable six varieties/strains of Lemongrass (*Cymbopogon spp.*) for oil yield across four years.

Muugani *et al.* (2007) also applied the method GGE biplots analysis on a multi-environment, mother-baby trial using ten pre-released maize hybrids and open pollinated varieties tested at fourteen sites across Zimbabwe.

4.10.8 Correlation and Path Analysis

The correlation between grain yield and panicle length was a positive and significant one (Table 4.2). The other agronomic trait characters used in the study did not have any significant effect on grain yield. The significant correlation of grain yield with panicle length is an indication that genotypes with longer panicle may prove effective in increasing yield potentials.

Days to 50% flowering was significantly positively correlated with days to maturity, plant height at maturity, panicle length and grain length. These results corroborates the findings of Babu *et al.* (2012), who obtained a significant positive correlation between days to 50% flowering with plant height, panicle length and number of filled grains per panicle for a path and correlation analysis using twenty one popular rice hybrids in India.

A significant negative correlation was observed for thousand grain weight with plant height at maturity, panicle length and grain length. This results agrees with the findings of Joshi (2005) who obtained a negative and significant correlation between thousand grain weight and plant height for Tartary buckwheat, but contravenes the results obtained by Oad *et al.* (2002), who had a positive significant correlation between thousand grain weight with panicle length and grain length for thirty rice cultivars evaluated under lowland condition in the Philippine.

Number of productive tillers was significantly correlated with plant height at maturity, but in the negative direction, suggesting a compromise in selecting for the optimum combination of these characters.

Days to maturity had a significant and positive correlation with plant height at maturity, panicle length and grain length. This might imply that plants that stay longer or takes a longer time to mature might have the tendency to produce more tillers and longer grains that might prove effective in improving yield.

Plant height at maturity had a positive and significant correlation with panicle length and grain length.

The correlation between panicle length and grain length was a positive and significant one. A positive significant estimates of these agronomic trait characters indicates a strong association of these characters with yield, therefore the selection of these traits will be useful in improving grain yield.

As simple correlation does not provide the true contribution of the characters towards the yield, these genotypic correlations were partitioned into direct and indirect effects through path coefficient analysis.

Days to maturity (0.435) and panicle length (0.374) exhibited a direct significant positive effect of low magnitude on grain yield. Grain length (-0.449) and days to 50% flowering (-0.441) however exhibited a negative significant direct effect of low magnitude on grain yield. The significant positive direct effect of panicle length on grain yield implied genotypes that had longer panicles might prove effective in improving yield, whilst a significant direct effect on grain yield by days to maturity might imply that genotypes that mature late might have the potential of increasing yield.

A negative direct effect of days to 50% flowering might imply, genotypes that delay in producing flowers might results in a drop in their yield output. Genotypes with shorter grain might also stand the chance of having lower yield, as exhibited by a negative direct effect of grain length on grain yield. These results are in unison with the findings of Meenakshi *et al.* (1999), Nayak *et al.* (2001), and Madhavilatha (2002).

Panicle length exhibited an indirect significant positive effect on grain yield through days to 50% flowering. Days to maturity on the other hand exhibited an indirect effect of low magnitude on grain yield through days to 50% flowering.

An indirect positive significant effect of low magnitude was exhibited by days to 50% flowering and panicle length on grain yield through days to maturity.

There was however no significant indirect effect of the agronomic trait characters on yield through plant height at maturity, thousand grain weight and grain length.

Number of productive tillers, days to maturity, plant height at maturity and grain length had a significant indirect effect on grain yield through panicle length. Days to 50% flowering on the other hand had exhibited a significant negative effect on grain yield through panicle length.

Critical analysis of the results obtained from the agronomic character trait association and path analysis indicated that panicle length possessed both positive association and high positive direct effects. Hence the selection of this agronomic trait could bring about improvements in yield and yield components.

The residual effects which determined how best the yield component accounted for the variability of the yield was 0.613, implying these agronomic traits characters accounted for about 39% of variability found in the grain yield.

4.10.9 Stochastic Frontier production function

The method of Maximum Likelihood Estimation (MLE) technique was used to estimate the production function for the rice farmers in the two hubs in order to obtain the farmers' level of efficiency. The Cobb-Douglas function linearized in log-form fitted for the estimation of the stochastic frontier framework, proposed by Aigner *et al.* (1977), and Meeusen and van den Broeck (1977).

Frontier estimates of parameters, standard errors and critical-z values of the Cobb-Douglas model are presented in table 4.8. In the stochastic frontier approach, the production function is estimated as efficient set of variables in the input category that would help to identify technical inefficiency by considering deviations from the frontier.

The production frontier model across the two rice producing hubs (Table 4.8) showed that with the exception of quantity of rice seeds planted, all inputs that were under consideration (Farm size, quantity of inorganic fertilizer and total labour), correlated negatively with the yield of rice. The coefficients of quantity of seeds and total labour were significant at the 5% level of significance, whilst farm size and quantity of inorganic fertilizer was not significant ($P > 0.05$).

The significant effect of quantity of seeds indicated that increasing the quantity of rice seeds sowed by farmers might increase the production efficiency of the farmers, whilst a significant effect of total labour also implied an increase in the number of labour force used on the farm might increase production output, thereby bringing about an increase in production efficiency. The farm size and quantity of inorganic fertilizer applied on the other hand did not significantly affect yield. This result agrees with the findings of Idiong (2007) who reported a non-significant effect of fertilizer on yield of swamp rice. Similarly, the results of the Cobb-Douglas maximum likelihood estimate given by Backman *et al.* (2009) showed that land, labour and seeds, among other factors significantly influenced rice production, while fertilizer had no significant effect.

The coefficient of sigma (0.802) which is the asymmetric error term denoting technical inefficiency indicated that 80.2% of variation in the output of rice in the two hubs was attributed to technical inefficiency, implying wastage of inputs and hence a reduction in efficiency. This means that 19.8% of the deviation output from the production frontier was occasioned by noise.

4.10.10 Technical Efficiency of rice farmers in the two hubs

The estimates of the Technical Efficiency (TE) of rice farmers in the two hubs are presented in Table 4.9. The technical efficiency of the farmers ranged from 7.8% to 95.1%, for the two hubs, which was the same as that for the Savelugu hub. The average technical efficiency for the two hubs was 55.2%. This implied on the average, farmers in the two hubs are producing 55.2% of the potential frontier output, given the present level of technology and input use. Hence, 44.8% of the potential frontier output is not realized. Rice farmers in the two hubs can therefore increase their production by 44.8 percent in the short run by adopting best rice farming practices. Similar results were obtained by Etwire *et al.* (2013) who obtained a mean technical efficiency of 53% for soybean farmers in the Sabobo and Cheriponi District of Northern Ghana. Tijani (2006), Donkor *et al.* (2013) and Ahmadu and Alufohai (2012), rather obtained mean technical efficiency score above 80% for rice farmers. The technical efficiency for farmers in the Navrongo hub ranged from 9.9% to 92.1% with an average technical efficiency of 51.9%. The average technical efficiency for rice farmers in the Savelugu hub was 58.5%. The mean technical efficiency for the two hubs indicates that given the level of technology and resources of the rice farmers, they still can increase production by about 44.8%. Farmers in the Navrongo hub would have to increase their technical production capacity to make up the difference of 48.1%, whilst farmers in the Savelugu hub will also need to increase their technical production capacity to also make up the difference of 41.5%. A high proportion of farmers across the two hubs had (40%) had efficiency scores less than 0.5. These results are in unison with the findings of Ewtire *et al.* (2013) who obtained a greater proportion (46.5%) of soybean farmers in the Sabobo and Cheriponi District of Northern Ghana producing below an efficiency score less than 0.5, but contravenes the findings of Idiong (2007), Tijani (2006), Donkor *et al.* (2013) and Sekhon *et al.* (2010). A greater proportion of farmers in the Navrongo hub (46%) scored less than 0.5 of the efficiency compared to farmers in the Savelugu hub (34%).

4.10.11 Technical Inefficiency Parameters of rice farmers in the two hubs

The technical inefficiency parameters estimated for the farmers in the two hubs (Table 4.8) showed that only number of extension contacts significantly ($p < 0.05$) influenced the technical inefficiency of the farmers. This agrees with the findings of Awunyo-Vitor *et al.* (2013) and Enweren and Ohajianya (2013), but contravenes the findings of Tijani (2006). All other variables (Age, education, household size, years of rice farming experience and membership of Farmer Based Organization (FBO)) were not significant, confirming the low level of technical inefficiency effects in the production of the farmers. The coefficient of the number of extension visits was negative, implying that farmers who receive advice from agricultural extension officers are more technical efficient than farmers who do not receive extension visits.

4.10.12 Generalized linear model

From the reduced model in Table 4.11, it was observed that water PH had a negative effect on yield of rice across the two hubs, hence a unit increase in water PH is likely to decrease yield by 1.231 t/ha.

The percentage of nitrogen in the soil plays an important role in contributing to the soil nutrient requirement by rice, thereby leading to an increase in the yield of rice. This can be seen clearly in Table 4.11 where the percentage of nitrogen in the soil has a positive effect on the yield of rice across the two hubs, implying a unit increase in the nitrogen content of the soil might lead to an increase in yield of rice by 0.427t/ha.

The proportion of organic matter content in the soil also plays a crucial role in the soil nutrient requirement level needed by crops. Hence an improvement of soil nutrient is enhanced through the crop residual left on the farm after harvesting, and rice is not an exception. Farmers across the two hubs often leave the residue of the rice on the field to decompose in order to increase the soil organic content, unlike the previously practice of burning the residues after harvesting. The result in the Table 4.7 is highly expected, since organic matter content in the soil has a positive effect on the yield of rice. Therefore a unit increase in the organic matter content of the soil would result in an increase in the yield of rice by 0.113 t/ha, other things being equal.

The proportion of clay in the soil also helps in enhancing the water retention capacity of the soil for crop use. The proportion of clay in the soil had a positive effect on the yield of rice (Table 4.7) and in maintaining the nutrient content of the soil. A unit increase in the proportion of clay in the soil increases yield by 0.061 t/ha across the two hubs.

The proportion of silt in the soil (Table 4.7) had a negative effect on yield, therefore a unit increase in the proportion of silt in the soil might reduce yield by 0.040 t/ha.

Minimum relative humidity had a positive effect on yield, whilst the maximum relative humidity affected yield negatively (Table 4.7). Therefore a unit increase in the relative humidity across the two hubs would increase yield by 0.036t/ha and a unit increase in the maximum relative humidity across the two hubs would reduce yield by 0.033t/ha.

The insignificant contribution of rainfall to grain yield corroborates the findings of Tannura *et al*. (2008).

CHAPTER FIVE

CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

The genotype *GH1837* had the highest yield (3.77 t/ha), higher than the overall average of 2.91 t/ha for all combined environments.

The study unearthed that the genotype *GH1837* and the genotype *Good and new (JP),* had higher yields in both combined rainfed and irrigated conditions.

On location specific basis, higher yields were recorded on genotypes *GH1837, Good and new (JP),* and GR18 red in the Gongnia environment, genotypes *GH1837* and *Perfume (short)* in Libga environment, genotypes *GH1837* and *Good and new (JP)* in Kologo environment and genotypes *Good and new (JP)* and GR18 red in the Boggu environment.

Additionally, the genotypes *Perfume (short)* and *GH1837* were observed to be stable in terms of yield performance across all environments. All four environment in the study were identified as mega environments.

The study also showed that the mean technical efficiency of rice farmers across the two hubs is 55.2% (7.8% - 95.1%). It also revealed that a high proportion (40%) of farmers across the two hubs obtained an efficiency score less than 0.5.

The study revealed that yield was significantly predicted by water PH, the proportions of nitrogen, organic matter, clay and silt in the soil, and the relative maximum and minimum humidity in the atmosphere across the two hubs.

5.2 Recommendations

Based on the findings of the work, the following recommendations are given;

i. Since the genotypes *GH1837*, Good and new (JP), *Perfume (short)* and IR72(Ph) were observed to be more stable and high yielding across the two hubs. Further evaluation based on on-farm trials should be carried out across the two hubs to assess their performance on farmer managed fields before recommending them for release.

ii. Since days to flowering has a negative indirect effect on grain yield but of low magnitude, farmers should resort to sowing their rice early to avoid a delay in the flowering of their rice crop which would have a negative toll on their yield.

iii. The Ministry of Agriculture should liaise with rural banks and financial institutions to give loans to farmers at reduced interest rates so as to enable them increase their production through expansion of their farm sizes and hire more labour on their farms.

iv. The evaluation of these fifteen (15) rice genotypes should be extended to other hubs within the country to assess favorable rice growing environments across the country for these genotypes.

v. Further research should be conducted to include nutrient and crop water requirement levels in the yield predictive model across the two hubs.

REFERENCES

Abeysiriwardena, D.S.de.Z., Buss, G.R., & Reese Jr., P.F. (1991). Analysis of multi environmental yield trials for testing adaptability of crop genotypes. *Tropical Agriculturist* 147, 85–97.

Ahmadu J., & Alufohai, G.O. (2012). Estimation of Technical Efficiency of Irrigated Rice Farmers in Niger State, Nigeria. *American-Eurasian J.Agric. & Environ. Sci.*, 12 (12): 1610-1616.

Aigner, D., Lovell, C.A.K., & Schmidt, P. (1977). 'Formulation and Estimation of Stochastic Frontier Production Function Models', *Journal of Econometrics* 6, 21-37.

Akbar, M., Khan, N.I., & Chowdhry, M.H. (1995). Variation and interrelationships between some biometric characters in wheat, Triticum aestivum L. *J. Agric. Res.*, 33, p. 247–54.

Akcura, M., Kaya, Y., & Taner, S. (2005). Genotype-environment interaction and phenotypic stability analysis for grain yield of durum wheat in the Central Anatolian region. *Turky Journal of Agriculture* 29: 369-375.

Alagarswamy, G., & Chandra, S. (1998). Pattern analysis of international sorghum multienvironment trials for grain-yield adaptation. Theor. *Appl. Genet*. 96, 397-405.

Amira, J.O., Ojo D.K., Ariyo, O.J., Oduwaye, O.A., & Ayo-Vaughan, M A. (2013). Relative Discriminating Powers Of GGE And AMMI Models In the Selection Of Tropical Soybean Genotypes. *Afr. Crop Sci. J.* (1): 67–73.

Anandan, R., Eswaran, T., Sabesan & Prakash, M. (2009). Additive Main Effects and Multiplicative Interactions Analysis of Yield Performance in Rice Genotypes under Coastal Saline Environments. *Advances in Biological Research* 3 (1-2): 43-47, 2009. ISSN 1992-0067 © IDOSI Publications, 2009

Annicchiarico, P. (2002).Genotype × environment interactions: Challenges and opportunities for plant breeding and cultivar recommendations. Available http://www.iao.florence.it/training/adaptation/references. php. FAO Plant Production and Protection Paper No. 174, FAO, Rome, 85–86.

Annicchiarico, P. (2002). Defining adaptation strategies and yield stability targets in breeding programmes. In Kang, M.S. (Ed.) *Quantitative genetics, genomics and plant breeding*, Wallingford, UK, CABI, pp. 365-383

Annicchiarico, P., & Perenzin, M. (1994). Adaptation patterns and definition of macro environment for selection and recommendation of common wheat in Italy. *Plant Breed*, 113:197-225.

Anputhas, M., Samita, S., & Abeysiriwarden, D.S. (2011). Stability and adaptability analysis of rice cultivars using environment-centered yield in two-way ANOVA model. *Communications in Biometry and Crop Science 6(2),* 80-86

Asenjo, C.A., Bezus, R., & Acciaresi, H.A. (2003). Genotype x environment interaction in rice (*Oryza sativa L.*) in temperate regions using the Joint Regression Analysis and AMMJ methods. *Cereal Research of Communication* 32:97-104.

Atnaf, M., Sisay, K., Seltene, A., & Zelalem, Fisha. (2013). GGE biplots to Analyze soybean multi-environment yield trial data in north Western Ethiopia. *Journal of Plant Breeding and Crop Science*. Vol. 5(12), pp. 245-254.

Awunyo-Vitor, D., Bakang, J., & Smith C. (2013). Estimation of Farm Level Technical Efficiency of Small-Scale Cowpea Production in Ghana. *American-Eurasian J. Agric. & Environ. Sci.*, 13 (8): 1080-1087, 2013 ISSN 1818-6769 © IDOSI Publications.

Babu, R.V., Shreya, K., Kuldeep, S.D., Usharani, G., & Siva, S.A. (2012). Correlation and Path Analysis Studies in Popular Rice Hybrids of India. *International Journal of Scientific and Research Publications*, Volume 2, Issue 3, March 2012. ISSN 2250-3153

Backman, S.K.M., Zahidul, I., & Sumelius, J. (2009). Determinants of Technical Efficiency of RiceFarms in North-Central and North-Western Regions in Bangladesh.www.perpustakaan.depkeu.go.id/ FOLDERJOURNAL/sawah.banglades.pdf. Accessed on 4th August, 2012.

Badu-Apraku, B., Lum, A. F. Fakorede, M.A.B., Menkir, A. Chabi, Y. The, C. Abdulai, M.Jacob, S.and Agbaje, S. (2008). Performance of early maize cultivars derived from recurrent selection for grain yield and *Striga* resistance. *Crop Science* 48:99-112

Badu-Apraku, B., & Lum, A.F. (2010). The pattern of grain yield response of normal and quality protein maize cultivars in stressed and non-stressed environments. *Agronomy Journal* 102:381-394.

Badu-Apraku, B., Akinwale, R.O., Menkir, A., Obeng-Antwi, K., Osuman, A.S., Coulibaly, N., Onyibe, J.E., Yallou, G.C., Abdullai, M.S., & Didjera, A. (2011). Use of GGE Biplot for targeting early maturing maize cultivars to mega-environments in West Africa. *African Crop Science Journal*, Vol. 19, No. 2, pp. 79 – 96

Bagi, F.S., & Haung, C.I. (1983). "Estimating production Technical Efficiency for individual farms in Tennessee. Canadian journal of Agricultural Economics, 31. 249-256.

Baker, R.J. (1988). Analysis of genotype-environmental interactions in crops. ISI *Atlas of Science: Animal and Plant Sciences* 1: 1-4.

Battese, G.E., & Coelli, T.J. (1995). A Model for Technical Inefficiency Effects in a Stochastic Frontier Production Function for Panel Data. *Empirical Economics* (1995) 20: 325-332.

Becker, H.C., & Leon, J. (1988). Stability analysis in plant breeding. Plant breeding 101:1-23.

Berzsenyi, Z., & Dang, Q.L. (2008). Effect of various crop production factors on the yield and yield stability Becker, H.C. and Leon, J. 1988. Stability analysis in plant breeding. Plant breeding 101:1-23.

Bhan, K., Pal, S., Rao, B.L., Dhar, A.K., & Kang, M.S., (2005). GGE Biplot Analysis of Oil Yield in Lemongrass (*Cymbopogon spp.*). *Journal of New Seeds*, Vol. 7(2).

Blanche, S.B., Utomo, H.S., Wenefrida, I., & Myers, G.O. (2009). Genotype × Environment Interactions of Hybrid and Varietal Rice Cultivars for Grain Yield and Milling Quality. Crop Science 49, 2011–2018.

Bose, L.K., Mohanty, A., Kar, M. K. & Nagaraju, M. (2004). Stability analysis of grain yield in rice under different agronomic practices. *Crop improvement* 6:26-29.

Bose, L.K., Jambhulkar, N.N., & Singh, O.N. (2014). Additive Main effects and Multiplicative Interaction (AMMI) Analysis of grain yield stability in early duration rice. *The Journal of Animal & Plant Sciences*, 24(6): 2014, Page: 1885-1897 ISSN: 1018-7081.

Bose, L.K, Nitiprasad, N. J., Kanailal, P., & Onkar, N.S. (2014). Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. *Chilean journal of Agricultural Research* 74(1) January-March 2014

Bouman, B.A.M., Peng, S., Castaòeda, A.R., & Visperas, R.M. (2005). Yield and water use of irrigated tropical aerobic rice systems. *Agricultural Water Management*, 74(2): 87–105.

Bravo-Vrata, B.E., & Evenson, R.E. (1994) Efficiency in agricultural production: The case of peasant farmers in eastern Paragnay, *Agricultural Economics*, 10(1): 27-37.

Casanoves, F., Macchiavelli, R., & Balzarini, M. (2005). Error variation in multi-environment Peanut trials: within-trial spatial correlation and between–trial heterogeneity. *Crop Science*. 45: 1927-1933.

Ceccarelli, S. (1989). Wide adaptation. How wide? *Euphytica* 40:197–205.

Chandrasiri, G .W .J. Abeysiriwardena, D.S., Pieris, B.L. & Jayathilake, H.M.C.K. (2002). Comparative evaluation of different statistical techniques on testing adaptability of rice varieties in varied environments. *Annals of the Sri Lanka Department of Agriculture* 4: 1-13.

Chavas, J-P., Petrie, R., & Roth, M. (2005). "Farm Household Production Efficiency: Evidence from The Gambia." *American Journal of Agricultural Economics* 87 (1), 160-179.

Coe Ric. (2012). Multi-Environment Trials: An Overview. Statistical Services Centre, University of Reading, UK and World Agroforestry Centre, Kenya 5 April 2012.

Cooper, M., & Delacy, I.H. (1994). Relationships among analytic methods used to study genotypic variation and genotype-by-environment interaction in plant breeding multi-environment trials. *Theor. Appl.* Genet. 88, 561-572.

Costa. e Silva, Dutkowski, G.W., & Glimour, A.R. (2001). Analysis of early tree height in forest genetic trials is enhanced by including a spatially correlated residual. *Can. J. For. Res* 31:1887-1893.

Coşge, B., Ipek, A., & Gürbüz, B. (2009). Some Phenotypic Selection Criteria to Improve Seed Yield and Essential Oil Percentage of Sweet Fennel (Foeniculum vulgare Mill. var. Dulce), Ankara Üniversitesi Ziraat Fakültesi, Tarim Bilimleri Dergisi, 15(2), p.127-133.

Craufurd, P., Peter, D., Alex, O-A., Koffi, D., Bimpong, I. & Koffi, M. (2000). Testing Drought-Tolerant plant types of upland rice in Ghana using participatory methods.

Crossa, J. (1990). Statistical analysis of multilocation trials. *Advances in Agronomy* 44:55-85.

Crossa, J., Gauch, HG., & Zobel, RW. (1990). Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Sci,* 30: 493-500.

Cullis, B. R., Gogel B.J, Verbyla A.P, & Thompson R. (1998). Spatial analysis of multi-environment early generation trials. *Biometrics* 54:1-18.

Dalkani, M., Darvishzadeh, R., & Hassani, A. (2011). Correlation and sequential path analysis in Ajowan (Carum copticum L.), *Journal of Medicinal Plants Research*, 5 (2), p.211-216.

Das, S., Mishra, R.C., & Sinha, S.K. (2008). Variation in seedling growth inhibition due to maleic hydrazide treatment of rice (O.sativa) and ragi (E coracana) genotypes and its relationship with yield and adaptability. *Journal of Crop Science and Biotechnology* 11(3):215-222.

Das, S., Misra, R.C., Das, S.R., Attnaik, M.C.P., & Sinha, S.K. (2011). Integrated analysis for genotypic adaptation in rice. *African Crop Science Journal*, vol. 19, No. 1, pp. 15 – 28.

Datt, G., & Ravallion, M. (1996). How important to India's Poor is the sectoral composition of growth? World Bank Economic Review 10 (1), 1–26.

Dawson, P.J. (1985). Measuring technical efficiency from production function: Some further estimates, *Journal of Agricultural Economics*, 38 (1): 27-37.

Dawson, P.J., & Lingard, J. (1989). 'Measuring Farm Efficiency over Time on Philippine Rice Farms', *Journal of Agricultural Economics* 40, 168-177.

Dawson, P.J., Lingard, J., & Woodford, C.H. (1991). "A generalized measure of farm specific technical efficiency". *America Journal of Agricultural Economics*. 2: 26: 1098–104.

Delacy, I.M., Redden, R.J., Butler, D.G., & Usher, T. (2000). Analysis of line x environment interactions for yield in navy beans. 3. Pattern analysis of environments over years. *Aust. J.Agric*. Res.51, 619-628.

Dewey, D.R., & Lu, K.H. (1959). A correlation and path coefficient analysis of components crested wheat grass and seed production, *Agron. J.*, 52, p.515–518.

Dhungana, R. B., Nuthall, P.L., & Nartea, G.V. (2004). "Measuring the Economic Inefficiency of Nepalese Rice Farms Using Data Envelopment Analysis." *The Australian Journal of Agricultural and Resource Economics*, 48 (2), 347-369.

Dingkuhn, M., Luquet, D., Kim H., Tambour, L., & Clement-Vidal, A. (2006). EcoMeristem, a model of morphogenesis and competition among sinks in rice. 2. Simulating genotype responses to phosphorus deficiency. *Functional Plant Biology* 33, 325-337.

Dixon, A.G.O., & Nukenine, EN. (1997). Statistical analysis of cassava yield trials with additive main effects and multiplicative interaction (AMMI) model. *Afr J Root Tuber Crops*, 3:46-50.

Dixon, B.L., Hollinger, S.E., Garcia, P., & Tirupattur, V. (1994). "Estimating Corn Yield Response Models to Predict Impacts of Climate Change." *Journal of Agricultural and Resource Economics* 19 (1994):58-68.

Donkoh, S.A., Sylvester, A., & Shamsudeen, A. (2013).Technical Efficiency of Rice Production at the Tono Irrigation Scheme in Northern Ghana. *American Journal of Experimental Agriculture* 3(1): 25-42, 2013.

Duarte, J.B., & Vencovsky, R. (1999). Interação genótipos x ambientes: uma introdução à análise"AMMI". Ribeirão Preto: Sociedade Brasileira de Genética, 1999. 60p. (Série monografias, n. 9).

Dutkowski, G. W., Costa e Silva, J., Gilmour, A.R., & Lopez, G.A. (2002). Spatial analysis methods for forest genetic trials. *Can. J. For. Res* 32:2201-2214.

Dutkowski, G. W., Costa e Silva, J., Gilmour, A.R., Wellendorf, H., & Aguiar, A. (2006). Spatial analysis enhances modeling of a wide variety of traits in forest genetic trials. *Can. J. For. Res*. 36: 1851-1870.

Eberhart, S.A., & Russell, W.A. (1966). Stability parameters for comparing varieties. *Crop Sci.*, 6:36-40.

Ebdon, JS., & Gauch, HG. (2002). Additive main effect and multiplicative interaction analysis of national turfgrass performance trials. II. Cultivar recommendations. *Crop Sci*, 42:497- 506.

Efron, B., & Tibshirani, R.J. (1993). An Introduction to the Bootstrap; Chapman & Hall, New York.

Enwerem, V.A., & Ohajianya, D.O. (2013). Farm Size and Technical Efficiency of Rice Farmers in Imo State, Nigeria. *Greener Journal of Agricultural Sciences*. ISSN: 2276-7770Vol. 3(2), pp. 128-136, February 2013.

Etwire, P.M., Martey, E., & Dogbe, W. (2013). Technical Efficiency of Soybean Farms and Its Determinants in Saboba and Chereponi Districts of Northern Ghana: A Stochastic Frontier Approach. *Sustainable Agriculture Research*; Vol. 2, No. 4; 2013 ISSN 1927-050X E-ISSN 1927-0518.

FAOSTAT. (2012). (available at: www.faostat.fao.org/).

Farrell, J.M. (1957). "The measurement of productive efficiency". *Journal Royal stats* 506 volume 120, Part III. Pp. 253-290

Farshadfar, E., Mahmodi, N., & Yaghotipoor, A. (2011). AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (Triticum aestivum L.). *Australasian Journal of Crop Science* 5: 1837-1844.

Farshadfar, E., & Sutka, J. (2006). Biplot analysis of genotype environment interaction in durum wheat using the AMMI model. *Acta Agron Hung* 54(4): 459–467

Farshadfar, E. (2008). Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. *Pakistan Journal of Biological Science* 11: 1791-1796.

Farshadfar, E., Mahdi, G., & Zahra, V. (2012). Chromosomal localization of QTLs controlling genotype × environment Interactions in barley. *Intl J Agri Crop Sci.* Vol., 4 (6), 317-324

Finlay, K.W., & Wilkinson, G.N. (1963). The analysis of adaptation in a plant- breeding programme. Aus. J. Agric. Res., 14: 742-754.

Francis, P .V., Kanakmany, M.T., Radhakrishnan, V .V., & Jaikumaran, U. (2005). Genotype x environment interaction in rice. Oryza 42: 174-178.

Friedl, H., & Stampfer, E. (2002a). Jackknife Resampling,Encyclopedia of Environmetrics, 2, Eds.: A. ElShaarawi, W. Piegorsch, Wiley:Chichester, pp. 1089-1098, Fu, Y. B., Yanchuk, A.D., & Namkoong, G. (1999). Spatial patterns of tree height variations in a series of Douglas-fir progeny trials: implications for genetic testing. *Can. J. For. Res.* 29:714-723.

Gabriel, K. R. (1971).The biplot graphic display of matrices with application to principal component analysis. *Biometrka* 58: 453–467.

Gallagher, P. (1986). "U.S. Corn Yield Capacity and Probability: Estimation and Forecasting with Non-Symmetric Disturbances." N. Cent. *J. Agr. Econ.* 8(1986): 109-22.

Garcia del Hoyo, J. J., Castilla, E.D., & Jimenez, T.R. (2004). Determination of technical efficiency of fisheries by stochastic frontier models: A case on the Gulf of Cadiz (Spain). *ICES Journal of Marine Science*, 61, 416-421.

Gauch, H.G., & Zobel, R.W. (1997). Identifying mega-environments and targeting genotypes. Crop Sci, 37:311-326.

Gauch, H.G. Jr. (1988). Model selection and validation of yield trials with interaction. *Biometrics,* 44, 705-715.

Gauch, H.G., & Zobel, R.W. (1996). Optimal replication in selection experiments. *Crop Science* 36:838–843.

Gauch, H.G., Zobel, R.W. (1997). Identifying mega-environments and targeting genotypes. *Crop Sci*, 37:311-326.

Ghana Business News (GBN). (2015). Ghana expect to import 600,000 tons of rice. General news lead. https://www.ghanabusinessnews.com/2015/01/14/ghana-expected-to-import-600000-tons-of-rice/

Ghana News Agency-Joy Online. (2012). Farmers fume over rice project delay. http://www.ghanaweb.com/GhanaHomePage/NewsArchive/artikel.php?ID=233113. Accessed March 21, 2013

Gilmour, A. R., B., Cullis, R., Wielham, S.J., & Thomson, R. (1999). ASREML reference manual NSW Agric. Biom, Bull. 3., New South Wales, Austrialia.

Golmirzaie, A.M., Schmidt, J.W., & Dreier, A.F. (1990).Components of variance and stability parameters in studies of cultivar x environment interactions in wheat (Triticum aestivumL.). *Cereal Res.* Cumm., 18: 249-256.

Gómez-Becerra, H.F., Morgounov, A., & Abugalieva, A. (2006). Evaluation of Grain Yield Stability, Reliability and Cultivar Recommendations in Spring Wheat (*Triticum Aestivum* L.) from Kazakhstan and Siberia. *Journal of Central European Agriculture*. Volume 7 (2006) No. 4 (649-660)

Greene, W.H. (1980a). Maximum likelihood estimation of econometric frontier functions, *Journal of Econometrics*, 13, pp. 27-56.

Greene, W.H. (1980b). On the estimation of a flexible frontier production model, *Journal of Econometrics*, 13, pp. 101-115.

Greene, W.H. (1990). A Gamma-distributed stochastic frontier model, *Journal of Econometrics*, 46, pp. 141-163.

Greene, W.H. (2008). The econometric approach to efficiency analysis, In H.O. Fried, C.A.K. Lovell and S.S. Schmidt (eds.). The Measurement of Productive Efficiency and Productivity Growth, Oxford: Oxford University Press, pp. 92-250.

Habibullah, M.S., & Ismail, M.M. (1994).Production frontier and technical efficiency: The case for Bee keeping farms in Malaysia. *Bangladesh Journal of Agricultural Economics* XVII (1&2):31-43.

Hamann, A., Koshy, M.P., & Namkoong, G. (2002). Improving precision of breeding values by removing spatially auto-correlated variation in forestry field experiments. Silvae Genet.

Hasan, M.J., Kulsum, M.U., Akter, A., Masuduzzaman, A.S.M., & Ramesha, M.S. (2011). Genetic Variability and Character Association for Agronomic traits in hybrid rice (*Oryza Sativa* L.). Bangladesh J. Pl. Breed. Genet, 24(1): 45-51.

Henderson, C. R. (1984). Application of linear models in animal breeding values. *Biometrics*. 32: 69-83

Hernandez, M.V., & Crossa, J. (2000). The AMMI analysis and graphing the biplot. In: Biometrics and Statistics Unit. CIMMYT INT. Mexico.

Heyman, M., & Chatterjee, S. (2014). Predicting crop Yield via Partial Linear Model with Bootstrap. 4th international workshop on Climate Informatics, September 25-26 2014.

Hossain, M. (1989). Green Revolution in Bangladesh: Impact on Growth and Distribution of Income. University Press Ltd, Dhaka.

Hohls, T. (1995). Analysis of genotype environment interactions. *South African Journal of Science* 91:121-124.

Hu, Q., & Buyanovsky, G. (2003). Climate effects on corn yield in Missouri. *Journal of Applied Meteorology* 42, 1626-1635

Huang, J., Wang, X., Li, X., Tian, H., & Pan, Z. (2013) Remotely Sensed Rice Yield Prediction Using Multi-Temporal NDVI Data Derived from NOAA's-AVHRR. PLoS ONE 8(8): e70816. doi:10.1371/journal. pone.0070816

Huff, F. A., & Neill, J.C. (1980). "Assessment of Effects and Predictability of Climate Fluctuations as Related to Agricultural Production." Final Rep., Phase I, State Water Survey Div., University of Illinois, Champaign.

Idiong, I.C. (2007). Estimation of Farm Level Technical Efficiency in Small scale Swamp Rice Production in Cross River State of Nigeria: A Stochastic Frontier Approach. *World Journal of Agricultural Sciences* 3 (5): 653-658, 2007 ISSN 1817-3047.

IRRI. (2006). Bringing hope, improving lives: Strategic Plan 2007–2015. Manila.61 p.

Iwunor, C. (1999). A Path Analysis of Correlates of Fertility and Infant mortality rates. A global outlook. *Nigerian Journal of Science* Volume 33 (1999) 185-198.

Jain, K.C., & Pandya, B.P. (1988). Relationship between mean performance and stability parameters in Chickpea. *Legume Res.*, 11(3): 103-108.

Jedynski, S. (2001). Heritability and path-coefficient analysis of yield components in Spring wheat, Grupy Problemowej Wodowli Pszenicy, Proceeding of Symposium, Zakopane, Poland, No. 218/219, p.203–209.

Jenny, C. A., Steven, B., Vijaya, R., & Peter, C.T. (2011): Center for Global Development "West Africa Experience with the World Rice Crises, 2007-2008". Working paper 242.

Jondrow, J., Lovell, C.A.K., Materov, I.S. & Schmidt, P. (1982). 'On the Estimation of Technical Inefficiency in the Stochastic Frontier Production Function Model',*Journal of Econometrics* 19, 233-238.

Jusuf, M., Rahayuningsih, S.A., Wahyuni, T.S., & Restuono, J. (2008). Adaptasi dan stabilitas hasil klon harapan ubi jalar. Jurnal Penelitian Pertanian Tanaman Pangan 27, 37-41.

Joshi, B.K. (2005). Correlation, regression and path coefficient analyses for some yield components in common and Tartary buckwheat in Nepal. Fagopyrum 22: 77-82.

Kalirajan, K.P., & Shand, R.T., (1989) A generalized measure of technical efficiency, *Applied Economics*, 21: 25-34.

Kalirajan, K.P., & Flinn, J.C. (1983). 'The Measurement of Farm-Specific Technical fficiency', *Pakistan Journal of Applied Economics* 2, 167-180.

Kang, M.S. (1998). Using genotype-by-environment interaction for crop cultivar development. *Adv. Agron.*, 35:199–240.

Kang, M. S. (2004). Breeding: genotype-by-environment interaction. Encyclopedia of Plant and Crop Science. (edt.) Goodman, R. M. New York Basel.218-221.

Kang, M.S., Aggarwal, V.D., & Chirwa, R.M. (2006). Adaptability and stability of bean Cultivars as determined via yield-stability statistic and GGE biplot analysis. *Journal of Crop Improvement* 15, 97–120

Kashif, M., & Khaliq, I. (2004). Heritability, correlation and path coefficient analysis for some metric traits in wheat, *International Journal of Agriculture & Biology*, 6, p. 138-142.

Kaya, Y., Palta, C., & Taner, S. (2002). Additive main effects and multiplicative interaction analysis of yield performances in bread wheat genotypes across environments. *Tur. J. Agric.* For., 26: 275-279.

Kaya, Y., Akcura, M., Ayaranci, R., & Taner, S. (2006). Pattern analysis of multi environment trials in bread wheat. *Commun. Biometry Crop Sci.* 1 (1), 63-71.

Kempton, R A. (1984). The use of biplots in interpreting variety by environment interaction. *J. Agric Sci,* 103:123-135.

Kenneth, J., & Hellevang, PE. (1995). Grain Moisture Content Effects and Management. NDSU Extension Service, North Dakota State University, Fargo, ND58105

Kinyua, M.G. (1992). Genotype x environment effects on wheat grown over multiple locations and years in Kenya. In: 7th Regional Wheat Workshop for Eastern, Central and Southern Africa. Nakuru, Kenya. ISBN 968-6127-62-3:103-107.

Krasachat. (2003). "Technical Efficiencies of Rice Farms in Thailand: a Non-Parametric Approach." Paper presented to the 2003 Hawaii International Conference on Business, Honolulu, June 18-21, 2003.

Kumbhakar, S.C., & Lovell, C.A.K. (2000). Stochastic Frontier Analysis, Cambridge: Cambridge University Press.

Larson, D.F., & Plessmann, F. (2002). 'Do Farmers Choose to be Inefficient? Evidence from Bicol, Philippines', *working paper in Agricultural, Land, Commodity Prices and Markets,* No. 2787, World Bank, Washington D.C.

Lestari, A.P., Abdullah, B., Junaedi, A., & Aswidinnoor, H. (2010). Yield Stability and Adaptability of Aromatic New Plant Type (NPT) Rice Lines. *Jurnal Agronomi Indonesia* 38(3), 199 – 204.

Lin, C.S., Binns, M.R & Lefkovitch, L.P. (1986). Stability analysis: Where do we stand? *Crop Sci.*, 26: 894-900.

Lingard, J., Castillo, L. & Jayasuriya, S. (1983). 'Comparative Efficiency of Rice Farms in Central Luzon, the Philippines', *Journal of Agricultural Economics* 34, 37-76.

Lone, A.A., Sofi, P.A., Warsi, M.Z., & Wani, S.H. (2009). Stability analysis in maize (*Zea mays L.*) for anthesissilking interval and grain yield. *Maize Genetics Cooperation Newsletter* 83, 1-9.

Madhavilatha, L. (2002). Studies on genetic divergence and isozyme analysis on rice (*Oryza sativa* L). M.Sc. (Ag.) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Mahalingam, L., Mahendran, S., Chandra, R., & Atlin, G. (2006). AMMI analysis for stability of grain yield in rice (O. sativaL.) *International Journal of Botany* 2:104-106.

Mahapatra, K.C., & Das, S. (1998). Approaches to analysis of genotypic adaptation in rice. *Indian Journal of Genetics and Plant Breeding* 58(3):297-306.

Magnussen, S. (1990). Application and comparison of spatial models in analyzing tree genetics yield trials. *Can. J. For. Res* 20.

Meenakshi, T., Amirthadevarathinam, A., & Backiyarani, S. (1999). Correlation and path analysis of yield and some physiological characters in rainfed rice. Oryza, 36 (2): 154-156.

Meeusen, W., & van den Broeck, J. (1977), 'Efficiency Estimation from Cobb-Douglas Production Functions with Composed Error', *International Economic Review* 18, 435-444.

Messina, C., Hammer, G., Dong, Z., Podlich, D., & Cooper, M. (2009). Modelling crop improvement in a GxExM framework via gene-trait-phenotype relationships. In: Sadras, V.O., Calderini, D. (Eds.), Crop physiology: Applications for Genetic Improvement and Agronomy. *Elsevier*, Netherlands, 235-265 p.

MiDA (Millennium Development Authority). (2010). Investment Opportunity in Ghana: Maize, Rice, and Soybean. Accra, Ghana: MiDA

Miller, R.G. (1974). The jackknife- a review, Biometrika, 61, pp. 1-15.

MoFA (Ministry of Food and Agriculture). (2007). District level agricultural production and price data.

MOFA (Ministry of Food and Agriculture). (2011). Agriculture in Ghana: Facts and Figures (2010). Accra, Ghana: Statistics Research and Information Directorate, MOFA

Mohammadi, R., Abdulahi, A., Haghparast, R., & Armion, M. (2007). Interpreting genotype-environment interactions for durum wheat grain yields using non-parametric methods. *Euphytica* 157: 239–251

Mohammadi, R., & Amri, A. (2008). Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. *Euphytica* 159: 419–432

Molla, F., Alemayehu, A. & Ketema, B. (2013). AMMI Analysis of Yield Performance and Stability of Finger Millet Genotypes across Different Environments. World *Journal of Agricultural Sciences* 9 (3): 231-237,

Mosavi, A.A., Jelodar, N.B., & Kazemitabar, K. (2013). Environmental Responses and Stability Analysis for Grain Yield of Some Rice Genotypes. *World Applied Sciences Journal* 21(1), 105-108.

Mugemangango, C., & Vinod, K. (2011). Correlation and Path Coefficient analysis of rice cultivars data. *Journal of Reliability and Statistical Studies*; ISSN (Print): 0974-8024, (Online):2229-5666 Vol. 4, Issue 2 (2011): 119-131.

Muir, W., Nyquist, W.E., & Xu, S. (1992). Alternative partitioning of the genotype-by environment interaction. *Theor. Appl. Genet.* 84: 193-200

Muungani, D., Peter, S., & Munyaradzi, D. (2007). Analysis of multi-environment, mother-baby trial data using GGE biplots. *African Crop Science Conference Proceedings* vol.8. pp. 103-112.

Nanita, D., H., Singh, N.B., Singh, M.R.K. & Sharma, P .R. (2006). Stability analysis of selected rice genotypes at varying spacing and sowing dates under rainfed lowland condition in Manipur Valley. Oryza43:20-24.

Nayak, A. R.., Chaudhary, D., & Reddy, J. N. (2001). Correlation and path analysis in scented rice (*Oryza sativa* L). *Indian Journal of Agricultural Research*, 35 (3): 186-189.

Nkegbe, P.K. (2012). Technical efficiency in crop production and environmental resource management practices in northern Ghana. *Environmental Economics,* Volume 3, Issue 4, 2012.

Nsowah-Nuamah, N.N.N. (2009). Design and Analysis of Experiments. A hand book of Basic Experimental Design. ACADEC Press, Accra 2009.

Nyquist, W. E. (1991). Estimation of heritability and prediction of selection response in plant populations. Critical Reviews in Plant Sciences. 10: 235-322.

Oad, F.C., Samao, M.A., Zia-Ul-Hasssan, Pompe, S.T.A., Crux & Oad, N.L. (2002). Quantitative characters of rice ratoon cultivars and advance lines / *Int. J. Agri. Biol.*, Vol. 4, No. 2, 2002.

Obwona, M. (2000). *Determinants of technical efficiency differentials amongst small and medium scale farmers in Uganda*: A *case of tobacco growers*. A final report presented at AERC bi-annual workshop at Grand Requency Hotel, Nairobi, Kenya.

Offutt, S. E., Garcia, P & Pinar, M. (1987). "Technological Advance, Weather, and Crop Yield Behavior." N. Cent. *J. Agr. Econ.* 9(1987):49-63.

Oliveira, E.J., & Godoy, I.J. (2006). Pod yield stability analysis of runner peanut lines using AMMI. *Crop Breeding and Applied Biotechnology* 6: 311-317.

Oliveira, E.J., Juan Paulo, Xavier de Freitas & Onildo, Nunes de Jesus. (2013). AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. *Sci. Agric.* v.71, n.2, p.139-145, Pandey, K.K., Rai, V.N., Sisodia, B.V.S., Bharti, A.K., & Gairola K.C. (2013). Pre -Harvest Forecast Models Based On Weather Variable And Weather Indices For Eastern U.P. *Advances in Bioresearch.* Adv. Biores., Vol4 (2) June 2013: 118- 122.

Patterson, H.D., & Thompson, R. (1971). Recovery of inter block information when block sizes are unequal. *Biometrika.* 58: 545-554.

Public Agenda. (2009). Controversy over Ghana's Rice Import Bill. March 2nd, 2009. ISSN0855-2061.

Purchase, J.L. (1997). Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat. Ph.D. Thesis. Department of Agronomy, Faculty of Agriculture of the University of the Free State, Bloemfontein, South Africa.

Purchase, J.L., Hatting, H., & Van Devendra, C.S. (2000). Genotype x environment interaction of winter wheat (Triticum aestivum L.) in South Africa: Stability analysis of yield performance. *South Africa Journal of Plant soil* 17:101-107.

Qari, M.S., Khan, N.I., & Bajwa, M.A. (1990). Comparison of wheat cultivars for stability in Yield performance. *Pak. J. Agric. Res.*, 11: 73-77.

Ragasa, C., Dankyi, A., Acheampong, P., Wiredu, A. N., Chapoto, A., Asamoah, M. & Tripp, R. (2013). Patterns of Adoption of Improved Maize Technologies in Ghana. GSSP Working Paper, IFPRI, Accra, Ghana.

Robertson, A. (1959). The sampling variance of the genetic correlation coefficient. *Biometrics.* 15: 469-485.

Rola, A., & Quintana-Alejandrino, J.T. (1993). 'Technical Efficiency of Philippine Rice Farmers in Irrigated, Rainfed Lowland and Upland Environments: A frontier Production Function Analysis', *Philippine Journal of Crop Science* 18, 56-69.

Romagosa, I., & Fox, P .N. (1993). Genotype x Environment interaction and adaptation. In Plant breeding: principles and prospects, edited by Hayward, Bosemark and Romagosa, Chapman and Hall, London, UK. pp. 373-390.

Romualdo, M., & Jesusa, D. O. (2014). Testing and Evaluation of Upland Rice Varieties In Sultan Kudarat Province. International Conference on Biological, Civil and Environmental Engineering (BCEE-2014) March 17-18, 2014 Dubai (UAE)

Royo, C., Aparicio, N., Blanco, R., & Villegas, D. (2004). Leaf and green area development of durum wheat genotypes grown under Mediterranean conditions, *European Journal of Agronomy*, 20(4), p.419-430.

Scheiner, S.M., Mitchell, R.J., & Callahan, H.S. (2000). Using path analysis to measure natural selection, *J. Evol. Biol.,* 13, p.423-433.

Sedghi-Azar, M., Ranjbar, G.A., Rahimian, H. & Arefi, H. (2008). Grain Yield Stability and Adaptability Study on Rice (*Oryza sativa*) Promising Lines. *Journal of Agriculture & Social Sciences* ISSN Print:1813–2235; ISSN Online: 1814–960X 07– 325/AKA/2008/04–1–27–30 http://www.fspublishers.org.

Sekhon, M.K., Amrit, K.M., Manjeet, K. & Sidhu, M.S. (2010). Technical Efficiency in Crop Production: A Region-wise Analysis. *Agricultural Economics Research Review* Vol. 23 July-December 2010 pp 367-374

Shapiro, S.S., & Wilk, M.B. (1965). An Analysis of Variance Test for Normality (Complete Samples). *Biometrika*, Vol. 52, No. 3/4 (Dec., 1965), pp. 591-611

Stevenson, R.E. (1980). Likelihood functions for generalized stochastic frontier estimation, *Journal of Econometrics*, 13, pp. 57-66.

Shafiq, M., & Rehman, T. (2000). "The Extent of Resource Use Inefficiencies in Cotton Production in Pakistan's Punjab: an Application of Data Envelopment Analysis." *Agricultural Economics* 22, 321-330.

Shapiro, K.H. (1983).Efficiency differentials in peasant agriculture and their implications for development policies. *Journal of Development Studies* 19(2):177-190.

Sharma, K. R., Leung, P., & Zaleski, H.M. (1999). "Technical, Allocative and Economic Efficiencies in Swine Production in Hawaii: A Comparison of Parametric and Nonparametric Approaches." *Agricultural Economics* 20, 23-35.

Sial, M.A., Arain, M.A., & Ahmad, M. (2000). Genotype environment interaction on bread wheat grown over multiple sites and years in Pakistan. *Pak. J. Bot.*, 32: 85-91.

Singh, I.P., Singh, S., & Pawar, I.S. (1987). Phenotypic stability in chickpea. ICN 16 pp.

Smith, A.B., Cullis, B.R., & Thompson, R. (2001). Analyzing variety by environment data using multiplicative mixed models and adjustments for spatial field trend. *Biometrics* 57:1138-1147

Smith, A. B., Cullis, B.R., & Thompson, R. (2005). The analysis of crop cultivar breeding and evaluation trials: an overview of current mixed model approaches. *Journal of Agricultural Science.* 143: 1-14.

Solís, D., Bravo-Ureta, B.E., & Quiroga, R.E. (2007). Soil conservation and technical efficiency among hillside farmers in Central America: a switching regression model, *Australian Journal of Agricultural and Resource Economics*, 51, pp. 491-510.

Son, T.V.H., Coelli, T., & Fleming, E. (1993). Analysis of the technical efficiency of state rubber farm in Vietnam. *Journal of Agricultural Economics* 9:183-201.

Sreedhar, S., Dayakar, T.R., & Ramesha, M.S. (2011). Genotype x Environment Interaction and Stability for Yield and Its Components in Hybrid Rice Cultivars (*Oryza sativa L.*). *International Journal of Plant Breeding and Genetics* 5(3), 194-208.

Syed, A.M., Rehana, A., & Ghulam, M. (2007). Yield stability analysis conferring adaptation of wheat to pre- and post-anthesis drought conditions. *Pak. J. Bot.*, 39(5): 1623-1637, 2007.

Tadesse, B., & Krishnamoorthy, S. (1997).Technical efficiency in paddy farms of Tamil Nadu: An analysis based on farm size and ecological zone. *Journal of Agricultural Economics* 16:185-192.

Tannura, M. A., Irwin, S.H., & Good, D.L. (2008) "Weather, Technology, and Corn and Soybean Yields in the U.S. Corn Belt." *Marketing and Outlook Research Report* 2008-01

Tariku, S., Taddesse, L., Mulugeta, B., & Mitiku, A. (2013). Genotype by environment interaction and grain yield stability analysis of rice (*Oryza sativa L.*) genotypes evaluated in north western Ethiopia. *Net Journal of Agricultural Science* Vol. 1(1), pp. 10-16, March 2013 Full Length Research Paper.

Teigen, L.D. (1991a) "Weather and Soybean Yield: A Regional Analysis." Oil Crops Situation and Outlook Report (OCS-31), *Economic Research Service*, U.S. Department of Agriculture. pp. 24-29.

Teigen, L.D. (1991b). "Weather, Climate, and Variability of U.S. Corn Yield." Feed Situation (FDS-320), Economic Research Service, U.S. Department of Agriculture, pp. 28-37.

Teigen, L.D., & Thomas M. (1995). "Weather and Yield, 1950-94: Relationships, Distributions, and Data." Staff Paper No. 9527, Commercial Agriculture Division, Economic Research Service, U.S. Department of Agriculture.

Tesemma, T., Tsegaye S., Belay G., Bechere E. and Mitiku D. (1998). Stability of performance of tetraploid wheat landraces in Ethiopian highland. *Euphytica*, 102: 301–8.

Thiam, A., Bravo-Ureta, B.E., & Rivas, T.E. (2001). "Technical Efficiency in Developing Country Agriculture: A Meta-Analysis." *Agricultural Economics* 25, 235-243.

Thompson, L.M. (1962). "An Evaluation of Weather Factors in the Production of Corn." Report No. 12T, Center for Agricultural and Rural Development, Iowa State University, 1962.

Thompson, L.M. (1963) "Weather and Technology in the Production of Corn and Soybeans." Report No. 17, Center for Agricultural and Rural Development, Iowa State University.

Thompson, L.M. (1969) "Weather and Technology in the Production of Corn in the U.S. Corn Belt." *Agronomy Journal* 61:453-456.

Thompson, L.M. (1970) "Weather and Technology in the Production of Soybeans in the Central U.S." *Agronomy Journal* 62:232-236.

Thompson, L.M. (1985). "Weather Variability, Climatic Change, and Soybean Production." *Journal of Soil and Water Conservation* 40: 386-389.

Thompson, L.M. (1986). "Climatic Change, Weather Variability, and Corn Production." *Agronomy Journal* 78: 649-653.

Thompson, L.M. (1988). "Effects of Changes in Climate and Weather Variability on the Yields of Corn and Soybeans." *Journal of Production Agriculture*1:20-27.

Tijani, A.A. (2006). Analysis of the technical efficiency of rice farms in Ijesha Land of Osun State, Nigeria. Agrekon, Vol 45, No 2.

Uddin, M.J., Mitra, B., Chowdhry, M.A.Z., & Mitra, B. (1997). Genetic parameters, correlation, path-coefficient and selection indices in wheat, Bangladesh J. Sci. Industrial Res., 32, p.528–38.

Ugwuanyi, C.A., Balogun, O.S., Akinyemi, O., Balogun, G.F., & Zungum, A. (2008). Cost and Returns of Small-Scale Locally Milled Rice Marketing in Uzo-Uwani LGA of Enugu State. Proceedings of 10

Viana, J.M.S., & Cruz, C.D. (2002). Analysis of stability and adaptability through different models of linear regression. *Cienc Agrotec Lavras,* 26: 455-462.

WARDA, Rice Trends in Sub-Saharan Africa, Third edition, Cotonou. (2005), p. 31 and FAOStat; IRRI, Rice Almanac, 3rd edition, Los Banos, 2002, p. 79.

Wadud, A., & White, B. (2000). "Farm Household Efficiency in Bangladesh: A Comparison of Stochastic Frontier and DEA Methods." *Applied Economics* 32, 1665-1673.

Wadud, A. (2003). "Technical, Allocative, and Economic Efficiency of Farms in Bangladesh: a Stochastic Frontier and DEA Approach." *The Journal of Developing Areas* 37 (1), 109-126.

World Bank. (2008). World Development report. Agriculture for development. http://web.worldbank.org/WBSITE/EXTERNAL/TOPICS/EXTPOVERTY/0.

Yan, W., Hunt, L.A., Sheng, Q., & Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Sci.* 40: 597-605.

Yan, W., & Hunt, L.A. (2001). Interpretation of genotype x environment interaction for winter wheat yield in Ontario. *Crop Science* 41, 19-25.

Yan, W. (2001). GGE biplot-A Windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agronomy Journal* 93:1111–1118.

Yan, W. & Kang, M. S. (2003). GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL.

Yan, W., & Tinker, N.A. (2005). An integrated biplot analysis system for display, interpreting, and exploring genotype x environment interaction. *Crop Science* 45:1004-1016.

Yan, W., Kang, M.S., Ma, B., Wood, S., & Cornelius, P.L. (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.* 47:643-655

Yan, W., Fregeau-Reid, J., Pageau, D., Martin, R., Mitchell-Fetch, J., Etienne, M., Rowsell, J., Scott, P., Price, M., de Haan, B., Cummiskey, A., Lajeunesse, J., Durand, J. & Sparry, E. (2010). Identifying essential test locations for oat breeding in Eastern Canada. *Crop Science* 50: 505-515.

Yang, R.C., & Baker, R.J. (1991). Genotype-environment interactions in two wheat crosses. *Crop Science*. 31: 83-87.

Yang, R.C. (2002). Likelihood-based analysis of genotype-environment interaction. *Crop Science*. 42: 1434-1440.

Zaeske, A.L. (2002). Water Use and Agricultural Production. A County Level Analysis of the Continental United States Prepared for EPA Contract Number EP-W-10- 002 "The Value of Water to the U.S. Economy".

Zobel, R.W., Wright, M.J., & Gauch, H.G. (1988). Statistical analysis of a yield trial. *Agronomy Journal* 80:388-393.

Zubair, M. & Ghafoor, A. (2001). Genotype × Environment interaction in mung bean. *Pakistan J.* Bot., 33(2): 187-190

APPENDIX

Appendix A

A1: Names and sources of germplasm materials used for the study

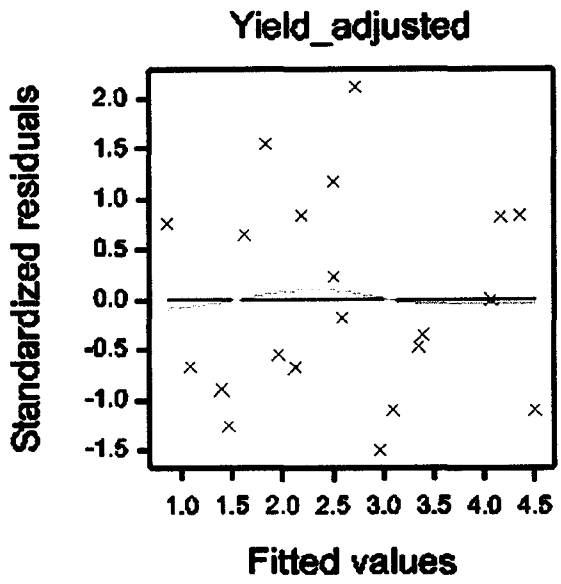
Genotype	Source
Basmati 370-1	IRRI, Philippines
GH1837	CSIR-PGRI, Ghana
Good and new (JP)	Japan
GR 18 RED	CSIR-PGRI, Ghana
IR 72 (Ph)	IRRI, Philippines
Kawawa red	CSIR-PGRI, Ghana
Koshihikari	Japan
Local Basmati – 2	IRRI, Philippines
Local red	Farmer collection
Matigey	CSRI-PGRI, Ghana
Perfume (short)	Thailand
Sebota1	Cameroun
Sebota33	Cameroun
Sebota41	Cameroun
Sebota69	Cameroun

A2: Shapiro Wilk Normality test

Variable	**Shapiro Wilk Statistic *W***	**Conclusion**
Yield adjusted 14 t/ha, combined (MET)	0.951	Normal
Yield adjusted 14 t/ha, Irrigated (MET)	0.893	Normal
Yield adjusted 14 t/ha, Rainfed (MET)	0.984	Normal
Yield adjusted 14 t/ha, Irrigated (Gongnia-MET)	0.922	Normal
Yield adjusted 14 t/ha, Irrigated (Libga-MET)	0.881	Normal
Yield adjusted 14 t/ha, Rainfed (Kologo-MET)	0.966	Normal

Yield adjusted 14 t/ha, Rainfed (Boggu-MET)	0.945	Normal
Yield adjusted 14 t/ha, (Yield Gap)	0.939	Normal
Days to 50% flowering	0.711	Normal
Number of productive tillers	0.959	Normal
Days to maturity	0.722	Normal
Panicle length	0.960	Normal
Hundred (100) grain weight	0.963	Normal
Grain length (mm)	0.906	Normal
Plant height at maturity	0.848	Normal
Water PH	0.985	Normal
Total Nitrogen (%)	0.911	Normal
Organic content (%)	0.896	Normal
Available Phosphorus (%)	0.873	Normal
Clay (%)	0.804	Normal
Silts (%)	0.946	Normal
Sand (%)	0.875	Normal

A3: Residual plots



Appendix B

B1: SAS syntax for normality test

```
proc univariate normal data=normality;
var DFF thou_GW Productive_tillers Days_mat PHM Panicle_length
Grain_Length      Yield;
run;


proc univariate normal data=normality;
var Water_PH Nitrogen Organic Phosphorus Clay Silt Sand
Rainfall_mm Min_temp Max_temp Min_RH Max_RH;
run;
```

B2: SAS syntax for Multi Environment analysis

```
proc glm data=combined;
class Location Rep Geno;
model Yld_t_ha=Location Geno Geno*Location/ss3;
run;

proc means mean stderr data=combined;
var Yld_t_ha;
run;
```

B3: SAS syntax for correlation analysis

```
proc corr data=correlation;
var DFF Prod_tiller Days_M PHM PAN_L thou_WT Grn_mm Yld_t_ha;
run;
```

B4: SAS syntax for Jackknife mean

```
proc surveymeans data=jackknife mean varmethod=jackknife mean var
clm;
strata Hub;
cluster Location;
var Yield_gap;
run;
```

B5: SAS syntax for Generalized Linear Model

```
/*Genmod for complete mode*/
proc genmod data=genmod;
model Yield_adjusted = Water_PH Nitrogen Organic Phosphorus Clay
Silt Sand
Rainfall_mm Min_temp Max_temp Min_RH Max_RH/dist=normal
link=identity;
run;

/*Genmod for reduced model*/
proc genmod data=genmod;
model Yield_adjusted = Water_PH Nitrogen Organic Clay Silt
Min_RH Max_RH/dist=normal link=identity;
run;
```

B6: SAS syntax for Variance Inflation Factor

```
proc reg data=genmod;
model Yield_adjusted = Water_PH Nitrogen Organic Clay Silt
Max_RH/tol VIF collin;
run;
```

B7: STATA syntax for descriptive statistics

```
clear

use "C:\Users\DESMOND\Desktop\Techeff_STATA\nesta.dta"

tab gender

tab educatio

tab member

tabstat age
```

tabstat hld

tabstat frmsz

tabstat seed

tabstat fertiliz

tabstat frmyrs

tabstat extensio

tabstat inc

tabstat lab

B8: STATA syntax for stochastic frontier model

```
clear

use "C:\Users\DESMOND\Desktop\Techeff_STATA\nesta.dta"

gen lyld=ln(myld)

gen lfrsiz=ln(mfrmsz)

gen lseed=ln(mseed)

gen lfert=ln(fertiliz)

gen ltlab=ln(mlab)

frontier lyld lfrsiz lseed lfert ltlab, dist (exponential) vhet(mage educatio mhld
extensio mfrmyrs member)
```

B9: STATA syntax for Path Analysis

```
clear

use "C:\Users\DESMOND\Desktop\PATH_STATA\nesta_nesta.dta"

sem (yield <- dff producti days_mat phm thou_gra grain_le panicle) ///

(dff yield <- producti days_mat phm thou_gra grain_le panicle) ///

(producti yield <- dff days_mat phm thou_gra grain_le panicle) ///
```

(days_mat yield <- dff producti phm thou_gra grain_le panicle) ///

(phm yield <- dff producti days_mat thou_gra grain_le panicle) ///

(thou_gra yield <- dff producti days_mat phm grain_le panicle) ///

(grain_le yield <- dff producti days_mat phm thou_gra panicle) ///

(panicle yield <- dff producti days_mat phm thou_gra grain_le)